National Symposium on Harnessing PGR of Peninsular India (NSPPI)

From Biodiversity Hotspot to Sustainable Bioresource Hub

BOOK OF ABSTRACTS

September 17-19, 2026

Organizers

ISPGR 1987

भाकृअनुप ICAR

taas
Progress Through Science

Co-Organizers

PPVFRA

Society for Promotion of Horticulture

Alliance Bioversity & CIAT

University of Agricultural Sciences, Bangalore

University of Horticultural Sciences, Bagalkot

ICRISAT

Venue: ICAR-Indian Institute of Horticultural Research, Hesaraghatta, Bengaluru



National Symposium on Harnessing PGR of Peninsular India (NSPPI)

From Biodiversity Hotspot to Sustainable Bioresource Hub

September 17-19, 2026

BOOK OF ABSTRACTS

ORGANIZERS

Indian Society of Plant Genetic Resources (ISPGR) New Delhi
ICAR-Indian Institute of Horticultural Research (ICAR-IIHR) Bengaluru
Trust for Advancement of Agricultural Sciences (TAAS) Bengaluru

CO-ORGANIZERS

Protection of Plant Varieties and Farmers Rights Authority (PPV&FRA) New Delhi
Society for Promotion of Horticulture (SPH) Bengaluru
Alliance of Bioversity International and CIAT
University of Agricultural Sciences (UAS) Bengaluru
University of Horticultural Sciences (UHS) Bagalkot
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Patancheru, Telangana

KNOWLEDGE PARTNERS

ICAR-Indian Institute of Spices Research (IISR), Kozhilkode
ICAR-Central Costal Agricultural Research Institute (CCARI), Goa
ICAR-Central Research Institue for Dryland Agriculture (CRIDA), Hyderabad
KSCSTE Jawarharlal Nehru Tropical Botanic Garden and Research Institute (JNTBGRI), Thiruvananthapuram
Universtiy of Agricultural Sciences (UAS), Dharwad
MS Swaminathan Research Foundation, Chennai

Venue: ICAR-Indian Institute of Horticultural Research, Hesaraghatta, Bengaluru

Cite as: Authors (2026). Title of the paper. In: Rohini M. R., Sherry Rachel Jacob, Pavan K. Malav, Anuradha Agrawal, R. K. Tyagi, R. C. Agrawal, Kuldeep Tripathi and T. K. Behera (eds.) Book of Abstracts of the National Symposium on Harnessing PGR of Peninsular India (NSPPI), Bengaluru, Karnataka, 17–19 September, 2026. Indian Society of Plant Genetic Resources, New Delhi, India, p. 176.

Publisher

Indian Society of Plant Genetic Resources (ISPGR)
Office Block A, 2nd Floor, National Agricultural Science Complex
Dev Prakash Shastri (DPS) Marg, New Delhi-110012, India
Email: ispgr2015@gmail.com
Website: https://ispgr.nbpgr.ernet.in/

Compiled and Edited

Rohini M. R, Sherry Rachel Jacob, Pavan K. Malav, Anuradha Agrawal, R. K.Tyagi, R. C. Agrawal, Kuldeep Tripathi, T. K. Behera

September 17-19, 2026

©Copyright 2026 - ISPGR, New Delhi

Disclaimer

This Abstract Book contains unprocessed or semi-processed data, which would form the basis of scientific papers in due course of time. The material contained in the report, therefore, may not be made use of without the written permission of the publisher/author except for citing as scientific reference.

Printers Details:
Shreya Printers and Publishers
#95, MNR Complex, Opp. Kurubarahalli Bus Stop
Kurubarahalli, Bengaluru - 560086
Mobile: 9538186800, 9513631213

PREFACE

We are delighted to present the Book of Abstracts of the National Symposium on Harnessing Plant Genetic Resources of Peninsular India (NSPPI–2026), which is being organized during September 17–19, 2026 at the ICAR–Indian Institute of Horticultural Research (ICAR–IIHR), Bengaluru. Peninsular India represents an exceptional repository of plant genetic diversity, encompassing diverse agro-ecological regions, biodiversity-rich landscapes, traditional farming systems and invaluable indigenous knowledge. The symposium provides a national platform to deliberate on the exploration, conservation, characterization, documentation and sustainable utilization of these precious genetic resources in the context of climate change, food and nutritional security, bioeconomy and equitable benefit sharing.

The three-day symposium features four thematic technical sessions, covering the exploration and conservation of plant genetic resources, PGR governance, benefit sharing and biosecurity, innovation and bioeconomy, and decoding diversity for sustainable use. This book presents the abstracts contributed by scientists, researchers and students from diverse disciplines, encompassing varied perspectives on the exploration, conservation, characterization and sustainable utilization of plant genetic resources; policy, biosecurity and access and benefit sharing; genomics and digital tools; climate resilience and nutritional security; grassroots innovations, value chains and livelihood opportunities; and the role of communities and stakeholders in conserving and harnessing biodiversity.

We sincerely thank all contributors for their valuable submissions and the members of the organizing and technical committees for their efforts in bringing this publication together. We hope that this Book of Abstracts will serve as a useful scientific record of the symposium and stimulate further research, collaboration and action towards the sustainable management of plant genetic resources.

Organizing Committee
NSPPI–2026

ACKNOWLEDGEMENTS

The National Symposium on Harnessing Plant Genetic Resources of Peninsular India (NSPPI–2026) is the outcome of the collective efforts, support and goodwill of numerous institutions and individuals committed to the conservation and sustainable utilization of plant genetic resources.

We express our sincere gratitude to the leadership of the Indian Council of Agricultural Research (ICAR), the Indian Society of Plant Genetic Resources (ISPGR), the ICAR–Indian Institute of Horticultural Research (ICAR–IIHR) and the Trust for Advancement of Agricultural Sciences (TAAS) for their guidance, encouragement and support in organizing this national symposium. We also gratefully acknowledge the valuable cooperation extended by the co-organizing institutions, knowledge partners and collaborating organizations, whose scientific and institutional support has enriched the scope and outreach of the symposium.

We extend our sincere gratitude to our esteemed Chief Patrons, Padma Bhushan Dr. R.S. Paroda, President, Indian Society of Plant Genetic Resources (ISPGR) and Chairman, Trust for Advancement of Agricultural Sciences (TAAS), New Delhi; Dr. Mangi Lal Jat, Secretary, DARE and Director General, ICAR, New Delhi; and Dr. T. Mohapatra, Chairperson, Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA), New Delhi, for their visionary guidance, encouragement and invaluable support towards the organization of NSPPI–2026.

We gratefully acknowledge the guidance and support of our esteemed Patrons, Dr. Sanjay Kumar Singh, Deputy Director General (Horticultural Sciences), ICAR, New Delhi; Dr. Devendra Kumar Yadava, Deputy Director General (Crop Sciences), ICAR, New Delhi; Dr. S.V. Suresha, Vice Chancellor, University of Agricultural Sciences, Bengaluru; and Dr. Vishnuvardhana, Vice Chancellor, University of Horticultural Sciences, Bagalkot. Their encouragement, support and commitment have been instrumental in strengthening the scientific and institutional outreach of the symposium.

We sincerely thank our Co-organizers – Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA), New Delhi; Alliance of Bioversity International and CIAT, India Office, New Delhi; International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad. Society for Promotion of Horticulture (SPH), Bengaluru; University of Agricultural Sciences (UAS), Bengaluru and University of Horticultural Sciences (UHS), Bagalkot for their support and valuable cooperation towards the successful organization of NSPPI–2026.

We specifically acknowledge and express our sincere gratitude for the financial support extended by the Indian Council of Agricultural Research (ICAR), New Delhi; Indian Society of Plant Genetic Resources (ISPGR), New Delhi; Trust for Advancement of Agricultural Sciences (TAAS), New Delhi; Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA), New Delhi; Alliance of Bioversity International and CIAT, India Office, New Delhi and International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad.

We place on record our sincere gratitude to Dr. T. K. Behera, Director, ICAR–IIHR, Bengaluru, for his constant encouragement, valuable guidance and wholehearted support in organizing NSPPI–2026 at ICAR–IIHR. We also express our sincere appreciation to Dr. E. S. Rao, Organizing Secretary, and Dr. G. R. Smitha, Co-organizing Secretary, ICAR–IIHR, for their dedicated efforts, valuable contributions, and wholehearted support towards the successful organization of the symposium. We also sincerely appreciate the dedicated efforts and wholehearted cooperation of the members of the Local Organizing Committee, ICAR–IIHR, whose commitment and teamwork have been instrumental in the successful conduct of the symposium.

The symposium has received an overwhelming response, with more than 250 delegates participating from diverse scientific and stakeholder organizations across the country. The delegates comprise participants from the Indian Council of Agricultural Research (ICAR) and its institutes, Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA), Alliance for Bioversity International and CIAT, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), State Agricultural Universities, Council of Scientific and Industrial Research (CSIR) institutions, private stakeholders, progressive farmers, entrepreneurs and other organizations. Their enthusiastic participation and valuable scientific contributions have significantly enriched the scope and outreach of NSPPI–2026. We warmly acknowledge all the authors and participants who contributed abstracts and scientific inputs to NSPPI–2026. Their enthusiastic response and diverse contributions form the core of this Book of Abstracts and reflect the growing national interest in the conservation and sustainable utilization of plant genetic resources.

We thank the editorial and compilation team for their meticulous efforts in receiving, reviewing, organizing and formatting the abstracts within the stipulated time. We also acknowledge the support of the administrative, technical and communication teams involved in the preparation of symposium materials and coordination with participants. Our sincere appreciation is extended to all sponsoring and supporting agencies whose encouragement and cooperation have contributed to the successful organization of the symposium.

Finally, we acknowledge the collective efforts of every individual associated with NSPPI–2026. The coming together of scientists, institutions, students and stakeholders from across the country represents a shared commitment towards safeguarding our rich plant genetic heritage and harnessing it responsibly for future generations.

Editors

CONTENTS

SI. No.	Particulars	Page No.
	ABSTRACTS	
	THEME - 1 Securing the Genetic Heritage of Peninsular India - from Exploration to Conservation	
ORAL PRESENTATIONS		
1.	***"Matoli"* - A unique ethno-botanical treasure of Goa and Konkan region** *Thangam M.* and *Preeti A. Perira*	2
2.	**Rediscovering *Linum mysorense* B. Heyne ex Wall: Germplasm Exploration and Conservation Imperatives in the Western Ghats** *Mamta Singh, Sunil Shriram Gomashe, Pavan K. Malav* and *Vikender Kaur*	3
3.	**Validation of DELTA (Description Language for Taxonomy) software for sugarcane genetic resources management** *Suganya A., Karthigeyan S.* and *Valarmathi R.*	4
4.	**Collection, conservation and domestication of native orchids of Kodagu in Western Ghats** *Sujatha A. Nair, Gowda J. M , Singh D. R., Muralidhara B. M., Awcharae C. M., Sankar V.* and *Lalduhsanga*	5
5.	**Habitat suitability modeling for conservation of *Naregamia alata* Wight and Arn. (Meliaceae): An endangered medicinal and ornamental plant, endemic to Western Ghats of Kerala, under different climatic scenarios** *Soujanya Halagatti, Sheron Fern*and*ez, Mini Sankar, Shelton Padua, Sreelatha U.* and *Simmy A. M.*	6
6.	**Species diversity of Abelmoschus in Western Ghats: prospects and issues in germplasm utilization** *Suma A., Joseph John K., Pradip Karmakar, P. P. Thirumalaisamy, Chithra Devi P*and*ey, Mamta Pathak, K. Senguttuvan, R. R. Acharya, Sushil P*and*ey, P. K. Singh, G. P. Singh*	7
7.	**Molecular Phylogenetics, Divergence Time Estimation and Historical Biogeography of Peninsular Indian Endemics of *Barleria* L. (*Acanthaceae*): Implications on PGR Conservation** *Sangoji Vasudha* and *Dr. Siddharthan S.*	8
8.	**Documentation and characterization of indigenous mango of Andaman and Nicobar Islands** *K. Abirami, M. Sankaran, V. Baskaran, B. A. Jerard* and *D. R. Singh*	9
9.	**Expedition of Wild Cajanus Species Diversity in Peninsular India** *Ravi Kishore Pamarthi, P. G. Gore, Kuldeep Tripathi, Bhaskar Bajaru, Sunil S. Gomashe, K. Prasad, A. Pradan, P. K. Singh* and *D. P. Semwal*	10
10.	**Germplasm Diversity and Conservation at ICAR-SBI Research Centre, Kannur: A Global Reservoir for Sugarcane Improvement** *Nisha M., Gopi R., Mahesh P., Dhanya V. G., Megaladevi P.* and *Govindraj P.*	11

11.	**Optimizing in vitro micro propagation and proliferation dynamics in *Piper longum* L.: mitigating hyperhydric stress for germplasm conservation** *Muhthasim K. V., Sharon Aravind, Nisthar E.* and *R. Sivaranjani*	12
12.	**Species associations in habitats of some threatened and endangered potential ornamentals of lateritic hillocks in Kerala** *Sheron Fern*and*ez, Soujanya Halagatti, Shelton Padua, Shravani J., Mini Sankar, Sreelatha U.* and *Shelton Padua*	13
13.	**Differential response of Oil Palm fruit forms to pollen desiccation and cryopreservation** *Rohini M. R., Diljith M. D., G. Somasundaram* and *Neema M.*	14
14.	**Safeguarding Mulberry Genetic Resources Through Exploration, Conservation, and Utilization** *Muthusamy Shankar, Mallegowdanakoppalu Channappa Thriveni, Raju Mondal, Manjunath N*and*an, Poojara Haleshsa* and *Narendra Kumar Bhatia*	15
15.	**Exploring Jamun (Sizijium cumini), Karonda (Carissa karonda) Jackfruit (Artocarpus app) and Kokum (Garcinia indica) Naturally occurring Biodiversity for Conservation and Development of Climate Resilient Cultivars in Konkan Region of Maharashtra** *Dr. B. P. Patil* and *Dr. B. M. Jamdagni*	16
16.	**Wild relatives of Solanum as store house for resistance to biotic and abiotic stresses in Western Ghats** *T. H. Singh* and *Mrs. Dr. Bhargavi H. A.*	17
17.	**Ploidy diversity in *Saccharum spontaneum* L., wild species of sugarcane, from Western Ghats of India** *V. P. Sobhakumari, P. Govindaraj* and *H. K. Mahadevaswamy*	18
18.	**Mapping Diversity for Future breeding: Germplasm Characterization of Jackfruit (*Artocarpus heterophyllus* Lam.)** *Abhishek Pratap, A. K. Srivastava, Om Prakash, S. V. Dwivedi, Vishal Chugh* and *Bhawna Singh*	19
19.	**Clonal propagation of strawberry guava (*Psidium cattleianum* Sabine) through stem cuttings: An approach for ex situ conservation** *Anushma P. L., Rafeekher M., Satisha J., Shivashankara K. S., Simi S., Vasugi C.* and *Sakthivel T.*	20
20.	**Emmer Wheat/Khapli (*Triticum dicoccum*): An emerging nutraceutical/functional food crop of Peninsular India** *Vikas V. K., Sivasamy M., Das B. K., Nisha R.* and *John Peter*	21
21.	**From Diversity to Discovery: Unlocking Genetic Resources for the Future of Chilli Improvement** *Naresh Ponnam, Smaranika Mishra, Lakshman Reddy D. C., S*and*eep Kumar G. M., Venkataravanappa V.* and *Prasanna Kumar N. R.*	22
22.	**Recent Trends in Conservation and Utilisation of Cashew Genetic Resources** *Mohana G. S., Eradasappa E.* and *Veena G. L.*	23
23.	**Morphological Delineation of Naturally Introgressed Eggplant Genotypes from Germplasm Collections: Implications for PGR Conservation and Management** *Kasireddy Sivasankarreddy, Thirumalaisamy P. P., Jiji Joseph, Venkatesan Kannan, Pradheep K., Madhavan Latha* and *Azhakan Suma*	24

24.	**Exploring Cucumber (*Cucumis sativus* L.) Diversity to Accelerate Genetic Improvement** *Vivek Hegde, Kavyashree K. R., Chithra Devi P*and*ey, Sushil P*and*ey, Koundinya A. V. V.* and *Hanume Gowda K.*	25
POSTER PRESENTATIONS		
1.	**Biodiversity to Table: Underutilized Vegetable Crops of Western Ghats of India for Health and Wellness** *R. Ramesh Babu, Bhanushree N.* and *Koundinya A. V. V.*	26
2.	**Exploration and Characterization of Acid Lime (*Citrus aurantifolia* S.) Germplasm for Conservation and Future Crop Improvement** *Bhawna Singh, Om Prakash, A. K. Srivastava, Subhash Ch*and*ra Singh, Abhishek Pratap* and *Abdullah Zaid*	27
3.	**Morphological Characterization and Assessment of Genetic Diversity in Dahlia (*Dahlia variabilis*) Genotypes** *Manchyala Divya, P. Naveen Kumar, P. T. Srinivas, Rajiv Kumar, Lakshman Reddy D. C.* and *M. Arivalagan*	28
4.	**Morphological Characterization and Distinctness, Uniformity, and Stability (DUS) Profiling of Carrot (*Daucus carota* L.) farmer variety 'Madhuvan Gajar'** *Padmini K.*	29
5.	**An epitome of vegetable crops diversity in Goa and adjoining Konkan region for posterity** *Thangam, M.., K. Ramach*and*rudu, S. C. Rana, S. A. Safeena, S. Priya Devi, R. Ramesh, V. S. Korikanthimath* and *N. P. Singh*	30
6.	**Effect of Cryo-Storage on Pollen Viability and Fertility in Taro (*Colocasia esculenta* L.)** *Vivek Hegde, Koundinya A. V. V., Sunitha S., M. N. Sheela, Asha Devi, K. Hanume Gowda* and *Sai Lekshmi N.*	31
7.	**Systematic exploration, documentation and conservation of Soursop (*Annona muricata* L.) genotypes from western ghats** *Roopendra Kumar, Anuradha Sane, Muralidhara B. M., Vasugi C., Laya P.* and *Nishant*	32
8.	**Potential Crop Landraces of Southern Western Ghats – PGR perspectives** *Latha M., K. Pradheep, A. Suma, K. Venkatesan, P. K. Singh* and *G. P. Singh*	33
9.	***In vitro* propagation through axenic seed culture for the conservation of an endangered species, *Exacum bicolor* Roxb.** *Shravani, J., Shajma Nafeesa Basheer, Mini Sankar, Deepa S. Nair, Rehna Augustine* and *Krishna Kumar G.*	34
10.	**Multi-Spectral Imaging (MSI) for seed viability prediction in sorghum germplasm conserved in the ICRISAT genebank** *Ovais Peerzada, Israr Majeed, Vetriventhan Mani, Senthil Ramach*and*ran, Kuldeep Singh* and *Raman Babu*	35
11.	**Exploring the cultivated and wild diversity of agriculturally important species in Western Ghats (Nashik, Thane and Palghar Districts) of Maharashtra State** *Sunil Shriram Gomashe, Kuldeep Tripathi, Ravi Kishore Pamarthi* and *Dipak Nivrutti Damse*	36

12.	**Identification of Novel Ideotypes of Okra (*Abelmoschus esculentus* L. Moench) Collected from the Western Ghats Region of Maharashtra Under Temperate Conditions** *Aftab M. Mulla, M. I. Makhdoomi, T. K. Behera* and *Hudda T. Syed*	37
13.	**Assessment of Morphological Variability in Kokum (*Garcinia indica* Choisy.) Germplasm from Western ghats of India** *Ruchitha T., Muralidhara B. M., Nayan Deepak G. and Deepa V. M.*	38
14.	**Development of an AI-Enabled Real-Time Mobile Application for Identification of Allium Crop Wild Relatives** *Ankur Tomar, Suresh Kumar, Akansha Bajpai* and *Kuldeep Tripathi*	39
15.	**An Integrated *In Vitro* Propagation and Seed Cryopreservation Strategy for Ex Situ Conservation of *Dendrobium heterocarpum* Wall. ex Lindl** *Lalduhsanga, Sujatha A. Nair, Rohini M. R.* and *Usha Rani T. R.*	40
	THEME - 2 PGR Governance: From Biosecurity to Benefit Sharing	
ORAL PRESENTATIONS		
1.	**Distribution of Phylotypes and Sequevars of *Ralstonia solanacearum* in India: Relevance to pathogen surveillance and Conservation of Plant Genetic Resources** *Sangeetha Ganesan, Madhuri Pattanaik, Satyaprakash Barik, D. K. Samuel* and *Sakthivel Krishnan*	42
2.	**Open Source Seeds as a "Protected Commons"** *Sridhar Gutam*	43
3.	**Defensive role of leaf trichomes in wild *Solanum* genetic resources against ash weevil, *Myllocerus subfasciatus* Guerin-Meneville** *Jayanthi Mala, B. R., Saravan Kumar P., Singh T. H., Shivashankara K. S., Naresh P., Samuel D. K.* and *Kamala Jayanthi P. D.*	44
4.	**Exploiting National Gene Bank Diversity for the Discovery of Novel Marker–Trait Associations (MTAs) Conferring Spot Blotch Resistance in Indian Wheat'** *Sundeep Kumar, S*and*eep Sharma, Manish Vishwakarma, Pradeep K. Bhati, Subhash Ch*and*ra, Mir Asif Iqbal, Dinesh Kumar, V. K. Mishra, Amit Kumar Singh* and *G. P. Singh*	45
5.	**Domestication of USDA pomegranate accession for bacterial blight resistance breeding** *Linta Vincent* and *Anuradha Sane*	46
6.	**Harnessing Brinjal Germplasm for Resistance to Root-Knot Nematode (*Meloidogyne incognita*): A Translational Approach for Crop Improvement and Sustainable Bioresource Development** *Devindrappa M., R. Umamaheswari, Singh T. H.* and *Bhargavi H. A.*	47
7.	**Exploring the Wild Tomato Genetic Resources for Volatile-Mediated Resistance Against the Two-Spotted Spider Mite** *Bhagyasree S. N., Prasanna H. C., Jayanth K. V.* and *P. D. Kamala Jayanthi*	48
8.	**Multi-varietal mango orchards offer enhanced ecosystem services with special reference to insect fauna** *P. Venkata Rami Reddy* and *M. Sankaran*	49

9.	**Evaluation of advanced breeding lines derived from IIHRBTG-144-1 for powdery mildew resistance in Bitter gourd (*Momordica charantia* L.)** *B. Varalakshmi, K. Hanume Gowda, G. M. S*and*eep Kumar, Vivek Hegde, M. Chaithra, Mahadev Kivati,* and *Tusar Kanti Behera*	50
10.	**CRISPR/Cas12a-based Rapid Diagnostic Assay for the Detection and Distinction of Important strains of *Tomato infecting Begomoviruses*** *Dhanvarsha M., Baskar S., Sheshadria S. A.* and *Basavaprabhu L. Patil*	51
11.	**Identification of Root-Knot Nematode-Resistant Chilli RILs Using Marker-Assisted Selection and Phenotypic–Genotypic Evaluation** *G. Santhosh, R. Umamaheswari, Naresh Ponnam, D. C. Lakshman Reddy* and *Devindrappa M.*	52
12.	**Mining Cowpea Core Collections for Bruchid (*Callosobruchus maculatus*) Resistance and its Association with Seed Physical, Chemical and Genetic Factors** *Chethan Kumar K. B., Kavita Gupta, Kuldeep Tripathi, Rakesh Bhardwaj* and *Dhammaprakash P*and*hari Wankhede*	53
POSTER PRESENTATIONS		
1.	**Genetic dissection of leaf rust resistance in a diversity panel of tetraploid wheat (*Triticum turgidum*)** *Jitendra Kumar Yadav, Shruti Sinha, Hariom Shukla, Ankur Singh, Tanmaya Kumar Sahu, Shailendra Kumar Jha, Jyoti Kumari, Manjusha Verma, Sundeep Kumar, Rakesh Singh, Gyanendra Pratap Singh* and *Amit Kumar Singh*	54
2.	**Identification of Turcicum leaf blight resistant sources among diverse maize germplasm and validation of SSR markers linked to resistance** *Kalyan Kumar P., Santosh K. Pattanashetti, Mahadevu P.* and *Sidramappa C. Talekar*	55
3.	**Genomic Insights into Papaya Ringspot Virus (PRSV-P) Resistance in Papaya (*Carica papaya* L.)** *Dodla Mamatha, Ravishankar K. V., Vasugi C.* and *D. K. Samuel*	56
4.	**Identification of novel sources of quick wilt resistance in black pepper (*Piper nigrum* L.)** *Navya B. L., Hiremath J. S., Kulkarni S., Sumangala K., Mahantesh N. B. N.* and *Mukund S.*	57
5.	**Phenotypic and molecular characterization of Capsicum germplasm for root-knot nematode (*Meloidogyne incognita*) resistance** *Sapana Gurupad Hegde, Smaranika Mishra, Uma Maheshwari R, Lakshmana Reddy D. C., Varsha V.* and *Prakash Singathiya*	58
6.	**Harnessing Wild Tomato Genetic Resources through Volatile Profiling for Sustainable Resistance against *Phthorimaea absoluta*** *Jayanth K. V., H. C. Prasanna* and *Pagadala Damodaram Kamala Jayanthi*	59
7.	**Identification of Tomato Leaf Curl New Delhi Virus tolerant ridge gourd (*Luffa acutangula* Roxb. L.) genotypes** *B. Varalakshmi, M. V. Dhananjaya, B. Mahesha, Mahadev Kivati* and *K. Hanume Gowda*	60
8.	**Biochemical characterization of defense responses in selected grape varieties (*Vitis* spp.) for resistance to grape rust disease** *Nishant, Satisha Jogaiah, Shamina Azeez, Sriram, S., Sanjay K. Singh, Linta Vincent, Debi Prasad Mohanty* and *Roopendra Kumar*	61

9.	**Screening of tuberose genotypes (*Agave amica* Medik.) for resistance to root knot nematode (*Meloidogyne incognita*)** *Sushmita Halagali, Umamaheshwari R., T. Usha Bharathi, Sujatha A. Nair, P. Naveen Kumar* and *Sreenivasa V.*	62
10.	**Optimizing Interspecific Hybridization and Revealing Genotype-Dependent Crossability for Introgression of Ascochyta Blight Resistance in Chickpea (*Cicer arietinum* L.)** *Swapnil Baraskar, Anuradha Chetukuri, Ramachandran Senthil, Ganesh Pawar, Vetriventhan Mani, Ovais Peerzada, Mamta Sharma, Himabindu Kudapa* and *Kuldeep Singh*	63
11.	**First report of CRISPR prime editing in a globally significant non-model organism, the fall armyworm, *Spodoptera frugiperda* (Lepidoptera: Noctuidae)** *Dhawane Yogi, Thalooru Shashikala, Geerthana Subramanian, Akshay Kumar, V. Kaninika, Maligeppagol Manamohan, M. N. Jithesh, Girish Kumar Jha, Ramasamy Asokan* and *Karuppannasamy Ashok*	64
12.	**Harnessing secondary gene pool wild relatives for introgressing stable late leaf spot resistance in groundnut** *H. V. Veerendrakumar, Srinivas Muluguri, U. N. Mangala, Chanakya Paidala, Hima Bindu Bhadragiri, Senthil Ramach*and*ran, Hari Kishan Sudini, Shivali Sharma, Nalini Mallikarjuna, Kuldeep Singh* and *Manish K. P*and*ey*	65
13.	**Haplotype-Based Mapping and Validation of Genomic Regions Controlling Aflatoxin Resistance in Groundnut** *Shilpi Dixit, Vinay Sharma, Hari K. Sudini, Pushpesh Joshi, Vanika Garg, Mangala Uppala, Sunil S. Gangurde, Pooja Soni, Prasad Bajaj, H. D. Upadhyaya, Kuldeep Singh, Rajeev K Varshney* and *Manish K. P*and*ey*	66
14.	**Screening of interspecific hybrids in guava for biotic stress tolerance** *C. Vasugi, S. Sriram, R. Umamaheswari* and *T. Veera Nagasupriya*	67
	THEME - 3 Innovation, Bioeconomy and Livelihood Enhancement	
ORAL PRESENTATIONS		
1.	**Lasoda (*Cordia myxa*) Mucilage as a Natural Cryo-Protectant: Lyophilisation of *Lactobacillus* spp and Formulation of Probiotic Beetroot Powder** *Neethu K., Ranjitha K., Preethi P., Pushpa C. K., Tiwari R. B., Karunakaran G., Shivashankara K. S., Abhishek M.* and *Anuradha S.*	69
2.	**From Forest Knowledge to Green Enterprise: A Scalable Biodiversity Based Livelihood Model among the Soliga community of Biligiri Rangana Hills** Sumangala H. P., Senthil Kumar R. and Sankar V.	70
3.	**Unlocking the Bio-economic Potential of Biodiversity: A Case of Farmer-Led Conservation of Red-Fleshed Jackfruit in India** Harishkumar H. V. and Ganesan Karunakaran	71
4.	**Integrated Farming Systems as Scalable Biodiversity-Based Livelihood Models: Evidence from Udupi and Shivamogga Districts of Karnataka** *Ramya H. R., M. C. A. Devi, Subash S.* and *Naveena N*	72

5.	**Community-Based Apiculture as a Scalable Livelihood Enterprise for Strengthening Livelihood Security of Smallholder Farm Women in Karnataka** *Ramya H. R., Vasanthi C., Bhagyashree S. N.* and *Balakrishna B.*	73
6.	**Who Protects the Protectors? Assessing the Awareness of Progressive Farmers on India's Biodiversity Governance and Farmers' Rights Framework** *Atheequlla G. A., Rohini M. R.* and *Senthil Kumar R.*	74
7.	**Global Production–Trade Dynamics and Economic Viability of Avocado (*Persea americana* Mill.): Evidence and Emerging Opportunities from India** *Raju R., Harish Kumar H. V.* and *Anbukkani Perumal*	75
8.	**Unlocking the Potential of Caryota urens for Sustainable Agroforestry Systems** *B. Augustine Jerard, Sumitha S., Beena Singh, Phani Kumar, P. C. Vengaiah* and *Elizabeth Mathew*	76
9.	**Demonstration and participatory evaluation of seed spices cultivation in the eastern Ghats of Koraput, Odisha** *Ramajayam, Devarajan, Jotirmayee Lenka, Saubhagya Kumar Samal, Saswat Kumar Kar, Ashish Khora* and *Sanjeev Patra*	77
10.	**Characterization of farmers' varieties and their conservation in indigenous minor fruit crops** *Anuradha Sane, Atheequlla G. A.* and *C. Vasugi*	78
11.	**Exploring the untapped potential of Barleria – an indigenous flower crop for their commercial utility** *Safeena S. A., Prerana S., P. Naveen Kumar, Sreenivasa V., Arivalagan M., Ch*and*rashekar N.* and *Chaithra M.*	79
12.	**Tapping the nutritional potential of karonda - a lesser known opportunity fruit by easily adoptable processing techniques** *S. Bhuvaneswari G. C. Sathisha* and *Anuradha Sane*	80
POSTER PRESENTATIONS		
1.	**Promoting the Competitiveness of Underutilized Fruits: Nutritional Analysis of Indigenous and Exotic Fruits in India** *T. R. Rupa, Anuradha Sane* and *P. C. Tripathi*	81
2.	**Leveraging livelihoods through participatory research: a case of Lakshmana Tamarind selection** *Atheequlla G. A., G. Karunakaran, Kanupriya, Senthil Kumar R.*	82
3.	**Screening of different genotypes of jackfruit (*Artocarpus heterophyllus* Lam.) for the preparation of different beverages and its storage stability** *Yadav Shivani Indrajeet* and *Dr. Sanjay Pathak*	83
4.	**Engineering Climate-Resilient Forest Restoration: A Hydrogel–Microbial–Biostimulant Approach for Timber Sapling Establishment** *Samwel Debbarma, Barun Rai, Pritiprasanna Samanta, Mohd. Asif Idrisi, Subhash Ch*and*ra Pradhan* and *Lingaraj Sahoo*	84
5.	**Field Evaluation of LEAFENERGY Biostimulant for Enhancing Growth, Yield, Quality, and Drought Tolerance in Tomato and Chilli under the Arid Conditions of Jharkhand** *Barun Rai, Samwel Debbarma, Pritiprasanna Samanta, Mohd. Asif Idrisi, Deepak Kumar, Subhash Chandra Pradhan* and *Lingaraj Sahoo*	85

THEME - 4 Decoding Diversity for Sustainable Use		
ORAL PRESENTATIONS		
1.	**Introgression of anthracnose fruit rot resistance from C. *baccatum* into C. *annuum* using marker-assisted genetic bridge strategy** *Pasupula Karishma, Sriram S., S*and*eep Kumar G. M., Madhavi Reddy K., Lakshamanareddy D. C., Manoj B. P., Mahebub Shaik, Sai Timmarao* and *Naresh Ponnam*	87
2.	**Unlocking the Breeding Potential of Maldandi Sorghum Landraces: Phenotypic Diversity, Yield Stability, and Adaptation Across Post-Rainy Seasons** *Parashuram Patroti, C. Aruna, B. Amasiddha, Baswaraj Raigond, T. Nepolean* and *C. Tara Satyavathi*	88
3.	**Assessment of bioactive constituents in *Garcinia indica* (Kokum for its potential as a nutraceutical source of hydroxycitric acid, anthocyanins, and phenolics** *Pritee Singh, T. K. Roy, C. Kanupriya, P. C. Tripathi* and *K. S. Shivashankara*	89
4.	**Harnessing Wild Relatives of Pearl Millet Conserved at the ICRISAT Genebank for Grain Quality and Disease Resistance Traits** *Vetriventhan M., Deekshitha B., Jagadeesh K., Naresh D., Rajan Sharma* and *Kuldeep Singh*	90
5.	**Integrative Multi-Omics Analysis Combining Meta-QTL, Comparative Genomics and Meta-Transcriptomics Reveals High-Confidence Candidate Genes for Heat Tolerance in Tomato (*Solanum lycopersicum* L.)** *Abhishek V. Karadagi, H. C. Prasanna, Shivashankaragouda Patil, S. A. Desai, P. L. Patil, T. K. Behera*	91
6.	**Screening of Pepper Germplasm for Heat Tolerance to Identify Promising Donors** *Prakash Singathiya, Smaranika Mishra, Laxman R. H., Naresh Ponnam, Prasanna H. C.* and *Lakshmana Reddy D. C.*	92
7.	**Exploring TOPLESS-RELATED PROTEIN 3 (TPR3) as a Genome Editing target for Fusarium Wilt resistance in Banana**	93
8.	**Harnessing Crop Wild Relatives for Improving Grain Protein Content in Sorghum** *Hari Haran R., Jagadeesh K., Deekshitha B., Naresh D., Vetriventhan M.* and *Kuldeep Singh*	93
9.	**"Genome-Wide Dissection of Adaptive Loci and Candidate Genes for Early Seedling Establishment under Moisture Deficit in Durum Wheat"** *Shashank H. G., Sherry Rachel Jacob, Manoj Kumar Patel, Jyoti Kumari, Krishnan P. Abhijith, Arun Kumar M. B., Sundeep Kumar, Rakesh Bharadwaj, Rahul Gajghate, Jayaluxmi Devi Khumukcham, R. S. Priyanga* and *Kiran Dasanal*	94
10.	**Characterization and evaluation for morpho-biochemical traits of soursop (*Annona muricata* L.) genotypes from western ghats** *Roopendra Kumar, Anuradha Sane, Muralidhara B. M., Vasugi C., Pushpa Chethan Kumar Laya P.* and *Nishant*	95
11.	**Enhancing Banana Genetic Diversity via Chromosome Doubling** *Kalpana Sathiamoorthy, Backiyarani Suthanthiram, Raju Karthic, S. Uma* and *R. Selvarajan*	96
12.	**Multi-Trait Selection Reprograms Metabolic and Transcriptional Networks Underlying Cis-Trans Nepetalactone Enrichment in Catmint (*Nepeta cataria* L.)** *Gunjan Tiwari, Trishna Chaturvedi, Yash P*and*ey* and *Anil Kumar Gupta*	97

13.	**Exploring Genetic Diversity for Nutritional and Biochemical Traits in Curry Leaf (*Murraya koenigii* L. Spreng) Genetic Resources** *B. R. Raghu, G. Chethan Kumar* and *K. S. N*and*ini*	98
14.	**Marker-Assisted Selection for Fusarium Wilt Resistance in Gladiolus progenies** *Priya Bhusaraddi, P. N*and*eesha, Priti Sonavane* and *T. Usha Bharathi*	99
15.	**Trait-Specific Characterization of Sweet Potato Germplasm for Identification of Superior Genetic Resources and Breeding Utilization** *C. Visalakshi Ch*and*ra, Shirly Raichal Anil, K. M. Senthilkumar, J. Sreekumar, T. Makeshkumar, S. Amalnath, P. S. Shameer, A. R. Anjitha, Senthil Muthukrishnan,* and *Pooja Krishnan*	100
16.	**Evaluation of Toxicity in *C. angustifolia*: A Potent Source for Antibacterial Drug** *N. Krishna Radhika, V. S. Keerthana, P. Murugesan, P. S. Sreejith,* and *C. V. S*and*hya*	101
17.	**Evaluation and Identification of Trait-Specific Foxtail Millet Germplasm for Climate-Resilient Breeding** *P. B. Manjunatha, Sunil Shriram Gomashe* and *K. Venkatesan*	102
18.	**Harnessing Wild Genetic Resources: Conservation, Characterisation and Utilisation of Wild Accessions for Broadening the Genetic Base and Climate-Resilient Agriculture in Rice** *Divya Balakrishnan, P. Magudeeswari, G. Pranay, K. S. Naresh, Amurutharao, V. Santosh, V. S*and*eep, T. Saketh, N. Nagamani, S. Suriya, P. Swetha, D. Saiprasanna, S. Michelle, T. Kishore, R. Priya, Y. G. Ravi, Y. Yogendra, N. Sarla, S. V. Sai Prasad* and *M. Sreenivas Prasad*	103
19.	**Exploring Heterozygosity for Genetic Diversity and Trait Improvement in Grapes** *Roshni R. Samarth, Anuradha Upadhyay, Pushpa Aher, Vidya Mane, Komal Thorat* and *Indu Sawant*	104
20.	**Coconut Genetic Resources-Status and Prospects in Breeding for Climate Resilience and Industrial Applications** *V. Niral, Y. Diwakar* and *K. B. Hebbar*	105
21.	**Genetic Diversity Studies for Yield, Nutritional Quality and Powdery Mildew Resistance in Sunflower (*Helianthes annuus* L.)** *N. Nagamani, D. Malarvizhi, R. Saraswathi, R. Sasikala* and *S. Harish*	106
22.	**Molecular Insights into Charantin and B-Carotene Biosynthesis in Bitter Gourd (Momordica charantia L.): Gene Expression Dynamics and Metabolite Profiling** *Banoth Tharun, Gograj Singh Jat, Manisha Mangal, Vishal Sunartiya, Sachin Kumar, Rakesh Bhardwaj, Naveen Singh, Jeetendra Kumar Ranjan, Avinash Tomer, Deepak Singh* and *Tusar Kanti Behera*	107
23.	**Collection, Characterization, Evaluation and Utilization of Appemidi Mango Genotypes of Westren Ghat** *M. Sankaran, M. R. Dinesh, K. S. Shivashankara, K. V. Ravishankar, G. L. Veena, K. Abirami, K. Ranjitha, C. Vasugi, Nishita Raj, Dharampal Singh* and *D. C. Sunil Gowda*	108
POSTER PRESENTATIONS		
1.	**Morphological Characterization and Fat Content Estimation of Different Avocado Accessions Collected from Kodagu Region of Karnataka** *P. Laya, Anuradha Sane, G. Karunakaran, B. M. Muralidhara* and *Roopendra Kumar*	109

2.	**Assessment of Watermelon Germplasm to Identify Lines with High Citrulline Content in Pulp of Fruit** *S. Sreelekshmi, E. Sreenivasa Rao* and *M. Arivalagan*	110
3.	**Characterization of Morphological, Floral and Phytochemical Diversity in *Clitoria ternatea* L. Germplasm** *Gajjala Vasavi Reddy, Rohini M. R., K. M. Yuvaraj, Arivalagan M.* and *Pushpa Chethan Kumar*	111
4.	**Honeycomb Design: A best method for plant architecture and ideotype development in okra {*Abelmoschus esculentus* (L) Moench}** *M. Pitchaimuthu, O. P. Dutta, Manjunatha Gowda, K. Padmini L. T. Chaithra,* and *G. V. Nagamani*	112
5.	**Genetic Dissection of Grain Yield, Protein and Essential Micronutrients in Pearl Millet [*Pennisetum glaucum* (L.) R. Br.] Through Line × Tester Analysis and SSR Marker-Assisted Diversity Assessment** *Ravi M. Jambukiya* and *Balvant C. Patel*	113
6.	**Morpho-Biochemical Characterization of Half-Sib Pummelo Progenies for Fruit Quality Improvement** *Bharti Thakur, M. Sankaran, K. Abirami, B. R. Raghu, T. Sakthivel, K. S. Shivashankara, M. Arivalagan, P. N*and*eesha, B*and*i Navya* and *P. S. Nitin*	114
7.	**Genetic Variability, Heritability and Correlation Studies in Gerbera (*Gerbera jamesonii* Adlam) Varieties Grown under Protected Cultivation** *Y. V. Bhavana, P. Naveen Kumar, Rajiv Kumar, S. A. Safeena, R. T. Anuradha* and *Veeresh*	115
8.	**Assessment of Morphological Diversity in Ridge Gourd (*Luffa acutangula* Roxb.) Genotypes through DUS Characterization** *V. Bhavitha, L. Mukunda Lakshmi, Syed Sadarunnisa, M. Jayaprada* and *T. Susila*	116
9.	**Dissecting the Genomic Regions for Root Nodulation Traits in Chickpea Through Genome Wide Association Mapping** *B. S. Ch*and*ana, Rohit Kumar Mahto, Rajesh Kumar Singh, Danakumar* and *Rajendra Kumar*	117
10.	**Evaluation of Advanced Breeding Lines of Chilli (*Capsicum Annuum* L.) for Deficit Moisture Stress Tolerance** *K. Bharath Ch*and*ra, R. H. Laxman, Naresh Ponnam, K. S. Shivashankara, M. D. Prathibha, Channappa Mahadevaiah, Ashwini Yadav* and *Hema Malini*	118
11.	**Genetic Analysis for Flower Yield and Quality Traits in Mutant Phenotypes of Royal Jasmine (*Jasminum grandiflorum* L.)** *S. M. Soundarya, M. Ganga* and *D. Malarvizhi*	119
12.	**Harnessing Genetic Diversity in CMS-Based Cauliflower for Heterosis Breeding and Sustainable Crop Improvement** *Mokkala Siva Prasad, Khushwant Singh, Neha Jamwal, Ankush Sharma* and *Shivani*	120
13.	**Assessment of Genetic Diversity in Barleria Genotypes using SSR Markers** *S. Prerana, S. A. Safeena, N. Ch*and*rashekar, P. Naveen Kumar, V. Sreenivasa, M. Arivalagan,* and *M. Chaithra*	121

14.	**Integrative Assessment of Fruit Quality, Bioactive Compounds, and Genetic Diversity in Indian Coffee Plum [*Flacourtia jangomas* (Lour.) Raeusch.] from Terai Ecosystems of West Bengal** *Prahlad Deb, P. K. Mukherjee, P. Das, U. Tudu, P. Sutradhar, A. Majumdar,* and *N. Bhowmick*	122
15.	**Decoding Genetic Diversity on Agronomic, Nutritional Traits and Dry Root Rot Resistance in Sesame (*Sesamum indicum* L.) Germplasm** *Ganesh Babu, S. R. V. N., R. Saraswathi, A. Mahalingam, M. Paramasivan, D. Uma* and *D. Malarvizhi*	123
16.	**Characterization of Mutant Progenies of Pummelo (*Citrus grandis* (L.) Osbeck)** *B*and*i Navya, M. Sankaran, K. Abirami, T. Sakthivel, K. S. Shivashankara, P. N*and*eesha, B. R. Raghu* and *Bharti Thakur*	124
17.	**Exploiting Genetic Variability and Heritability for Quantitative and Qualitative Improvement in Mango (*Mangifera indica* L.)** *Rachapally Prashanth, Rajasekhar Marri, V. Suchitra, P. Saidaiah, P. Harikanth* and *P. Gouthami*	125
18.	**Morphological and Biochemical Characterization of Interspecific Hybrids of Guava** *C. Vasugi, T. Veera Nagasupriya* and *M. Arivalagan*	126
19.	**Fruit Morpho-Biochemical Characterization of Some Tamarind (*Tamarindus indica* L.) Genotypes Under Sriniketan Block, Birbhum, West Bengal** *Pradipto Kumar Mukherjee, Biman Ghosh, Tanni Paul, Urmila Tudu* and *Prahlad Deb*	127
20.	**Integrative Assessment of Phenotypic Divergence and Molecular Diversity in Tomato (*Solanum lycopersicum* L.) Germplasm** *B. H. Patel, K. C. Patel* and *Lalita Kumari*	128
21.	**Genetic Architecture, Trait Association, and Diversity Assessment of China Aster [*Callistephus chinensis* (L.) Nees.] Genotypes using PCA and Cluster Analysis** *N. R. Poojashree, Rajiv Kumar, T. Usha Bharathi, M. R. Rohini, C. Mahadevaiah, K. V. Ravishankar, R. Venugopalan* and *Sridhar Gutam*	129
22.	**Comparative Analysis of Diosgenin Accumulation in Fruit Tissues of Various Southern Indian Accessions of *Balanites roxburghii* Planch.** *Guggalada Govardhana Yadav* and *Hosakatte Niranjana Murthy*	130
23.	**CRISPR/Cas9-Mediated Induction of Male Sterility for Use in Plant Breeding** *A. Vijeth Gowda* and *B. R. Raghu*	131
24.	**Heterosis, Combining Ability and Gene Action Studies for Yield, Quality Traits and TOLCD Resistance in Tomato (*Solanum lycopersicum* L.)** *Raju Sarkar, Zakir Hussain, P. K. Singh, R. Selvakumar, Navinder Saini* and *Alka Joshi*	132
25.	**Evaluation of Fertility Levels and Water-Soluble Fertilizers for Sustainable Utilization of Brinjal (*Solanum melongena* L.) var. GJLB-4** *Sabhaya Nirali Bharatbhai* and *M. V. Patel*	133
26.	**Morphological, Biochemical, and Molecular Characterization of *Syzygium cumini* (L.) Skeels Collections from South India** *Kirti Saini, Kanupriya Chaturvedi, Karunakaran Ganesan, Pritee Singh, Lakshmana Reddy,* and *Channappa Mahadevaiah*	134

27.	**Phytochemical Profiling and Antioxidant Activity of *Jasminum* Species** *V. Siva Teja, Anupama T. V., Mini Sankar, Shajma Nafeesa Basheer, Parvathi M. Sreekumar* and *Asish I. Edakkalathur*	135
28.	**Integrated Multivariate Characterization and Multi-Trait Selection of Finger Millet Genotypes for Yield and Nutritional Improvement** *Mihir A. Hansalia, Vikas Pali, Hemanthkumar Koorakula, Parth Patel* and *Ahwan Sanket Pradhan*	136
29.	**Genome Analysis in Pre-Breeding Lines derived from Greengram × Ricebean Crosses** *P. Venkatesh* and *P. Jayamani*	137
30.	**Screening Avocado (*Persea americana* Mill.) Accessions from Kodagu Region of Karnataka for Low-Browning Genotypes** *P. Laya, Anuradha Sane, G. Karunakaran, B. M. Muralidhara* and *Roopendra Kumar*	138
31.	**Harnessing indigenous Finger millet (*Eleusine coracana* (L.) Gaertn.) germplasm through integrated genetic variability and diversity analysis for sustainable crop improvement** *Koorakula Hemanth Kumar, Shweta, Mihir A. Hansalia* and *Kalva Santhi Kumari*	139
32.	**Genetic Variability for Rind Citrulline Content and Yield Traits in Diverse Watermelon (*Citrullus lanatus* L.) Germplasm** *M. S. Varshini, Eguru Sreenivasa Rao* and *M. Arivalagan*	140
33.	**Multivariate Analysis of Morphological Diversity in Bitter Gourd (*Momordica charantia* L.) Germplasm** *A. Adithya, Tusar Kanti Behera, B. Varalakshmi, K. Hanumegowda, Vivek Hegde,* and *Mahadev Kivati*	141
34.	**Bridging Genetic Bottlenecks in Chickpea through Exploiting Wild *Cicer* Gene Pools for Sustainable Crop Improvement** *Ramach*and*ran Senthil, Swapnil Baraskar, Ganesh Pawar, Vetriventhan Mani, Ovais Peerzada* and *Kuldeep Singh*	142
35.	**Harnessing Plant Genetic Resources for Hybrid Development in Bell Pepper (*Capsicum annuum* L.)** *Pratibha Singh, Devinder Kumar Mehta, Ramesh Kumar Bhardwaj, Rajesh Kumar Dogra* and *Meenu Gupta*	143
36.	**Estimation of Heterosis for Yield and Yield-Attributing Traits in Okra (*Abelmoschus esculentus* L. Moench)** *Sristi Sharma, Happy Dev Sharma, Devinder Kumar Mehta, Rajesh Kumar Dogra* and *Vipin Sharma*	144
37.	**Protocol Optimization of *In Vitro* Regeneration in Rice utilized for Genetic Transformation Studies in Rice Varieties Suited for Konkan Region** *Tanmay B. Kamble, S. V. Sawardekar* and *S. H. Sherkar*	145
38.	**Reproductive Trait Characterisation of Annona Plant Genetic Resources:** **A Comparative Study of Pollen Germination, Pollen Viability and Stigma Receptivity** *Madhumathi, T. Sakthivel, M. Sankaran, P. L. Anushma, G. Karunakaran, K. S. Shivashankara, D. C. Lakshmana Reddy* and *C. Mahadevaiah*	146

39.	**Characterization and Evaluation of Yellow Mangosteen (*Garcinia xanthochymus*) accessions for Morpho-Biochemical Traits** *Akriti Tiwari, Anuradha Sane, Roopendra Kumar* and *A. Vithiyalakshmi*	147
40.	**Character Association and Path Coefficient Analysis for Yield and its Components in Pigeonpea (*Cajanus cajan* L. Millsp.)** *M. Jeya Varshini, D. Malarvizhi, A. Thanga Hemavathy, D. Amirtham* and *L. Karthiba*	148
41.	**Development and Genetic Evaluation of Anthocyanin-Rich Okra (*Abelmoschus esculentus* L.) Hybrids for Yield and Yield Attributes** *B. N. Anjali* and *Prakash Kerure*	149
42.	**Decoding Rice Germplasm Diversity for biofortification and climate-resilient rice breeding: Integrating Phenotypic, Biochemical and Molecular Characterization** *Shuvendu Shekhar Mohapatra, Torit Baran Bagchi, Shaswati Rout, C. Anilkumar,* and *Krishnendu Chattopadhyay*	150
43.	**Heterosis, combining ability and gene action studies for yield, quality traits and ToLCD resistance in tomato (*Solanum lycopersicum* L.)** *Raju Sarkar, Zakir Hussain, P. K. Singh, Selvakumar R., Navinder Saini* and *Alka Joshi*	151
44.	**Genetic Analysis of Heterosis, Combining Ability and Molecular Diversity in Gynoecious Parthenocarpic Cucumber (*Cucumis sativus* L.) under Protected Cultivation** *Yamini Yadav, S. S. Dey, K. K. Gangopadhyay, Shrawan Singh, Prolay Kumar Bhowmick, Manjusha Verma and Vikrant Tomar*	152
45.	**Exploring Gamma Ray-Induced Variability in Jackfruit CV. Tubagere through Multi-Level Characterization** *S. Ambrish, Prakash Patil, Kundapura V. Ravishankar* and *Kodthalu Seetharamaiah Shivashankara*	153
46.	**Collection, Conservation and Characterization of Jackfruit (*Artocarpus heterophyllus* Lam.) Germplasm in Peninsular India under AICRP on Fruits** *S. Priya Devi, J. Monisha, Dicto Jose, S. Muthulakshmi, P. Ashok* and *Prakash Patil*	154
47.	**Genetic Diversity Analysis of M_3 Mutant Lines of Mothbean (*Vigna aconitifolia* (Jacq. Marechal) for Yield and Yield Contributing Traits** *A. Jaikeerthi, Bangaremma S. Wadyer, G. M. Sajjanar, Sidharam Patil* and *N. Rekhamani*	155
48.	**Phenotypic Characterization and Multivariate Assessment of Diversity in Coconut (*Cocos nucifera* L.) Germplasm** *Y. Diwakar* and *V. Niral*	156
49.	**Assessment of Genetic Variability for Yield and Yield-Contributing Traits in Horse Gram [*Macrotyloma uniflorum* (Lam.) Verdc.] Germplasm** *N. Rekhamani, Bangaremma S. Wadyer, G. M. Sajjanar, Sidharam Patil* and *A. Jaikeerthi*	157
50.	**Identification of Stable Horse Gram [*Macrotyloma uniflorum* (Lam.) Verdc.] Germplasm Across Different Sowing Dates Using AMMI and GGE Biplot Analysis** *N. Rekhamani, Bangaremma S. Wadyer, G. M. Sajjanar, Sidharam Patil* and *A. Jaikeerthi*	158
51.	**Biochemical Characterization of Sugar Apple (*Annona squamosa* L.) Genotypes based on Fruit Traits for Crop Improvement** *Shivam Kumar Rajpoot, Mahesh Kumar Dhakar, Vishal Nath* and *Chavlesh Kumar*	159

52.	**Unlocking the Genetic Diversity of Shankhpushpi (*clitoria ternatea* L.) Genotypes: Insights into Morphological and Phytochemical traits** *V. Sreenivasa, M. R. Rohini, K. Hima Bindu, R. Gowthami, C. S. Karthik, K. S. Divya,* and *Shivan* and *D. Ainapur*	160
53.	**Integrative Morphological, Quantitative and Molecular Characterization of Contrasting Rice Genetic Resources and F_1 Hybrids reveals Breeding Potential for Marker-Assisted Improvement** *T. J. Shree Bhavatharani, Rose Mary Francies, Jiji Joseph, E. R. Aneena, A. G. Kiran,* and *Jauhar Ali*	161
54.	**Developing Bridge Species through Complementary Strategies to Overcome Ploidy Bottlenecks in Wild Germplasm** *Madhvi Sharma, Srinivas Muluguri, Senthil Ramach*and*ran, Kuldeep Singh* and *Manish K. P*and*ey*	162
55.	**Agro-Morphological Characterization and Yield Evaluation of Parents and F_1 Hybrids Derived from Crosses between KAU Manuratna and Green Super Rice (GSR) Donor accessions in Rice (*Oryza sativa* L.)** *P. Harshitha, Jiji Joseph, Rose Mary Francies* and *Jauhar Ali*	163
56.	**BLUP-Based Genotype-by-Yield*Trait Analysis for Identification of Groundnut Germplasm lines with In-situ Germination Tolerance and Superior Agronomic Performance** *M. Jayanth, B.N. Motagi, Mahesh S. Hullur, B. Rajanna, Akshatha, R. Gurumurty, Kiran Dasanal* and *Ramesh S. Bhat*	164
57.	**Evaluation of Oriental Pickling Melon (*Cucumis melo* L. var conomon) Genotypes Growth and Yield Traits** *Supriya Jaiswal* and *D. C. Manjunathagowda*	165
58.	**Characterization of root distribution and mineral profiling of the *Annona* Hybrid 'Arka Sahan' grafted onto different rootstocks** *Roja H. S., J. Satisha, T. Sakthivel, S. Sujatha, Anuradha Sane, K. V. Ramesh, D. Kalaivanan* and *Vasantha S. V.*	166
59.	**Evaluation of Morpho-Physiological and Anatomical Adaptations in Coconut Genotypes for Climate Resilience** Rithika A., Niral V., U. K. Gayathri, K. M. Ashwitha, P. Ashitha, S. V. Ramesh, K. B. Hebbar	167

THEME - 1

Securing the Genetic Heritage of Peninsular India - from Exploration to Conservation

ORAL PRESENTATIONS

OP-1-01

"*Matoli*"- A unique ethno-botanical treasure of Goa and Konkan region

Thangam M.[1]* and Preeti A. Perira[2]
[1]*Division of Vegetable Crops, ICAR-IIHR, Hesaraghatta Lake Post, Bengaluru, Karnataka*
[2]*School of Biological Science &Biotechnology, Goa University, Taleigao Plateau, Goa*
*Corresponding author email: thangamgoa@gmail.com

ABSTRACT

The "*Matoli"*- an important plant-based arrangement made in wooden canopy and placed over the head of clay idol of Lord Ganesha during the celebration of Ganesh Chaturthi in every household in Goa and Konkan region of Western India. It is an ethno-botanical representation of plant diversity during monsoon season which indicate the traditional richness of diversity of local flora. It is very common in Goa Since, the state of Goa experiences warm and humid climate with annual rainfall ranging from 3000-5000mm, which keeps Goa rich in *flora and fauna*. Primarily the "*Matoli*" consists of all types of wild fruits, vegetables, roots and tubers available during the monsoon season. The seasonally available above plants are collected from the neighbouring forest areas and tied using the fibre extracted from Indian Screw tree (*Helicteres isora*). The collection itself is an ethno-botanical tour to the family members of the region. The elderly people in the house would take their children into the nearby forest areas and educate them the all the useful wild plants available in their locality for its medicinal value and how to conserve the nature for future generations. The six month of Hindu calendar coincides with peak of south west monsoon in Konkan region in general and it exhibits various facets of Goa's rich biodiversity. The important "*Matoli*" items include cultivated plants like coconut, banana, arecanut, apple, sapota, guava *etc.* and season vegetables like okra, cucumber, musk melon *etc.,* minor fruits *viz.,* hog plum, pineapple, citrus *etc.* in addition to numerous wild edible and non-edible plant species collected from forest. On an average, each "*Matoli*" will represent not less than 20-25 plant species and the total number of plant item exceeds 100 in number is not uncommon. The diversity and richness of plants used in "*Matoli*" also significantly varies in different places of Goa state. The taluks proximity to western ghats *viz.,* Sanguem, Sattari, Quepem and Canacona exhibits huge diversity of edible plants used in the arrangements indicating its availability in its natural habitat in the forest regions of ghat area. Meanwhile coastal taluks *viz.,* Tiswadi, Bardez, Mormagoa, Margao exhibits less wild plants diversity with more of commonly available fruits, vegetables and other plants.

In order to promote the cultural identity like "*Matoli*"-which also represents the biological diversity of the region, the government departments like Art and Culture conducts "*Matoli"* competition for public and it awarded a "*Matoli"* with as high as 400 items of wild and edible plant parts used. Unfortunately, due to fast development, urbanization and dwindling forest areas with plant diversity signifies the renewed emphasis for conservation and sustainable utilization of plant genetic resources in the diversity hot spots like Western Ghat regions of India.

Keywords: *Matoli,* ethno-botanical, Goa, Konkan.

OP-1-02

Rediscovering *Linum mysorense* B. Heyne ex Wall: Germplasm Exploration and Conservation Imperatives in the Western Ghats

Mamta Singh[1*], Sunil Shriram Gomashe[2], Pavan K. Malav[1] and Vikender Kaur[1]
[1]*ICAR, National Bureau of Plant Genetic Resources, New Delhi, India*
[2]*ICAR, National Bureau of Plant Genetic Resources, RS-Akola, Akola, India*
*Corresponding author email: mail2mamta.s@gmail.com; mamta.singh@icar.org.in

ABSTRACT

Linum mysorense B. Heyne ex Wall*,* a lesser-known wild flax species native to India, remains significantly underrepresented in national germplasm collections and largely absent from conservation discourse. The scarcity of scientific studies on the ecological and biochemical aspects of this species underscores the need for focused research and scientific exploration. This study documents a targeted exploration of *L. mysorense* across the Western Ghats of Maharashtra—specifically in Ratnagiri, Kolhapur, Sindhudurg, and Satara districts—guided by gap analysis of existing flax accessions and studies of herbarium records. Field surveys conducted during the flowering season (October 2021) revealed scattered populations inhabiting moist forest edges and rocky plateaus, with notable morphological variation in plant stature, flower pigmentation, and capsule traits. Seven germplasm samples were collected, five of which were successfully deposited in the ICAR-NBPGR gene bank. Herbarium vouchers containing flowers, capsules and, seeds were prepared in the field according to conventional herbarium methods and deposited for inclusion in the National Herbarium of Cultivated Plants (NHCP), ICAR-NBPGR, New Delhi with sample ID HS-25628 and HS-25629 to support taxonomic validation and future records. Preliminary fatty acid profiling via GC-MS indicated high linoleic and moderate linolenic acid content, reinforcing the species' potential for nutritional and taxonomic studies in future. The exploration highlights urgent conservation needs, given habitat degradation, poor seed germination, and limited natural competitiveness. The exploration findings underscore the species' vulnerability to habitat degradation and its ecological niche within the Western Ghats flora. This exploration contributes to biodiversity documentation, highlights the *in-situ* conservation and further need to assess the impact of climate shifts on the occurrence of this species, and opens avenues for integrating wild germplasm into climate-resilient crop strategies.

Keywords: *Linum mysorense*, Wild flax, Western Ghats flora, Germplasm exploration, Biodiversity documentation.

OP-1-03

Validation of DELTA (Description Language for Taxonomy) software for sugarcane genetic resources management

Suganya A.*, Karthigeyan S. and Valarmathi R.
ICAR-Sugarcane Breeding Institute Coimbatore-641007 India
*Corresponding author email: suganyamuns@rediff.com

ABSTRACT

The DELTA (DEscription Language for TAxonomy) system is a flexible data-coding format for taxonomic descriptions, and an associated set of programs for producing and typesetting natural-language descriptions and keys, for interactive identification and information retrieval, and for conversion of the data to formats required for phylogenetic and phenetic analysis. About 800 grass genera has been automatically described using DELTA software in terms of more than 500 characters. It was adopted as a standard for data exchange by Biodiversity Information Standards (TDWG) (http://deltaintkey.com/www/overview.htm). It is highly advantageus in plant genetic resources management in digitization, identification, automated descriptions and exclusion of duplicates and phylogenetic studies. However this software has been used limitedly only/ in *Psidium* and *Festuca* germplasm. In this study the software is validated for sugarcane germplasm management. About 96 Indian clones of *Erianthus arundinaceus* of wild genera of sugarcane were characterised based on 37 standard descriptors and descriptor states. The data incorporated into the input file/ DELTA edit and images were uploaded. E- database has been created and documented. The data sets exported to intkey (interactive key) menu/ to retrieve individual clone database, for automated description, to generate difference between clones and identification; to identify the duplicates. The automated description of the clone SES 288 is as follows: Stem Colour [EX] Dark purple. Stem colour [UEx] Greenish purple. Internode shape Cylindrical. Internode alignment Straight. Internode diameter 14 cm. Internode pithiness PRESENT. Internode C.S Oval. Internode waxiness ABSENT. Mode swelling PRESENT. Root zone colour [EX] Purple. Root zone colour [UEX] purple. Number of root eyes 1. alignment regular. Bud size 0.3 cm. Bud shape Oval. Bud Cusion Absent. Bud groove Absent. Growth ring colour light orange. Leaf length 102 cm. Mid rib width 0.06 cm. Leaf sheath hair Absent. Leaf sheath wax Absent. Ligule shape Arch. Ligule hair Absent. Plant height 246 Cm. No. internodes 25. Identification key can be prepared through intkey or manually also prepared depending on the satisfaction of delimitation of clones**.** Among the clones SES 288 was distinct with dark purple coloured internodes. EA thornless was deviated with conoidal shaped internodes. Majority of the clones (83.3%) had straightly alighned internodes. The internodes of SES 159 and IND 99-884 had shown Zig-Zag alighnment. Bud shape in 64.5% of the clones were oval. Beaked buds observed only in the clones IND 99-871 and IND 99-873. All clones were found to be distinct.No duplicates have been indicated by the software. This successful validation of DELTA software implies that the available manual database of different crops can be retrieved with this DELTA software for the effective utilization of crop genetic resources. In addition this software also useful for any database of natural resources and living organisms.

Keywords: DELTA software; Taxonomic description; Sugarcane germplasm; *Erianthus arundinaceus*; Germplasm characterization; Digital documentation.

OP-1-04

Collection, conservation and domestication of native orchids of Kodagu in Western Ghats

Sujatha A. Nair[1], Gowda J. M [2], Singh D. R.[3], Muralidhara B. M.[4],
Awcharae C. M.[4], Sankar V. [4] and Lalduhsanga[1]
ICAR–Indian Institute of Horticultural Research, Hesaraghatta, Bengaluru – 560089, India
* Corresponding author email: Duhsanga14@gmail.com

ABSTRACT

The Western Ghats, a UNESCO-recognised biodiversity hotspot, is home to a remarkable diversity of orchids, representing nearly one-third of the endemic orchids of India. The Kodagu district of Karnataka, with its sacred groves, evergreen forests, and coffee-based agroforestry systems, harbours more than seventy-five species of wild orchids. However, rapid habitat loss, unregulated collection, and anthropogenic pressures have rendered several native species vulnerable, necessitating urgent conservation efforts. This study was undertaken at the ICAR–Central Horticultural Experiment Station (CHES), Chetalli, and ICAR–IIHR, Bengaluru, in collaboration with the National Research Centre on Orchids, Pakyong, Sikkim. It aims to collect, conserve and domesticate native orchids of Kodagu. Epiphytic and terrestrial orchids were established in controlled environments in a naturally ventilated polyhouse, shade-net house and open orchidarium at both CHES, Chetalli and IIHR, Bengaluru. Morphological characterisation and phenological documentation were conducted to evaluate adaptability and horticultural potential. Over twenty-five species across twelve genera, including *Aerides*, *Dendrobium*, *Coelogyne*, *Phaius*, and *Vanda*, were successfully domesticated. Species such as *Rhynchostylis retusa*, *Cymbidium aloifolium*, and *Dendrobium ovatum* demonstrated ornamental and medicinal value, highlighting their potential for sustainable floriculture and ethnobotanical use. The findings provide an effective, sustainable model for conserving the rich orchid diversity of the Western Ghats.

Keywords: Native orchids, Western Ghats, Kodagu, conservation, ex situ, domestication, orchid diversity, sustainable floriculture.

OP-1-05

Habitat suitability modeling for conservation of *Naregamia alata* Wight and Arn. (Meliaceae): An endangered medicinal and ornamental plant, endemic to Western Ghats of Kerala, under different climatic scenarios

Soujanya Halagatti[1]*, Sheron Fernandez[1], Mini Sankar[1], Shelton Padua[2], Sreelatha U.[1] and Simmy A. M.[1]
[1]*Department of Floriculture and Landscaping, College of Agriculture, Vellanikkara, Kerala Agricultural University, KAU P.O., Thrissur, Kerala, India - 680656.*
[2]*Department of Marine Biodiversity and Fishery Environment Management Division, Kochi, Kerala, India, ICAR-Central Marine Fisheries Research Institute, Kochi, Kerala, India - 682018.*
*Corresponding author email: soujanyahalagatti1820@gmail.com

ABSTRACT

Naregamia alata Wight and Arn*.,* a native endangered medicinal plant found in the Indian subcontinent, is widely distributed in lateritic hillocks of Kerala. Due to overexploitation for medicinal purposes, *N. alata* has become a rare species in its natural habitat. Due to its increasing demand driven by its valuable medicinal properties, it is crucial to preserve its genetic diversity through a holistic approach. The main objective of species conservation planning is to identify the current population and distribution. In order to support conservation efforts, suitable habitats can be identified by using Ecological Niche Modeling (ENM) to predict a geographic distribution of species. Maximum Entropy or MaxEnt model was used to estimate the potential distribution of *N. alata* in the state of Kerala, India under present and future climatic scenarios. A total of 22 parameters including bioclimatic, soil types, agroecological zones and topographical variables were used to predict habitat suitability under present climatic scenario using the MaxEnt model. Model output indicated habitat suitability for the species to the tune of approximately 1525 km^2 mainly in the northern part of Kerala. It was seen that the parameters like soil type, precipitation of driest quarter (Bio17), annual precipitation (Bio12), solar radiation (January, March, July and September), agro-ecological zones, Topographic Position Index (TPI), Terrain Ruggedness Index (TRI) and elevation were the most influencing factors determining the distribution of *N. alata.* The habitat suitability for the future scenarios for the periods 2020-2040, 2040-2060, 2060-2080, and 2080-2100 under different Shared Socioeconomic Pathways (SSPs 126, 245, 370, and 585) were also estimated. A substantial decline in the extent of highly suitable area under SSP245 and SSP585 with 21.5 % and 2.09 % reduction respectively during the period 2080-2100, was noticed which could be due steep increase in temperature and decrease in rainfall.

Keywords: Conservation planning, Genetic diversity, Lateritic hillocks, MaxEnt model, Shared Socioeconomic Pathways.

OP-1-06

Species diversity of *Abelmoschus* in Western Ghats: prospects and issues in germplasm utilization

Suma A.[1]*, Joseph John K.[1], Pradip Karmakar[2], P. P. Thirumalaisamy[1], Chithra Devi Pandey[3], Mamta Pathak[4], K. Senguttuvan[5], R. R. Acharya[6], Sushil Pandey[3], P. K. Singh[3], G. P. Singh[3]

[1]*ICAR- National Bureau of Plant Genetic Resources, Regional Station, Vellanikkara, KAU. P. O, Thrissur, Kerala – 680656*

[2]*ICAR-Indian Institute of Vegetable Research, Varanasi, UP - 221005*

[3]*ICAR- National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi - 110012*

[4]*Punjab Agricultural University, Ludhiana, Punjab – 141004*

[5]*Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu – 641003*

[6]*Anand Agricultural University, Anand, Gujarat - 388110*

*Corresponding author email: suma.a@icar.gov.in; sumaagri@gmail.com

ABSTRACT

'Western Ghats' is a biodiversity hotspot renowned for the occurrence of potential crop wild relatives, high endemism and diverse ecosystems. Out of the 13 *Abelmoschus* species occurring in India, seven are reported as naturally occurring in this region. They include two cultivated (*A. esculentus*, *A. caillei*) and five wild species (*A. angulosus, A. moschatus, A. tetraphyllus, A. ficulneus* and *A. enbeepeegeearensis*). The species diversity of *Abelmoschus* in Western Ghats is characterized by the niche specificity of endemic taxa like *A. enbeepeegeearensis*, *A. angulosus* var. *angulosus*, var. *grandiflorus* and var. *purpureus*. These wild species are gene rich sources for tolerance towards biotic and abiotic stresses, prolificacy, extended bearing, reduced fruit length (consumer preferred trait), high mucilage content (medicinal value), perennating tendency, and ornamental value. The repeated use of elite breeding lines has led to narrowing of the genetic base of the okra crop, which was overcome by utilizing these wild species in the wide hybridization progammes. As early as 2013-14 itself, ICAR-NBPGR, Regional Station, Thrissur initiated the interspecific hybridization using *A. enbeepeegeearensis, A. caillei, A. tetraphyllus,* and *A. angulosus* var*. grandiflorus* for transferring the genes conferring tolerance to YVMV disease. Recently, as part of the screening work done under the CRP-AB project during 2021-22, *A. moschatus* was also reported to be resistant to YVMV disease. Though, the fruit set percentage and no. of seeds per fruits were 65.00 and 69.80 percentage in Pusa Sawani x *A. enbeepeegeearensis* (IC649278) and 31.82 and 53.75 percentage in Pusa Sawani x *A. mochatus* (IC433550), the seeds were found to be less viable. Further, the ornamental potential of *A. moschatus* and *A. sagittifolius* was also tapped and the red flowered F_1 hybrid was registered as genetic stock (INGR16036). The F_2 derivatives of this cross were also found to produce flowers with different shades of yellow, pink and red, which can directly be utilized as ornamentals. The issues related to the wild species are with respect to their seed conservation (due to niche specificity), and failure to develop cross derivatives involving species like *A. moschatus* and *A. enbeepeegeearensis* (as they belong to tertiary genepool). Adopting *in-situ* conservation approaches and employing embryo rescue techniques are the ways out to tackle these constraints. Further, the wild flora is threatened by deforestation and habitat loss, urbanization and monoculture, invasive species, unethical seed collection etc. Concerted efforts need to be attempted to regenerate and multiply rare and niche specific taxa like *A. angulosus* subsp. *angulosus* and subsp. *purpureus*.

Keywords: Okra, Crop wild relatives, Pre-breeding, Wide hybridization, Plant genetic resources.

OP-1-07

Molecular Phylogenetics, Divergence Time Estimation and Historical Biogeography of Peninsular Indian Endemics of *Barleria L.* (*Acanthaceae*): Implications on PGR Conservation

Sangoji Vasudha and Dr. Siddharthan S.*
Department of Plant Sciences, School of Life Sciences, University of Hyderabad.
*Corresponding author email: sid@uohyd.ac.in

ABSTRACT

The genus *Barleria* L. (*Acanthaceae*) forms an important component of the wild plant genetic resources of Peninsular India and includes ecologically resilient, medicinal, and ornamental species distributed across the Western Ghats, Eastern Ghats, and Deccan Plateau. Despite its ecological and economic significance, the evolutionary history, divergence times, and biogeographic origin of Peninsular Indian endemic species remain poorly understood because many regional taxa have been underrepresented in global molecular studies. In addition, traditional classifications based on capsule and seed characters are vulnerable to morphological homoplasy.

In the present study, a comprehensive molecular phylogeny of *Barleria* was reconstructed using a combined dataset of nuclear ribosomal ITS and chloroplast intergenic spacer regions (*ndh-rpl32-trnL* and *trnS-trnG*) representing 109 taxa, including major Peninsular Indian endemics such as *B. grandiflora*, *B. montana*, *B. tomentosa*, *B. courtallica*, *B. mysorensis* etc., Divergence times were estimated using an uncorrelated relaxed lognormal clock in BEAST, and ancestral area reconstruction was performed using BioGeoBEARS.

Phylogenetic analyses confirmed the monophyly of *Barleria* and resolved two major subgenera, subgenus *Barleria* and subgenus *Prionitis*. The results further demonstrated that *B. tomentosa* belongs to section *Somalia* within subgenus *Prionitis*, indicating that some morphological characters previously used for classification are homoplasious. Molecular dating showed that the two subgenera diverged during the Late Miocene (~9.18 Ma), while the Western Ghats endemic *B. courtallica* diverged around 8.51 Ma, suggesting that the humid forests of the Western Ghats acted as long-term climatic shelter during Neogene aridification. Biogeographic analyses supported an African origin for the genus and indicated that *Barleria* entered India through multiple independent dispersal events. Section *Somalia* underwent rapid diversification during the Early Pliocene (~4.48 Ma), accompanied by the evolution of adaptive traits such as spines and dense leaf indumentum in response to seasonally dry environments.

Overall, this study provides a molecular framework for the phylogeny, evolution, and biogeography of *Barleria*. The results improve species delimitation, support accurate identification of medicinally important taxa, help reduce adulteration in herbal trade, and provide a scientific basis for the conservation of endemic *Barleria* species and fragile habitats in Peninsular India.

OP-1-08

Documentation and characterization of indigenous mango of Andaman and Nicobar Islands

K. Abirami*, M. Sankaran, V. Baskaran, B. A. Jerard and D. R. Singh
ICAR-Central Island Agricultural Research Institute (CIARI), Sri Vijaya Puram, India
*Corresponding author email: abirami78@gmail.com

ABSTRACT

The Andaman and Nicobar Islands represent an important centre of diversity for the genus *Mangifera*. Six species of mango are distributed that includes the five wild species and the cultivated *Mangifera indica.* Exploratory surveys were undertaken across the Island to document the diversity and documentation of wild and indigenous germplasm of *Mangifera indica.* The endemic and indigenous species, namely *Mangifera griffithii*, *M. camptosperma*, *M. andamanica*, *M. nicobarica*, and *M. sylvatica*, were found to occur in geographically restricted habitats. *M. nicobarica* was found to be distributed only in the Nicobar group of Islands. Morphological characterization of the identified wild species was carried out using the NBPGR minimal descriptors, generating baseline information for their identification, evaluation, and conservation. The cultivated mango (*Mangifera indica*) of the Andaman and Nicobar Islands exhibits remarkable genetic diversity, comprising elite seedling types, multi-season flowering genotypes and polyembryonic accessions that possess considerable value for crop improvement. A total of 104 cultivated mango were identified and characterized under field conditions using standard descriptor-based observations. Based on their desirable horticultural attributes, 12 elite genotypes were selected and established in the field gene bank for detailed evaluation and long-term conservation. Fourteen polyembryonic accessions were collected from diverse locations in South Andaman, including Manjeri (2), Neil Island (4), Guptapara (3), Garacharma (1), and Manglutan (4). These accessions were systematically characterized and conserved to facilitate the identification of superior rootstock candidates with desirable traits such as uniformity, vigour, and tolerance to biotic and abiotic stresses. The exploration also resulted in the identification of a unique farmer variety 'Chinta', from Neil Island, which is registered under Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA), recognizing its value as a protected genetic resource. The cultivated and wild *Mangifera* germplasm of the Andaman and Nicobar Islands together represents an important repository of genetic diversity with immense potential for mango genetic improvement. Systemic conservation efforts of this island mango diversity will ensure their sustainable utilization for future mango breeding initiatives.

Keywords: Andaman and Nicobar Islands, Conservation, Wild Mango, Polyembryony, indigenous.

OP-1-10

Expedition of Wild Cajanus Species Diversity in Peninsular India

Ravi Kishore Pamarthi[1]*, P. G. Gore[2], Kuldeep Tripathi[2], Bhaskar Bajaru[3], Sunil S. Gomashe[4], K. Prasad[5], A. Pradan[6], P. K. Singh[2] and D. P. Semwal[2]

[1]*Department of Plant Genetic Resources, The Graduate School, ICAR-Indian Agricultural Research Institute, New Delhi, India*

[2]*ICAR-National Bureau of Plant Genetic Resources, New Delhi, India*

[3]*ICAR-National Bureau of Plant Genetic Resources, Regional Station, Hyderabad, India*

[4]*ICAR-National Bureau of Plant Genetic Resources, Regional Station, Akola, India*

[5]*Department of Botany, Sri Venkateswara College (DU), Dhaula Kuan, New Delhi, India*

[6]*Department of Agronomy, Indira Gandhi Krishi Viswa Vidyalaya, Raipur, India*

*Corresponding author email: ravi.pgr10024@gmail.com

ABSTRACT

The genus Cajanus is an important member of the family Fabaceae, comprising 34 accepted species worldwide (POWO, 2026). In India, the genus is represented by 18 taxa, including 16 wild species, one cultivated species (Cajanus cajan), and two varieties (Sanjappa, 2020). Among these, C. cajanifolius, C. sericeus, and C. villosum are endemic to India (Sanjappa, 2020). Peninsular India, encompassing the Eastern and Western Ghats, the Deccan Plateau, and the adjoining plains, is one of the country's richest centres of plant diversity, harbouring numerous cultivated and wild crop species. To strengthen the collection and conservation of wild pigeonpea relatives, six systematic exploration and germplasm collection missions were undertaken during 2024–2026 across remote and underexplored regions of Peninsular India. Wild populations of Cajanus albicans, C. cajanifolius, C. crassus, C. platycarpus, and C. scarabaeoides were surveyed and collected from the Eastern Ghats, whereas C. heynie, C. lineata, and C. trinervius were collected from the Western Ghats of Tamil Nadu and Kerala. In addition, C. sericeus was explored and collected from Nashik district, Maharashtra. Among these, the two endemic species, C. cajanifolius and C. sericeus, are considered among the most valuable crop wild relatives of pigeonpea in India because of their restricted distribution and potential utility in genetic improvement. Cajanus cajanifolius exhibits a narrow distribution in the Eastern Ghats, extending from the Bailadila Hills of Chhattisgarh through Koraput district of Odisha to the Dummakonda region of Alluri Sitharama Raju (ASR) district, Andhra Pradesh. The collected accessions have been established under field conditions, characterized using standard taxonomic descriptors, and successfully acclimatized under natural environmental conditions. Detailed taxonomic characterization, supported by diagnostic keys and morphological illustrations, enabled the delineation of nine Cajanus species. While most collections corresponded well with earlier taxonomic descriptions, certain populations exhibited distinct morphological features that may indicate the presence of a previously unrecognized taxon within the genus, warranting further investigation using comprehensive morphological and molecular approaches. The newly collected germplasm represents a valuable addition to the national repository of pigeonpea genetic resources and constitutes an important source of novel alleles for broadening the genetic base of cultivated pigeonpea. These crop wild relatives hold immense potential for utilization in pre-breeding and future pigeonpea improvement programmes aimed at enhancing resistance to biotic and abiotic stresses, productivity, and climate resilience.

OP-1-11

Germplasm Diversity and Conservation at ICAR-SBI Research Centre, Kannur: A Global Reservoir for Sugarcane Improvement

Nisha M.[1]*, Gopi R.[2], Mahesh P.[2], Dhanya V. G.[1], Megaladevi P.[1] and Govindraj P.[2]
[1]*ICAR-Sugarcane Breeding Institute, Research Centre, Kannur, Kerala*
[2]*ICAR-Sugarcane Breeding Institute, Coimbatore, India*
*Corresponding author email: nishathanima@yahoo.com

ABSTRACT

Sugarcane (*Saccharum* spp.) genetic diversity is pivotal for breeding resilient, high-yielding, and climate-adaptable commercial cultivars. The ICAR-Sugarcane Breeding Institute Research Centre (ICAR-SBIRC) at Kannur maintains a globally significant collection of sugarcane germplasm. Situated in an isolated region free from commercial sugarcane, maize, and sorghum cultivation, the Centre provides ideal phytosanitary conditions for long-term clonal field gene bank conservation.

The world collection at ICAR-SBIRC, Kannur, currently comprises 3,382 accessions representing wild species, cultivated progenitor species, interspecific hybrids, and allied genera

- Cultivated Species: *Saccharum officinarum* (757), the high-sugar "noble" cane primarily originating from New Guinea; *S. barberi* (42) and *S. sinense* (30), stress-tolerant historic cultivars derived from natural hybridization.
- Wild Progenitors: *S. robustum* (129), high-biomass ancestral forms including flood-tolerant *f. sanguineum* types; *S. edule* (16), noted for aborted edible inflorescences; and *S. spontaneum* (384), offering extensive ploidy and biotic/abiotic stress resilience.
- Hybrids: Indian hybrids/Co canes (1,042); Exotic hybrids (614 accessions representing 24 countries, notably the USA, Barbados, Fiji, and Australia); and Indo-American (IA) hybrids (130).
- Allied Genera: 240 accessions comprising *Erianthus*, *Miscanthus*, *Narenga*, *Sclerostachya*, *Neyraudia*, and *Vetiveria* (152 exotic, 88 indigenous).

The collection is vegetatively propagated on an annual basis under strict phytosanitary and quarantine protocols. Accessions are systematic evaluated for morphological, yield, quality, and stress-tolerance traits according to standardized sugarcane descriptors, with data digitized into accessible germplasm databases.

This diverse germplasm repository serves as an indispensable genetic resource for pre-breeding and introgressing novel genes into commercial sugarcane programs globally, ensuring crop security against evolving climate and environmental challenges.

OP-1-12

Optimizing *in vitro* micro propagation and proliferation dynamics in *Piper longum* L.: mitigating hyperhydric stress for germplasm conservation

Muhthasim K. V.*, Sharon Aravind, Nisthar E. and R. Sivaranjani
ICAR-Indian Institute of Spices Research, Kozhikode 673012, Kerala
*Corresponding author email: muhthasimkv123@gmail.com

ABSTRACT

Piper longum L. (Long Pepper) is a pharmacologically invaluable medicinal plant facing severe population decline due to destructive over exploitation in the Western Ghats. To ensure long term germplasm conservation and mitigate ecological strain, this study established a highly efficient, reproducible *in vitro* micro propagation protocol. Morphogenic potential and proliferation dynamics were systematically evaluated using node, leaf, root, and shoot tip explants across Murashige and Skoog (MS) and Woody Plant Medium (WPM) regimes at ICAR-Indian Institute of Spices Research, Kozhikode, Kerala.

Our findings reveal a definitive correlation between the moisture profiles established during primary induction and subsequent biomass accumulation in secondary culture. Across all explant types, excessive tissue water retention (>95%) induced by high hormone concentrations, such as MS + 4 mg/L 6-benzylaminopurine (BAP) and MS + 3 mg/L Naphthalene Acetic Acid (NAA) severely restricted cellular respiration and division, resulting in suboptimal secondary Growth Indexes (GI) as low as 91.86%. Conversely, moderate standalone cytokinin treatments effectively regulated primary osmotic status and prevented hyperhydric degradation.

Specifically, MS + 2 mg/L BAP emerged as the universal physiological optimizer for callogenesis. In leaf explants, it maintained a well-regulated primary moisture content 91.55%, yielding a peak GI of 548.16% and 1.033 g of secondary dry matter. For nodal and root cultures, lower primary moisture levels 78.75% and 76.65% primed the tissue for explosive biomass expansion, achieving peak GIs of 1963% and 1076.04%, respectively. Shoot tip explants on MS+ 2 mg/L BAP similarly resisted waterlogging, securing a dominant secondary dry weight of 0.602 g and a GI of 1006.18%. Established calli from all treatments were transferred to an optimized regeneration medium (MS + 2.0 mg/L BAP) for high frequency indirect organogenesis which exhibited the highest morphogenic potential with a mean yield of 13.00±1.73 multiple shoots, 33.33±3.05 leaves, 9.33±0.57 roots, and a leaf length of 2.167±0.15 cm per clump.

During the subsequent *ex vitro* hardening phase, a substrate combination of vermiculite and perlite (3:1) promoted robust growth kinetics, achieving a maximum average plantlet height of 13.27 cm. Ultimately, this optimized micro propagation protocol provides a high frequency mass multiplication system that bypasses hyperhydric physiological stress offering a powerful tool for repository-based conservation and regional biodiversity restoration to offset wild harvesting.

Keywords: Callogenesis, Hyperhydricity, 6-Benzylaminopurine (BAP), Germplasm Conservation, Western Ghats.

OP-1-13

Species associations in habitats of some threatened and endangered potential ornamentals of lateritic hillocks in Kerala

Sheron Fernandez[1*], Soujanya Halagatti[2], Shelton Padua[3], Shravani J.[4],
Mini Sankar[4], Sreelatha U.[4] and Shelton Padua[2]
[1]*AICRP (VC), College of Agriculture, Vellanikkara, Kerala Agricultural University, KAU P.O., Kerala.*
[2]*Department of Floriculture and Landscaping, Indian Agriculture Research Institute, N. Delhi*
[3]*Department of Fishery Biodiversity and Environment Management Division,*
Central Marine Fisheries Research Institute, Kochi
[4]*Department of Floriculture and Landscaping, College of Agriculture, Vellanikkarara, KAU P.O., Thrissur*
*Corresponding author email: sheron.fernandez@kau.in

ABSTRACT

Survey and habitat analysis was carried out in twelve locations of lateritic hillocks of Kerala to study the biodiversity and environment. The locations were Thalakottukara and Puranattukara from Thrissur district, Kumbla, Puthige, Dharmatadaka, Kudalmarkala, Neerchal, Seethangoli and Cheemeni from Kasargod district, Periyaram from Kannur district and Kannamvettikavu and Vazhayur from Malappuram district. Phytosociological quantitative analysis of frequency (F), density (D), relative frequency (RF), relative density (RD), and importance value index (IVI) of each location was identified which are essential for understanding species associations, dominance hierarchies, and vegetation patterns. The study revealed the specific association of certain endangered species such as *Exacum bicolor* and *Ishimum* spp. showing highest IVI value in lateritic locations such as Thalakottukara, Puranattukara, Puthige, Dharmatadaka, Neerchal, Seethangoli. Characteristic association of *Habenaria diphylla* and *Curculigo orchiodes* showing highest IVI were observed in locations such as Thalakottukara, Puthige, Kudalmarkala, Cheemeni, and Periyaram. Close association between with *Naregamia alata* and *Ixora coccinea* was found in Kumbla, Dharmatadaka, Cheemeni and Kannamvettikavu. These indices reveal the adaptive potential and ecological status of species distributed across heterogeneous lateritic soils, which are marked by severe nutrient limitations and distinctive microhabitats.

High IVI values consistently highlight dominant taxa, while assessment of RF and RD facilitates the identification of indicator and rare species, thus informing conservation priorities and community dynamics in these edaphically challenging habitats. Environmental variables with a correlation coefficient of less than 0.8 were selected and provided as input into the MaxEnt software. The key environmental variables which contributed to the habitat modeling of these species were annual precipitation (Bio12), precipitation of the driest quarter (Bio17), mean diurnal range (Bio2), precipitation seasonality (Bio15), solar radiation (January, March, July, and September), and water vapor pressure (January). Topographic variables such as elevation (Digital Elevation Model), Topographic Position Index (TPI), Terrain Ruggedness Index (TRI), slope and aspect. Additionally, agroecological zones, soil types, and Normalized Difference Vegetation Index (NDVI). Out of these variables, critical variables that contributed to the MaxEnt model for the current distribution of *Exacum bicolor* were Bio 17, Bio 12, Bio 2, TPI, solar radiation (March) and slope. For *Habenaria diphylla,* Bio 12, Bio 2, Bio 17, TPI and solar radiation (March) had significant contribution. Soil types, Bio 17, Bio 12, solar radiation, elevation (DEM), TPI and TRI had contributed to the habitat suitability of *Naregamia alata*.

Keywords: Relative frequency, Importance value index, Digital elevation model, NDVI.

OP-1-14

Differential response of Oil Palm fruit forms to pollen desiccation and cryopreservation

Rohini M. R., Diljith M. D., G. Somasundaram and Neema M.
ICAR-Indian Institute of Oil Palm Research, Research Centre, Palode
*Corresponding author email: rohu20@gmail.com

ABSTRACT

Oil palm (*Elaeis guineensis* Jacq.) is the world's leading oilseed crop, and the availability of viable pollen is essential for controlled hybridization and hybrid seed production. However, the short viability of fresh pollen under ambient conditions restricts its use in breeding programmes. Cryopreservation in liquid nitrogen (−196°C) offers an effective approach for long-term pollen conservation, provided that pollen is desiccated to an optimum moisture content before storage. The present study evaluated the differential response of the three oil palm fruit forms, Dura, Tenera, and Pisifera to pollen desiccation and cryopreservation to identify optimum desiccation conditions for each. Fresh pollen was collected from male inflorescences of six oil palm genotypes comprising two Dura, two Tenera, and two Pisifera palms and desiccated for 0, 1, 2, 3, 4, and 5 hours. At each desiccation interval, pollen moisture content and *in vitro* germination percentage were assessed before and after cryopreservation. Fresh pollen moisture content ranged from 20–27% in Dura, 11–12% in Tenera and 20–21% in Pisifera exhibiting distinct initial moisture levels. Fresh pollen maintained high germination (80–95%) before cryopreservation in all the fruit forms. In contrast, cryopreserved pollen exhibited marked differences among the fruit forms. Without adequate desiccation, post-cryopreservation germination was low in Dura and Pisifera (0–20%), whereas Tenera retained comparatively higher germination (40–45%). A progressive increase in post-cryopreservation germination was observed with decreasing pollen moisture content, confirming the importance of pre-desiccation for successful cryostorage. Maximum post-cryopreservation germination (80–100%) was obtained when pollen moisture content was reduced to 6–10%. However, the optimum desiccation duration varied among the fruit forms: Tenera achieved optimum moisture content after 3 hours of desiccation, whereas Dura and Pisifera required 4 hours. These findings demonstrate distinct differences in desiccation requirements and cryotolerance among oil palm fruit forms and highlight the need for fruit form-specific cryopreservation protocols

Keywords: Oil Palm, cryopreservation, pollen, viability, desiccation.

OP-1-15

Safeguarding Mulberry Genetic Resources Through Exploration, Conservation, and Utilization

Muthusamy Shankar*, Mallegowdanakoppalu Channappa Thriveni,
Raju Mondal, Manjunath Nandan, Poojara Haleshsa and Narendra Kumar Bhatia
CSB-Central Sericultural Germplasm Resources Centre, Central Silk Board,
Ministry of Textiles, Hosur, Tamil Nadu
*Corresponding author email: shankarpgr@gmail.com

ABSTRACT

The Central Sericultural Germplasm Resources Centre (CSB-CSGRC), Hosur, functions as the national repository for mulberry genetic resources and plays a pivotal role in their conservation, characterization and strategic utilization for sericulture improvement. Over more than three decades, the centre has developed and maintained a robust field gene bank comprising 1,352 mulberry accessions collected through 84 exploratory trips across diverse agroecological regions. The collection represents genetic diversity from 29 countries and 31 states and union territories of India, of which 1,067 accessions are indigenous and 285 are exotic. All accessions have been assigned National Accession Numbers by ICAR-NBPGR, New Delhi, thereby ensuring proper identity, documentation, and long-term genetic security. The mulberry germplasm conserved at CSB-CSGRC, Hosur has been systematically evaluated for propagation traits, growth and yield attributes and biochemical parameters. Till now, 1,292 accessions have been characterized using 19 morphological, 14 anatomical and 26 reproductive descriptors generating a comprehensive phenotypic database for effective utilization in crop improvement programmes. This extensive characterization has facilitated the identification of trait-specific accessions with superior agronomic and adaptive value. Promising genotypes include those with high leaf yield and biomass (20), high harvest index (17), high water retention capacity (20), high rooting ability (30) and superior performance for multiple growth traits (15). Accessions adapted to tropical alkaline irrigated conditions (09), tropical hot and high humid conditions (04), cold tolerance (04), drought tolerance (17), salinity tolerance (20) and resistance/tolerance to Tukra (08) and powdery mildew (20) have also been identified. In addition to field conservation, CSB-CSGRC has established a safety backup through cryopreservation with 338 accessions conserved in the National Cryo-Gene Bank at ICAR-NBPGR, New Delhi. This integrated conservation strategy enhances the resilience of the collection against biotic, abiotic, and climatic threats. Beyond conservation, the germplasm is being utilized to support breeding, pre-breeding, and region-specific varietal development aimed at improving leaf productivity, stress resilience and input-use efficiency. These efforts contribute directly to the sustainability of sericulture and the livelihood security of farmers dependent on mulberry-based silk production. Thus, CSB-CSGRC serves as a critical national institution linking biodiversity conservation with climate-smart utilization and long-term sericultural advancement.

Keywords: Characterization, Cryopreservation, Mulberry Germplasm, Trait-Specific Accessions, Sericulture Livelihoods.

OP-1-16

Exploring Jamun (Sizijium cumini), Karonda (Carissa karonda) Jackfruit (Artocarpus app) and Kokum (Garcinia indica) Naturally occurring Biodiversity for Conservation and Development of Climate Resilient Cultivars in Konkan Region of Maharashtra

Dr. B. P. Patil[1]* and Dr. B. M. Jamdagni[2]
[1]*Ex ADR RFRS, Vengurla and Head Agronomy, DBSKKV, Dapoli*
[2]*Ex Pulses Breeder and Plant Physiologist MPKV, Rahuri, Maharashtra*
*Corresponding author email: bhimraoppatil49@gmail.com

ABSTRACT

Natural plant diversity has been developed over centuries of cross pollination by natural pollinators ,mainly, honey bees, birds, insects, wind and water through natural selection and survival of the fittest mechanism. The natural diversity of plants within and between species has been the basic principle for sustainability, survival and natural perpetuation . Eventually, these plants are resiliant to changeing climate and accompanied inadvertent changes in the entire growing environment of the plant. Exploring such naturally stabilized (natural selection) useful plants, especially, fruit plants, having specific nutritional traits and medicinal values, is the need of the present days of rapid, uncertain and unprecedented changes in climate as these plants are naturally resiliant to changeing climate. In view of this Jamun (Sizijium cumini) , Karonda (Carissa karonda), Jackfruit (Artocarpus app), Kokum (Garcinia indica) biodiversity was explored from Western Ghat, the world's mega biodiversity centre in the state of Maharashtra. The bold type (20 to 22g fruit wt) Jamun, naturally stabilized genotype was selected (Village Bahadoli ,Palghar district), studied for various fruit traits and evaluated to release as Konkan Bahadoli cultivar in 2005. Eventhogh, it's polyembryonic in nature, it can be successfully propagated and mass multiplied ,as true to type, by soft wood wedge grafting on top of non discript jamun seedlings. Lakhs of grafted plants of this cultivar have been supplied to farmers. Similarly, bold Karonda types were collected from Sindhudurg district(village Amboli) and after studying and evaluating various characteristics it was released as Konkan Bold Karonda cultivar in the year 2005.Its rich in iron and anti oxidants with deep red and purple edible pigment .Standard vegetative propagation method using mature cuttings treated with root inducing hormone ,IBA, has been developed for mass multiplication. The naturally occurring variability of jackfruit in Western Ghats is vast and needs conservation and exploration for commercial exploitation in the form of a commercial cultivar , was long over due. Konkan Prolific ,a table purpose variety of Jackfruit has been out come of such scientific exploitation of jackfruit biodiversity in Konkan. Mass multiplication of this climate resilient genotype has been done by soft wood grafting technique since 2005.Garcinia is another fruit used widely as garnishing agent in various vegetarian dishes and specially, in fish curries and is rich in hydroxy citric acid (anti cholesterol agent) and deep red food grade pigment in its rind. The seeds contain edible fat characteristically solid at room temperature. Garcinia's naturally occurring wide biodiversity exploration and conservation studies led to development of early fruiting first cultivar, Konkan Amruta, which is mass multiplied by soft wood top grafting on any kokum seedling. It's plagiotrophic branches develop into plagiotrophic dwarf plants providing opportunities

for high density planting and harvesting by hand . However, grafting orthotrophic branches leads to upright tall conical plants. Even the exposed roots of garcinia can give rise to mother plant like progeny. Development of hermaphrodite garcinia cultivar from naturally occurring biodiversity is in progress by conservation and exploration. The Western Ghat Kokum Foundation based in Goa is promoting Garcinia research and development in Maharashtra , Goa, Karnataka and Kerala as a super food of future. All the above nutri-medico-spice- fruit crops are rainfed , highly drought tolerant and resilient to climate change and perfectly fitting the organic and natural foods of present and the long future.

OP-1-17

Wild relatives of *Solanum* as store house for resistance to biotic and abiotic stresses in Western Ghats

T. H. Singh* and Mrs. Dr. Bhargavi H. A.
Division of Vegetable crops, ICAR-Indian Institute of Horticultural Research,
Hesaraghatta lake Post, Bengaluru-560089
*Corresponding author email: ttejavathu41@gmail.com

ABSTRACT

Brinjal (*Solanum melongena* L.) is one of the most widely cultivated annual vegetable crops belonging to the family Solanaceae mainly grown for its edible immature and tender fruits in tropical and subtropical regions of the world. Eggplant originated in India and with secondary centers of origin as China and South East Asia. In India, eggplant is cultivated in almost all parts of the country (except at higher at higher altitude where it succumbs to frost injury). In India the eggplant is grown in an area of 6, 77,000 hectares with the production of 12.77 million tonnes. Brinjal is rich source of acids such & chlorigenic, choline, trigonellline, flavanoids,, phosphorous, calcium, potassium, vitsminB, vitaminC, vitamin A &B. Eggplant has major pharmaceutical actions such as cholesterol lowering, antiatherogenic, diuretic, cholagogue, and antioxidant, anti rheumatic. It contains some of the therapeutic indicators such as Hypercholesterolemia, atherosclerosis, hepatobiliary dyskineiasis, rheumatic pains, lower cholesterol & skin conditions and minerals. Other compounds such as anthocyanins, phenols, glycoalkaloids (solasodine), free-reducing sugars and amide proteins are high in eggplant. Eggplant is an excellent source of medicine for liver complaints and diabetic problems.

Brinjal (Eggplant, Aubergine) is a traditional and indigenous crop of India. The Genus ***Solanum*** comprises approximately 2000 species, which include both tuber bearing and non-tuber bearing form Solanum melongena is an important edible species under non-tuber bearing form of which 22 wild species are of domesticated types of which ***Solanum macrocarpon***(perennial brinjal) , ***Solanum nigram*****, (used as remedy for stomach ace)** ***Solanum torvum*** sundekayee) **, Solanum viarum** and **Solanum mammosum** are widely grown in western Ghats of Indian and they posses many genes for resistance to both biotic and abiotic stresses have lot of biodiversity with respect fruit shape size and colour. The following wild species namely ***S. incanum*** (Resistant to Shoot

and fruit borer), ***S. sisymbriifolium*** *(*Resistant to Root-knot nematode), ***S. nigrum (resistant*** **to Bacterial wilt*)* *S. mammosum*** (resistant to Epilachana beetle), ***S. torvum*** (resistant to Spotted beetle, RKN& BW)**,** ***S. gilo*** (resistant Phomopsis blight)**,** ***S. xanthocarpum (*** Resistant to Fruit rot), ***S. macrocarpon*** (Shoot and fruit borer**)** and **Solanum seaforthianum,Solanum viarum,Solanum mammosum,Solanum sisymbrifolium, Solanum torvum were found as resistant and Solanum capsicoides** was tolerant to mylocerus root grub/ ash weevil. An extensive research work carried out at ICAR-IIHR has led in maintence, utilization and transfer of genes from wild to cultivated species background. Apart from wild species there some heirlooms species such Mattugulla (GI tagged) WCGR (west coast green round) are widely cultivated in Western Ghats). These heirlooms types have been extensively used in characterizatio**n**, evaluation**,** and utilization for Sustainable Development as store houses of genes resistance to many biotic and abiotic stresses, as rootstocks for combating many soil borne diseases Brinjal.

OP-1-18

Ploidy diversity in *Saccharum spontaneum* L., wild species of sugarcane, from Western Ghats of India

V. P. Sobhakumari*, P. Govindaraj and H. K. Mahadevaswamy
Crop Improvement Division, ICAR-Sugarcane Breeding Institute, Coimbatore - 641 007, Tamil Nadu, India
*Corresponding author email: vpsobhakumari@rediffmail.com

ABSTRACT

Saccharum spontaneum, a wild species of sugarcane, is highly valuable and diverse among the *Saccharum* species and the genetic material from the species is vital for improving modern sugarcane cultivars as it offers traits such as drought tolerance, pest and disease resistance and potential for tillering and ratoonability. The world collection of sugarcane germplasm maintained by ICAR- Sugarcane Breeding Institute, Coimbatore, is the largest collection at present. This collection includes more than 20 cytotypes of *S. spontaneum* collected from the distributional areas in the country and outside. While reviewing the germplasm collection, a gap in the Western Ghats area was observed and accordingly an exploration was carried out during 2019 for the collection and ex-situ conservation of *S. spontaneum* from the vulnerable area of Western Ghats especially from high altitude regions. The expedition area covers the Western Ghats travers south through the states of Maharashtra, Goa, Karnataka, Kerala and Tamil Nadu. This targeted exploration resulted in the collection of 39 *S. spontaneum* accessions. The largest collection was from Maharashtra (18 collections) followed by Karnataka (9 collections), Kerala (5 collections), Goa (4 collections) and Tamil Nadu (3 collections). Characterization of collected *Saccharum* genetic resources is necessary for its efficient utilization. Cytological characterization has been done in 39 *S. spontaneum* accessions. Accessions having somatic chromosome number 2n=64 were maximum in this collection (67%). The ploidy of this cytotype is octoploid (8x) and it is the most prevalent ploidy type of *S. spontaneum* in India. Accessions with 2n=72 (23%) and 2n=80 (10%) were also identified from this collection. Considering the basic chromosome number of *S. spontaneum* as

X=8, the collection of this species from Western Ghats included three different types of ploidies. i.e., 8x, 9x and 10x with three different cytotypes as 2n=64, 2n=72 and 2n=80 respectively.

Genetic diversity along with the chromosomal polymorphism existing in *S. spontaneum* collection evidenced the natural variation preserved in the less disturbed virgin forest areas of Western Ghats. The collection of this wild species from Western Ghats will serve as a new source of genes for base broadening in pre breeding programmes and also to develop new, more resilient sugarcane varieties.

OP-1-20

Mapping Diversity for Future breeding: Germplasm Characterization of Jackfruit (*Artocarpus heterophyllus* Lam.)

Abhishek Pratap[1], A. K. Srivastava[2*], Om Prakash[3], S. V. Dwivedi[2], Vishal Chugh[3] and Bhawna Singh[1]
Department of Fruit Science, College of Horticulture,
Banda University of Agriculture and Technology, Banda Uttar Pradesh
*Corresponding author email: srivastavahort@yahoo.com

ABSTRACT

Jackfruit (*Artocarpus heterophyllus* Lam.) is an economically vital evergreen tree cultivated extensively throughout India across altitudinal gradients ranging from 45 to 1200 m. While India ranks as the world's second-largest jackfruit producer—with major cultivation spanning West Bengal, Tamil Nadu, Karnataka, Odisha, Kerala, Assam, Bihar, Tripura, and Uttar Pradesh—systematic documentation of its genetic diversity remains limited. Due to its cross-pollinated nature and predominant propagation via seeds, the species exhibits profound natural variability in physico-chemical traits. However, this genetic resource base faces significant risks due to selective cultivation driven by market demand. Currently, well-defined commercial varieties are lacking, and production relies on a few indigenous landraces (e.g., Champa, Gulabi, Rudrakshi, Hazari) categorized by their distinct yield and morpho-cultural attributes. Consequently, identifying superior genotypes is critical for crop improvement.

While vast wild diversity persists in the evergreen forests of the Western Ghats, this study focused on characterizing domestic variations in Northern India. A germplasm survey was conducted during the 2023–24 cropping season across several districts of Uttar Pradesh, including Banda, Ayodhya, Sultanpur, Varanasi, Fatehpur, Lalganj, Pratapgarh and Ghazipur. Morphological characterization was performed using standardized IPGRI guidelines. Significant phenotypic divergence was observed among the collected genotypes regarding tree architecture, bark patterns, leaf and fruit morphology, spine traits, and latex exudation. A wide range of variability also noted for fruit quality attributes (fruit weight 0.07-11.94 kg, fruit length 5.8-51.3 cm, fruit width4.6-25.4 cm, number of flakes per fruit 12-606, average weight of flakes 7-18 g, flake length 2.28-5.22 cm, flake width 1.57-4.04 cm, number of seeds per fruit 7-591, average weight of seeds 3.8-10.4 g, seed length 1.81-3.39 cm, seed width 1.3-2.4 cm, TSS 7-32 °Brix).

Keywords: Jackfruit (*Artocarpus heterophyllus* Lam.), germplasm, variability, diversity, characterization.

OP-1-22

Clonal propagation of strawberry guava (*Psidium cattleianum* Sabine) through stem cuttings: An approach for ex situ conservation

Anushma P. L.[1]*, Rafeekher M.[2], Satisha J.[1], Shivashankara K. S.[1], Simi S.[2], Vasugi C.[1] and Sakthivel T.[1]
[1]*ICAR-Indian Institute of Horticultural Research, Hesaraghatta Lake Post, Bengaluru, Karnataka, India*
[2]*College of Agriculture, Vellayani, Thiruvananthapuram, Kerala, India*
*Corresponding author email: anushma.p.l@gmail.com

ABSTRACT

Psidium cattleianum Sabine (strawberry guava) is an underutilized wild *Psidium* species of considerable value as a genetic resource for guava improvement. The species possesses potential importance as a source of resistance to soil-borne pathogens, particularly the guava wilt and root-knot nematode complex**,** and can serve as a potential clonal rootstock for cultivated guava (*P. guajava* L.). The present study was undertaken to standardize clonal propagation of *P. cattleianum* through stem cuttings by use of growth regulators. Softwood and herbaceous cuttings were treated with different concentrations of indole-3-butyric acid (IBA), paclobutrazol, spermidine and hydrogen peroxide (H_2O_2) in a completely randomized design with 30 replications. Softwood cuttings showed better sprouting, shoot growth and rooting performance compared with herbaceous cuttings. Growth regulator treatment successfully induced rooting and sprouting in strawberry guava, which was previously reported to be difficult to root. The results demonstrate that selection of appropriate cutting type growth regulator treatments could substantially improve clonal multiplication of *P. cattleianum*. An efficient stem-cutting propagation protocol can facilitate rapid multiplication and ex situ conservation of genetically uniform germplasm**,** supporting the establishment of filed gene banks and clonal repositories. Thus, clonal propagation provides a practical approach for both conservation and sustainable utilization of this valuable but underexploited *Psidium* species.

Keywords: Wild guava, plant growth regulators, adventitious rooting, clonal repository.

OP-1-23

Emmer Wheat/Khapli (*Triticum dicoccum*): An emerging nutraceutical/functional food crop of Peninsular India

Vikas V. K.[1]*, Sivasamy M.[1], Das B. K.[2], Nisha R.[1] and John Peter[1]
[1]*ICAR-Indian Agricultural Research Institute Regional Station, Wellington - 643 231, Tamilnadu, India.*
[2]*Mutation Breeding Section, Bhabha Atomic Research Centre, Mumbai - 400 085, Maharashtra, India.*
*Corresponding author email: vkvikaswtn@gmail.com

ABSTRACT

Emmer wheat (*Triticum dicoccum*), popularly known as "Khapli" is grown in the state of Maharashtra and Karnataka of the Peninsular India. It is an old crop with hulled grain and has been cultivated during seven millennia. It has been largely replaced by hulless species and is a minor crop with exception of some countries like India, Ethiopia and Yemen where its grain is used for preparing traditional food. It is gaining importance as functional/therapeutic food because of the low glycemic index (<55), slow digestibility, high satiety value coupled with resistant starch, high protein (16%) and fibre. These quality attributes are considered vital for the dietary management of diabetes and cardiovascular risks. In recent years, India is recognised as 'Diabetic Capital of the world". Rigid architecture in the starch granules of dicoccum wheat provides resistant nature to starch. Incorporation of dicoccum wheat in the diet of diabetic patients resulted in reduction in total lipids, triglycerides and LDL-cholesterol concentration, Thus the current view of dietary carbohydrates as simply providing us with energy should be reconsidered. Traditional varieties/landraces of emmer are tall, susceptible to lodging and low yielding with high quality (NP200, 201 &202), however modern semi dwarf cultivars are high yielding with low quality. Most of the currently cultivated semi dwarf dicoccum cultivars derived their dwarfing genes from *Triticum durum* (cultivated tetraploid species) and has strong linkage drag in altering the quality traits. This necessitates the need to search for new sources to create variability among the dicoccum gene pool wherein mutation, inter specific hybridization etc., could help. Gamma irradiation of traditional variety, NP201 provided a semi dwarf line with high yield, stable in performance and comparable quality was released as variety, HW1098 for cultivation for the farmers of dicoccum cultivating areas of India (Peninsular India). Interspecific hybridisation between *T. dicoccum* and *T.carthalicum* (wild tetraploid species) resulted in a transgressive segregant with high yield and quality which is under field testing. Emmer wheat, a minor cereal today should know a new development due to the nutritional value of its grain.

Keywords: Emmer wheat; *Triticum dicoccum;* Functional food; Resistant starch; Diabetes.

OP-1-24

From Diversity to Discovery: Unlocking Genetic Resources for the Future of Chilli Improvement

Naresh Ponnam*, Smaranika Mishra, Lakshman Reddy D. C.,
Sandeep Kumar G. M., Venkataravanappa V. and Prasanna Kumar N. R.
ICAR-Indian Institute of Horticultural Research, Bengaluru
*Corresponding author email: ponnam.naresh@icar.org.in

ABSTRACT

Chilli (*Capsicum* spp.) is an important commercial spice crop with immense economic value and diverse applications in the food, spice, animal feed, cosmeceutical, pharmaceutical, and traditional medicinal industries. The unique bioactive compounds present in chilli fruits, particularly capsaicinoids, capsanthin, and capsorubin, have further enhanced its industrial significance and demand. India, a major centre of *Capsicum* diversity and the world's leading producer and exporter of dry chilli, possesses a rich reservoir of genetic resources, including diverse landraces and more than 5,000 germplasm accessions conserved in national gene banks. This genetic wealth provides tremendous opportunities for developing varieties and F1 hybrids tailored to specific industrial applications, consumer preferences, fruit quality attributes, and resilience to emerging production challenges. Despite substantial progress in chilli improvement, breeding programmes have largely focused on *C. annuum*, with limited exploitation of other domesticated species, wild relatives, and indigenous landraces. These underutilized genetic resources represent an untapped reservoir of novel alleles for resistance to emerging pests and diseases, abiotic stresses, and desirable fruit and bioactive traits. Their systematic exploration, characterization, and deployment in breeding programmes are therefore essential for broadening the genetic base and enhancing the productivity, quality, and resilience of cultivated chilli. Recent advances in genomics, next-generation sequencing, molecular markers, marker-assisted selection, and precision breeding provide powerful tools for accelerating the identification and utilization of valuable genetic variation. Further research is needed to elucidate the genetic architecture and develop molecular markers linked to resistance against emerging pests and diseases and key fruit quality traits in Indian germplasm.

OP-1-25

Recent Trends in Conservation and Utilisation of Cashew Genetic Resources

Mohana G. S.*, Eradasappa E. and Veena G. L.
ICAR-Directorate of Cashew Research, Puttur, Karnataka
*Corresponding author email: mohangs2007@gmail.com

ABSTRACT

ICAR- Directorate of Cashew Research, Puttur, Karnataka, is the nodal centre for cashew research in the country and houses 603 cashew germplasm accessions collected from different parts of India and other countries. So far, five germplasm catalogues have been published, and a germplasm database management system has been developed. Through this software, it is possible to select a particular accession based on multiple characters, for subsequent utilisation in breeding programs. Statistical analysis involving correlation, frequency distribution, skewness, and kurtosis of various characters has been worked out, giving an idea of the extent of alleles and direction of dominance.

A core collection comprising 49 accessions has been developed, deploying the advanced maximisation strategy with a heuristic approach. Polyclonal hybrids from these core accessions have been produced and are under evaluation. The Cashew Nut Shell Liquid (CNSL) content of 428 germplasm accessions has been estimated, and both CNSL-rich and free types have been identified. Three wild species belonging to the *Anacardium* genus have been conserved and utilised to develop interspecific hybrids. Further, seven accessions of *Semacarpus anacardium* have been recently collected. In addition, *Semecarpus kurzii* was used as the male parent to develop intergeneric hybrids utilising cryopreservation techniques. The recent work covering these aspects will be discussed in detail.

OP-1-26

Morphological Delineation of Naturally Introgressed Eggplant Genotypes from Germplasm Collections: Implications for PGR Conservation and Management

Kasireddy Sivasankarreddy[1], Thirumalaisamy P. P.[2], Jiji Joseph[1], Venkatesan Kannan[2], Pradheep K.[2], Madhavan Latha[2] and Azhakan Suma[2]

[1]*Department of Plant Breeding and Genetics, College of Agriculture, Kerala Agricultural University, Thrissur, India.*

[2]*ICAR-National Bureau of Plant Genetic Resources, Regional Station, Thrissur, India.*

*Corresponding author email: sivagpb@gmail.com

ABSTRACT

Natural introgression between wild and cultivated *Solanum* species within germplasm collections represents a significant yet often overlooked challenge for plant genetic resources (PGR) management. Eggplant (*Solanum melongena* L.), one of India's most widely cultivated vegetable crops, has its primary domestication centre in the Indian subcontinent. Three closely related species — *S. melongena*, *S. incanum*, and *S. insanum* co-exist in India, where spontaneous hybridization between the wild progenitor *S. insanum* and cultivated *S. melongena* generated naturally introgressed genotypes within germplasm collections. Despite their significance for PGR management, no morphological key had previously been established to distinguish these introgressed genotypes from cultivated and wild forms under field conditions.

The present study characterized 157 eggplant germplasm accessions conserved at ICAR-NBPGR Regional Station, Kerala, classifying them into three distinct groups: 117 cultivated eggplants (*S. melongena*), 30 naturally introgressed genotypes, and 10 wild progenitors (*S. insanum*). Key morphological traits reliably differentiating introgressed genotypes included prickliness of stem, petiole, calyx and pedicel, leaf base shape, and fruit shape and size. Fruit length, breadth and mesocarp texture provided additional discriminatory support. Quantitative analysis revealed substantial variability, with fruit length-to-breadth ratio exhibiting the highest coefficient of variation (73.87%), followed by fruit length (54.73%) and average fruit weight (53.50%). Frequency distribution of 14 qualitative traits confirmed the presence of all character states, reflecting rich phenotypic diversity within the collection. These findings establish a reliable morphological framework for field-level identification of naturally introgressed eggplant genotypes, with direct applications for gene bank curators, taxonomists and germplasm explorers in maintaining germplasm purity, accurate documentation and sustainable PGR management.

Keywords: Eggplant germplasm; natural introgression; morphological key traits; Peninsular India; plant genetic resources management; *Solanum insanum*; *Solanum melongena.*

OP-1-27

Exploring Cucumber (*Cucumis sativus* L.) Diversity to Accelerate Genetic Improvement

Vivek Hegde*, Kavyashree K. R., Chithra Devi Pandey[1],
Sushil Pandey[1], Koundinya A. V. V.[2] and Hanume Gowda K.
ICAR - Indian Institute of Horticultural Research, Hesaraghatta, Bengaluru 560089
[1]ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi
[2]Central Horticultural Experiment Station, ICAR-IIHR, Bhubaneswar - 751019
[3]ICAR-CTCRI, Regional Centre, Bhubaneswar 751019, Odisha, India
*Corresponding author email: vivekhegde25@gmail.com

ABSTRACT

Cucumber is a popular vegetable across the globe, consumed both fresh, commonly in salads and in processed forms such as pickles or cooked mature fruits. The species exhibits substantial genetic diversity in traits including yield, fruit morphology (shape, size, and color), spine pigmentation, and vine growth patterns. In this study, 98 cucumber germplasm lines were evaluated using the minimal descriptor guidelines provided by NBPGR, New Delhi for 44 characters. At the marketable stage, fruit colour varied widely, ranging from cream and light green to dark green and brown, while flesh colour spanned white and green. Notable differences were observed in fruit length, diameter, number of fruits per plant, and overall yield per plant. Fruit length at harvest ranged from 5.67 cm in genotype G46 to 29.67 cm in G83, with significant variation also noted in fruit breadth and shape. The number of fruits per plant ranged from 0.20 (G77) to 19.20 (G53), and yield per plant varied from 20 g (G77) to 3412 g (G97). Cluster analysis grouped the genotypes into six distinct clusters, with the greatest Euclidean distance (577.51) observed between clusters V and VI. Using a combination of the Multi-trait Genotype-Ideotype Distance Index (MGIDI), principal component analysis, factor analysis, and the Smith-Hazel selection index, five superior genotypes, G57, G26, G88, G79, and G69 were identified for potential use in future cucumber breeding programs.

Keywords: Cucumber improvement, Multi-trait genotype ideotype distance index (MGIDI), Principal component analysis, Cluster analysis, Smith-Hazel selection index.

POSTER PRESENTATIONS

PP-1-01

Biodiversity to Table: Underutilized Vegetable Crops of Western Ghats of India for Health and Wellness

R. Ramesh Babu[1], Bhanushree N.[2] and Koundinya A. V. V.[3]
[1]*Division of Horticulture, ICAR-IIHR, CHES, Chettalli*
[2]*Division of Horticulture, ICAR-IIHR, CHES, Chettalli*
[3]*Division of Horticulture, ICAR-IIHR, CHES, Bhubaneshwar*
*Corresponding author email: rathod.ramesh89@gmail.com

ABSTRACT

The Western Ghats region of India is bestowed with the most congenial climatic conditions for growing underutilized vegetable crops. The wild and locally available underutilized crops include various leafy greens (water spinach, common purslane, Indian pennywort, wild Amaranthus), tuberous herbs (Colocasia leaves, Yams (Dioscorea sps.), wild gourds (spine gourd, sweet gourd, wild cucumber) and legumes (winged bean, sword bean, velvet bean, tree bean) which are considered as essential source of vitamins, minerals and antioxidants that support overall health and wellness, as well as possessing significant nutritional and medicinal properties. These crops are adapted to the unique growing conditions of the Western Ghats, making them more resilient to environmental stresses. They have a role in conserving agrobiodiversity and have the potential to improve household food security and income. Promoting the cultivation of these crops helps to preserve the rich genetic diversity of the region's horticultural heritage. Moreover, these crops are valuable to local communities as ethno-medicines and can serve as raw materials for different industries. They also act as reservoirs of traits for various biotic and abiotic stress resistance. A comprehensive approach is necessary to explore, domesticate, and incorporate these unique crops into sustainable agriculture, thereby providing broader health and economic benefits. Additionally, these crops are more adaptable and can be considered climate-resilient amid the current changing climate scenario.

Keywords: Underutilized vegetables, agrobiodiversity, nutrition security, climate resilience.

PP-1-02

Exploration and Characterization of Acid Lime (*Citrus aurantifolia* S.) Germplasm for Conservation and Future Crop Improvement

Bhawna Singh[1], Om Prakash[4*], A. K. Srivastava[2],
Subhash Chandra Singh[3], Abhishek Pratap[1] and Abdullah Zaid[1]
Department of Fruit Science, College of Horticulture,
Banda University of Agriculture and Technology, Banda, Uttar Pradesh
*Corresponding author email: opji.2007@rediffmail.com

ABSTRACT

Acid lime (*Citrus aurantifolia* S.) is an economically important citrus fruit crop widely cultivated in India for its nutritional, medicinal, and commercial value. Despite the existence of considerable genetic variability, particularly in diverse agro-climatic regions, systematic exploration and conservation of acid lime germplasm have remained inadequate. The present study was undertaken to survey, collect, characterize, and conserve diverse acid lime genotypes from Bundelkhand and its adjoining districts of Uttar Pradesh. Extensive surveys were conducted for the collection of promising genotypes exhibiting desirable horticultural traits. The collected germplasm was characterized using morphological and biochemical parameters to assess the extent of variability and identify superior genotypes. The collected accessions were conserved through suitable ex situ conservation methods to ensure their long-term utilization in crop improvement programmes.

The study revealed considerable variability among the collected genotypes with respect to vegetative growth, fruit morphology, yield attributes, and biochemical characteristics. Several promising genotypes possessing desirable traits such as high juice content, thin rind, better fruit quality, and comparatively fewer seeds were identified. A few accessions also exhibited tolerance to major biotic stresses, including citrus canker, and adaptability to the semi-arid conditions of the Bundelkhand region. The collected germplasm was successfully conserved as a valuable genetic resource for future breeding and crop improvement programmes. The findings highlighted the rich genetic diversity present in the region and provided a strong foundation for the development of superior acid lime cultivars with enhanced productivity, quality, and stress tolerance.

Keywords: Acid lime (*Citrus aurantifolia* Swingle), Germplasm, Genetic variability, Characterization and Conservation.

PP-1-06

Morphological Characterization and Assessment of Genetic Diversity in Dahlia (*Dahlia variabilis*) Genotypes

Manchyala Divya[1], P. Naveen Kumar[1]*, P. T. Srinivas[2],
Rajiv Kumar[3], Lakshman Reddy D. C.[4] and M. Arivalagan[5]

[1]*Ph. D. Scholar, Department of Floriculture and Landscaping, College of Horticulture, Anantharajupeta, Dr. Y. S. R. Horticultural University, Annamayya district, Andhra Pradesh - 516101*

[1]**Principal scientist & Head, Division of flower and medicinal crops, ICAR-Indian Institute of Horticultural Sciences, Bengaluru, Karnataka - 560089*

[2]*Associate Dean, College of Horticulture, Anantharajupeta, Dr. Y. S. R. Horticultural University, Annamayya district, Andhra Pradesh – 516101*

[3]*Principal scientist, Division of flower and medicinal crops, ICAR-Indian Institute of Horticultural Sciences, Bengaluru, Karnataka – 560089*

[4]*Principal scientist, Division of Basic sciences, ICAR-Indian Institute of Horticultural Sciences, Bengaluru, Karnataka - 560089*

[5]*Scientist, Division of Basic sciences, ICAR-Indian Institute of Horticultural Sciences, Bengaluru, Karnataka - 560089*

*Corresponding author email: naveeniari@gmail.com

ABSTRACT

Dahlia variabilis (family Asteraceae), native to Mexico and Central America, is among the most economically important ornamental crops worldwide, prized for its exceptional diversity in flower colour, form, size and plant architecture. The genus comprises numerous species and thousands of cultivars, encompassing a wide range of flower types including single, semi-double, double, cactus, decorative and pompon forms, making it a valuable model for studying floral trait variation and a major commercial crop for cut flowers, potted plants and landscape use. Owing to this extensive phenotypic diversity and its clonal propagation through tubers, dahlia germplasm possesses considerable for untapped genetic variability that remains inadequately documented. Systematic characterization of available germplasm is therefore essential for effective conservation, utilization, and genetic improvement of this crop. The present study was undertaken to assess morphological diversity among 40 dahlia genotypes under field conditions in a Randomized Block Design with 3 replications. Observations were recorded on key qualitative and quantitative traits, including plant height, number of branches, number of flowers per plant, flower diameter, flower weight, days to first flower bud emergence, days to 50% flowering, days to full bloom, flowering duration and vase life. Significant variability was observed among genotypes for most traits studied. IIHRDV 23 has recorded maximum plant height, flower diameter and flower weight, IIHRDV 5 has more number of branches and number of flowers per plant, IIHRDV 27 showed the earliest flower bud emergence, 50% flowering and full bloom. Whereas, IIHRDV 33 as recorded the longest flowering duration and high vase life. This study indicates the presence of substantial genetic variability within the germplasm and reflects independent trait segregation rather than coordinated trait expression. The study highlights the significance of comprehensive

morphological characterization as a reliable approach for evaluating genetic diversity in dahlia germplasm. The identified diverse genotypes constitute valuable genetic resources for breeding programmes aimed at developing high-yielding cultivars with superior ornamental traits and wider adaptability.

Keywords: Dahlia, genotypes, flowering, diversity and ornamental traits.

PP-1-07

Morphological Characterization and Distinctness, Uniformity, and Stability (DUS) Profiling of Carrot (*Daucus carota* L.) farmer variety 'Madhuvan Gajar'

Padmini K.
Principal Scientist (Horticulture), Division of Vegetable Crops,
ICAR-Indian Institute of Horticultural Research, Bengaluru
Corresponding author email: Padmini.K@icar.org.in,veghybrid@rediffmail.com

ABSTRACT

Comprehensive morphological profiling based on Distinctness, Uniformity, and Stability (DUS) guidelines is essential for genetic purity testing and variety identification in carrot (*Daucus carota* L.). A study on morphological characterization of the farmer variety 'Madhuvan Gajar' was conducted at ICAR-Indian Institute of Horticultural Research, Bengaluru, during the period 2021-2023, to evaluate 32 UPOV DUS characteristics. Morphological analysis of foliage revealed broad crown width, erect leaf attitude, very long leaf length with coarse division, dark green leaves and distinct red-purple petiole anthocyanin pigmentation. Root characterization demonstrated medium-length, broad roots featuring a narrow obtriangular shape with a very strong conical tendency, flat-to-rounded shoulder, strongly pointed tip, and medium surface ridging. Uniquely, the root skin displays prominent purple pigmentation with minimal green shoulder coloration. Internal cross-sectional profiling indicated a large core diameter relative to total root diameter, displaying a dark yellow core contrasted against a dark orange cortex. Reproductive traits showed a weak bolting tendency, tall primary umbels at flowering, and intermediate male sterility of the brown anther type. These distinctive phenotypic descriptors provide a robust reference standard for establishing genetic purity, ensuring seed quality, and safeguarding plant variety protection for 'Madhuvan Gajar'.

Keywords: *Madhuvan Gajar, Daucus carota, DUS testing, Genetic purity, UPOV descriptors, Root morphology, Anthocyanin pigmentation, Male sterility.*

PP-1-08

An epitome of vegetable crops diversity in Goa and adjoining Konkan region for posterity

Thangam, M.[1]*., K. Ramachandrudu[2], S. C. Rana[3], S. A. Safeena[4],
S. Priya Devi[5], R. Ramesh[6], V. S. Korikanthimath[7] and N. P. Singh[8]
[1]*Division of Vegetable Crops, ICAR-IIHR, Hesaraghatta Lake Post, Bengaluru, Karnataka
[2]ICAR-Indian Institute of Oil palm Research, Pedavegi, West Godavari, Andhra Pradesh
[3]ICAR-IARI Regional Station, Karnal, Haryana
[4]Division of Flower crops, ICAR-IIHR, Hesaraghatta Lake Post, Bengaluru, Karnataka
[5]PC Unit, ICAR-IIHR, Hesaraghatta Lake Post, Bengaluru, Karnataka
[6]Division of Crop Protection, ICAR-Sugarcane Breeding Institute, Coimbatore, Tamil Nadu
[7]Director (Retired), ICAR Research Complex for Goa, Ela, Old Goa, Goa
[8]Director (Retired), ICAR-NIASM, Baramati, Maharashtra
*Corresponding author email: thangamgoa@gmail.com

ABSTRACT

Goa is a small state situated in Western Ghat area in the West Coast of India. It experiences warm and humid climate with annual rainfall ranging from 3000-5000mm, which keeps Goa rich in *flora and fauna*. Though cultivation of vegetable crops in Goa is limited, there is tremendous variability in okra, brinjal, chilli, vegetable cowpea, Amaranthus, Cucurbits *etc.* Therefore, there is a scope for collection, conservation and utilization of these vegetables. Brinjal, having originated in India, exhibits wide variability. There are two popular land races viz., *Taleigao* and *Agassaim.* The *Taleigao* produces violet, round fruits, the average fruit weight being 350g and per plant yield about 2.5-3.5kg. The *Agassaim* type yields violet purple, elongated fruits of 300g and gives about 2.0-2.5kg per plant. Okra forms an important vegetable in Goan cuisine. The evaluation study in okra at ICAR -CCARI revealed that, there are significant variation in terms of crop duration, fruit length, weight and colour. Majority of the local types are long fruited, tender and light green in colour, which retains their tenderness, even when they attain length of 20-22cm. Popular types in okra are *Saathpaani* and *Aaatpaani* (node at which first fruit appears). Chilli (both hot and sweet pepper) was first introduced by Portuguese to India, more particularly to Goa. Presently there are three types viz., *Tarwatti*, *Lovongi* and *Portugali*. The *Tarwatti* type is perennial and seeds are disseminated through birds. The fruits are small and pungent. This type may be a source of virus resistance.

Systematic collection, conservation, evaluation and improvement of important vegetable crop genetic resources in Goa from 1998 onwards have resulted in release of high yielding varieties in Amaranthus (Goa Tambdi Bhaji-1), Okra (Goa Bhendi-1), Brinjal (Goa Brinjal-1 to 4) for the state of Goa. In addition to this, the valuable genetic resources in crops like brinjal (42), Chilli (55), Amaranth (36), Okra (14), Vegetable Cowpea (28) were characterized and conserved for utilization in future crop improvement programme. Other important aspect of registration under Geographical Indicators (GI) have resulted in three vegetable cultivars under GI category from Goa viz., *Agassaim Vayingim* (Brinjal), *Kholla* and *Harmal* (Chilli) which indicates the potential of vegetable genetic resources in the state of Goa.

Minor/under-utilized other edible crops like tuber crops (Colacasia,Chinese Potato, Disocorea), Mangrove Fern, Bamboo *etc.* needs further attention for its collection and conservation. The vegetables mentioned above are very much preferred by the local people because of its taste and they got acclimatized well under this condition. Systematic study on these crops may give some value added germplasm for future breeding programme.

PP-1-10

Effect of Cryo-Storage on Pollen Viability and Fertility in Taro (*Colocasia esculenta* L.)

Vivek Hegde*, Koundinya A. V. V.[2], Sunitha S.[3], M. N. Sheela[3],
Asha Devi[3], K. Hanume Gowda and Sai Lekshmi N.[3]
[1]*ICAR - Indian Institute of Horticultural Research, Hesaraghatta, Bengaluru 560089*
[2]*Central Horticultural Experiment Station, ICAR-IIHR, Bhubaneswar - 751019*
[3]*ICAR-Central Tuber Crops Research Institute, Thiruvananthapuram - 695 017, India*
*Corresponding author email: vivekhegde25@gmail.com

ABSTRACT

Taro (*Colocasia esculenta* (L.) Schott) is a significant tuber crop widely cultivated across tropical and subtropical regions, where nearly all parts of the plant are consumed as a vegetable. However, traditional breeding efforts are often limited by irregular flowering patterns and various structural and functional barriers associated with its reproductive behaviour. The successful use of cryopreserved pollen in taro could greatly facilitate targeted genetic improvement of this economically valuable crop. Therefore, this study was conducted to explore effective methods for storing taro pollen. A portion of the inflorescence with staminate (male) flowers of the taro variety *Muktakeshi* was collected one day before anther dehiscence. These were kept overnight under laboratory conditions. The following morning, pollen grains were gently extracted from the male flowers by tapping and immediately placed in cryo-vials for storage at various temperatures. The viability of both fresh and stored pollen was assessed using acetocarmine staining and *in vitro* germination tests. Freshly collected pollen showed 90.15% staining and 48.50% germination under laboratory conditions. However, pollen stored at room temperature and at 4 °C lost viability after six days. In contrast, cryopreserved pollen stored for 30 days retained 81.45% staining and 40.09% *in vitro* germination. Hand pollination in the field was performed on female flowers of the same variety *Muktakeshi* using both fresh and cryo-stored pollen. Normal fruit set and viable seeds were observed in both cases.

Keywords: Taro, long-term storage, pollen conservation, cryo-preservation, pollen viability.

PP-1-12

Systematic exploration, documentation and conservation of Soursop (*Annona muricata* L.) genotypes from western ghats

Roopendra Kumar[1], Anuradha Sane[1]*, Muralidhara B. M.[2], Vasugi C.[1], Laya P.[1] and Nishant[1]
[1]*ICAR-Indian Institute of Horticulture of Research, Hessaraghatta-Bengaluru-560089*
[2]*ICAR- IIHR- Central Horticultural Experiment Station, Chettalli, Kodagu-571248, Karnataka*
*Corresponding author email: anusane@rediffmail.com

ABSTRACT

Soursop (*Annona muricata* L.) is an underutilized tropical fruit crop gaining increasing attention for its nutritional richness, therapeutic properties, and potential as a commercial fruit in southern India. Despite its importance, systematic exploration, documentation and conservation of soursop genetic resources remain limited. Passport data collection is a crucial first step in germplasm management, as it provides essential baseline information on the origin, geographical distribution, and cultivation practices associated with genotypes. The present study was undertaken for systematic survey and exploration in Kodagu and Dakshina Kannada districts of Karnataka, and Wayanad district of Kerala to locate unique, local traditional types. This has resulted in the identification of 12 unique soursop types of these regions. The data were recorded, covering details such as geographical coordinates (latitude, longitude, and altitude), site characteristics, source and mode of collection, and information on local nomenclature, cultivation practices, and associated traditional knowledge. Considerable variability was observed in the distribution pattern of genotypes, reflecting the influence of ecological conditions and farmer preferences in different locations. Efforts were made to multiply and conserve unique type at IIHR-CHES, Chettalli. The compilation of this passport data forms a valuable resource for the conservation and sustainable utilization of soursop genetic diversity. Furthermore, the documentation strengthens the prospects of utilizing soursop genotypes in future crop improvement programs aimed at enhancing productivity, fruit quality, and adaptability.

Keywords: Soursop, passport data, Kodagu, Wayanad, geographical coordinates.

PP-1-13

Potential Crop Landraces of Southern Western Ghats – PGR perspectives

Latha M.[1]*, K. Pradheep[1], A. Suma[1], K. Venkatesan[1], P. K. Singh[2] and G. P. Singh[2]
[1]*ICAR-National Bureau of Plant Genetic Resources Regional Station, KAU (P.O.), Vellanikkara, Thrissur, Kerala 680 656, India*
[2]*ICAR-National Bureau of Plant Genetic Resources, Pusa campus, New Delhi 110012, India*
*Corresponding author email: m.latha@icar.org.in

ABSTRACT

Landraces are invaluable reservoirs of vital genes needed for crop improvement and those available from biodiversity hotspot are still more special as they maintain high genetic diversity and niche adaptation. Southern Western-Ghats comprising South Goa to Kanyakumari region covering all districts except one of Kerala, seven each of Karnataka and Tamil Nadu. Under National Exploration Plan, ICAR-National Bureau of Plant Genetic Resources Regional Station, Thrissur has collected a total of 8209 samples in 199 genera comprising 266 species from this region since 1978. Rice, the predominant crop, a total of 876 named germplasm samples were collected which include 250 unique landraces. Their names often reflect season of cultivation, crop duration, used in various religious and cultural occasions, peculiar morphological features. Unique types include *Chennellu, Chennelthondi, Chenthadi, Chitteni, Gandhakasala, Kalladiaryan, Mallikuruva, Aryan, Ramli, Thondi, Vedantham* and *Veliyan* (flood tolerant); *Komban* – (from Idukki dt., with ten months duration) used only for Pooja purposes; *Kothanden* – (a nearly extinct landrace of rice of Wayanad district), tolerant to biotic stress with high rice bran content. Among millets, specific landraces in finger millet, fox tail millet and little millet (38 accessions) have been conserved in NGB from Muthuvan tribes of Idukki district. They include *Chanagili, Arakanachi, Periyapoovan, Undapoovan, Cholakambili, Meenkanni, Kadampara, Selakambili, Palakin, Aruvi, Poothalchi, Uppulusi, Neelakanni*in finger milet*, Muliyanthina* and *Kambanthina* in foxtail millet. With respect to vegetables, ample variability collected and evaluated. Specific landraces in yard long bean are *Karkoondal, Kurutholapayar, Kanjikuzhipayar, Vakkachan, Arikozhinjipayar*, named after their morphological feature and cooking quality. Among other vegetables, *Vlanthangaracheera* in Chinese spinach (late bolting and tolerant to leaf spot disease), *Sambar southekkai*, *Kallanvellari*, M*ikkikkai*, *Kanivellari, Puna vellari* in melon (exclusively used for curry preparation), In okra, *Anaikomban* with extra-long fruit is a notable one. Small fruited brinjal (*Cheruvazhuthina*) and ashgourd (N*eykumbalam*) used in ayurvedic medicine preparation. *Vengeri vazhuthina* and *Illi vazhuthina* (in brinjal), Chengalikodan, *Chundilakannan*, *Padalimoongi*, (among 18 known in banana), *Moovandan, Kilichundan, Chandrakaran, Tholikaipan* in mango among 25, *Thamarachakka, Theanvarikka, Muttomvarikka*, Chembaruthi *chakka* (jackfruit), *Kudiraivalli, Karimunda, Thekkan, Thothumuriyan* (in black pepper) are other notable ones. In tuber crops, about 50 are conserved in field gene bank which include accessions in taro without acridity and edible even in raw stage, *Neichena* in elephant foot yam. Landraces not only represent the cultural heritage and traditional knowledge of local communities but also provide critical genetic resources for future crop improvement. Despite challenges in validation, continued conservation, characterization, and utilization remain essential to harness their benefits.

PP-1-15

In vitro propagation through axenic seed culture for the conservation of an endangered species, *Exacum bicolor* Roxb.

Shravani, J.[1*], Shajma Nafeesa Basheer[1], Mini Sankar[1],
Deepa S. Nair[2], Rehna Augustine[3] and Krishna Kumar G.[3]
[1]*Department of Floriculture and Landscaping, College of Agriculture, Kerala Agricultural University, Thrissur - 680 656*
[2]*College of Agriculture, Vellayani, Kerala Agricultural University, Thrissur - 695 522*
[3]*College of Agriculture, Vellanikkara, Kerala Agricultural University, Thrissur - 680 656*
*Corresponding author email: shravani-2023-22-013@student.kau.in

ABSTRACT

Exacum bicolor Roxb. (Gentianaceae) is an endangered species endemic to the lateritic hillocks of Kerala, a unique ecological niche within the Western Ghats of Peninsular India. Its natural population is under severe threat due to habitat destruction, laterite mining, soil erosion, and overexploitation for its attractive bicoloured flowers. Hence *ex situ* conservation is the right strategy for preserving this beautiful, ornamental and medicinal herb. Although it is feasible to propagate plants from seeds, the seedlings typically necessitate an extended period of six months in nursery before they are ready for transplantation. Propagation of *Exacum* by stem cutting is rather slow and time consuming. In this context, the present study was undertaken in the Department of Floriculture and Landscaping, to develop an efficient *in vitro* propagation protocol and evaluate the potential of micropropagation as a tool for *ex situ* conservation and restoration of this threatened species. *In vitro* cultures of axenic seeds were established using semi matured capsule as the explant. Results revealed that explants sterilized with 3% NaOCl for 5 minutes recorded the best balance between low contamination and high survival rate and ½ MS+1.0 mg/L GA+3% maltose as the best treatment with respect to days taken for *in vitro* germination and emergence of 1st leaf primordium. Nodal explants from *in vitro* healthy plants were collected and cultured on MS media supplemented with various concentrations of BA and Kinetin for multiple shoot induction and different concentrations of NAA and IBA for root induction. Optimal multiple shoot induction was achieved on MS media containing BA 2.0 mg/L+0.4 mg/L Kinetin combination, producing maximum mean shoot length and a greater number of shoots per explant. Rooting was successfully induced on ½ MS media supplemented with 1.0 mg/L IBA which recorded maximum number of roots and mean root length before hardening. The regenerated plantlets exhibited vigorous growth and phenotypic uniformity under *in vitro* conditions. Following *in vitro* development, *ex vitro* acclimatization posed notable challenges. Modifications in the hardening regime, such as gradual reduction in humidity, maintenance under shade, and the use of a potting mixture comprising of cocopeat and perlite (1:1), significantly improved survival rates. These results demonstrate that *in vitro* propagation provides a reliable, rapid, and season independent strategy for the mass multiplication and conservation of *E. bicolor*. Thus, integrating micropropagation with habitat restoration can significantly support the re-establishment of natural populations and help preserve the genetic diversity of this endemic species in Western Ghats of Peninsular India.

Keywords: *Exacum bicolor*, Endemic, *In vitro* propagation, Endangered ornamental, Western Ghats, Peninsular India.

PP-1-16

Multi-Spectral Imaging (MSI) for seed viability prediction in sorghum germplasm conserved in the ICRISAT genebank

Ovais Peerzada*, Israr Majeed, Vetriventhan Mani,
Senthil Ramachandran, Kuldeep Singh and Raman Babu
International Crops Research Institute for the Semi-Arid Tropics, Patancheru - 502324, Telangana
*Corresponding author email**:** Ovais.peerzada@icrisat.org

ABSTRACT

Seed viability assessment is a critical component of genebank management, ensuring the long-term conservation and effective use of plant genetic resources. It measures the capacity of stored seeds to germinate and develop into normal, healthy seedlings under favourable conditions, thereby serving as a key indicator of seed quality, longevity and regeneration need. Conventional germination testing is widely used for seed viability assessment, which is labour-intensive, time-consuming, and requires substantial seed quantities. Therefore, rapid, non-destructive, and reliable methods for viability prediction are essential for efficient genebank operations. ICRISAT genebank conserves more than 132,000 accessions of eight millets and three legumes. In this study, we evaluated the potential of Multi-Spectral Imaging (MSI) technology for predicting seed viability in sorghum germplasm conserved at the ICRISAT genebank. Over 8000 seeds were randomly sampled from different seed lots with differences in germination status (viable and non-viable) and analysed using MSI under VideometerLab across multiple wavelengths spanning the visible to near-infrared spectra (365-960 nm). Spectral and morphological features, including seed reflectance, texture, colour parameters, and fluorescence-related indices, were extracted and correlated with standard germination tests. Statistical and machine learning approaches were employed to classify viable and non-viable seeds and to develop predictive models for viability estimation. The results demonstrated significant differences in spectral signatures between viable and non-viable seeds. MSI-based models showed high accuracy in predicting seed viability, with the Support Vector Machine (SVM) model showing the highest accuracy of 93.5% during model training and development and 88% on an independent dataset. These findings indicate that the MSI can serve as a rapid and non-destructive alternative to conventional germination assays. Further validation using larger and more diverse sample sets, along with model fine-tuning, is ongoing. Adoption of MSI-based viability prediction can enhance the efficiency of germplasm conservation programs by reducing testing time, labour requirements, and seed consumption while improving the management of valuable sorghum genetic resources conserved at the ICRISAT genebank.

Keywords*:* Seed Viability, MSI, VideometerLab, reflectance, fluorescence, SVM.

PP-1-17

Exploring the cultivated and wild diversity of agriculturally important species in Western Ghats (Nashik, Thane and Palghar Districts) of Maharashtra State

Sunil Shriram Gomashe[1]*, Kuldeep Tripathi[2], Ravi Kishore Pamarthi[2] and Dipak Nivrutti Damse[3]
[1]*ICAR-National Bureau of Plant Genetic Resources, Regional Station, Akola, Maharashtra*
[2]*ICAR-National Bureau of Plant Genetic Resources, New Delhi*
[3]*AICRP on Niger, Zonal Agriculture Research Station, Igatpuri, Nashik, Maharashtra*
*Corresponding author email: sunil.gomashe@icar.org.in

ABSTRACT

An exploration for collection of Millets, Linseed, *Cajanus, Vigna sps*, and other CWR was undertaken from Nashik, Thane and Palghar districts of Maharashtra during 01- 08 November 2023. This Western Ghats Region encompasses great diversity for many species of agricultural importance. During exploration, a total of 61 germplasm samples consisting *Panicum sumatranse (10), Oryza sativa (07), Eluecine coracana (05), Vigna mungo (02), Cucumis melo (02), Cucumis hardwikii (02), Niger (03), Cajanus cajan (01), Cajanus scarabdoides (03), Cajanus platycarpus (01), Luffa acutangula (02), Macrotyloma uniflorum (01), Vigna unguiculata (02), Vigna radiata (01), Sorghum bicolor (01), Dolichos lablab (01)* and others CWRs (17) were collected. Good variability was observed in Sorghum for biomass, plant type, earliness and popping character. Tremendous potential of little millet and finger millet was also observed in these areas as being grown for their consumption and selling in local markets as an earning source. Rare germplasm (Landraces) considered *Mahodi, Kal Bhat, Wada kolum* of Paddy were also collected from these areas. Good variability in *Cucumis* sps, *Abelmoschus* sps, paddy landraces and *Vigna* sps was observed during the exploration of germplasm. *Cajanus sericius*, and *Vigna yadavii* endemic species of Sahyadri hills also recorded for documentation.

PP-1-19

Identification of Novel Ideotypes of Okra (*Abelmoschus esculentus* L. Moench) Collected from the Western Ghats Region of Maharashtra Under Temperate Conditions

Aftab M. Mulla[1]*, M. I. Makhdoomi[2], T.K. Behera[3] and Hudda T. Syed[4]
[1&3]*Division of Vegetable Crops, ICAR-IIHR, Hessaraghatta, Bengaluru, Karnataka - 560089*
[2&4]*Division of Vegetable Science, SKUAST-K, Shalimar (J&K) - 190025*
*Corresponding author email: aftabmulla129@gmail.com

ABSTRACT

The cultivation of okra (*Abelmoschus esculentus* L. Moench) in temperate regions faces challenges due to the crop's natural sensitivity to cold and the absence of varieties that meet both climatic conditions and consumer preferences for smaller pods. This research aimed to identify innovative okra ideotypes with traits suitable for sustainable agriculture in temperate and cold-prone areas, such as those found in North India. We screened 120 landraces during the 2022-23 and 2023-24 growing seasons, focusing on key traits including dwarf stature, early fruiting, higher number of nodes, shorter internodal length, higher number of branches, good fruit quality and cold tolerance.

Significant findings from the study include the characterization of genotypes featuring a unique cream-colored fruit, a trait not currently described in DUS guidelines, thereby enhancing their novelty. The research identified determinate growth types (MH-09-01 and MH-09-02), showcasing a rare and advantageous architecture for synchronised harvesting. Significantly, genotypes MH-09-03 and MH-09-04 exhibited considerable cold tolerance, permitting fruit development at a minimum of 6°C. While flowering was even observed at 0°C, though physiological activities decelerated. These plants can endure low temperatures for more than a month; however, exposure to -3°C proved lethal. This resilience renders them particularly suitable for cultivation in temperate regions and the North Indian plains, where winter chilling restricts production. Additionally, these accessions exhibited prolific cluster-bearing through complex sympodial and cymose branching patterns. The identification of these genotypes establishes a foundational germplasm resource for breeding innovative, climate-resilient okra ideotypes aimed at enhancing yield and quality within sustainable production systems across diverse agroclimatic zones.

Keywords: Okra, ideotype, cold tolerance, cluster bearing, determinate growth, sympodial, cream fruit, DUS guidelines.

PP-1-21

Assessment of Morphological Variability in Kokum (*Garcinia indica* Choisy.) Germplasm from Western ghats of India

Ruchitha T.*, Muralidhara B. M., Nayan Deepak G. and Deepa V. M.
ICAR-IIHR-Central Horticulture Experimental Station, Chettalli, Kodagu (D), Karnataka
*Corresponding author email: ruchithat.hrt@gmail.com

ABSTRACT

Kokum (*Garcinia indica* Choisy.), a tropical evergreen fruit tree belonging to the family Clusiaceae, is native to the Western Ghats of India and is valued for its culinary, medicinal, and processing uses. The crop shows considerable variation in fruit and rind characteristics, making the evaluation of available germplasm important for identifying superior accessions for crop improvement. The present study was conducted at the ICAR-IIHR, Central Horticultural Experiment Station, Chettalli, Kodagu, Karnataka, during 2024-2025 and 2025-2026 to evaluate 25 kokum accessions for their morphological variation. The accessions were assessed for fruit weight, fruit length, fruit breadth, rind weight, fruit dry weight, rind recovery, moisture content, seed length, seed breadth, seed dry weight, number of fruits per tree and yield per tree. Significant variation was observed among the accessions for all the traits studied. Fruit weight ranged widely among the accessions, indicating substantial diversity in fruit size. Accession R_6P_8 recorded the highest fruit weight (73.09 g), fruit breadth (5.38 cm), rind fresh weight (43.14 g), rind dry weight (13.55 g), rind recovery (26.89%), number of fruits per tree (645), yield per tree (51.53 kg) and lower moisture content (73.10%), which showed good horticultural trait. The highest fruit length (4.05 cm) was observed in accession $R_{14}P_7$. The highest seed dry weight (5.76 g) was observed in $R_{14}P_8$ and highest seed length (17.89 mm) and seed breadth (9.16 mm) was observed in $R_{14}P_7$. The lowest number of seeds (6.20) was observed in the accession R_7P_4. The differences observed among the accessions indicate the presence of useful variability that can be utilized in further breeding programme. Among the evaluated accessions, R_6P_8 consistently performed better for most of the economically important fruit traits, particularly those related to rind yield and dry matter.

Keywords: Kokum; improvement; morphological variation; rind recovery.

PP-1-22

Development of an AI-Enabled Real-Time Mobile Application for Identification of Allium Crop Wild Relatives

Ankur Tomar[1]*, Suresh Kumar[1], Akansha Bajpai[2] and Kuldeep Tripathi[2]
[1]*Manav Rachna International Institute of Research and Studies, Faridabad, Haryana.*
[2]*ICAR-National Bureau of Plant Genetic Resources, New Delhi.*
*Corresponding author e-mail: ankur.tomar@icar.org.in

ABSTRACT

Crop Wild Relatives (CWRs) represent valuable reservoirs of genetic diversity for crop improvement, adaptation and long-term food security. However, their effective conservation and utilization depend on accurate species identification, which can be challenging when closely related taxa exhibit similar morphological characters or when available plant material is incomplete. Recent advances in artificial intelligence provide an opportunity to support taxonomic identification and improve the accessibility of Plant Genetic Resources (PGR) information. The present study developed an AI-enabled real-time mobile application for species-level identification of *Allium* CWRs using images of authenticated herbarium specimens and live plants.

A curated image dataset was prepared through taxonomic verification, image organization and species-wise labelling. Deep-learning models were evaluated for image-based identification, and a lightweight MobileNet architecture was selected for mobile deployment because of its suitability for computationally efficient inference. The trained model was converted to TensorFlow Lite format and integrated into an Android application. The application allows a user to capture a plant image directly through the mobile camera or select an existing image from the device. The image is processed according to the model input requirements, followed by real-time inference and species-label mapping. The predicted *Allium* species and corresponding confidence score are displayed to the user, providing rapid preliminary identification at the point of use.

The developed application demonstrates how deep-learning-based CWR identification can be translated from laboratory model development into a practical mobile tool. Its smartphone-based design reduces dependence on specialized computational infrastructure and offers potential utility during field exploration, germplasm documentation, herbarium-based studies and preliminary taxonomic screening. The approach is particularly relevant for PGR management because reliable identification is a fundamental step in documenting, conserving and subsequently utilizing crop wild diversity.

The present work also provides a scalable foundation for future expansion to additional CWR taxa as larger authenticated datasets become available. Further strengthening through broader field validation, increased representation of populations and image domains, and integration with passport, geographical and genebank information could enhance its practical value. Overall, the study illustrates the potential of lightweight artificial intelligence and mobile technologies to support digital approaches for CWR identification and PGR management. Such tools can contribute to improved documentation and accessibility of wild genetic resources and strengthen the pathway from biodiversity exploration to

conservation, characterization and future crop-improvement programmes in India. This deployment-oriented framework can support faster field-level decisions while maintaining a clear pathway for expert validation and subsequent integration with institutional PGR systems.

Keywords: Crop Wild Relatives; *Allium*; Plant Genetic Resources; Deep Learning; MobileNet; TensorFlow Lite; Mobile Application.

PP-1-23

An Integrated *In Vitro* Propagation and Seed Cryopreservation Strategy for Ex Situ Conservation of *Dendrobium heterocarpum* Wall. ex Lindl

Lalduhsanga*, Sujatha A. Nair, Rohini M. R. and Usha Rani T. R.
ICAR- Indian Institute of Horticultural Research, Bengaluru - 560089
*Corresponding author email: duhsanga14@gmail.com

ABSTRACT

Dendrobium heterocarpum Wall. ex Lindl. is a fragrant and medicinal orchid of considerable horticultural importance that is increasingly threatened by habitat destruction and anthropogenic exploitation. The present study developed an integrated *in vitro* propagation and cryopreservation protocol for ex situ conservation. Asymbiotic seed germination was optimised using Murashige and Skoog (MS) media, where half-strength liquid MS medium recorded the highest seed germination (89.00%) and protocorm-like body (PLB) establishment (74.75%), with PLB formation within 35.25 days. Subsequent differentiation and multiplication of PLBs demonstrated that half-strength MS supplemented with 1.5 mg L^{-1} BAP produced the highest number of shoots (7.00 per explant), whereas 1.0 mg L^{-1} BAP induced the greatest rooting response (4.50 roots per shoot). Organic supplementation enhanced plantlet development, where 100 g L^{-1} banana pulp combined with 4 mg L^{-1} BAP produced the longest shoots (3.80 cm), while 50 g L^{-1} banana pulp without BAP generated the highest number of leaves (7.25). While, 50 g L^{-1} banana pulp supplemented with 2 mg L^{-1} BAP resulted in the greatest shoot multiplication (27.50 shoots). For long-term germplasm conservation, vitrification-based cryopreservation showed that PVS2 treatment for 60 min before liquid nitrogen exposure achieved the highest post-cryogenic seed germination (58.63%), whereas shorter exposure durations resulted in poor or no recovery. The integrated protocol developed in this study provides an efficient framework for rapid propagation, production of high-quality planting material, and long-term germplasm conservation of *D. heterocarpum*, supporting conservation and sustainable utilization of this threatened orchid species.

Keywords: *Dendrobium heterocarpum*; asymbiotic seed germination; protocorm-like bodies; banana pulp; BAP; cryopreservation; vitrification; orchid conservation.

Theme - 2

PGR Governance: From Biosecurity to Benefit Sharing

ORAL PRESENTATIONS

OP-2-02

Distribution of Phylotypes and Sequevars of *Ralstonia solanacearum* in India: Relevance to pathogen surveillance and Conservation of Plant Genetic Resources

Sangeetha Ganesan[1]*, Madhuri Pattanaik[2], Satyaprakash Barik[3], D. K. Samuel[1] and Sakthivel Krishnan[4]

[1]*Division of Crop Protection, ICAR-Indian Institute of Horticultural Science, Bengaluru - 560089, India*

[2]*ICAR-IIHR-Central Horticultural Experiment Station, Bhubaneswar - 751019, India*

[3]*Department of Agriculture and Allied Sciences, CV Raman Global University, Bhubaneswar - 752054, Odisha, India*

[4]*ICAR-Indian Institute of Oilseeds Research, Telangana - 500030, India*

Corresponding author email:* G.Sangeetha@icar.org.in; sangeethaau@hotmail.com

ABSTRACT

Bacterial wilt, caused by *Ralstonia solanacearum*, is one of the destructive diseases affecting solanaceous vegetable crops, causing severe yield losses. Understanding the genetic diversity and geographical distribution of pathogen population is essential for pathogen surveillance and protection of plant genetic resources. In the present study, the genetic and phenotypic diversity of *R. solanacearum* populations was investigated using isolates collected from the major solanaceous vegetable-growing regions of Karnataka (inland plains, South India) and Odisha (coastal plains, eastern India). Twenty-one isolates obtained from wilt-infected tomato and brinjal plants were characterized using a polyphasic approach. All isolates produced typical bacterial wilt symptoms, inducing complete wilting of tomato and brinjal plants. Molecular identification using species-specific PCR primers confirmed all isolates as *R. solanacearum*, while multiplex PCR classified them under Phylotype I. To understand the distribution of epidemiologically important lineages, sequence analysis of the virulence-associated endoglucanase (*egl*) gene was performed for sequevar determination. The analysis revealed the predominance of Sequevar 48, accounting for 76% of the isolates across the surveyed regions. Five isolates—KA-VIII-22 from Karnataka and OD-JAJ-B-22, OD-GAJ-B-22, OD-MAL-C-22, and OD-MAL-B-22 from Odisha—could not be assigned to any previously described sequevar, indicating the occurrence of novel or uncharacterized lineages. These findings suggest ongoing genetic diversification within Phylotype I population and possible regional adaptation might be driven by local agroecological conditions. Identification of dominant and emerging sequevars provides valuable baseline information for pathogen surveillance. Furthermore, knowledge of the distribution of *R. solanacearum* phylotypes and sequevars will support resistance breeding programs by facilitating the deployment of representative pathogen populations for disease screening, thereby contributing to the protection and conservation of solanaceous plant genetic resources in India.

Keywords: Bacterial wilt, *Ralstonia solanacearum,* Solanaceous vegetable, phylotype, sequevars.

OP-2-03

Open Source Seeds as a "Protected Commons"

Sridhar Gutam
ICAR-Indian Institute of Horticultural Research, Bengaluru 560089
Corresponding author email: gutam2000@gmail.com

ABSTRACT

For millennia, Plant Genetic Resources for Food and Agriculture (PGRFA) functioned as a shared biophysical commons, enabling the evolution and conservation of the agro-biodiversity that underpins resilient food systems. The global expansion of intellectual property rights (IPRs), particularly utility patents and the restrictive provisions of the UPOV 1991 Convention, has progressively enclosed these shared resources, facilitating corporate control over seeds while undermining cultivated biodiversity and restricting farmers' customary rights to save, exchange, and improve seed. Although India's sui generis Protection of Plant Varieties and Farmers' Rights (PPV&FR) Act, 2001 seeks to balance breeders' interests with farmers' rights, practical implementation challenges remain. The emergence of Digital Sequence Information (DSI) further complicates governance by enabling the use of genetic information without physical access to biological material, thereby weakening existing access and benefit-sharing mechanisms and raising concerns over "digital biopiracy." In response to these governance limitations, the Open Source Seed (OSS) movement has emerged as a legally innovative and decentralised alternative. Through copyleft-inspired pledges and civil-law licensing mechanisms, OSS transforms intellectual property tools into a "protected commons" that guarantees four fundamental seed freedoms: the freedom to save, share, study, and improve seeds. Importantly, all derivative varieties developed from OSS-licensed material must remain permanently free from exclusive proprietary restrictions, thereby preventing future enclosure. This paper argues that the OSS framework offers a practical and socially equitable governance model for the rich PGR landscape of Peninsular India. By connecting community seed banks, traditional farmer-breeders, indigenous knowledge systems, and public research institutions, OSS networks can safeguard endemic landraces and associated traditional knowledge from corporate appropriation while promoting collaborative innovation. Unlike conventional multilateral benefit-sharing systems that often face difficulties in monitoring commercialisation and distributing benefits, OSS ensures immediate and continuous non-monetary benefit-sharing by maintaining unrestricted community access to germplasm. Integrating open-source principles alongside national legislation such as the PPV&FR Act can therefore strengthen farmers' rights, enhance agrobiodiversity conservation, and reposition plant genetic resources as a sustainable shared heritage rather than an exclusively commercial commodity.

Keywords: Open Source Seeds; Plant Genetic Resources for Food and Agriculture (PGRFA); Protected Commons; Farmers' Rights; Benefit-Sharing; PPV&FR Act; Digital Sequence Information (DSI).

OP-2-04

Defensive role of leaf trichomes in wild *Solanum* genetic resources against ash weevil, *Myllocerus subfasciatus* Guerin-Meneville

Jayanthi Mala, B. R.[1]*, Saravan Kumar P.[1], Singh T. H.[2],
Shivashankara K. S.[3], Naresh P.[2], Samuel D. K.[1] and Kamala Jayanthi P. D.[1]
*[1]*Division of Crop Protection, [2]Division of Vegetable Crops, [3]Division of Basic Sciences,*
ICAR-Indian Institute of Horticultural Research,
Hesaraghatta Lake Post, Bengaluru, 560 089, India.
*Corresponding author email: entjaya@gmail.com; jayanthimala.br@icar.org.in

ABSTRACT

Trichomes are specialized epidermal appendages that serve as both physical and chemical barriers, effectively deterring herbivore attacks. In the present study, we investigated the biochemical mechanisms underlying the feeding interactions between various *Solanum* species and the folivorous ash weevil, *Myllocerus subfasciatus*, focusing on trichome morphology and associated secondary metabolites. Comprehensive analyses were conducted on leaf trichome diversity and biochemical composition in 11 wild *Solanum* species (*S. mammosum*, *S. viarum*, *S. macrocarpon*, *S. sisymbriifolium*, *S. indicum*, *S. aethiopicum*, *S. gilo*, *S. torvum*, *S. capsicoides*, *S. seaforthianum*, and *S. nigrum*) as well as one cultivated *S. melongena*. These studies aimed to elucidate the chemical basis for host plant defense (feeding antixenosis) observed against *M. subfasciatus*.

A total of seven trichome types were identified, comprising three glandular (Types IV, VI, and VII) and four non-glandular (Types II, III, V, and VIII) forms. *Solanum* species possessing glandular trichomes were markedly less preferred by *M. subfasciatus*, while the more susceptible species predominantly featured Type VIII non-glandular trichomes and lacked glandular types entirely.

Biochemical profiling through Gas Chromatography Mass Spectrometry (GCMS) for volatile organic compounds (VOCs) and Liquid Chromatography Tandem Mass Spectrometry (LCMS/MS) for phenolic acids and acyl sugars revealed distinct metabolite signatures associated with glandular trichomes. Elevated levels of acyl sugars and phenolic acids were correlated with enhanced feeding antixenosis and higher glandular trichome density. Among the 46 VOCs detected, principal component analysis (PCA) indicated that acetic acid (2-benzothiazolylthio)-ethyl ester, Z-9-octadecenoic acid, and 2-(3-chloropropyl)-1,3-dioxolane were key contributors to feeding deterrence. In contrast, n-hexadecanoic acid predominantly associated with non-glandular trichomes was linked to higher susceptibility in *Solanum* species.

OP-2-05

Exploiting National Gene Bank Diversity for the Discovery of Novel Marker–Trait Associations (MTAs) Conferring Spot Blotch Resistance in Indian Wheat

Sundeep Kumar[1]*, Sandeep Sharma[2], Manish Vishwakarma[3], Pradeep K. Bhati[3], Subhash Chandra[4], Mir Asif Iqbal[5], Dinesh Kumar[5], V. K. Mishra[2], Amit Kumar Singh[1] and G. P. Singh[1&4]

[1]ICAR-National Bureau of Plant Genetic Resources, New Delhi (INDIA) -110012

[2]Banaras Hindu University, Varanasi (INDIA)- 221005

[3]Bourlong Institute of South Asia, Ludhiana (INDIA)- 141008

[4]Acharya Narendra Dev University of Agriculture & Technology, Ayodhya (INDIA)- 224 229

[5]ICAR-Indian Agricultural Statistics Research Institute, New Delhi (INDIA) -110012

*Corresponding author email: Sundeep.Kumar@icar.org.in

ABSTRACT

Spot blotch is a major foliar disease caused by *Bipolaris sorokiniana*, which limits wheat production in warm and humid regions of South Asia and other parts of the world. In the current study, 6,031 wheat germplasm accessions from the National Gene Bank at ICAR-NBPGR, were phenotyped for spot blotch severity (AUDPC) across three locations (Varanasi, Ayodhya, and Samastipur) over two years. These accessions were genotyped using the 35K Axiom® Wheat Breeders Array, generating 13,957 high-quality SNPs after quality filtering, providing a dense marker platform for genome-wide association mapping. The GWAS analysis was carried out for the full panel and three subsets (Indian landraces, Mexican landraces, and released varieties) using six models (GLM, MLM, CMLM, MLMM, FarmCPU, and BLINK). The analysis resulted in identification of 63 unique marker-trait associations (MTAs) including 47 potential novel MTAs. The analysis also identified 5 novel MTAs within the Indian landrace subset that underscores the value of indigenous germplasm as a reservoir of population-specific resistance alleles. Allele stacking study showed a substantial negative association between the number of favorable alleles and AUDPC. Haplotype analysis also revealed two blocks on Chromosome 5A and 5B indicating that specific haplotypes were associated with significantly lower AUDPC levels. Candidate gene analysis 1 Mb window of significant SNPs found 1329 genes including 61 differently expressed during infection including defense signaling, jasmonic acid pathways and receptor kinase activity genes. Four MTAs on chromosomes 1D, 2B, 3B and 5D were validated using KASP markers in an independent panel of 86 wheat lines, indicating considerable allelic differentiation between resistant and susceptible genotypes ($p < 0.001$). These findings, including 5 novel MTAs within Indian germplasm, provide new insights into the genetic architecture of spot blotch resistance and deliver validated markers for marker-assisted selection in the national wheat breeding program.

OP-2-06

Domestication of USDA pomegranate accession for bacterial blight resistance breeding

Linta Vincent[1]* and Anuradha Sane[2]
[1]Senior Scientist, [2]Principal Scientist, Division of Fruit Crops, ICAR-IIHR, Bengaluru
*Corresponding author email: linta.vincent7@gmail.com

ABSTRACT

Pomegranate (*Punica granatum* L.), a crop naturally suited to the Mediterranean climate, is increasingly cultivated in non-traditional regions of India where it tends to adopt evergreen or semi-deciduous growth patterns. While this physiological shift can offer certain production advantages, it also exposes the crop to severe disease pressures, particularly bacterial blight caused by *Xanthomonas axonopodis* pv. *punicae*. This pathogen affects all aerial parts of the plant and can result in up to 80% yield loss during epidemics, underscoring the importance of identifying and deploying resistant germplasm. To address this challenge, ICAR–Indian Institute of Horticultural Research (IIHR), Bengaluru initiated a breeding programme by introducing diverse pomegranate germplasm from USDA. Among the exotic accessions, 99A was identified as a promising source of resistance to bacterial nodal blight. However, its deciduous habit and complete lack of flowering under Bengaluru conditions posed significant limitations to its use as a parent in hybridization.

To overcome these constraints, a range of flowering induction strategies was evaluated. Treatments included application of growth regulators (paclobutrazol, GA_3, and NAA), cold treatments ranging from 200 to 800 hours, cold treatment of scions prior to top-working onto the commercial variety 'Bhagwa', systematic pinching at monthly intervals, and staggered planting throughout the year. Among these, planting during August–September was particularly effective, resulting in vigorous vegetative growth and the development of 32–38 leaves per m^2 compared with only 12–20 leaves per m^2 in long-standing control plants that had remained non-flowering for nearly a decade. Enhanced leaf production is presumed to have contributed to successful floral induction between November and January.

The induced flowers of 99A exhibited a single whorl of petals and included hermaphrodite, intermediate, and male forms, often borne in clusters. Pollen viability studies indicated 50–60% germination in 15% sucrose solution, confirming the functional reproductive competence of the accession under induced conditions. These findings demonstrate that targeted physiological and environmental interventions can successfully overcome the flowering barrier in 99A, enabling its integration into pomegranate breeding programmes.

The study highlights the potential of accession 99A as a valuable source of bacterial blight resistance maybe through possible epigenetic modulation. Its successful flowering induction lays the foundation for its effective use in developing resilient cultivars tailored to emerging pomegranate production zones.

Keywords: Pomegranate, USDA accession 99A, Bacterial blight resistance, Flower induction, Domestication.

OP-2-07

Harnessing Brinjal Germplasm for Resistance to Root-Knot Nematode (*Meloidogyne incognita*): A Translational Approach for Crop Improvement and Sustainable Bioresource Development

Devindrappa M.[1]*, R. Umamaheswari[1], Singh T. H.[2] and Bhargavi H. A.[2]
[1]*Division of Crop Protection, ICAR–Indian Institute of Horticultural Crops, Bengaluru*
[2]*Division of Vegetable Crops, ICAR–Indian Institute of Horticultural Crops, Bengaluru*
*Corresponding author email: dnayak4505@gmail.

ABSTRACT

Plant genetic resources (PGR) constitute the foundation for developing resilient crop varieties capable of addressing emerging biotic stresses. Root-knot nematode (*Meloidogyne incognita*) is a major constraint to brinjal production, causing severe yield losses and limiting sustainable cultivation. The present study aimed to identify resistant brinjal germplasm that can serve as a valuable genetic resource for nematode resistance breeding. Thirty five brinjal accessions were evaluated under artificial inoculation in pot culture during January–April 2026 using the standard gall index (0–5) described by Taylor and Sasser. Plant growth traits, root galling, egg mass production, and resistance reactions were recorded. Significant variability was observed among the germplasm, indicating substantial genetic diversity for nematode resistance. Among the evaluated germplasm, Arka Harshitha exhibited a highly resistant reaction (Gall Index = 1), with only 2.0 root galls and 0.4 egg masses per plant, coupled with superior shoot growth (55.3 cm). Pusa Safed Long showed moderate resistance (Gall Index = 3), whereas the remaining accessions were classified as susceptible or highly susceptible, with gall indices of 4-5 and extensive nematode multiplication. The identified resistant germplasm represents an important genetic resource for developing nematode-resistant brinjal cultivars through conventional breeding and molecular approaches. Exploitation of these resistance sources will reduce dependence on chemical nematicides, enhance crop productivity, and support environmentally sustainable horticulture.

Keywords: Brinjal germplasm, Plant genetic resources, *Meloidogyne incognita*, Host plant resistance, Crop improvement, Sustainable horticulture.

OP-2-08

Exploring the Wild Tomato Genetic Resources for Volatile-Mediated Resistance Against the Two-Spotted Spider Mite

Bhagyasree S. N.*, Prasanna H. C., Jayanth K. V. and P. D. Kamala Jayanthi
ICAR-Indian Institute of Horticultural Research Bengaluru-560089
*Corresponding author email: bhagyashree.sn@gmail.com

ABSTRACT

The two-spotted spider mite, *Tetranychus urticae* Koch (Acari: Tetranychidae), is one of the most destructive arthropod pests of tomato, causing severe yield and quality losses worldwide. The identification of resistant genetic resources and their defence mechanisms is essential for developing sustainable mite management strategies. In the present study, wild tomato genetic resources were evaluated to identify resistance against *T. urticae* and to investigate the behavioural responses of mites to constitutive and herbivore-induced plant volatiles. Initially, 14 wild tomato accessions were screened under greenhouse and open-field conditions for mite infestation. Considerable variation in susceptibility was observed among the accessions, with several wild species exhibiting little or no infestation under field conditions, indicating their potential as valuable sources of resistance. Healthy (constitutive) and herbivore-induced plant volatiles (HIPVs) were subsequently collected from selected resistant accessions and assessed using a four-arm olfactometer bioassay. The behavioural responses of adult mites were evaluated based on the time spent and the number of entries into odour-treated and control arms. Significant differences in mite preference were observed among volatile blends from different wild tomato species. Constitutive volatiles from *Solanum chilense* (LA1970) elicited the strongest repellent response, towards *T. urticae*, with significantly lower residence time and fewer entries than the control. Herbivore-induced volatiles elicited an even stronger behavioural response, with HIPVs from *S. galapagense, S. habrochaites*, *S. chmielewskii* and *S. pennellii* significantly reducing mite preference compared with controls ($P < 0.05$). These findings indicate that herbivore attack enhances the emission of defensive volatile blends that influence host selection by *T. urticae*. The study demonstrates that wild tomato genetic resources harbour both constitutive and inducible volatile-mediated defence mechanisms that can be exploited for crop improvement. Resistant accessions identified in this study constitute valuable germplasm for breeding mite-resistant tomato cultivars and provide promising candidates for the identification of bioactive semiochemicals that can be integrated into environmentally sustainable pest management strategies.

Keywords: Wild tomato germplasm, Herbivore-induced plant volatiles (HIPVs), Four-arm olfactometer, Host plant resistance, Semiochemicals, Integrated pest management.

OP-2-09

Multi-varietal mango orchards offer enhanced ecosystem services with special reference to insect fauna

P. Venkata Rami Reddy[1]* and M. Sankaran[2]
[1]Division of Crop protection, [2]Division of Fruit Crops
ICAR-Indian Institute of Horticultural Research, Hesaraghatta Lake, Bengaluru – 560089
*Corresponding author email: pvreddy2011@gmail.com

ABSTRACT

Mango (*Mangifera indica* L.), an indigenous fruit crop represented by hundreds of genotypes and cultivated across diverse agro-climatic regions of India, offers an ideal system for evaluating ecosystem services. a concept that has received limited attention in Indian horticulture. Insects play a pivotal role in orchard ecosystems as pests, pollinators and natural enemies, contributing to essential ecological functions such as pollination and natural pest regulation. Field studies were undertaken to assess the ecosystem services provided by multi-varietal mango orchards through crop associated biodiversity (weeds, arthropods, birds, etc.) compared with mono-varietal orchards. The study was conducted in Chittoor district of Andhra Pradesh, where twenty multi-varietal orchards, each comprising approximately ten mango varieties, and six mono-varietal orchards were selected.

Multi-varietal orchards, consisting of varieties with staggered flowering periods, provided an extended availability of floral resources for pollinators compared with mono-varietal orchards. The inclusion of traditional local cultivars such as *Punasa*, an off-season bearer, further prolonged floral resource availability and helped sustain pollinator populations beyond the regular flowering season. In contrast, mono-varietal orchards, predominantly planted with commercial cultivars such as Totapuri, Banganapalli and Neelam, were managed under intensive clean cultivation and received higher pesticide inputs. Consequently, these orchards supported fewer off-season floral resources and lower pollinator abundance. The diversity of non-crop vegetation within and surrounding the orchards was positively associated with pollinator abundance. Multi-varietal orchards recorded higher weed species richness (25 species) and greater pollinator activity (2.35 pollinators per 10 panicles per minute) than mono-varietal orchards (1.86 pollinators per 10 panicles per minute). Across all orchards, dipteran pollinators, particularly syrphid and calliphorid flies, constituted nearly 70% of the pollinator community, followed by Apis florea and stingless bees.

Significant variations in mango hopper populations too were observed among orchards. The lower hopper incidence in multi-varietal orchards may be attributed to the relatively higher population of natural enemies besides the varietal diversity. However, this aspect needs further studies. Overall, the study demonstrates that multi-varietal mango orchards not only serve as valuable repositories of genetic diversity but also promote ecological sustainability by supporting richer pollinator communities and greater associated biodiversity.

Keywords: Mango, multi varietal orchards, pollinators, ecosystem services.

OP-2-10

Evaluation of advanced breeding lines derived from IIHRBTG-144-1 for powdery mildew resistance in Bitter gourd (*Momordica charantia* L.)

B. Varalakshmi*, K. Hanume Gowda, G. M. Sandeep Kumar,
Vivek Hegde, M. Chaithra, Mahadev Kivati, and Tusar Kanti Behera
ICAR-Indian Institute of Horticultural Research, Bengaluru-560089, Karnataka, India
*Corresponding author email: Varalakshmi.B@icar.org.in, vara1965@gmail.com

ABSTRACT

Powdery mildew is one of the most destructive foliar diseases of bitter gourd causing severe reductions in photosynthetic activity, fruit quality and marketable yield. Development of resistant cultivars is the most economical and environmentally sustainable strategy for disease management. A resistant donor parent, IIHR BTG-144-1, previously identified through systematic screening, was utilized to introgress powdery mildew resistance into elite bitter gourd backgrounds. In the present investigation, twenty-six advanced breeding lines derived from IIHR BTG-144-1were evaluated under natural epiphytotic conditions during two consecutive seasons (2025–26 and 2026–27). Disease severity was recorded at regular intervals and quantified using Percent Disease Index (PDI) and Area Under Disease Progress Curve (AUDPC). Significant variation among the breeding lines was observed for disease severity and disease progression, indicating successful transfer and segregation of resistance from the donor parent. Based on pooled field screening data, IIHR PMR-IP-24-2, IIHR PMR-IP-24-6, IIHR PMR-IP-24-7, IIHR PMR-IP-24-9, IIHR PMR-IP-24-11, IIHR PMR-IP-24-14, IIHR PMR-IP-24-24 and IIHR PMR-IP-24-25 consistently recorded lower PDI and AUDPC values and were classified as resistant. In addition to disease resistance, fruit quality and horticultural performance were considered for selecting superior lines for validation under artificial inoculation conditions. Accordingly, IIHR PMR-IP-24-6, IIHR PMR-IP-24-7 and IIHR PMR-IP-24-14, along with the resistant donor IIHR BTG-144-1, were selected as resistant entries, whereas IIHR BTG IP-20-146, IIHR-BTG IP-20-156 and Arka Harit were included as susceptible checks. Artificial screening clearly differentiated resistant and susceptible genotypes. The resistant entries IIHR PMR-IP-24-6, IIHR PMR-IP-24-7 and IIHR BTG-144-1 exhibited low disease development and restricted disease progression throughout the observation period, whereas the susceptible checks IIHR BTG IP-20-146, IIHR-BTG IP-20-156 and Arka Harit showed rapid disease development with substantially higher PDI and AUDPC values. The results confirmed the reliability of field screening and validated the resistance expressed by the selected breeding lines under controlled disease pressure. The consistent performance of IIHR PMR-IP-24-6, IIHR PMR-IP-24-7 across field and artificial screening conditions demonstrates successful introgression of powdery mildew resistance from IIHR BTG-144-1 into elite bitter gourd backgrounds. These lines constitute valuable genetic resources for varietal development and can be effectively utilized as parental stocks for breeding high-yielding, powdery mildew-resistant bitter gourd cultivars.

Keywords: Bitter gourd, powdery mildew, IIHR BTG-144-1, advanced breeding lines, PDI, AUDPC, artificial screening.

OP-2-11

CRISPR/Cas12a-based Rapid Diagnostic Assay for the Detection and Distinction of Important strains of *Tomato infecting Begomoviruses*

Dhanvarsha M.[1,2], Baskar S.[1,2], Sheshadria S. A.[2] and Basavaprabhu L. Patil[1*]
[1]*ICAR-Indian Institute of Horticultural Research, Bengaluru, 560089, Karnataka, India*
[2]*Jain University, Bengaluru, 560027, Karnataka, India*
*Corresponding author email: dhanvarsha.mr@gmail.com

ABSTRACT

Tomato leaf curl New Delhi virus (ToLCNDV) and Tomato leaf curl Palampur virus (ToLCPalV), bipartite begomoviruses belonging to the family *Geminiviridae*, are among the major viral pathogens causing tomato leaf curl disease, resulting in significant yield losses in tomato cultivation. Early, rapid, and accurate detection of these closely related viruses is essential for effective disease surveillance, timely management, and the production of virus-free planting material. In this study, a CRISPR/Cas12a-based diagnostic assay was developed for the rapid and specific detection of ToLCNDV and ToLCPalV. Virus-specific guide RNAs targeting the coat protein (CP) and replication initiation protein (Rep) were designed based on sequence-confirmed isolates of ToLCNDV and ToLCPalV, respectively. An *in vitro* Cas12a cleavage assay was performed using virus-specific PCR amplicons to evaluate target-specific cleavage activity. The developed assay demonstrated high sensitivity, detecting virus-specific PCR amplicons of ToLCNDV and ToLCPalV at concentrations as low as ≤1-10 ng. Furthermore, the assay successfully detected ToLCNDV and ToLCPalV genomic DNA at low concentration without prior PCR or isothermal amplification, demonstrating its potential for direct virus detection. Owing to its high specificity, rapid turnaround time, and minimal instrumentation requirements, the CRISPR/Cas12a-based assay represents a promising molecular diagnostic platform for early disease diagnosis and timely disease management in resource-limited agricultural field conditions.

Keywords:Tomato; CRISPR/Cas12a ; ToLCNDV ; ToLCPalV; Molecular diagnosis.

OP-2-12

Identification of Root-Knot Nematode-Resistant Chilli RILs Using Marker-Assisted Selection and Phenotypic–Genotypic Evaluation

G. Santhosh, R. Umamaheswari*, Naresh Ponnam, D. C. Lakshman Reddy and Devindrappa M.
ICAR-Indian Institute of Horticultural Research, Bengaluru
*Corresponding author email: umanema369@gmail.com

ABSTRACT

Chilli (*Capsicum annuum* L.), an economically important vegetable and spice crop in India, suffers substantial yield losses due to the root-knot nematode (*Meloidogyne incognita*). Host plant resistance, particularly mediated by resistance genes such as *Mi-1*, offers an environmentally sustainable and cost-effective strategy for nematode management. In the present study, 99 recombinant inbred lines (RILs) derived from the crosses IIHR BHP130 × CM334 and Anugraha × CM334 were evaluated for resistance to *M. incognita* using integrated phenotypic and molecular approaches. Phenotypic screening identified 38 resistant RILs. Genotyping with sequence-characterized amplified region (SCAR) markers linked to resistance genes (*Me1, Me3, Me4,* and *Me7*) revealed varying levels of agreement with phenotypic responses: SCAR B94 (74.74%), SCAR N (66.66%), SCAR CD (64.64%), 20-24 (56.56%), and ZY6-13 (53.53%). Among these, SCAR B94, linked to the *Me3–Me4* locus, exhibited the highest predictive accuracy, whereas ZY6-13 (*Me1*) showed the lowest. Twelve RILs from the IIHR BHP130 × CM334 population at the F_5 generation, including RIL 189, RIL 130, RIL 171, and RIL 122, along with ACRIL90, ACRIL70, and ACRIL48 from the Anugraha × CM334 population, consistently exhibited resistance under both phenotypic and genotypic evaluations. These findings demonstrate the utility of marker-assisted selection (MAS) for developing root-knot nematode-resistant chilli cultivars. However, the moderate concordance between molecular markers and phenotypic performance indicates the need for complementary strategies such as gene pyramiding and multi-location validation to enhance the stability and durability of resistance. The identified resistant RILs constitute valuable genetic resources for breeding multiple disease-resistant chilli cultivars and support sustainable chilli improvement programmes.

Keywords: Chilli, *Meloidogyne incognita*; *Mi-1* gene, recombinant inbred lines (RILs), SCAR markers, resistance breeding.

OP-2-13

Mining Cowpea Core Collections for Bruchid (*Callosobruchus maculatus*) Resistance and its Association with Seed Physical, Chemical and Genetic Factors

Chethan Kumar K. B.[1]*, Kavita Gupta[2], Kuldeep Tripathi[2],
Rakesh Bhardwaj[2] and Dhammaprakash Pandhari Wankhede[2]
[1]*ICAR-National Bureau of Plant Genetic Resources, Regional Station, Hyderabad - 500030, Telangana, India*
[2]*ICAR-National Bureau of Plant Genetic Resources, New Delhi, 110012, New Delhi, India*
*Corresponding author email**:** chethanreddykb@gmail.com, chethankumar.kb@icar.org.in

ABSTRACT

Cowpea, *Vigna unguiculata* L. Walp, known as Lobia, Boda, cowpea gram, Cuba bean and asparagus bean has diverse uses as a vegetable, dal, green manure and feed crop. As a legume, it enriches soil nitrogen and improves fertility. However, its yield potential is constrained by insect-pests and diseases. Among storage pests, pulse beetle (*Callosobruchus maculatus*) causes significant quantitative and qualitative losses. The adverse effects of pesticides necessitate ecofriendly pest management approaches, including host plant resistance. Therefore, cowpea core germplasm was evaluated for differential reaction to *C. maculatus* to identify resistance sources, followed by biochemical assessment and Genome Wide Association Studies (GWAS). Accessions were screened under no-choice artificial infestation, revealing significant variation in Oviposition, Mean Development Period (MDP), Adult Emergence Percent (AEP), Emergence Holes (EH), Weight Loss Percent (WLP) and Growth Index (GI). GI ranged from 0 to 6.83 and accessions were classified as highly resistant (22 accessions; GI 0–1.366), moderately resistant (37 accessions; GI 1.367–2.732), moderately susceptible (111 accessions; GI 2.732–4.098), susceptible (193 accessions; GI 4.098–5.464) and highly susceptible (11 accessions; GI 5.464–6.830). Based on screening results, 91 accessions (22 highly resistant, 7 resistant, 31 moderately susceptible and 31 highly susceptible) were selected for biochemical analysis. Correlation analysis showed negative associations of Total Dietary Fiber (TDF) and starch with AEP, GI, WLP and MDP. Phenol, phytic acid and amylose was found to have a negative correlation with AEP, GI and WLP and a positive correlation with MDP. Phenol was found to have positive correlation with seed hardness. Protein and TSS was found to have a positive and significant correlation with AEP, GI and WLP. GWAS was conducted to identify genomic regions associated with bruchid resistance. Genotyping by Sequencing (GBS) identified 17,703 high-quality SNPs (MAF ≥0.05, read depth ≥10 and ≤20% missing data) from 522,926 SNPs. The linkage disequilibrium was assessed with an r^2 value of 0.25. Multilocus GWAS using six models (mrMLM, FASTmrMLM, FASTmrEMMA, pLARmEB, ISIS EM-BLASSO and pKWmEB; LOD≥3) identified 28 significant QTNs across four traits, explaining 2.11–12.59% phenotypic variation. Mean Development Period, Growth Index and Weight Loss Percent each had nine significant QTNs with mrMLM and pKWmEB being most effective. Gene annotation was performed for highly significant and consistent QTNs considered reliable across environments. The findings can support bruchid-resistant variety development, marker-assisted breeding and value addition to national and international gene banks.

Keywords: Cowpea, *Callosobruchus maculatus*, Bruchid resistance, Host plant resistance, Biochemical traits, Genome Wide Association Studies (GWAS).

POSTER PRESENTATIONS

PP-2-01

Genetic dissection of leaf rust resistance in a diversity panel of tetraploid wheat (*Triticum turgidum*)

Jitendra Kumar Yadav[1,3], Shruti Sinha[1], Hariom Shukla[2], Ankur Singh[1], Tanmaya Kumar Sahu[1], Shailendra Kumar Jha[2]*, Jyoti Kumari[1], Manjusha Verma[1], Sundeep Kumar[1], Rakesh Singh[1], Gyanendra Pratap Singh[1] and Amit Kumar Singh[1]*

[1]*ICAR-National Bureau of Plant Genetic Resources, New Delhi*

[2]*ICAR-Indian Agricultural Research Institute, New Delhi*

[3]*Graduate School, Indian Agricultural Research Institute, New Delhi*

*Corresponding author email: amit.singh5@icar.gov.in; jhashail78@gmail.com

ABSTRACT

Leaf rust, caused by Puccinia triticina Erikss. (Pt), remains one of the most devastating diseases limiting wheat productivity worldwide. Rapid evolution of virulent Pt races frequently overcomes deployed resistance genes, highlighting the need to identify novel and durable sources of resistance from genetically diverse wheat germplasm. In the present study, a subset of 189 accessions from the Global Durum Wheat Panel (GDP), representing diverse tetraploid wheat species, was evaluated at the seedling stage against five predominant Indian leaf rust pathotypes, namely 77-5 (121 R 63- 1), 77-6 (121 R 55- 1), 77-9 (121 R 60- 1), 12-5 (29 R 45), and 104 (17 R 23), to elucidate the genetic basis of resistance through genome- wide association analysis. Substantial phenotypic variation was observed across the panel, with approximately 45% of the accessions exhibiting immune to moderately resistant reactions against pathotypes 77-5, 77-6, and 104, whereas 23–27% displayed comparable resistance against pathotypes 77-9 and 12-5. A genome- wide association study (GWAS) employing six multi- locus models identified 89 significant quantitative trait nucleotides (QTNs), of which 22 were consistently detected across multiple models and considered highly reliable. These included four QTNs associated with pathotype 77-5, six with 12-5, three with 77-9, seven with 104, and two with 77-6. Comparative genomic analysis revealed that ten of these reliable QTNs co- localised with previously reported leaf rust resistance loci, whereas the remaining twelve represented potentially novel genomic regions associated with resistance. Candidate gene mining within the genomic intervals flanking all significant QTNs identified more than 300 annotated genes, including 62 genes implicated in disease resistance and defence- related pathways. Furthermore, in silico transcriptome analysis identified two nucleotide- binding leucine- rich repeat (NBS- LRR) genes, TRITD 6 Bv 1 G 224600 on chromosome 6B near QTN RAC 875 _ c 35430 _ 373, and TRITD 6 Av 1 G 225060 on chromosome 6 A adjacent to QTN Excalibur _ c 77841 _ 224, which exhibited significantly higher expression in the resistant genotype during the early stages of P. triticina infection, indicating their potential role in mediating host resistance. Collectively, these findings provide new insights into the genetic architecture of leaf rust resistance in tetraploid wheat and identify novel resistance- associated genomic regions and candidate genes that can be exploited for marker- assisted selection and genomic breeding to develop wheat cultivars with durable and broad- spectrum resistance against leaf rust.

Keywords: *Puccinia triticina*, tetraploid wheat, durum wheat, leaf rust, genome-wide association study, quantitative trait nucleotides, candidate genes, NBS-LRR, marker-assisted breeding.

PP-2-02

Identification of Turcicum leaf blight resistant sources among diverse maize germplasm and validation of SSR markers linked to resistance

Kalyan Kumar P.[1], Santosh K. Pattanashetti[1]*, Mahadevu P.[2] and Sidramappa C. Talekar[3]
[1*]*Department of Genetics and Plant Breeding, College of Agriculture, KSNUAHS, Shivamogga*
[2]*AICRP (Maize), Zonal Agricultural Research Station, V.C. Farm, UAS, Mandya*
[3]*AICRP (Maize), Main Agricultural Research Station, UAS, Dharwad*
*Corresponding author email: santoshpattanashetti@uahs.edu.in

ABSTRACT

Maize is a major cereal worldwide grown for food, feed and industrial value. Globally, its cultivation is hampered by several biotic and abiotic stresses causing significant yield losses. Turcicum leaf blight (TLB) is a major foliar fungal disease that affects maize productivity in several states of India including Karnataka causing yield loss up to 28-91%. Identification of diverse sources of resistance is a pre-requisite for development of TLB resistant cultivars. Towards this, diverse maize inbreds (65) coming from different genetic background were tested under field condition at College of Agriculture, Shivamogga. To create artificial epiphytotic conditions, conidial suspension of the pathogen (*Exserohilum turcicum* (Pass) K.J. Leonard and E.G. Suggs) was sprayed at 40 days after sowing (DAS) and humid conditions were ensured for disease progress. The disease severity among germplasm was assessed by disease rating scale (1–9) and per cent disease index (PDI 0-100%) at 60 and 75 DAS, and used to classify germplasm into resistant (1-3, <33.3%), moderately resistant (4-5, 33.4-55.5%), moderately susceptible (6-7, 55.6-77.7%) and susceptible (8-9, ≥77.8%), respectively. Out of 65 inbred lines evaluated for TLB response, 18 lines were found resistant, 27 lines moderately resistant, and 14 lines moderately susceptible to TLB disease. Inbreds such as MMI-2, GI2208, VL-111354 and GI2264 recorded low disease severity (< 3 score, < 33.3% PDI) and higher grain yield, which could serve as valuable donor parents in resistance breeding programmes. To validate previously reported SSR markers (20) associated with TLB resistance, 32 genotypes including 24 resistant, 4 moderately resistant, and 4 susceptible genotypes were analysed. The analysis of molecular variance indicated higher variation within groups (87.77%) but lesser among groups (12.23%) i.e., resistant, moderately resistant, and susceptible groups. The fixation index (ΦST = 0.122) was significant (p = 0.011), indicating moderate but statistically significant genetic differentiation among groups. Four SSR markers (phi330507, bnlg1267, phi109642 and phi-085) were polymorphic showing significant marker-trait association (p ≤ 0.05) and consistently differentiated resistant and susceptible genotypes. The present study identified diverse TLB resistant sources and validated SSR markers associated with resistance that would help in rapid development of TLB resistant hybrid cultivars for commercial cultivation.

Keywords: Field screening, Maize, Resistant, SSR markers, Turcicum leaf blight, Validation.

PP-2-03

Genomic Insights into Papaya Ringspot Virus (PRSV-P) Resistance in Papaya (*Carica papaya* L.)

Dodla Mamatha*, Ravishankar K. V., Vasugi C. and D. K. Samuel
PhD Scholar, Division of Basic Sciences, Indian Institute of Horticultural Research
*Corresponding author email: dodlamamatha09@gmail.com

ABSTRACT

Papaya (*Carica papaya* L.) is an economically important fruit crop widely cultivated in tropical and subtropical regions of the world. However, its production is severely constrained by papaya ringspot virus (PRSV-P), one of the most destructive viral diseases affecting its cultivation globally often resulting in total yield loss. Conventional management practices, including vector control and cultural methods, have limited effectiveness, making the development of resistant cultivars a promising and eco-friendly strategy for long-term disease management. Thus, the emergence of new viral strains necessitates the discovery for identifying genomic regions associated with resistance to PRSV-P using a segregating population developed from a cross between resistant (*Vasconcelea cauliflora*) and susceptible (Arka Prabhath) parental lines. By employing advanced sequencing-based approaches, genomic variation between resistant and susceptible groups was analysed to detect loci linked to disease resistance. This approach enabled the identification of specific genomic regions located on Chr 04 associated with PRSV-P resistance, providing insights into the genetic architecture underlying this important trait. The study also facilitated the discovery of molecular markers linked to PRSV resistance.

These genomic insights provide a foundation for Marker-Assisted Selection (MAS) and genome editing strategies aimed at developing durable, non-transgenic PRSV-P resistance. These findings bridge the gap between structural genomics and practical breeding applications to ensure sustainable papaya production.

Keywords: *Carica papaya,* PRSV-P, Sequencing based approaches, Molecular markers.

PP-2-04

Identification of novel sources of quick wilt resistance in black pepper (*Piper nigrum* L.)

Navya B. L., Hiremath J. S., Kulkarni S., Sumangala K., Mahantesh N. B. N. and Mukund S.
University of Horticultural Sciences, Bagalkot
*Corresponding author email: navyablnrp@gmail.com

ABSTRACT

Black pepper (*Piper nigrum* L.), an economically important spice crop and a native genetic resource of the Western Ghats biodiversity hotspot, harbours substantial genetic variability with immense potential for crop improvement. Among the major biotic constraints limiting its productivity, quick wilt caused by *Phytophthora capsici* Leon. remains the most destructive disease, necessitating the identification of resistant germplasm for sustainable breeding programmes. The present study evaluated twenty-one black pepper genotypes, including indigenous landraces, cultivated varieties, and resistant and susceptible checks, for their reaction to *P. capsici* under controlled polyhouse conditions. The pathogen was isolated from naturally infected vines, identified based on cultural and morphological characteristics, and its pathogenicity was confirmed following Koch's postulates. Rooted cuttings were artificially inoculated with actively growing mycelial plugs, and disease severity was assessed 72 h after inoculation by recording leaf and stem lesion development and calculating the disease severity index (DSI). Significant variability was observed among the genotypes, with leaf and stem lesion sizes ranging from 1.75–14.48 mm and 2.41–27.24 mm, respectively. The resistant check IISR Shakthi recorded the lowest total DSI (20.31%), followed by the genotypes Sigandini (24.22%) and RMH (27.34%), whereas SV-19 (85.16%) and V-3 (84.38%) exhibited the highest disease severity. Based on DSI, only Sigandini and RMH, in addition to the resistant check, were classified as resistant, while the remaining genotypes were susceptible. The identification of resistance in indigenous germplasm underscores the importance of this biodiversity-rich region as a reservoir of valuable alleles for disease resistance. These genotypes represent promising donor parents for resistance breeding and genetic enhancement programmes aimed at developing durable quick wilt-resistant black pepper cultivars while promoting the conservation and effective utilization of plant genetic resources.

PP-2-05

Phenotypic and molecular characterization of Capsicum germplasm for root-knot nematode (*Meloidogyne incognita*) resistance

Sapana Gurupad Hegde[1], Smaranika Mishra[1], Uma Maheshwari R[2],
Lakshmana Reddy D. C.[3], Varsha V.[1,4] and Prakash Singathiya[1]
[1]Division of Vegetable Crops, [2]Division of Crop Protection and [3]Division of Basic Sciences,
ICAR - Indian Institute of Horticultural Research, Bangalore - 560089,
[4]University of Horticultural Sciences, Bagalkot - 587101
*Corresponding author email: sapanagh5@gmail.com

ABSTRACT

Root-knot nematode (*Meloidogyne incognita*) is a major soil-borne endoparasite that limits Capsicum production worldwide. Identification of resistant germplasm and validation of resistance-linked molecular markers are essential for accelerating marker-assisted breeding. In this study, 52 diverse Capsicum germplasm accessions were evaluated for root-knot nematode resistance through artificial inoculation, and four reported SCAR markers (SCAR N, SCAR B94, SCAR Pm6a, and SCAR CD) associated with root-knot nematode resistance were validated. The phenotypic data were further analysed using correlation analysis, principal component analysis (PCA), hierarchical clustering, and the Multi-trait Genotype–Ideotype Distance Index (MGIDI) to identify superior donor genotypes. Analysis of variance revealed highly significant ($P < 0.01$) differences among genotypes for all growth and nematode-related traits, indicating substantial genetic variability for resistance. Based on gall index and egg mass index, CM-334 (G2) was identified as the only resistant genotype, whereas the remaining accessions exhibited varying levels of susceptibility. Correlation analysis revealed strong positive associations among gall formation, egg mass production, and nematode reproduction traits, while plant growth traits were positively correlated with one another. The first two principal components explained 64.35% of the total phenotypic variation, clearly separating plant growth traits from nematode infection and reproduction traits. Hierarchical clustering grouped the germplasm into three distinct clusters, while MGIDI identified CM-334 (G2) as the genotype closest to the ideotype, with G17, G21, G23, G46, G51, and G52 emerging as promising donor lines for resistance breeding. Molecular validation demonstrated that SCAR N, SCAR B94, SCAR Pm6a, and SCAR CD consistently differentiated the resistant genotype CM-334 from susceptible germplasm through distinct amplification profiles, confirming their utility as diagnostic markers for marker-assisted selection. The integration of phenotypic screening, multivariate analysis, and SCAR marker validation provides a robust framework for identifying elite resistance sources and accelerating the development of root-knot nematode-resistant Capsicum cultivars.

Keywords: *Capsicum annuum*, *Meloidogyne incognita*, SCAR markers, Marker-assisted selection, MGIDI, Resistance breeding.

PP-2-08

Harnessing Wild Tomato Genetic Resources through Volatile Profiling for Sustainable Resistance against *Phthorimaea absoluta*

Jayanth K. V.[1,2], H. C. Prasanna[3*] and Pagadala Damodaram Kamala Jayanthi[4]
[1]*Ph. D Scholar, Department of Vegetable Science, UHS, Bagalkot, Karnataka*
[2]*Research Scholar, Division of Vegetable Crops, ICAR-IIHR, Bengaluru, Karnataka*
[3]*Principal Scientist and Head, Division of Vegetable Crops, ICAR-IIHR, Bengaluru, Karnataka*
[4]*Principal Scientist, Division of Entomology, ICAR-IIHR, Bengaluru, Karnataka*
*Corresponding author email: prasannahc@yahoo.com

ABSTRACT

Wild crop relatives represent invaluable plant genetic resources (PGR) for broadening the genetic base of cultivated crops and enhancing resilience against emerging biotic stresses. Tomato (*Solanum lycopersicum* L.) has undergone extensive domestication, resulting in a narrow genetic base and increased susceptibility to the invasive tomato leaf miner, *Phthorimaea absoluta*. In contrast, wild tomato species possess diverse morphological, biochemical, and molecular traits that remain largely unexplored for sustainable insect resistance. The present study aimed to characterize wild tomato genetic resources for volatile-mediated resistance against *P. absoluta* and identify promising donor accessions for tomato pre-breeding. Seventeen wild tomato accessions representing different *Solanum* species were evaluated for resistance using detached leaf bioassays and field validation. Resistant and susceptible accessions were further characterized through volatile profiling using Gas Chromatography–Mass Spectrometry (GC–MS). Behavioural responses of *P. absoluta* adults were assessed using Y-tube olfactometer assays, followed by detached leaf bioassays employing synthetic volatile compounds to validate their biological activity. Significant variation was observed among the wild accessions for insect resistance and volatile composition, highlighting the rich genetic diversity present within tomato wild relatives. Resistant accessions exhibited distinct volatile fingerprints compared with susceptible genotypes. Several volatile organic compounds demonstrated strong repellence towards *P. absoluta* in olfactometer assays. Bioassay validation further confirmed that compounds such as (+)-2-Carene, Longifolene and 1-Tridecene substantially reduced larval feeding damage compared with untreated controls, indicating their potential role in host plant resistance. The study demonstrates that volatile metabolites associated with wild tomato genetic resources constitute valuable biochemical markers for resistance breeding. Integrating volatile profiling with phenotypic screening provides an efficient strategy for identifying superior donor parents and accelerates the utilization of wild germplasm in crop improvement programmes. The identified resistant accessions and bioactive volatile compounds offer promising resources for developing climate-resilient and pest-resistant tomato cultivars while reducing dependence on chemical insecticides. This work highlights the importance of conserving and harnessing wild plant genetic resources for sustainable agriculture and future food security.

Keywords: Plant genetic resources, wild tomato relatives, volatomics, host plant resistance.

PP-2-09

Identification of Tomato Leaf Curl New Delhi Virus tolerant ridge gourd (*Luffa acutangula* Roxb. L.) genotypes

B. Varalakshmi*, M. V. Dhananjaya, B. Mahesha, Mahadev Kivati and K. Hanume Gowda
[1]*ICAR-Indian Institute of Horticultural Research, Bengaluru - 560089, Karnataka, India*
*Corresponding author email: Varalakshmi.B@icar.org.in, vara1965@gmail.com

ABSTRACT

Tomato Leaf Curl New Delhi Virus (ToLCNDV) is a major viral disease causing severe yield losses and limiting ridge gourd production in India. The present study was undertaken to identify ToLCNDV-tolerant ridge gourd genotypes through field screening and artificial sap inoculation. Six promising ridge gourd genotypes exhibiting varying levels of ToLCNDV tolerance were selected through an initial screening trial and subsequently evaluated across four environments. The genotypes were assessed for flowering, fruit, yield and disease-related traits. Pooled analysis of variance revealed significant effects of genotype, environment and genotype × environment interaction for most of the traits studied, indicating substantial variability and differential genotype responses across environments. Pearson's correlation analysis revealed that ToLCNDV incidence was negatively associated with fruit and yield-related traits, indicating the adverse effect of disease severity on productivity. Principal component analysis showed that the first three principal components accounted for 98.9% of the total variation, with PC1, PC2 and PC3 contributing 56.2%, 24.0% and 18.6%, respectively. Factor analysis grouped the evaluated traits into three major factors comprising flowering, yield and fruit-related traits, highlighting their contribution to genotype differentiation. Under field conditions, the genotype IIHR RV-28-1 recorded the lowest mean ToLCNDV incidence (26.81%), whereas the susceptible check Arka Prasan exhibited a significantly higher mean disease incidence of 45.49%. Artificial screening through sap inoculation further confirmed the tolerance of IIHR RV-28-1, wherein only one out of six inoculated plants developed disease symptoms (16.7% incidence), while the susceptible check Arka Prasan recorded 100% infection with all fifteen inoculated plants exhibiting typical ToLCNDV symptoms. Molecular confirmation using PCR revealed negative amplification in the resistant bulk of IIHR-RV-28-1, whereas the susceptible bulk of Arka Prasan showed positive amplification, confirming the presence of ToLCNDV infection. Selection differential analysis indicated favourable genetic gains for number of fruits per plant (20.6%), yield per plant (10.8%) and yield per hectare (10.8%). Based on field screening, artificial inoculation and molecular confirmation, genotype IIHR-RV-28-1 was identified as a promising source of ToLCNDV tolerance with superior agronomic performance. The genotype can serve as a valuable donor parent in resistance breeding programmes and for the development of ToLCNDV-resilient ridge gourd cultivars.

Keywords: Ridge gourd, Tomato Leaf Curl New Delhi Virus, disease screening, Pearson correlation, Principal component analysis, factor analysis.

PP-2-10

Biochemical characterization of defense responses in selected grape varieties (*Vitis spp.*) for resistance to grape rust disease

Nishant[1], Satisha Jogaiah[1], Shamina Azeez[1], Sriram, S.[1], Sanjay K. Singh[2],
Linta Vincent[1], Debi Prasad Mohanty[1] and Roopendra Kumar[1]
[1]*ICAR-Indian Institute of Horticultural Research, Bengaluru – 560089*
[2] *Division of Horticultural Science, Indian Council of Agricultural Research,*
Krishi Anusandhan Bhawan- New Delhi – 110 012
Corresponding author email: satilata@gmail.com

ABSTRACT

The study on the biochemical mechanisms of defense responses in rust resistance was conducted in 2024-25 at the Indian Institute of Horticultural Research, Bengaluru. Leaf samples from eight-year-old vines of 16 different genotypes were collected. Healthy and diseased leaves were sampled to estimate various biochemical parameters, namely chlorophyll a, chlorophyll b, and total chlorophyll, total soluble sugar, non-enzymatic antioxidants such as total phenols, total flavonoids, proline, and enzymatic antioxidants such as peroxidase (POD), polyphenol oxidase (PPO), phenyl ammonia lyase (PAL), and chitinase. The standard disease scoring technique (0-5 scale) was followed to estimate the percent disease index during disease progression. Among 16 grape varieties, Flame Seedless, Fantasy Seedless, Thompson Seedless, Gulabi, Manjari Medika, Crimson Seedless were moderately resistant; Arkavati, Sharad Seedless, Arka Chitra, Anab-e-Shahi, Tas-A-Ganesh, Red Globe, Arka Kanchan, Manjari Naveen, and Dilkush were moderately susceptible; and Bangalore Blue was extremely susceptible. There was a consistent increase in the activities of defense-related enzymes such as peroxidase (POD), polyphenol oxidase (PPO), phenyl ammonia lyase (PAL), and chitinase, and other defense-related secondary metabolites like total phenols, total flavonoids, and biochemical parameters such as total soluble sugar and proline, in moderately resistant varieties. There was a sharp decrease in chlorophyll content in susceptible varieties such as Bangalore Blue. These results suggested that the faster and stronger activation of the defense system is associated with resistance against rust in the grapevine varieties.

Keywords: Grapes, rust, resistance, antioxidant and non-antioxidant enzymes.

PP-2-11

Screening of tuberose genotypes (*Agave amica* Medik.) for resistance to root knot nematode (*Meloidogyne incognita*)

Sushmita Halagali*, Umamaheshwari R., T. Usha Bharathi,
Sujatha A. Nair, P. Naveen Kumar and Sreenivasa V.
ICAR-Indian Institute of Horticultural Research, Bengaluru - 560089, India
*Corresponding author email: sushmita.halagali9@gmail.com

ABSTRACT

Tuberose (*Agave amica* Medik.), formerly known as *Polianthes tuberosa* L., is a well-known perennial bulbous ornamental crop that belongs to the family Asparagaceae and is native to Mexico. Root knot nematode (*Meloidogyne incognita*) is a plant-parasitic nematode known to cause up to 13–14% yield reduction in tuberose. Gall formation on the roots is the diagnostic symptom of root knot nematode infection. Infected plants exhibit various symptoms such as reduced height and biomass, wilting, swollen roots, damaged plasma membranes, chlorosis, and necrosis. An experiment was conducted at ICAR-IIHR, Bengaluru, during 2025 to screen 50 tuberose genotypes for root knot nematode resistance using a Completely Randomized Design with three replications. The uniform, disease free bulbs are planted in the polythene bag (5x7 inch) and each plant was artificially inoculated with *M. incognita* at the rate of 1000 juveniles (J_2) at 15 days after planting. The study revealed that the genotype IIHR-20-8-18B was recorded as highly resistant reaction with the least number of galls per root (1.66), and genotypes IIHR-20-1-77A, IIHR-20-8-114, and IIHR-20-05 43 were also found to be resistant with a gall index of 2. Thirteen genotypes showed a tolerant reaction to *M. incognita* with a gall index ranging from 2.33 to 3 and 32 genotypes with susceptible reaction. The study revealed significant variation among the tuberose genotypes in response of to root knot nematode infestation. These resistant genotypes can be valuable resources for breeding, contribute to sustainable crop production and can also be employed as a component of integrated nematode management.

Keywords: Tuberose, root knot nematode, artificial inoculation, resistant.

PP-2-14

Optimizing Interspecific Hybridization and Revealing Genotype-Dependent Crossability for Introgression of Ascochyta Blight Resistance in Chickpea (*Cicer arietinum* L.)

Swapnil Baraskar[1,2], Anuradha Chetukuri[2], Ramachandran Senthil[1], Ganesh Pawar[1], Vetriventhan Mani[1], Ovais Peerzada[1], Mamta Sharma[1], Himabindu Kudapa[1] and Kuldeep Singh[1]*
[1]*International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, Telangana, India*
[2] *Professor Jayshankar Telangana Agricultural University, Hyderabad, Telangana, India*
*Corresponding author email: kuldeep.singh@icrisat.org

ABSTRACT

Wild *Cicer* species represent valuable sources of alleles for improving disease resistance in cultivated chickpea (*Cicer arietinum* L.). Ascochyta blight is among the major diseases affecting the chickpea crop, while resistance within the cultivated germplasm remains limited. Screening of *C. pinnatifidum,* belonging to the tertiary gene pool of the cultivated chickpea, identified resistance accessions. Subsequent validation confirmed ICC 20228 and ICC 20239 exhibiting the highest levels of resistance. However, their effective use in crop improvement is constrained by poor interspecific crossability due to strong pre- and post-zygotic reproductive barriers. Previous hybridization studies have generally relied on one or a few cultivated genotypes as female parents, leaving limited information on genetic variation for crossability within the cultivated germplasm. This study was conducted at ICRISAT, aimed to optimize an interspecific hybridization protocol, assess crossability across diverse cultivated germplasm. A total of 1,707 crosses involving 20 cultivated accessions (10 desi and 10 kabuli) and five

C. pinnatifidum accessions were performed across five consecutive seasons in the glasshouse. Simultaneous morning emasculation and pollination successfully overcame the pre-zygotic barrier associated with stigma desiccation. To address the post-zygotic incompatibility, two plant growth regulator formulations containing GA_3, NAA and kinetin were evaluated. The optimized formulation (75:10:10 ppm) significantly increased overall pod set from 1.65% to 13.32% (an 8.07-fold improvement), with the highest pod set (18.84%) during the post-rainy season of 2024. Recovery of shrivelled interspecific seeds across several crossing combinations demonstrated partial mitigation of post-zygotic barriers. Substantial genotype-dependent variation in crossability was observed among cultivated accessions, with nine accessions consistently showing superior crossing success across seasons. No significant difference was detected between desi and kabuli groups, suggesting that crossability is governed primarily by genotype rather than market class. Overall, this study establishes an integrated pre-breeding framework that combines validated resistant donor parents, an optimized interspecific hybridization protocol and identification of highly crossable cultivated germplasm. Molecular markers can be further employed to confirm the hybridity of putative F_1 progenies generated from these crosses. This is the first study to evaluate interspecific crossability of chickpea germplasm accessions over multiple seasons, suggesting that crossability may be genetically regulated and providing a foundation for identifying crossability-associated genes, while facilitating future introgression of beneficial alleles from wild *Cicer* species into cultivated chickpea.

Keywords: Chickpea, Interspecific hybridization, Ascochyta blight, Crossability, Pre-breeding.

PP-2-15

First report of CRISPR prime editing in a globally significant non-model organism, the fall armyworm, *Spodoptera frugiperda* (Lepidoptera: Noctuidae)

Dhawane Yogi[1,2]*, Thalooru Shashikala[1], Geerthana Subramanian[1], Akshay Kumar[1], V. Kaninika[1], Maligeppagol Manamohan[1], M. N. Jithesh[2], Girish Kumar Jha[3], Ramasamy Asokan[1] and Karuppannasamy Ashok[1,4]

[1]*ICAR–Indian Institute of Horticultural Research, Bengaluru 560089, Karnataka, India*

[2]*Jain University, Bengaluru 560027, Karnataka, India*

[3]*ICAR–Indian Agricultural Statistics Research Institute, New Delhi - 110012, India*

[4]*ICAR–Indian Agricultural Research Institute, New Delhi - 110012, India*

*Corresponding author email: yogidhawane@gmail.com

ABSTRACT

The power of CRISPR/Cas9 mediated genome editing has been harnessed in different facets of entomological research, particularly useful in developing genetic pest management strategies. The edits thus obtained are robust and results in a loss-of-function of the target gene. Recently the development of newer editing approach called Prime editing is yet another addition in the insect editing tool-box. In this regard, the prime editing offers a transformative approach to precise genome manipulation by enabling targeted insertions, deletions, and nucleotide substitutions without double-strand break or donor template. While its application has been explored in mammalian system and plants, its deployment through the delivery of ribonucleoprotein complex (RNP) has been demonstrated for the first-time in the globally significant pest, *Spodoptera frugiperda*. Using a Cas9 (H840A)-reverse transcriptase fusion protein (PE2) and a customized prime editing guide RNA (pegRNA), we targeted exon 3 of the *Tryptophan 2,3-dioxygenase* (SfTO) gene to introduce a premature stop codon. Recombinant PE2 protein was expressed in *E. coli*, purified, and validated functionally through RT-PCR. The Ribonucleoprotein complex was microinjected into G0 eggs and subsequent genotyping revealed successful edits, including perfect and imperfect prime edits, as well as unintended mutations. Phenotyping revealed the mutants with altered eye pigmentation, and chromatographic analysis confirmed disruption in ommochrome biosynthesis, validating functional consequences of Prime editing. This study provides a foundational proof-of-concept for Prime editing in insect pests, opening new avenues for functional genomics and designing next-generation pest management strategies.

Keywords: *Spodoptera frugiperda*; Prime editing; CRISPR/Cas9; pegRNA; Insect functional genomics.

PP-2-16

Harnessing secondary gene pool wild relatives for introgressing stable late leaf spot resistance in groundnut

H. V. Veerendrakumar, Srinivas Muluguri, U. N. Mangala, Chanakya Paidala, Hima Bindu Bhadragiri, Senthil Ramachandran, Hari Kishan Sudini, Shivali Sharma, Nalini Mallikarjuna, Kuldeep Singh and Manish K. Pandey*

[1]*Accelerated Crop Improvement & Center for Pre-Breeding Research (CPBR), International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India - 502324*

*Corresponding author email: Manish.Pandey@icrisat.org

ABSTRACT

Groundnut (*Arachis hypogaea* L.) is a vital global oilseed crop, yet its productivity is severely constrained by late leaf spot (LLS), caused by *Phaeoisariopsis personata*, which incurs yield losses of up to 50%. Host-plant resistance provides the most economical and environmentally sustainable strategy for LLS management; however, global resistance breeding has mostly relied on a narrow genetic base, predominantly derived from *Arachis cardenasii* (GPBD 4). Recent field reports of resistance breakdown in GPBD 4 highlight an urgent need to diversify genetic defenses using groundnut wild relatives. In this study, 148 introgression lines (ILs), developed in the elite background of ICGV 87846 using synthetic amphidiploids ISATGR 265-5A [*A. kempff-mercadoi* (ICG 8164)/ *A. hoehnei* (ICG 8190)] and ISATGR 278-18 [*A. duranensis* (ICG 8138)/ *A. batizocoi* (ICG 13160)], were evaluated under field conditions with artificial inoculation across two consecutive rainy seasons (2024–2025). Ten superior ILs (ICGIL 22308, ICGIL 22421, ICGIL 22484, ICGIL 22105, ICGIL 22107, ICGIL 22101, ICGIL 22112, ICGIL 22115, ICGIL 22247, and ICGIL 22124) exhibited high resistance, recording disease score of 3 to 5 (on a 9-point scale) and significantly outperforming the resistant check GPBD 4 (score 6.0). Among these, ICGIL 22308 (score 3.0, derived from *A. batizocoi*) and ICGIL 22421 (score 4.0, derived from *A. kempff-mercadoi / A. hoehnei*) were notably superior and emerged as the most promising LLS donors. Furthermore, QTL-seq analysis of the ISATGR 265-5A mapping population uncovered a novel, major genomic region controlling LLS resistance on Chromosome 2, physically distinct from the resistant locus of *A. cardenasii*. These superior introgression lines offer invaluable donor sources for breeding resilient cultivars, while the newly mapped Chromosome 2 genomic region facilitates targeted introgression for stable LLS resistance.

Keywords: Groundnut, late leaf spot, wild species, genes, stable resistance.

PP-2-17

Haplotype-Based Mapping and Validation of Genomic Regions Controlling Aflatoxin Resistance in Groundnut

Shilpi Dixit[1], Vinay Sharma[1], Hari K. Sudini[1], Pushpesh Joshi[1], Vanika Garg[1,2], Mangala Uppala[1], Sunil S. Gangurde[1], Pooja Soni[1], Prasad Bajaj[1], H. D. Upadhyaya[1], Kuldeep Singh[1], Rajeev K Varshney[1,2] and Manish K. Pandey[1*]

[1]*Accelerated Crop Improvement (ACI) and Centre for Pre-Breeding Research (CPBR), International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad, India*

[2]*Centre for Crop and Food Innovation, WA State Agricultural Biotechnology Centre, Food Futures Institute, Murdoch University, Murdoch, Western Australia, Australia*

*Corresponding author email: manish.pandey@icrisat.org

ABSTRACT

Aflatoxin contamination caused by *Aspergillus flavus* is a major food safety and trade constraint in groundnut (*Arachis hypogaea* L.), particularly in tropical and semi-arid regions. Developing resistant cultivars through genomics-assisted breeding offers a sustainable approach to mitigate pre-harvest aflatoxin contamination (PAC). To dissect the genetic basis of resistance, a genome-wide association study (GWAS) was conducted using four seasons of phenotypic data for *A. flavus* infection and aflatoxin content, together with 691,194 high-quality SNP markers from the ICRISAT groundnut minicore collection. Significant genomic regions associated with resistance to *A. flavus* infection were identified on chromosome 12, while loci associated with reduced aflatoxin accumulation were detected on chromosomes 7, 9, 14, 15, and 18. Candidate gene analysis revealed 60 putative genes linked to fungal infection resistance and 36 genes associated with aflatoxin resistance, many of which are involved in plant defense pathways. Haplotype analysis identified superior haplotypes from 37 candidate genes for infection resistance and 17 genes for aflatoxin resistance. Furthermore, 34 Kompetitive Allele-Specific PCR (KASP) markers were developed and validated for deployment in marker-assisted breeding. To validate these loci, haplotype mining across 1,500 diverse groundnut accessions identified 17 promising lines carrying 8-13 favorable resistance-associated SNPs. These accessions are currently being evaluated under PAC sick-plot conditions, and aflatoxin quantification is underway. The identified genomic regions, favorable haplotypes, and validated KASP markers provide valuable resources for accelerating the development of aflatoxin-resistant groundnut cultivars and improving food safety.

Keywords: Groundnut, aflatoxin, *Aspergillus flavus*, GWAS, haplotypes, KASP markers.

PP-2-20

Screening of interspecific hybrids in guava for biotic stress tolerance

C. Vasugi[1]*, S. Sriram[2], R. Umamaheswari[3] and T. Veera Nagasupriya[1a]
[1]*Principal Scientist, Division of Fruit Crops*
[2]*Principal Scientist, Division of Crop protection*
[3]*Principal Scientist, Division of Crop protection*
[1a]*PhD Scholar, Division of Fruit Crops*
ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka - 560089
*Corresponding author email: vasugiperumal@gmail.com

ABSTRACT

Guava (Psidium guajava L.) is one of the important commercial fruit crops of the tropical and subtropical regions of the world. Its production faces significant yield losses due to various biotic stresses viz., wilt disease (Fusarium oxysporum f. sp. psidii) and the root-knot nematode (Meloidogyne enterolobii) which make it complex. As there is no resistance available in the cultivated species for these biotic stresses, interspecific hybridization involving resistant wild species is a viable option for long term sustainable production and use . Hence, the present study was carried out at ICAR-IIHR to develop the interspecific hybrids involving wild relatives Psidium cattleianum var. cattleianum and Psidium cattleianum var. lucidum.The interspecific hybrid progenies were screened for nematode and wilt under controlled conditions. The results revealed that three interspecific hybrids: ISHG-3 (Arka Poorna× and Psidium cattleianum var. lucidum), ISHG-10(Arka Poorna× and Psidium cattleianum var. lucidum), ISHG-12(Arka Poorna× and Psidium cattleianum var. cattleianum) exhibited combined resistance to both nematode and wilt disease. They recorded a minimum gall index of 2, low number of egg masses (0 to 3.33), maximum reduction in nematode population (0 to 0.83) and number of females (0 to 0.25) as compared to susceptible Psidium guajava with highest gall index of 5, more number of egg masses (148.6 to 374) with maximum mean nematode population (4.67 to 306.00) and mean number of females (41.5 to 230). The rhizosphere colonization confirmed the presence of the wilt pathogen Fusarium oxysporum f. sp. psidii in the roots and it was observed to an extent of 29 to 33 % for the interspecific hybrids as against the susceptible Psidium guajava which has recorded highest value of 95%. Thus, the findings resulted in identification of three promising hybrids having combined resistance to both nematode and wilt for sustainable guava production.

Keywords: Psidium guajava, Interspecific Hybridization, Biotic Stress tolerance, wild species, resistance, screening.

Theme - 3
Innovation, Bioeconomy and Livelihood Enhancement

ORAL PRESENTATIONS

OP-3-01

Lasoda (*Cordia myxa*) Mucilage as a Natural Cryo-Protectant: Lyophilisation of *Lactobacillus* spp and Formulation of Probiotic Beetroot Powder

Neethu K.[1]*, Ranjitha K.[2], Preethi P.[2], Pushpa C. K.[2], Tiwari R. B.[2], Karunakaran G.[3], Shivashankara K. S.[4], Abhishek M.[5] and Anuradha S.[6]

Ph. D Scholar, Department of Post Harvest Technology and Agricultural Engineering
ICAR-IIHR, Hessarghatta, Bengaluru, Karnataka, India
*Corresponding author email: neethukunnikrishnan22@gmail.com

ABSTRACT

The present work explores the potential application of lasoda (Cordia myxa) mucilage as a natural cryo-protectant and stabilizing agent for the lyophilisation of *Lactobacillus* spp.**,** with the ultimate aim of developing a functional probiotic beetroot powder. Lasoda mucilage, rich in polysaccharides and bioactive compounds, exhibits strong water-binding, film-forming, and protective properties, making it a promising alternative to conventional synthetic cryo-protectants. In this study, lasoda mucilage was incorporated into *Lactobacillus* cultures prior to freeze-drying to evaluate its ability to enhance bacterial viability, survival during storage, and rehydration efficiency. The mucilage-based lyophilised cultures were subsequently blended with cabinet-dried beetroot powder to formulate a probiotic product with improved stability, color retention, and functional attributes. Initial findings suggest that lasoda mucilage supports higher post-lyophilisation viability of *Lactobacillus* cells, likely due to its capacity to form a protective matrix that reduces cellular stress during freezing and dehydration. The resulting probiotic beetroot powder demonstrates favorable physicochemical properties, antioxidant potential, and viable cell counts within the recommended therapeutic range. This study highlights lasoda mucilage as a sustainable, plant-based product that can enhance probiotic stability and facilitate the development of value-added functional foods.

Keywords: Lasoda mucilage; *Cordia myxa*; lyophilisation; *Lactobacillus* spp.; cryo-protectant; probiotic powder; beetroot powder; cabinet drying; functional foods; microbial viability; natural stabilizers.

OP-3-02

From Forest Knowledge to Green Enterprise: A Scalable Biodiversity Based Livelihood Model among the Soliga community of Biligiri Rangana Hills

Sumangala H. P.*, Senthil Kumar R. and Sankar V.
ICAR-Indian Institute of Horticultural Research, Bengaluru -560089
*Corresponding author email: Sumangala242@gmail.com

ABSTRACT

The Biligiri Rangana Hills (B.R. Hills), located at the unique ecological junction of the Western and Eastern Ghats in Karnataka, are recognized for their remarkable biological richness, high levels of endemism, and deep cultural heritage. This landscape also sustains the traditional livelihoods of the indigenous Soliga community, whose knowledge and way of life are closely connected with forest resources. However, increasing habitat degradation, unsustainable extraction of plant resources, and changing land-use practices are placing considerable pressure on this fragile ecosystem and its valuable plant genetic resources. In this context, the present study explores a community-centered approach for conserving native ornamental plant diversity while creating sustainable livelihood opportunities for the Soliga community through bioeconomic interventions.

Field explorations were carried out across different altitudinal zones of B.R. Hills to document native ornamental plant species possessing aesthetic appeal, ecological relevance, and commercial potential. Selected species were subjected to propagation trials using seeds, stem cuttings, rhizome divisions, and clump separations under low-cost nursery conditions utilizing locally available substrates such as coir pith, compost, and forest soil. The objective was to develop simple, affordable, and scalable propagation techniques that could be easily adopted by local communities.

Alongside technical interventions, participatory training programs, hands-on demonstrations, and skill development workshops were conducted to strengthen community capacities in plant propagation, nursery management, value addition, and small-scale enterprise development. Baseline socio-economic assessments helped understand existing livelihood patterns, indigenous knowledge, and the community's dependence on forest resources, enabling the design of interventions aligned with local needs and aspirations.

A significant outcome of this initiative has been the gradual transformation of community participation into community ownership. With continuous technical support, confidence building, and entrepreneurial mentoring over the years, the Soliga beneficiaries have successfully established and are now independently managing a fully functional multipurpose ornamental nursery in B.R. Hills. This experience demonstrates that when traditional knowledge is meaningfully integrated with scientific interventions and market-oriented opportunities, biodiversity conservation can become a viable pathway for long-term livelihood enhancement. The study highlights a practical and replicable model for transforming biodiversity-rich tribal landscapes into resilient, community-driven bioresource hubs.

OP-3-03

Unlocking the Bio-economic Potential of Biodiversity: A Case of Farmer-Led Conservation of Red-Fleshed Jackfruit in India

Harishkumar H. V.[a] and Ganesan Karunakaran[b]
[a]*Division of Social Sciences and Training, ICAR-Indian Institute of Horticultural Research, Bengaluru*
[b]*Division of Fruit Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru*
*Corresponding author email: harishkumar.hv@icar.org.in

ABSTRACT

Many individual farmers in India play a vital role in conserving agricultural biodiversity by preserving and propagating indigenous plant genetic resources. However, the true societal value of these resources is realized only when they are scientifically characterized, improved, and commercialized. This study documents the conservation of red-fleshed jackfruit by farmers in Karnataka and demonstrates how institutional support from ICAR–Indian Institute of Horticultural Research (ICAR-IIHR) transformed these farmer-conserved genetic resources into commercially viable cultivars through characterization, registration, and large-scale propagation. As a result, red-fleshed jackfruit now occupies 62.9% of the jackfruit cultivation area in Karnataka. Economic analysis revealed that although the cost of cultivation of red-fleshed jackfruit is higher than that of conventional yellow-fleshed varieties, its substantially higher market price results in a net return of ₹5.45 lakh ha^{-1}, compared with ₹3.66 lakh ha^{-1} for yellow-fleshed jackfruit. Discounted cash flow analysis further confirmed its superior financial viability, with higher net present value, internal rate of return, and faster payback period. The commercialization of these cultivars has generated direct economic incentives for conserving farmers through royalty income while significantly enhancing the profitability of commercial growers. Beyond primary production, women-led self-help groups have created additional livelihood opportunities through value addition and processing of red-fleshed jackfruit into diversified products, thereby increasing rural incomes. Consumer surveys indicated high awareness, strong preference, and a willingness to pay a premium for red-fleshed jackfruit owing to its distinctive taste, attractive colour, and nutritional benefits. Nevertheless, constraints such as an underdeveloped supply chain and limited market integration continue to hinder its full commercial potential. Strengthening branding, ensuring a reliable supply chain, promoting value-added products, and exploring export markets could substantially expand market opportunities for this indigenous crop. The study demonstrates that biodiversity conservation by individual farmers, when complemented with scientific validation, institutional support, and market linkages, creates a sustainable bio-economy model that delivers multiplier benefits to society. These include enhanced incomes for conserving and commercial farmers, royalty benefits, employment generation through women-led enterprises, increased availability of nutritious food, and long-term conservation of valuable plant genetic resources. The red-fleshed jackfruit model offers a scalable pathway for integrating biodiversity conservation with livelihood enhancement and sustainable rural development.

Keywords: Farmers' variety, Red fleshed jackfruit, biodiversity conservation, Bio-economy, Livelihood enhancement, Value addition, Consumer preference.

OP-3-04

Integrated Farming Systems as Scalable Biodiversity-Based Livelihood Models: Evidence from Udupi and Shivamogga Districts of Karnataka

Ramya H. R.[1], M. C. A. Devi[2], Subash S.[3] and Naveena N[4]
[1]Scientist, ICAR-IIHR, Bengaluru, [2&3]Principal & Senior Scientist ICAR-SRS-NDRI, Bengaluru,
[4]Data Scientist, Rakuten ltd

ABSTRACT

Integrated Farming Systems (IFS) offer an innovative pathway for sustainable agriculture by integrating complementary farm enterprises that enhance resource-use efficiency, farm profitability, and livelihood resilience. The present study evaluated IFS models in the Coastal (Udupi) and Hilly (Shivamogga) agro-climatic zones of Karnataka. A total of 100 IFS farmers (50 from each district) were selected through random sampling from two taluks in each district, and data on the eight predominant IFS models were analysed for their socio-economic impact.

The predominant IFS models integrated plantation crops (arecanut, coconut and rubber); horticultural crops (banana, mango, jackfruit, pineapple and vegetables); spices and plantation intercrops (black pepper, betel vine, ginger, turmeric, vanilla, nutmeg and cinnamon); livestock enterprises (dairy, sheep & goats and fodder); and, in several farms, cocoa, medicinal and aromatic plants, thereby creating highly diversified production systems. The cropping pattern was predominantly plantation-based multi-tier and mixed cropping, wherein black pepper and betel vine were cultivated on live standards within arecanut and coconut gardens, while banana, pineapple, vegetables, fodder and medicinal plants were grown as intercrops, ensuring year-round resource use and diversified income. Udupi models additionally incorporated fishery and apiary, whereas Shivamogga models exhibited greater integration of field crops (paddy and maize), commercial crops and agroforestry, resulting in enhanced enterprise diversification and efficient recycling of farm resources.

The most successful IFS model in Udupi (Plantation crops + Spices + Horticulture + Commercial crops + Field crops + Dairy + Fodder + Agroforestry + Apiary) generated a net income of ₹14.20 lakh and 830 man-days of employment from a 5-acre farm, while the leading model in Shivamogga (Plantation + Field crops + Horticulture + Spices + Commercial crops + Dairy + Fodder + Sheep & Goat + Agroforestry + Apiary) recorded a net income of ₹12.90 lakh and 770 man-days of employment from a 9-acre farm, demonstrating the economic viability of diversified farming systems. Strong stakeholder linkages in Udupi and moderate linkages in Shivamogga further highlighted the importance of extension support and institutional convergence. The study establishes IFS as a successful and scalable biodiversity-based livelihood model that conserves crop diversity, enhances nutrient recycling through farm residues, and creates opportunities for value addition, employment generation and sustainable bioeconomy. The findings provide a replicable framework for promoting biodiversity-based farming systems in the Western Ghats, contributing to innovation-driven, climate resilience sustainable agricultural development.

Keywords: Integrated Farming System, Bioeconomy, Agrobiodiversity, Livelihood Enhancement, Enterprise Diversification, Udupi, Shivamogga.

OP-3-05

Community-Based Apiculture as a Scalable Livelihood Enterprise for Strengthening Livelihood Security of Smallholder Farm Women in Karnataka

Ramya H. R.[1], Vasanthi C.[2], Bhagyashree S. N.[3] and Balakrishna B.[4]
[1&3]Scientist, [2]Senior Research Fellow, [4]Principal Scientist ICAR-IIHR, Bengaluru

ABSTRACT

Apiculture is a sustainable farm-based enterprise that enhances income, nutrition and ecosystem services while strengthening rural livelihoods. ICAR-IIHR under a DST funded project introduced apiculture as a livelihood intervention among smallholder farm women in panasachowdanahalli and Nayanahalli villages in Chikkaballapura and Kurubrahalli and Ancharahalli villages in Bengaluru Rural districts of Karnataka. The present study evaluated the economic viability of the enterprise and documented farmers' perceptions of its livelihood and ecological benefits.

The study was conducted among ten women beneficiaries using structured interviews, field observations and enterprise-level economic analysis. Continuous technical support was provided through pluralistic extension approaches, including training, demonstrations, diagnostic visits, farmer-scientist interactions, exposure visits and digital advisories. The apiaries were established within diversified horticultural production systems comprising flowering avenue trees such as Pongamia, neem and eucalyptus, plantation crops such as arecanut and coconut, vegetable crops including cucurbits, drumstick, brinjal and chilli and fruit crops including mango, banana, guava, jamun and rose apple. The continuous availability of floral resources contributed to the production of good-quality honey and sustained bee colonies throughout the year.

The enterprise proved economically viable among 10 studied farm women with an average investment of ₹50,000, annual honey production of 380 litres, gross income of ₹1.91 lakh and net income of ₹1.21 lakh, resulting in a Benefit-Cost Ratio of 3.81. Nearly 25% of the profits were reinvested for enterprise expansion, indicating its sustainability. Regular household consumption of honey improved nutritional security, while income from honey and hive products strengthened household livelihoods. Farmers also perceived increased honey bee activity, resulting in improved pollination of nearby horticultural crops (80.00%), better flowering (80.00%), enhanced fruit set (70.00%) and perceived improvements in crop productivity (60.00%). By promoting plant reproduction and increasing the production of fruits and seeds, apiculture also supported agricultural food webs by providing greater food resources for birds, beneficial insects and other organisms, thereby enhancing agroecosystem resilience

Additionally, the intervention also enhanced women's social security, confidence, entrepreneurial orientation and decision-making ability, enabling beneficiaries to evolve from technology adopters to entrepreneurs and community resource persons who encouraged neighbouring farm women to adopt apiculture.

The study demonstrates that community-based apiculture simultaneously generates economic, nutritional, ecological and social benefits. Supported through pluralistic extension approaches and integrated with diversified horticultural farming systems, the intervention offers a practical and scalable model for strengthening women's entrepreneurship, promoting rural bioeconomy and enhancing livelihood security among smallholder farm women.

Keywords: Apiculture, livelihood security, women entrepreneurship, pluralistic extension, pollination services.

OP-3-06

Who Protects the Protectors? Assessing the Awareness of Progressive Farmers on India's Biodiversity Governance and Farmers' Rights Framework

Atheequlla G. A.[1]*, Rohini M. R.[2] and Senthil Kumar R.[3]
[1&3]*Senior Scientist & Principal Scientist, Division of Social Sciences and Training ICAR- Indian Institute of Horticultural Crops, Hesaraghatta, Bengaluru*
[2]*Senior Scientist, ICAR- IIOPR, RC, Palode*
*Corresponding author email: atheeq.agriextn@gmail.com

ABSTRACT

India's rich agrobiodiversity has been conserved by farming communities through the cultivation, selection, and preservation of traditional crop varieties. Progressive farmers have played a significant role in conserving plant genetic resources and promoting sustainable agriculture. To recognize these contributions, the Government of India enacted the Biological Diversity Act (2002), the National Biodiversity Action Plan (NBAP), and the Protection of Plant Varieties and Farmers' Rights Act (PPV&FRA), 2001. However, the effectiveness of these frameworks depends on farmers' awareness and participation. The present study assessed the awareness of progressive farmers regarding the Biological Diversity Act, NBAP, and PPV&FRA, with emphasis on farmers' rights, plant variety registration, protection of traditional knowledge, and access and benefit-sharing mechanisms. A cross-sectional survey was conducted using a structured interview schedule. An awareness index was developed to measure respondents' knowledge across the three policy frameworks, and statistical analyses were employed to identify the determinants of awareness and existing knowledge gaps. The findings revealed substantial disparities in awareness despite the farmers' active role in biodiversity conservation. Awareness was significantly influenced by socio-economic characteristics, institutional linkages, and access to information sources. Critical knowledge gaps were observed in legal provisions, registration procedures, and benefit-sharing mechanisms. The study recommended targeted extension interventions, policy communication strategies, and capacity-building programmes to improve legal literacy among progressive farmers. Integrating biodiversity governance into agricultural extension systems can strengthen farmers' participation in conservation efforts, protect indigenous genetic resources and traditional knowledge, and enhance the effective implementation of national biodiversity policies while promoting sustainable agriculture and livelihood security.

Keywords: Biological Diversity Act, PPV&FRA, National Biodiversity Action Plan, agro biodiversity, progressive farmers, innovator farmers, farmers' rights, biodiversity governance, agricultural extension.

OP-3-07

Global Production–Trade Dynamics and Economic Viability of Avocado (*Persea americana* Mill.): Evidence and Emerging Opportunities from India

Raju R.*, Harish Kumar H. V. and Anbukkani Perumal
Division of Social Science and Training, ICAR–Indian Institute of Horticultural Research (IIHR), Bengaluru, Karnataka, India
*Corresponding author email: rajukrshimoga@gmail.com

ABSTRACT

Avocado (Persea americana Mill.), a nutrient-dense subtropical fruit native to Mexico and Central America, has emerged as one of the fastest-growing horticultural commodities in global trade over the past two decades. This studd examines the global production and trade scenario of avocado, traces its evolving footprint in India, and presents a detailed economic analysis of avocado cultivation based on farm-level data from Karnataka, India. Global area, production and productivity of avocado stood at 8.72 lakh ha, 88.10 lakh tonnes and 10.11 t/ha, respectively, in 2021, with Mexico alone contributing over 29 per cent of world output. Trade remains highly concentrated, with Mexico, Peru and the Netherlands together accounting for about 69 per cent of global exports, while the USA, Netherlands and Spain dominate import demand. In India, where avocado is popularly known as 'butter fruit', cultivated area and import volumes have expanded rapidly, albeit from a small base, with Karnataka, Kerala, Tamil Nadu and Sikkim as the principal growing states. Farm-level economic analysis reveals a total establishment cost of ₹6.20 lakh per acre, an average annual net return of ₹4.23 lakh per acre, a benefit–cost ratio of 3.67, an internal rate of return of 39.96 per cent and a payback period of five years, confirming strong economic feasibility. High initial establishment cost, non-availability of quality planting material, price fluctuation and marketing constraints were identified as the principal barriers to expansion. The paper further synthesises secondary evidence on India's rapidly growing avocado import demand, changing consumption patterns, and untapped agro-climatic potential to outline concrete opportunities for domestic production, processing and value addition, and offers a demand outlook for the Indian avocado sector through the next decade. The findings provide an evidence base for policymakers, investors and horticultural planners seeking to position India within the expanding global avocado economy.

Keywords: *Avocado; economic feasibility; benefit-cost ratio; India; horticultural trade.*

OP-3-08

Unlocking the Potential of *Caryota urens* for Sustainable Agroforestry Systems

B. Augustine Jerard, Sumitha S.*, Beena Singh, Phani Kumar, P. C. Vengaiah and Elizabeth Mathew
ICAR-AICRP on Plantation, ICAR-CPCRI, Kasaragod 671124, Kerala
*Corresponding author email: sumithasundaram12@gmail.com

ABSTRACT

Caryota urens L. (fishtail palm) is an underutilized, multipurpose palm with considerable potential for sustainable agroforestry, biodiversity conservation, and rural livelihood enhancement. In India, the species is widely distributed across the southern states, particularly along the Western and Eastern Ghats, where it occurs naturally in forests and traditional agroforestry systems, often in association with the wild date palm (*Phoenix sylvestris*). *C. urens* is a monocarpic species that remains in the vegetative phase for several years before flowering. Flowering progresses sequentially from the uppermost to the lowermost inflorescences, after which the palm dies. The species is traditionally tapped for its sweet sap (neera), which is processed into jaggery, palm sugar, syrup, and fermented beverages. In addition, it provides edible pith (sago), fibre, timber, leaves for thatching and handicrafts, making it an important resource for rural communities. Beyond its economic importance, *C. urens* plays a significant role in carbon sequestration, soil conservation, biodiversity enhancement, and ecosystem resilience, making it a valuable component of sustainable agroforestry systems. The palm also possesses considerable ethnobotanical significance. In the Bastar region of Chhattisgarh, several tribal communities regard *C. urens* as a culturally significant and sacred tree associated with traditional beliefs and rituals. Furthermore, larvae of the red palm weevil (*Rhynchophorus ferrugineus*) developing in naturally senescent or felled palms are traditionally harvested and consumed as a protein-rich food source. Interestingly, the same insect is one of the most destructive pests of coconut and arecanut plantations, illustrating a unique plant–insect–human interaction. Despite its ecological, cultural, and economic importance, *C. urens* remains an underexplored plant genetic resource. Systematic collection, characterization, conservation, and utilization of its genetic diversity are essential for identifying superior genotypes, strengthening climate-resilient agroforestry systems, conserving indigenous knowledge, and promoting sustainable livelihood opportunities in Peninsular India.

OP-3-09

Demonstration and participatory evaluation of seed spices cultivation in the eastern Ghats of Koraput, Odisha

Ramajayam, Devarajan*, Jotirmayee Lenka, Saubhagya Kumar Samal,
Saswat Kumar Kar, Ashish Khora and Sanjeev Patra
[1]*ICAR-Indian Institute of Soil and Water Conservation, Research Centre, Koraput, Odisha*
*Corresponding author email: ramajayamd@gmail.com

ABSTRACT

India is the largest producer, consumer and exporter of seed spices in the world. Non-traditional areas like Odisha is having suitable climatic conditions during the winter season for the cultivation of these seed spices. Also, introduction and evaluation of improved high-yielding varieties of seed spices and their value addition will be beneficial for the livelihood of tribes dominated farmers. In collaboration with ICAR-NRCSS and funding from Koraput district administration, the ICAR-IISWC, Regional Centre, Koraput Odisha demonstrated cultivation of seed spices *viz*., coriander, fennel, nigella and fenugreek in 70 acres of land covering 153 farmers' fields spread across 20 villages in seven blocks of Koraput district of Odisha.

The participatory evaluation study of coriander in the randomly selected farmers field revealed statistically significant differences in plant height (36.4 to 57.0 cm), No. of branches per plant (5.3 to 7.3), No. of seeds per branches (15.2 to 169) and yield (630.0 to 875.0 Kg/ha) while plant spread (11.5 to 15.6 cm) recorded statistically non-significant. Similarly, fennel recorded significant differences only with respect to number of branches per plant (4.1 to 7.4) and no. of seed per branches (69.7 to 1958.5). However, fenugreek recorded non-significant differences for all the growth and yield parameters. The growth and yield attributes of coriander and fennel were significant across the villages/blocks. Girligumma village recorded highest coriander and fennel yield (kg/ha) of 843.3±33.9 and 1545.0±160.1, respectively while the lowest yield of coriander (630.0±28.3) and fennel (990.0±127.3) was recorded at Sundhiput village. When compared the yield at block level, the highest yield of 843.3±33.9 (coriander) and 1545.0±160.1 (fennel) was recorded in Dasmanthpur and lowest of 727.5±117.3 and 1182.5±238.4) were recorded for coriander and fennel respectively, in Semiliguda. Fennel recorded non-significant differences for both growth and yield traits with respect to farmers/villages/block level. The yield (Kg/ha) of fennel varied between 1260.0 to 1310.0 and 1255.0 to 1317.5 in different farmers and villages/blocks, respectively. Other seed spices like Cumin, Nigella and Ajwain did not perform satisfactorily in the farmers fields.

The performance of seed spices like coriander, fennel and fenugreek were satisfactory as per the participatory evaluation trials in the farmers fields across Koraput district, Odisha. *Jhola* land with irrigation facility during *Rabi* season could be ideal for the cultivation of seeds spices after the paddy harvest.

Keywords: Seed spices, Eastern Ghats, Coriander, Fennel, Fenugreek.

OP-3-10

Characterization of farmers' varieties and their conservation in indigenous minor fruit crops

Anuradha Sane[1]*, Atheequlla G. A.[2] and C. Vasugi[1]
Division of Fruit Crops, Division of Social Sciences, ICAR-IIHR, Bengaluru
*Corresponding author email: anukeerti06@gmail.com

ABSTRACT

Indigenous fruit crops maintained by farmers constitute an important reservoir of genetic diversity and possess unique horticultural traits with significant potential for crop improvement, livelihood enhancement, and biodiversity conservation. The present study aimed to identify and characterize elite farmer-maintained genotypes of indigenous fruit crops exhibiting distinct agronomic and fruit quality attributes. Extensive field surveys were conducted in farmers' orchards and homesteads in different locations in Karnataka to identify superior trees of indigenous fruit crops like Ber and Jamun based on fruit quality, yield, consumer preference, and off season bearing behaviour. The selected crop varieties were characterized using standardized morphological, and biochemical descriptors. The Jamun elite genotype exhibited the unique ability to produce off-season and biannual fruiting with desirable fruit quality, thereby providing an extended harvesting period and improved market opportunities. The Ber farmers' variety exhibited a high sweet-to-acid balance, superior fruit quality, high yield, and served as a major source of livelihood for the farming family. The identified farmer's varieties represent valuable genetic resources with considerable potential for commercial cultivation, breeding programmes, and registration under the Protection of Plant Varieties and Farmers' Rights (PPV&FR) Act. Their conservation and utilization will not only safeguard indigenous fruit diversity but also enhance farmers' income through the promotion of superior locally adapted varieties.

Keywords: In situ evaluation, Farmers' conserved varieties, Fruit yield, fruit quality, *Syzygium cumini, Ziziphus.*

OP-3-11

Exploring the untapped potential of Barleria – an indigenous flower crop for their commercial utility

Safeena S. A., Prerana S., P. Naveen Kumar, Sreenivasa V.,
Arivalagan M., Chandrashekar N. and Chaithra M.
ICAR-Indian Institute of Horticultural Research, Bengaluru
*Corresponding author email: safeenaicar@gmail.com

ABSTRACT

Barleria, being the third -largest genus in Acanthaceae, has received substantial attention from both horticulturists and landscape architects for its ornamental characteristics and its enormous applications in landscaping. This plant serves as the flagship species for ornamental cultivation due to its dense, upright growth habit and prominent, funnel-shaped flowers with striking color variations. Because of the ecological and economic significance of Barleria, and also its medicinal value, it is important to characterize Barleria germplasm in detail. The present study which focusses on investigating the untapped potential of Barleria for its commercial utility was carried out at ICAR–IIHR, Bengaluru during 2023 to 2026. Twenty-six genotypes were characterized based on sixty-three qualitative and quantitative characters under open field conditions in a randomized complete block design with three replications. The evaluation included plant habit, stem features, leaf morphology, thorn characters, inflorescence types, and floral characters. Wide variation was observed in genotypes for the majority of traits examined. Growth habit ranged from erect to spreading types, and pubescence on the stems ranged from glabrous to highly hairy. Leaf shape, leaf size and floral features exhibited great diversity. Flower colours ranged from violet, red, purple, pink, orange and yellow forms, while the size of flowers varied from small to large types. Quantitative characters such as plant height, number of branches, leaf area, flowering period and qualitative characters such as, stem colour, stem hairiness etc. showed statistically significant variation among genotypes. The study showed that there was high morphological diversity in Barleria germplasm collection. This variation in both the qualitative and quantitative traits offers critical data for identifying superior quality genotypes with the preferred characteristics. The extensive dataset generated from the study ascertain both the genetic diversity and associated phenotypic characters, for conservation, utilization, and identification of elite lines with superior ornamental and medicinal traits in Barleria.

OP-3-12

Tapping the nutritional potential of karonda - a lesser known opportunity fruit by easily adoptable processing techniques

S. Bhuvaneswari* G. C. Sathisha and Anuradha Sane
ICAR-Indian Institute of Horticultural Research, Bengaluru
*Corresponding author email :bhuvanaiihr@gmail.com

ABSTRACT

Karonda (*Carissa carandas* L.), a member of the Apocynaceae family, is an evergreen, spiny shrub widely distributed across India. It is well-suited to arid and semi-arid tropical regions. It thrives on marginal and wastelands, making it ideal for low-input cultivation. Karonda is rich in iron and vitamin C. Its antiscorbutic properties and used in treating anaemia and supporting overall health. Mature fruits are highly valued in the international market for making jelly, jam, squash, sauce, and syrup. In order to harness the nutritive potential of this future fruit, research was conducted at ICAR-IIHR to convert karonda fruit into karonda fruit powder by standardization of drying techniques using tray drying and spray drying method. Pulp extraction, drying conditions for tray and spray drying methods and pulverization protocol for processing karonda fruit were optimized using standard procedures. Physico chemical properties of karonda powder were analysed as per standard methods. It was found from the studies that the average powder yield of karonda from tray drying method and spray drying methods were 12% and 11% respectively. Spray dried karonda powder had higher retention of Iron (6.9%) Zinc (23.86%) Vitamin C (39.25%) Flavonoids (27.64%) and antioxidants (8.07%) calcium (6%) and magnesium(23.86%) than tray dried karonda powder. Hence this, bright purple coloured karonda powder rich in nutrition can be used as natural food colourant alternative to the unpermitted synthetic colour prohibited by Food Safety and Standards Regulations 2011.

POSTER PRESENTATIONS

PP-3-01

Promoting the Competitiveness of Underutilized Fruits: Nutritional Analysis of Indigenous and Exotic Fruits in India

T. R. Rupa*, Anuradha Sane and P. C. Tripathi
ICAR-Indian Institute of Horticultural Research, Hesaraghatta Lake post, Bengaluru – 560 089, Karnataka
*Corresponding author email: sairupa.tr@gmail.com

ABSTRACT

Underutilized fruits are highly nutritive with medicinal attributes. They are a rich source of vitamins, minerals, fats, proteins, and dietary fiber. The underutilized fruit crops have not received adequate research attention in their mineral composition. This study, conducted at the ICAR-Indian Institute of Horticultural Research over five years (2020-21, 2021-22, 2022-23, 2023-24 and 2024-25), aimed to assess the accumulation of macro-elements *viz.,* nitrogen ((N), phosphorus (P), potassium (K), calcium (Ca), magnesium (Mg), and sulphur (S); and micro-elements *viz.,* iron (Fe), manganese (Mn), copper (Cu), and zinc (Zn) in indigenous and exotic underutilized fruits. The trees were planted in 2006, and the study included 22 underutilized fruits: Bael, Wood-apple, Rose-apple, Mountain-Sweet-Thorn, Loquat, Egg-fruit, Rough-lemon, Pumello, Surinam-cherry, West-Indian-cherry, Amla, Soursop, Milk-fruit, Rough-lemon, Tree-tomato, Jackfruit, Ceylon-Olive, Strawberry-Guava, Kokum, Karonda, Bilimbi and Lasoda. Data analysis revealed significant differences among the fruits in terms of mineral nutrients content. The fruits were rich in K, N, Ca, and Mg, but had relatively low levels of S and P. Among the micro-elements, Fe was the most abundant, while Cu was the least abundant. The highest nitrogen content (>1.0%) was found in Bilimbi, Lasoda, Wood-apple and Bael fruits. Red Kokum (E1-R17PI) had the highest phosphorus content (1.47%). The fruits with the highest potassium content were Soursop P-1 (4.8%), Bael (4.6% and 4.4%), Lasoda B-2 (4.5%) and Amla R1P30 (4.4%). Karonda-R7P10, Bael-P1 and Soursop fruits were very rich in calcium (>4.0%). Karonda-R7P10, Bael-P1 and Ceylon-Olive fruits had high magnesium content (>0.80%). Manila Tamarind, Bael, Wood-apple, and Strawberry-Guava fruits had relatively higher sulfur content (>0.20%). Underutilized fruits offer a wide range in the micronutrient content to choose and use as a dietary source of minerals. The Fe content was highest in bael (587.6 ppm) and the lowest was recorded in Yellow Kokum-R16P1 (11.8 ppm). The Mn content ranged between 103.3 ppm in bael and loquat to 0.1 ppm in Yellow Kokum-R16P1. The Zn content on the other hand ranged between 415.6 ppm in loquat to

3.91 ppm in Karonda-R3P1. The Cu content varied from 198.1 ppm in bael to 0.11 ppm Karonda-R3P1. The results demonstrated that certain underutilized fruit cultivars contain higher levels of minerals compared to ranges reported in international studies on other types of commercial fruits. This indicates that these underutilized-fruits possess higher nutritional value and greater health benefits than their commercial counterparts.

Keywords: Mineral nutrients, underutilized fruits, exotic fruits.

PP-3-03

Leveraging livelihoods through participatory research: a case of Lakshmana Tamarind selection

Atheequlla G. A.[1], G. Karunakaran[2], Kanupriya[3], Senthil Kumar R.[4]
[1&4]*Scientist & Principal Scientist, Division of Social Sciences and Training*
[2&3]*Principal Scientists, Division of Fruit Crops*
ICAR- Indian Institute of Horticultural Crops, Hesaraghatta, Bengaluru
*Corresponding author email: atheeq.agriextn@gmail.com

ABSTRACT

Participatory research has emerged as an effective approach for identifying and validating superior horticultural genetic resources while ensuring farmer participation in technology development and dissemination. The present study highlights the successful identification and promotion of the tamarind (Tamarindus indica L.) selection 'Lakshamana', developed through participatory selection involving researchers of ICAR-Indian Institute of Horticultural Research (ICAR-IIHR) and a progressive farmer from Nandihalli village, Tumakuru district, Karnataka. The study aimed to identify a superior tamarind accession with enhanced yield, fruit quality, and livelihood potential through on-farm evaluation and farmer participation.The selected accession exhibited significantly superior performance over local tamarind types, recording a mean annual yield of 251.4 kg tree^{-1}, compared to 165.0 kg tree^{-1} in local trees. It produced long, curved pods (25.4 cm × 3.8 cm) with only 24 pods kg^{-1}, indicating larger fruit size. The variety recorded an impressive 43% pulp recovery, substantially higher than the 28% observed in local types, with low fibre content (5%) and attractive light-brown pulp preferred by consumers. Nutritional profiling revealed 29.78% total sugars, 20% acidity, and 18.61 g 100 g^{-1} tartaric acid, confirming its superior processing quality.The participatory approach extended beyond varietal selection to livelihood enhancement through primary processing and value addition. Harvesting coincides with the agricultural lean season (February–April), creating off-season employment opportunities for farm families. Processing 15–20 kg of pods per day can generate an income of approximately

₹400 per person per day. In addition, processed pulp, seeds, and shell fetch remunerative prices, with seeds sold at ₹17 kg^{-1} and shell chips at ₹2.50 kg^{-1}, thereby maximizing returns from the produce.The Lakshamana tamarind selection demonstrates how participatory research can bridge scientific innovation with farmer knowledge to identify high-value genetic resources that enhance productivity, promote value addition, generate rural employment, and improve livelihood security. The approach provides a scalable model for farmer-centric varietal selection and commercialization of underutilized horticultural crops, contributing to sustainable agriculture and rural prosperity.

Keywords: Tamarind, Participatory Research, Farmer Participation, Variety Selection, Rural Livelihoods, Horticultural Innovation, Technology Dissemination, Genetic Resources.

PP-3-04

Screening of different genotypes of jackfruit (*Artocarpus heterophyllus* Lam.) for the preparation of different beverages and its storage stability

Yadav Shivani Indrajeet[1]* and Dr. Sanjay Pathak[2]
[1]*Ph.D. Scholar (Fruit Science), Department of Horticulture, B.A.C.A. Anand agricultural University, Anand*
[2]*Retd. Dean, COH&F, Acharya Narendra Deva University of Agriculture and Technology*
*Corresponding author email: shivaniyadav0499@gmail.com

ABSTRACT

A comprehensive investigation was conducted at the MES Horticulture, Department of Fruit Science, College of Horticulture and Forestry, Acharya Narendra Deva University of Agriculture and Technology during 2022–2023. The investigation comprised three experiments, and the data were analyzed under a Completely Randomized Design (CRD) with three replications.

The primary objective of this research was to screen different genotypes of Narendra Jackfruit for the preparation of various beverages and assess their storage stability. Different genotypes were evaluated for fruit characteristics and chemical qualities. NJ-4 exhibited maximum fruit weight, length, and diameter; fruit weight, length, and diameter ranged from 3.74-19.00 kg, 22.67-58.27 cm, and 14.77-26.33 cm, respectively. Rind and pulp percentages ranged from 21.76-41.11% and 22.41-46.04%, respectively, with NJ-5 exhibiting the minimum rind percentage. The number of seeds ranged from 46.66 - 219.66 per fruit, with maximum seeds observed in NJ-4. NJ-15 exhibited the best chemical attributes, with the significantly highest TSS (30° Brix). TSS, reducing sugars, acidity, and total sugars across genotypes ranged from 16.00 - 30.00° Brix, 5.19-6.81%, 0.20-0.35%, and 15.40-23.52%, respectively.

The study investigated the development of a blended ready-to-serve (RTS) drink prepared from different jackfruit genotypes using a 70:30 ratio of jackfruit juice to aloevera juice. Genotype NJ-15 was found most suitable for the blended RTS drink. During a 3-month storage study, the RTS drink exhibited slight increase in TSS, acidity, and sugar content, while non-reducing sugars, ascorbic acid, and organoleptic scores declined. Overall, product quality remained acceptable throughout the storage period.

Additionally, Jaffee, a coffee like beverage prepared from jackfruit seeds, as a potential substitute for commercial coffee. Two preparation methods, 1. boiled-roasted and 2. sundried-roasted were compared. Organoleptic evaluation revealed that Jaffee resembled commercial coffee in color, aroma, and texture, with the boiled-roasted method yielding superior results. Genotype NJ-6 was identified as the most promising for Jaffee production using the boiled-roasted method, while NJ-5 was suitable for the sundried-roasted method. NJ-6 was recommended for commercial Jaffee production based on organoleptic score, and higher seed count. These findings have important implications for the cultivation, processing, and commercialization of jackfruit and its derived value added products.

Keywords: *Jackfruit, Artocarpus heterophyllus, genotype evaluation, Jaffee, ready-to-serve drink, value added products, beverage.*

PP-3-06

Engineering Climate-Resilient Forest Restoration: A Hydrogel–Microbial–Biostimulant Approach for Timber Sapling Establishment

Samwel Debbarma, Barun Rai, Pritiprasanna Samanta,
Mohd. Asif Idrisi, Subhash Chandra Pradhan and Lingaraj Sahoo
Department of Biosciences and Bioengineering, IIT Guwahati, Guwahati-781039

ABSTRACT

Climate change, land degradation, and persistent water scarcity increasingly constrain forest restoration efforts by reducing the post-transplantation survival and establishment of tree saplings. In India, inadequate soil moisture retention, declining soil fertility, and disruption of beneficial rhizosphere microbial communities remain major barriers to the success of large-scale afforestation programmes. These challenges are particularly severe in the semi-arid landscapes of Deoghar, Jharkhand, where harsh climatic and edaphic conditions restrict the establishment of rare, endangered, and commercially valuable timber species. The present study evaluates an integrated, bio-augmented soil-conditioning framework designed to improve sapling survival, growth, physiological performance, and ecological establishment under moisture-limited conditions. The framework combines a water-retaining hydrogel with a multifunctional microbial consortium comprising Azotobacter, arbuscular mycorrhizal fungi, Streptomyces, and Trichoderma, supplemented with a plant biostimulant. The hydrogel functions as a localized soil-water reservoir, enhancing moisture retention and maintaining water availability within the rhizosphere during intermittent drought periods. It also provides a supportive matrix for the gradual release and persistence of beneficial microorganisms and bioactive compounds in the root zone. The microbial consortium is expected to promote biological nitrogen fixation, nutrient mobilization, root development, stress tolerance, disease suppression, and improved soil biological activity. Concurrently, the biostimulant may enhance plant metabolic activity, nutrient-use efficiency, antioxidant defence, and acclimation to environmental stress. The synergistic interactions among the hydrogel, beneficial microorganisms, and biostimulant are anticipated to provide greater restoration benefits than individual soil amendments by simultaneously addressing water limitation, nutrient deficiency, rhizosphere dysfunction, and transplant stress. This integrated strategy represents a holistic and potentially scalable approach to climate-resilient afforestation. Its application could improve timber sapling establishment, reduce transplant mortality, enhance resource-use efficiency, and accelerate ecosystem rehabilitation in degraded and water-limited landscapes. The framework may therefore contribute to the development of sustainable, biologically supported restoration practices for strengthening the long-term effectiveness of plantation and forest recovery programmes.

PP-3-07

Field Evaluation of LEAFENERGY Biostimulant for Enhancing Growth, Yield, Quality, and Drought Tolerance in Tomato and Chilli under the Arid Conditions of Jharkhand

Barun Rai*, Samwel Debbarma, Pritiprasanna Samanta, Mohd. Asif Idrisi,
Deepak Kumar, Subhash Chandra Pradhan and Lingaraj Sahoo
Indian Institute of Technology Guwahati
*Corresponding author email: barun.rai@iitg.ac.in

ABSTRACT

Excessive dependence on chemical fertilizers remains a major challenge in modern agriculture, particularly in high-value vegetable crops such as tomato (*Solanum lycopersicum* L.) and chilli (*Capsicum annuum* L.). Although conventional fertilizers supply essential nutrients and support crop productivity, their prolonged and indiscriminate use can deteriorate soil health, reduce nutrient-use efficiency, disrupt ecological balance, and produce diminishing yield benefits. Plant biostimulants offer a promising complementary approach for improving crop performance while reducing dependence on excessive chemical inputs. The present field study evaluates the efficacy of the commercial biostimulant LEAFENERGY in improving the growth, yield, quality, and stress resilience of tomato and chilli under the agroclimatic conditions of Deoghar, Jharkhand. The experiment comprises eight treatment combinations: an untreated control, the recommended NPK fertilizer treatment, NPK supplemented with 1.0% LEAFENERGY, and five foliar concentrations of LEAFENERGY—0.125%, 0.25%, 0.50%, 0.75%, and 1.0%. This dose-response design is intended to determine the optimal application concentration and assess the potential interaction between LEAFENERGY and conventional fertilization. Biostimulant efficacy is being assessed through an integrated evaluation of phenotypic, physiological, biochemical, yield-related, and molecular parameters. Plant growth and productivity are monitored using plant height, number of branches, stem diameter, leaf area, flowering behaviour, fruit characteristics, and final yield. Physiological performance following foliar application is evaluated through photosynthetic efficiency, total chlorophyll content, Water Band Index, Plant Senescence Reflectance Index, and Photochemical Reflectance Index. Fruit quality and metabolic responses are examined by estimating total soluble sugars, organic acids, carotenoids, and antioxidant capacity. Molecular analyses are additionally being undertaken to identify the regulatory mechanisms associated with biostimulant-induced improvements in plant performance and stress adaptation. The study is expected to establish an effective and agronomically suitable concentration of LEAFENERGY for tomato and chilli cultivation. The findings will provide field-level evidence regarding its potential to enhance crop productivity and nutritional quality, improve physiological resilience, increase nutrient-use efficiency, and reduce excessive dependence on chemical fertilizers under the agroclimatic conditions of Jharkhand.

THEME - 4
Decoding Diversity for Sustainable Use

ORAL PRESENTATIONS

OP-4-02

Introgression of anthracnose fruit rot resistance from C. *baccatum* into C. *annuum* using marker-assisted genetic bridge strategy

Pasupula Karishma[1], Sriram S.[2], Sandeep Kumar G. M.[2], Madhavi Reddy K.[1], Lakshamanareddy D. C.[3], Manoj B. P.[1], Mahebub Shaik[1], Sai Timmarao[3] and Naresh Ponnam[1*]

[1] *Division of Vegetable Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, India.*
[2]*Division of Crop Protection, ICAR–Indian Institute of Horticultural Research, Bengaluru, Karnataka, India.*
[3]*Siksha O Anusandhan University, Bhubaneshwar, Orissa, India.*

ABSTRACT

Chilli (*Capsicum annuum* L.) is an important vegetable-cum-spice crop grown extensively in tropical and subtropical regions across the globe. India is the largest producer, consumer, and exporter, with production of approximately 5.36 million metric tonnes (MT) of green chilli and 2.64 million MT of dry chilli (NHB, 2024–25). Chilli contributes significantly to the Indian economy, accounting for about 39.8% of total spice exports, with earnings of USD 1.37 billion during 2023–24 (Spices Board). Anthracnose fruit rot, caused by *Colletotrichum truncatum* and *C. gloeosporioides*, leads to yield losses of up to 80%, particularly during fruit ripening and storage. Fungicide application at the ripening stage raises food safety concerns, making host plant resistance a sustainable and eco-friendly solution. Resistance sources have been identified in *Capsicum baccatum* (PBC80, PBC81) and *C. chinense* (PBC932). However, interspecific incompatibility between *C. baccatum* and *C. annuum* restricts direct gene transfer. The present study employed a genetic bridge-cross strategy using *C. chinense* to introgress anthracnose fruit rot resistance from *C. baccatum* (PBC81) into *C. annuum* (IIHR-B-HP-A21). Viable F_1 hybrids derived from *C. annuum* × *C. chinense* were crossed with *C. baccatum* to generate a three-way hybrid (TWH), which was subsequently backcrossed to *C. annuum* to develop the BC_1-TWH population. The progenies exhibited variation in floral morphology and reproductive traits, including corolla spot intensity, petal colour, pollen viability (5–51%), and embryo abortion. Artificial inoculation with *C. truncatum* (Ct1 isolate) at red-ripe stage and *C. gloeosporioides* (Cg1 isolate) at green stage revealed phenotypic variation ranging from highly resistant to susceptible. Foreground selection using seven SSR markers showed resistance allele detection accuracy of 70–82%, while background selection indicated 79.05% genome recovery of the recurrent parent (*C. annuum*). The three-way bridge-cross strategy IIHR-B-HP-A21 (*C. annuum*) × IIHR-4652 (*C. chinense*)] × PBC81 (*C. baccatum*) achieved a cross-compatibility index of 93%. Marker-assisted backcrossing enabled effective introgression of QTLs associated with anthracnose fruit rot resistance. BC_1-TWH plants carrying both target QTLs were identified through foreground selection, while background SSR analysis and phylogenetic assessment revealed that BC_1-TWH-4, BC_1-TWH-57, and BC_1-TWH-66 were closely aligned with *C. annuum*, indicating high recurrent parent genome recovery. Advancement to BC_2 and screening under natural epiphytotic conditions led to identification of five progenies (BC_2TWH-7, BC_2TWH-17, BC_2TWH-33, BC_2TWH-40, and BC_2TWH-43) exhibiting 0% disease severity index (DSI), indicating strong resistance. This study demonstrates effective utilization of wild *Capsicum* genetic resources for broadening the genetic base of cultivated chilli and developing anthracnose-resistant lines through genomics-assisted breeding. The identified pre-bred lines hold significant potential for varietal development and sustainable disease management.

Keywords: *Capsicum*, plant genetic resources, anthracnose fruit rot resistance, genetic bridge-cross, marker-assisted selection, interspecific hybridization.

OP-4-03

Unlocking the Breeding Potential of Maldandi Sorghum Landraces: Phenotypic Diversity, Yield Stability, and Adaptation Across Post-Rainy Seasons

Parashuram Patroti[1]*, C. Aruna[2], B. Amasiddha[2], Baswaraj Raigond[1], T. Nepolean[2] and C. Tara Satyavathi[2]
[1]*ICAR-Indian Institute of Millets Research, Regional station, Centre on Rabi Sorghum, Shelgi, Solapur, Maharashtra - 413006, India*
[2]*ICAR-Indian Institute of Millets Research, Rajendranagar, Hyderabad, Telangana - 500030, India*
*Corresponding author email: parashuram@millets.res.in

ABSTRACT

Maldandi sorghum landraces represent a unique and invaluable reservoir of genetic diversity that has evolved through generations of farmer-led selection under the moisture-limited and stress-prone environments of peninsular India. Renowned for their superior grain quality, excellent chapati-making characteristics, fodder value, and adaptation to post-rainy season cultivation, these landraces hold immense potential for broadening the genetic base of rabi sorghum breeding programs. However, comprehensive information on their phenotypic diversity, yield stability, and breeding utility remains limited. The present study evaluated 136 maldandi sorghum landraces at the ICAR–Indian Institute of Millets Research, Centre on Rabi Sorghum, Solapur, Maharashtra, India, across three consecutive post-rainy seasons (2022–2024) to assess genetic variability, adaptation, and breeding potential for key agronomic and yield-related traits. Pooled analysis of variance revealed highly significant genotypic and environmental effects for all traits, indicating substantial variability within the germplasm and a strong influence of seasonal conditions. Grain yield per plant exhibited the highest variability (CV = 49.81%), reflecting considerable scope for selection, whereas 100-seed weight showed comparatively low variability and greater stability across environments. Principal component analysis indicated that the first two principal components explained 59.44% of the total variation and revealed strong positive associations among grain yield, plant height, and fodder yield, suggesting opportunities for simultaneous improvement of grain and biomass productivity. Hierarchical cluster analysis grouped the landraces into distinct divergent clusters, highlighting broad phenotypic diversity and the availability of genetically diverse parental material. AMMI analysis identified several stable and widely adapted landraces, including EP16, EP87, EP81, EP13, and EP91 for grain yield, and EP92, EP45, EP60, and PU29 for fodder yield. The study demonstrates that maldandi landraces possess rich adaptive diversity, stable performance, and significant breeding value, making them strategic genetic resources for developing climate-resilient, high-yielding, and farmer-preferred post-rainy season sorghum cultivars under changing climatic conditions.

Keywords: Maldandi sorghum landraces, phenotypic diversity, genotype × environment interaction, yield stability, AMMI analysis, post-rainy season sorghum breeding.

OP-4-04

Assessment of bioactive constituents in *Garcinia indica* (Kokum for its potential as a nutraceutical source of hydroxycitric acid, anthocyanins, and phenolics

Pritee Singh*, T. K. Roy, C. Kanupriya[1], P. C. Tripathi[1] and K. S. Shivashankara
Division of Basic Sciences, ICAR-Indian Institute of Horticultural Research (IIHR), Hessarghatta Lake Post, Bengaluru 560089, Karnataka, India.
[1]Division of Fruit Crops, ICAR-Indian Institute of Horticultural Research (IIHR), Hessarghatta Lake Post, Bengaluru 560089, Karnataka, India.
*Corresponding author email: pritee.siingh@gmail.com

ABSTRACT

The growing demand for natural ingredients in the food and pharmaceutical sectors has stimulated interest in indigenous and underexploited fruits and vegetables as alternative sources of valuable bioactive compounds. *Garcinia indica* is one such species that has attracted attention because of its traditional medicinal importance and promising phytochemical profile. The present study aimed to comprehensively characterize the bioactive constituents of *Garcinia indica* fruits, with particular emphasis on hydroxycitric acid, anthocyanins, and phenolic compounds. Metabolite profiling of the ripe fruit rind was carried out using liquid chromatography–mass spectrometry (LC–MS). The analysis revealed a high concentration of hydroxycitric acid, ranging from 15.60% to 22.92%, indicating the potential of the fruit as a natural source for weight-management formulations. The fruit rind also contained substantial levels of anthocyanins (4.47–7.08 mg g^{-1}), exceeding those commonly reported in many fruits and vegetables and suggesting its suitability as a natural food colorant. In addition, the elevated phenolic content highlights the antioxidant potential of the fruit. A total of 38 anthocyanin compounds were identified, several of which are reported here for the first time. The predominant anthocyanins were cyanidin-3-sambubioside, peonidin-3-arabinoside, and pelargonidin-3-glucoside. Furthermore, 30 individual phenolic compounds were characterized, among which ortho/para-coumaric acid, narinenin, and apigenin were particularly abundant and possess significant industrial relevance. Two-way hierarchical clustering and heat-map analysis enabled the identification of superior accessions for specific bioactive compounds. Overall, the findings demonstrate that *Garcinia indica* is a rich and sustainable source of hydroxycitric acid, anthocyanins, and phenolic compounds, with considerable potential for applications in the food, nutraceutical, pharmaceutical, and allied industries.

OP-4-05

Harnessing Wild Relatives of Pearl Millet Conserved at the ICRISAT Genebank for Grain Quality and Disease Resistance Traits

Vetriventhan M.*, Deekshitha B., Jagadeesh K., Naresh D., Rajan Sharma and Kuldeep Singh
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT),
Patancheru - 502324, Hyderabad, Telangana, India.
*Corresponding author email: Vetriventhan.mani@icrisat.org

ABSTRACT

Pearl millet improvement increasingly requires novel genetic variation to enhance nutritional quality and resilience to major biotic stresses under changing climatic conditions. Crop wild relatives (CWRs) constitute an invaluable reservoir of novel alleles for broadening the narrow genetic base of cultivated crops. Pre-breeding enables the introgression of genes for productivity, nutritional quality, and climate resilience traits from wild species into cultivated backgrounds. The ICRISAT genebank conserves the world's largest collection of pearl millet, including 859 wild-species accessions representing diverse taxa and eco-geographical regions, providing an invaluable resource for pre-breeding and trait discovery. Systematic characterization and evaluation of *Pennisetum glaucum* subsp. *monodii* have identified valuable donor accessions for grain quality traits and disease resistance. Screening identified promising sources of high grain protein, low rancidity, and blast and downy mildew resistance. To convert these trait sources into usable pre-breeding material, promising inbreds were developed by selfing individual plants from selected wild-species accessions using the single-seed descent method. Inbreds derived from wild species accessions such as IP 21628 and IP 21656 for high grain protein (~18-20%), IP 21662 and IP 21772 for low rancidity (low Acid Value), and IP 21987 and IP 22160 for resistance to blast and downy mildew showed promising potential for trait improvement. These inbreds are now being used for trait introgression and genetic mapping studies. Overall, the findings demonstrate that pearl millet CWRs conserved at the ICRISAT Genebank represent a largely untapped reservoir of novel alleles for improving grain quality and resistance to major diseases. Integrating systematic conservation, targeted phenotyping, pre-breeding, and genomic tools will accelerate the development of climate-resilient, nutrient-rich pearl millet cultivars to support sustainable agricultural productivity and food security.

Keywords: Crop wild relatives, food security, protein, millets, pre-breeding, Genetic Stocks.

OP-4-06

Integrative Multi-Omics Analysis Combining Meta-QTL, Comparative Genomics and Meta-Transcriptomics Reveals High-Confidence Candidate Genes for Heat Tolerance in Tomato (*Solanum lycopersicum* L.)

Abhishek V. Karadagi[1,2], H. C. Prasanna[3]*, Shivashankaragouda Patil[1],
S. A. Desai[4], P. L. Patil[5], T. K. Behera[6]

[1]*Ph. D Scholar, Department of Genetics and Plant Breeding, UAS, Dharwad, Karnataka*

[2]*Research Scholar, Division of Vegetable Crops, ICAR-IIHR, Bengaluru, Karnataka*

[3]*Principal Scientist and Head, Division of Vegetable Crops, ICAR-IIHR, Bengaluru, Karnataka*

[4]*Dean (Agri) and Campus Head, College of Agriculture, Hanumanmatti, UAS, Dharwad, Karnataka*

[5]*Former Vice- Chancellor, UAS, Dharwad, Karnataka*

[6]*Director, ICAR-IIHR, Bengaluru, Karnataka*

*Corresponding author email: prasannahc@yahoo.com

ABSTRACT

Heat stress is a major environmental constraint limiting tomato (*Solanum lycopersicum* L.) productivity, particularly during reproductive development, by adversely affecting pollen viability, fruit set and yield. Although numerous quantitative trait loci (QTLs) associated with heat tolerance have been reported, their practical utilization in breeding has been hindered by inconsistent genomic positions, broad confidence intervals and limited validation across independent studies. To overcome these limitations, we employed an integrative multi-omics strategy combining meta-QTL (MQTL) analysis, comparative genomics and meta-transcriptomics to identify stable genomic regions and high-confidence candidate genes associated with heat tolerance. A total of 112 heat tolerance-related QTLs from seven independent studies were compiled, of which 69 QTLs were successfully projected onto a high-density consensus genetic map comprising 10,375 markers. Meta-analysis identified 10 MQTLs distributed across chromosomes 1, 2, 4, 7 and 8, reducing the average confidence interval by 2.24-fold relative to the original QTLs. Several MQTLs co-localized with previously reported genome-wide association study (GWAS), genomic regions, providing independent genetic support for their stability and biological relevance. The MQTL regions encompassed 1,649 annotated genes, of which 79 high-confidence candidate genes were prioritized through integration with published plasticity QTL (pQTL) candidate genes. Comparative transcriptomic analysis at reproductive stage further identified 32 conserved heat-responsive genes consistently differentially expressed under heat stress, strengthening candidate gene prioritization. Gene Ontology enrichment analysis revealed significant enrichment of genes involved in DNA replication, cell-cycle regulation, transcriptional regulation, protein degradation, intracellular transport, hormone signalling and cellular homeostasis. Comparative genomic analysis between the heat-tolerant genotype E42 and the heat-susceptible cultivar MoneyMaker identified three prioritized non-coding sequence variants associated with selected candidate genes. Furthermore, promoter sequence analysis revealed a putative cis-regulatory polymorphism resulting in the predicted gain of a Dof (DNA-binding with One Finger) transcription factor binding site in the promoter of *Solyc04g080710*, suggesting a potential regulatory mechanism

underlying heat tolerance. Overall, this integrative multi-omics framework provides robust MQTLs, high-confidence candidate genes and regulatory variants that constitute valuable genomic resources for functional validation, marker development and genomics-assisted breeding of climate-resilient tomato cultivars.

Keywords: Heat tolerance; meta-QTL; pQTLs; meta-transcriptomics; Climate resilience breeding; genomics-assisted breeding.

OP-4-07

Screening of Pepper Germplasm for Heat Tolerance to Identify Promising Donors

Prakash Singathiya, Smaranika Mishra*, Laxman R. H., Naresh Ponnam,
Prasanna H. C. and Lakshmana Reddy D. C.
ICAR-Indian Institute of Horticultural Research, Bengaluru, 560 089, India
*Corresponding author email: mishrasmaranika@gmail.com

ABSTRACT

In the present scenario of global climate change, frequent occurrence of heat stress significantly affects the reproductive phase of pepper cultivation, exhibiting substantial yield loss. To mitigate this challenge, the current study was designed to evaluate pepper genotypes for their response under heat stress and control conditions. The objective was to identify donor lines for heat tolerance and to pinpoint the important traits linked to stress resilience. Significant variability was observed among the genotypes for physiological, biochemical, and yield-related parameters. Heat stress significantly affected each trait compared to the control condition. Correlation analysis revealed a positive association between physiological and biochemical parameters observed in the vegetative phase, while they were negatively correlated with the reproductive parameters. Reproductive parameters such as pollen viability, pollen germination, pollen tube growth, fruit set percentage, and healthy seed set percentage exhibited strong positive inter-correlations under heat stress. Further, the Principal Component Analysis (PCA) biplot identified the genotypes AVPP9905, CHT3-2, and EC-1118086 as highly heat-tolerant with excellent reproductive parameters. Cluster analysis further confirmed the role of pollen parameters in conferring heat stress tolerance. The heat-tolerant genotypes identified in this study are valuable genetic resources for the improvement of heat tolerance in pepper.

OP-4-08

Exploring TOPLESS-RELATED PROTEIN 3 (TPR3) as a Genome Editing target for Fusarium Wilt resistance in Banana

ABSTRACT

Fusarium wilt, caused by *Fusarium oxysporum* f. sp. *cubense* (Foc), poses a major threat to global banana production. Successful infection depends on the secretion of effector proteins, including Secreted in Xylem (SIX) proteins, which manipulate host cellular processes to facilitate disease development. TOPLESS (TPL) and TOPLESS-RELATED (TPR) proteins are conserved transcriptional co-repressors that regulate hormone signaling pathways associated with plant growth, development, and immunity. To investigate their potential role in banana–Foc interactions, bioinformatics analyses identified conserved LisH, CTLH, CRA, and WD40 domains in Musa TPL/TPR proteins and revealed strong evolutionary conservation and synteny across diverse plant species. Protein–protein docking using HADDOCK predicted a stronger interaction between the Foc effector SIX1 and banana TPR3 than with SIX6, suggesting that TPR3 may serve as a potential host target during Fusarium infection. The TPR3 gene was isolated from banana cv. Neypoovan, and sequence analysis confirmed its identity through BLAST. These findings identify TPR3 as a promising candidate for functional characterization and precision genome editing to disrupt effector–host interactions while preserving native gene function. This study provides a foundation for developing durable Fusarium wilt resistance in banana through targeted manipulation of host susceptibility mechanisms.

OP-4-09

Harnessing Crop Wild Relatives for Improving Grain Protein Content in Sorghum

Hari Haran R.[1,2], Jagadeesh K.[1], Deekshitha B.[1], Naresh D.[1], Vetriventhan M.[1]* and Kuldeep Singh[1]

[1]*International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru - 502 324, Hyderabad, Telangana, India.*

[2]*Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore - 641003.*

*Corresponding author email: Vetriventhan.mani@icrisat.org

ABSTRACT

Malnutrition remains one of the most pressing global health challenges, affecting nearly two billion people worldwide, with over one billion people having chronically insufficient protein intake, and remains a major nutritional concern. It is particularly prevalent in regions where cereal grains are the primary staple food. As cereals provide a substantial share of the daily diet for a large proportion of the global population, improving their nutritional quality, particularly grain protein content, offers a sustainable strategy for addressing malnutrition. Plant-derived proteins account for nearly 65%

of global dietary protein intake and are the primary, and often the sole, source of protein in many developing countries. Among cereal crops, Sorghum [*Sorghum bicolor* (L.) Moench], the world's fifth most important cereal after wheat, rice, maize, and barley, serves as a staple food for millions of people across Africa and Asia. In these regions, sorghum grain is extensively utilized for both human consumption and livestock feed, underscoring its significance in ensuring food and nutritional security. Grain protein content is a key nutritional quality trait in sorghum for both food and feed. Its improvement primarily depends on the assessment and effective utilization of genetic variability available in germplasm resources. Evaluation of grain protein content in over 240 wild-species accessions of sorghum conserved at the ICRISAT Genebank revealed significant variability, ranging from 12% to 21%, with a mean of 16%. A selected set of high-protein accessions was subsequently validated at two nitrogen levels, leading to the identification of stable high-protein wild-species accessions. These accessions represent valuable genetic resources for sorghum improvement and provide promising donors for breeding programs aimed at introgression of favorable alleles into cultivated backgrounds to develop nutritionally enhanced sorghum cultivars.

Keywords: Sorghum, Grain protein, Crop wild relatives, Genetic variability.

OP-4-10

"Genome-Wide Dissection of Adaptive Loci and Candidate Genes for Early Seedling Establishment under Moisture Deficit in Durum Wheat"

Shashank H. G.[1], Sherry Rachel Jacob[2]*, Manoj Kumar Patel[2], Jyoti Kumari[2], Krishnan P. Abhijith[3], Arun Kumar M. B.[1], Sundeep Kumar[2], Rakesh Bharadwaj[2], Rahul Gajghate[4], Jayaluxmi Devi Khumukcham[1], R. S. Priyanga[1] and Kiran Dasanal[2]

[1]*ICAR–Indian Agricultural Research Institute (IARI), New Delhi, India*

[2]*ICAR–National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India*

[3]*ICAR–Indian Agricultural Research Institute (IARI), Assam, India*

[4]*ICAR–Indian Agricultural Research Institute (IARI), Regional Station, Indore, Madhya Pradesh, India*

*Corresponding author email: sherryracheljacob@gmail.com

ABSTRACT

India is the world's second-largest producer of durum wheat (*Triticum turgidum* ssp. *durum*), predominantly cultivated in the rainfed, arid, and semi-arid regions of Peninsular India, where moisture deficit frequently constrains crop establishment and productivity. Early seedling vigour traits, including coleoptile length (CL), root length (RL), root number (RN), and root angle (RA), are critical determinants of seedling establishment, water acquisition, and drought adaptation. However, the genetic architecture governing these adaptive traits remains inadequately understood, limiting the effective utilization of durum wheat plant genetic resources.To decipher adaptive genomic diversity, a genome-wide association study (GWAS) was conducted using a diversity panel of 250 genetically

diverse durum wheat genotypes evaluated under control and 12% PEG-6000-induced moisture-deficit conditions across Delhi, Indore, and Jodhpur. Moisture stress significantly reduced CL (9–10 to 6–7 cm), RL (14 to 9–11 cm), RN (5.0 to 4.2–4.7), and RA (41° to 29–38°). Genome-wide association analysis identified 102 significant marker–trait associations (MTAs), including 12 stable adaptive loci across environments. Stable loci on chromosomes 6B, 5A, 3B, and 7B revealed key candidate genes, including *TRITD6Bv1G054010 (PSKR1)* regulating peptide signalling and coleoptile elongation, TRITD5Av1G103660 (SCL3) and *TRITD5Av1G103710 (RING Finger Protein 10)* governing gibberellin signalling and root architecture, *TRITD3Bv1G102340 (MADS-box Transcription Factor 3)* associated with root development, and *TRITD7Bv1G027130 (β-Glucosidase 24)* and *TRITD7Bv1G027250 (Thioredoxin-like Protein)* involved in ABA signalling and redox homeostasis. These findings decode adaptive genomic diversity conserved in durum wheat germplasm and provide robust molecular resources for marker-assisted selection, functional genomics, and genomics-assisted breeding, facilitating the sustainable utilization of plant genetic resources for developing climate-resilient durum wheat cultivars adapted to the moisture-deficit agroecosystems of Peninsular India.

Keywords: *Durum wheat,GWAS, moisture deficit, early seedling vigour, adaptive loci, candidate genes.*

OP-4-11

Characterization and evaluation for morpho-biochemical traits of soursop (*Annona muricata* L.) genotypes from western ghats

Roopendra Kumar[1], Anuradha Sane[1]*, Muralidhara B. M.[2],
Vasugi C.[1], Pushpa Chethan Kumar[1], Laya P.[1] and Nishant[1]
[1]*ICAR-Indian Institute of Horticulture of Research, Hessaraghatta-Bengaluru - 560089*
[2]*ICAR- IIHR- Central Horticultural Experiment Station, Chettalli, Kodagu - 571248, Karnataka*
*Corresponding author email: anusane@rediffmail.com

ABSTRACT

Soursop (*Annona muricata* L.) is an underutilized tropical fruit tree valued for its nutritional and medicinal properties. Soursop plants are traditionally cultivated through seeds which has resulted in wide variability with respect to morphological and biochemical traits. The present study aimed at *In-situ* characterization and evaluation of soursop genotypes collected from Kodagu and Dakshina Kannada districts in Karnataka and Wayanad in Kerala. A total of 12 selected genotypes were assessed for morpho-biochemical attributes to understand the extent of variability present. Significant variation was observed in fruit characteristics *viz.,* fruit size, fruit weight, pulp percentage, and seed content. The biochemical attributes including total soluble solids (TSS), acidity and total acetogenin content also exhibited considerable variation among the genotypes. Based on the evaluation, the genotype RK/MBM-1 has been identified for high pulp recovery (82.44%) and genotype RK-2 was found highest in total soluble solids (18.56°B) coupled with low acidity content (0.53%). However, genotype RK/MBM-4 was found highest in total acetogenin content (1.46 mg/g dw) whereas lowest

was recorded in RK/MBM-1 (0.34 mg/g dw). The identified unique genotype has potential for future crop improvement and commercial utilization. The study highlights the importance of conserving local soursop germplasm and provides baseline information for selecting promising genotypes suitable for cultivation, value addition, and genetic enhancement programs in the region.

Keywords: Soursop, Kodagu, Wayanad, variability, genotype.

OP-4-13

Enhancing Banana Genetic Diversity via Chromosome Doubling

Kalpana Sathiamoorthy[1]*, Backiyarani Suthanthiram[1], Raju Karthic[1], S. Uma[1] and R. Selvarajan[1]
[1]*Crop Improvement Division, ICAR-National Research Centre for Banana,*
Tiruchirappalli, Tamil Nadu - 620102, India
*Corresponding author email: ramajayamkalpana@gmail.com

ABSTRACT

Banana breeding is significantly constrained by limited genetic diversity, sterility barriers, and complex polyploid genetics, restricting the development of improved cultivars with resilience to biotic and abiotic stresses. Diploid bananas, particularly those with AB and BB genomic constitutions, represent untapped reservoirs of valuable traits including fruit quality, vigour, and stress tolerance. However, their direct utilization in hybridization is limited by narrow ploidy compatibility. Chromosome doubling provides a powerful strategy to overcome these constraints and expand the genetic resource base available for breeding. In the present study, chromosome doubling was induced in elite AB (Kunnan), AA (cvRose & Pisang Lilin) and BB (Athiakol) diploid bananas using optimized *in vitro* oryzalin treatments. Putative tetraploids were identified through a combination of morphological screening, stomatal analysis, and flow cytometry. The induced tetraploids exhibited distinct phenotypic traits including increased leaf and stomatal size, reduced stomatal density, thicker and broader leaves, and enhanced overall vigour, confirming successful ploidy enhancement and clear differentiation from diploid controls. These new tetraploid lines are now being evaluated for fertility restoration and use as bridge parents to generate improved triploid hybrids. The study demonstrates the role of induced polyploidy as an efficient tool to **broaden usable genetic diversity** and enable hybrid development pathways that support **sustainable banana improvement.** The tetraploid resources developed represent a valuable addition to breeding programmes targeting seedless, high-yielding, and climate-resilient triploid cultivars.

Keywords: Banana, Chromosome doubling, Polyploidy, AB and BB diploids, Genetic diversity, Flow cytometry, Sustainable breeding.

OP-4-14

Multi-Trait Selection Reprograms Metabolic and Transcriptional Networks Underlying Cis-Trans Nepetalactone Enrichment in Catmint (*Nepeta cataria* L.)

Gunjan Tiwari[1]*, Trishna Chaturvedi[1], Yash Pandey[1] and Anil Kumar Gupta[1]
[1]*Division of Plant Breeding and Genetic Resource Conservation, CSIR-Central Institute of Medicinal and Aromatic Plants, P.O. CIMAP, Lucknow, India*
*Corresponding author email: gunjantiwari.cimap@csir.res.in

ABSTRACT

Catmint (*Nepeta cataria* L.) is an economically important medicinal and aromatic plant valued for its essential oil, particularly the bioactive iridoid monoterpene cis-trans nepetalactone (CTN). Despite its commercial importance, the genetic and molecular mechanisms governing CTN improvement through breeding remain largely unresolved. In this study, we integrated quantitative genetics, metabolomics, transcriptomics, and molecular marker discovery to elucidate the biological basis of CTN enrichment in a half-sib breeding population evaluated across four cycles of recurrent multi-trait selection. Selection simultaneously improved biomass, essential oil yield, and CTN content, while correlation analyses revealed strong positive relationships among CTN, oil yield, oil content, and leaf biomass, demonstrating that phytochemical enhancement can be achieved without compromising plant productivity. BLUP-based selection indices consistently identified NCS3 as the superior genotype and NCS15 as the contrasting low-performing genotype. Comparative metabolomic profiling revealed extensive reprogramming of amino acid, carbohydrate, organic acid, and terpenoid metabolism associated with CTN accumulation. Transcriptome analysis further identified coordinated upregulation of genes involved in carbon metabolism, stress adaptation, redox homeostasis, and iridoid biosynthesis, including GES, G8H, ISY/CYC2, NEPS, and MLPL, in the elite genotype. Integrated gene–metabolite network analysis highlighted NEPS1, MLPL, and P5CS as central regulatory hubs linking primary metabolism with CTN biosynthesis, whereas co-expression analysis identified MYB124, NAC56, and WRKY23 as candidate transcriptional regulators of iridoid metabolism. Furthermore, transcriptome-derived SSR and SNP markers associated with key biosynthetic and regulatory genes provide valuable genomic resources for marker-assisted breeding. These findings demonstrate that multi-trait selection reprograms the metabolic and transcriptional networks that underlie CTN enrichment, providing mechanistic insights and genomic tools to develop high-value catmint cultivars and advance the genetic improvement of medicinal and aromatic plants.

Keywords: *Nepeta cataria*; catmint; BLUP; selection index; nepetalactone; stereoisomers; transcriptomics; metabolomics; omics-assisted breeding.

OP-4-15

Exploring Genetic Diversity for Nutritional and Biochemical Traits in Curry Leaf (*Murraya koenigii* L. Spreng) Genetic Resources

B. R. Raghu*, G. Chethan Kumar and K. S. Nandini
Division of vegetable Crops, ICAR-IIHR, Bengaluru
*Corresponding author email: ragubr@gmail.com

ABSTRACT

Curry leaf (*Murraya koenigii* L. Spreng), an aromatic and nutritionally important leafy spice of the family Rutaceae, is valued for its culinary, medicinal, and industrial uses. However, comprehensive information integrating nutritional and biochemical diversity remains limited. This study evaluated the genetic variability of ten mineral nutrients, essential oil (EO) yield, and EO composition in 80 curry leaf accessions conserved ex situ at the ICAR–Indian Institute of Horticultural Research (ICAR-IIHR), Bengaluru, India. The accessions were collected from diverse agro-ecological regions, including the Western Ghats, Himalayan region, and other parts of India.

Substantial genotypic variation was observed for all traits, demonstrating rich nutritional and biochemical diversity. Calcium (0.30–5.97%), potassium (0.09–3.52%), and phosphorus (0.11–0.77%) were the predominant macronutrients, whereas iron (51.71–439.16 ppm) and boron (26.02–143.38 ppm) exhibited the greatest variation among micronutrients. High phenotypic and genotypic coefficients of variation, high heritability (>70%), and substantial genetic advance indicated strong prospects for genetic improvement through selection. Significant positive correlations among calcium, magnesium, copper, and manganese suggested opportunities for simultaneous enhancement of multiple nutrients. Principal component analysis explained 73.04% of the total variation, while cluster analysis grouped accessions into three major clusters reflecting genetic and geographical differentiation. Essential oil analysis revealed extensive biochemical diversity. Cultivated accessions exhibited significantly higher EO yield than wild types. A total of 80 volatile compounds, comprising six major and 74 minor constituents, were identified. Among the major compounds, α-pinene, γ-terpinene, and α-selinene were highly variable and contributed to chemotype differentiation, whereas trans-caryophyllene and α-humulene predominated across accessions. Regional associations of valencene and γ-terpinene, together with higher concentrations of α-pinene, bornyl acetate, and camphene in wild accessions, indicated the influence of geography and domestication on EO composition. Four major chemotypes were identified, including three reported for the first time in curry leaf.

Elite accessions, including IC652403, IC652419, IC652461, and IC652517, combined superior mineral nutrition with desirable biochemical attributes, representing valuable genetic resources for biofortification, chemotype-based selection, and the development of nutritionally enriched, high-quality curry leaf cultivars. This study provides the first integrated assessment of mineral nutrient and essential oil diversity in Indian curry leaf germplasm.

Keywords: *Murraya koenigii; ex situ conservation; mineral nutrients; essential oil; chemotypes; genetic diversity; heritability; biofortification*.

OP-4-16

Marker-Assisted Selection for Fusarium Wilt Resistance in Gladiolus progenies

Priya Bhusaraddi[1,2]*, P. Nandeesha[2], Priti Sonavane[2] and T. Usha Bharathi[2]
[1]*ICAR- Indian Agricultural Research Institute, New Delhi - 110012, India*
[2]*ICAR- Indian Institute of Horticultural Research, Bengaluru- 560089, India*
*Corresponding author email: bhusaraddipriya@gmail.com

ABSTRACT

Gladiolus is a popular bulbous ornamental crop, stands out for its majestic appearance and radiant colours. The 220 gladiolus progenies derived from 4 different cross combinations were evaluated for morphological traits and Fusarium wilt resistance. *A total of 24 resistance gene analogue (RGA) markers are used to screen the 12 parental gladiolus genotypes and RGA marker* GhRGA10 *exhibited polymorphism. The polymorphic marker generated 2 alleles with an average polymorphic information content (PIC) value of* 0.42*. Marker-trait association analysis identified* GhRGA10 *marker significantly associated with Fusarium wilt resistance with the LOD score value of 12. Resistant genotypes consistently amplified the allele with size 120bp, whereas, susceptible genotypes lacked the corresponding allele.* F-test and T-test for alleles exhibited highly significant differences with the moderate recombination frequency (9.83 to 15) and higher prediction efficiency (85.00% to 90.17%), suggests the moderate linkage between the marker and trait. *Along with markers assisted selection,* multi-trait genotype–ideotype distance index (MGIDI) analysis identified superior progenies by simultaneously considering the morphological, yield and disease resistance traits. Progenies with the lowest MGIDI values exhibited the closeness to the ideotype and 32 progenies were identified as the most desirable candidates for utilization in further varietal screening. The identified GhRGA10 marker can be used as an efficient tool for marker-assisted selection for future gladiolus breeding programmes aimed at wilt resistance.

Keywords: RGA Markers, *resistance gene analogue*, Fusarium wilt, resistance, MGIDI.

OP-4-17

Trait-Specific Characterization of Sweet Potato Germplasm for Identification of Superior Genetic Resources and Breeding Utilization

C. Visalakshi Chandra*, Shirly Raichal Anil, K. M. Senthilkumar, J. Sreekumar, T. Makeshkumar, S. Amalnath, P. S. Shameer, A. R. Anjitha, Senthil Muthukrishnan, and Pooja Krishnan
ICAR-Central Tuber Crops Research Institute, Sreekaryam, Thiruvananthapuram, Kerala, India
*Corresponding author email: visalakshi.ctcri@gmail.com

ABSTRACT

Sweet potato (*Ipomoea batatas* L.) is a versatile, climate-resilient root crop valued for its high productivity, adaptability to diverse agro-ecological conditions, and nutritional richness as a source of complex carbohydrates, dietary fibre, vitamins, and β-carotene. With an annual global production of 93.51 million tonnes, it is one of the world's most important tuber crops. In India, it is widely cultivated in the eastern and southern regions and is popularly known as the "poor man's rich food" owing to its affordability and nutritional value. Fifty sweet potato accessions were characterized using 30 morphological descriptors following the IPGRI descriptor. Significant variability was observed for all traits across two seasons, indicating substantial phenotypic diversity. UPGMA cluster analysis grouped the accessions into six major clusters and sixteen sub-clusters. Accessions S1403, S1462, and S1803 were highly divergent with unique morphological features, whereas S1436, S1439, S1440, S1441, S1455, S1511, S1526, S2075, and S2079 exhibited high similarity. Yield evaluation conducted with the released variety Sree Arun as the check, identified S1695 as the highest-yielding accession (26.42 t ha^{-1}), followed by S2086 (23.12 t ha^{-1}), S1686 (19.00 t ha^{-1}), and S1455 (17.86 t ha^{-1}), all significantly outperforming the check. Boiled tuber evaluation based on consistency, texture, and sweetness identified S1514, S1695, and S1456 as superior cooking types. The mean dry matter content was 21.28%, while S1686, S2076, S1433, and S1455 recorded >35%, indicating their suitability for processing. Weevil screening identified 18 accessions with <10% tuber damage, indicating tolerance to sweet potato weevil. Virus indexing revealed Sweet potato feathery mottle virus (SPFMV) as the most prevalent virus, detected in 45 accessions, followed by Sweet potato leaf curl virus (SPLCV) in 10 accessions and Sweet potato chlorotic stunt virus (SPCSV) in three accessions. The study identified promising trait-specific germplasm combining high yield, superior cooking quality, high dry matter, weevil tolerance, and distinct morphological diversity. These accessions represent valuable donor parents for sweet potato breeding and provide an important genetic resource for developing high-yielding, nutritionally superior, pest tolerant, and end use specific cultivars, while also supporting efficient germplasm conservation and utilization.

Keywords: Sweet potato, characterisation, weevil resistance, breeding.

OP-4-19

Evaluation of Toxicity in *C. angustifolia*: A Potent Source for Antibacterial Drug

N. Krishna Radhika[1]*, V. S. Keerthana[1], P. Murugesan[1], P. S. Sreejith[2], and C. V. Sandhya[2]
[1]*ICAR Central Tuber Crops Research Institute*
[2]*Multidisciplinary research Unit Govt. Medical College, Thiruvananthapuram*
*Corresponding author email: krishna.rn@gmail.com

ABSTRACT

Curcuma angustifolia (East Indian arrow root) is a rhizomatous crop that comes under the family Zingiberaceae, used traditionally for nutritional and medicinal purposes due to its phytochemical composition and rich starch content. It commonly known as East Indian arrowroot , and is consumed as a food, rather than spice. Its starch is used in preparation of burfi, pudding etc, and consumed by people at times of fast, when they avoid eating cereals. The *C. angustifolia* is having antibacterial effects. The extract prepared from C. angustifolia, showed antibacterial effects towards an range of bacteria including methicillin resistant *S. aureus*. In order to develop a drug from *C. angustifolia*, it is essential to evaluate its toxicity, and the level of lethality. The present study assesses the toxicity in the methanolic extract of two variants of *C. angustifolia,* namely IC 641835 and Chhattisgarh Tikhur-1, using zebrafish (*Danio rerio*) as the model organism. The rhizomes of both plants are dried and powdered to make the methanolic extract, and stock solutions are made with DMSO for the embryo exposure. The fertilised zebrafish embryos were exposed to various extract concentrations ranging from 200 to 1600 µg. The parameters such as survival and mortality, hatching rate, heart rate and developmental abnormalities were observed and recorded at 24, 48, 72, 96, 120 and 144 hours post-fertilisation. Both the plant extracts possess the embryos of normal growth and development at low to moderate concentrations (200–1200 µg). However, there was a clear concentration-dependent embryotoxic effect recorded at the higher concentration of IC 641835, which caused complete embryo mortality, but Chattisgarh Tikhur-1 did not show any effect at the same concentration, indicating accession-specific variation in toxicity. These findings depict that *C. angustifolia* extracts are generally safe within a low to moderate dosage range but exhibit accession-dependent toxicity at elevated concentrations, underscoring the need for dose-dependent studies for future pharmaceutical or nutraceutical applications related to these species.

Keywords: *Curcuma angustifolia*, genetic resource, antimicrobial effect, toxicity, Zebrafish.

OP-4-20

Evaluation and Identification of Trait-Specific Foxtail Millet Germplasm for Climate-Resilient Breeding

P. B. Manjunatha[1]*, Sunil Shriram Gomashe[1] and K. Venkatesan[2]
[1]*ICAR–National Bureau of Plant Genetic Resources (ICAR-NBPGR), RS Akola -444104, India*
[2]*ICAR–National Bureau of Plant Genetic Resources (ICAR-NBPGR), RS Thrissur -680656, India*
*Corresponding author email: pb.manjunatha@icar.org.in

ABSTRACT

Foxtail millet (*Setaria italica* (L.) P. Beauv.) is one of the oldest domesticated crops and is known for its highly valued for nutritional traits, stress tolerance, enormous seed production, potential bioenergy source and ability to grow in unfavourable semi-arid regions of Southern India. This diploid panicoid crop plant has short life cycle, performs C_4 type of photosynthesis. Landraces represent valuable plant genetic resources due to their regional adaptation and the presence of unique alleles that confer tolerance to adverse environmental conditions under local farming systems. However, genetic diversity within these resources has been declining in recent years because of genetic erosion. We hypothesized that foxtail millet germplasm collected from semi-arid climatic regions harbors novel alleles that can be exploited to develop climate-resilient, high-yielding foxtail millet cultivars. Keeping in view, there is an urgent need for conservation of genetic resources. This study was initiated to explore the phenotypic diversity and identify trait-specific germplasm for agronomic traits from heterogeneous mixture of foxtail millet accessions collected from farmer fields. One ninety accessions together with seven checks were evaluated for eight descriptors at two agro-ecologically diverse locations in India during the 2024 & 2025 rainy season. The experiment was conducted in an augmented block design with one of the seven checks repeated after every five-test entries at other locations. The accessions showed significant diversity in all the studied traits. A number of diverse germplasm accessions with agronomically (1000 seed weight and earliness superior traits) were identified for use in foxtail millet breeding. We identified accessions IC97194 (3.31g), IC97189 (3.11g) and IC120247 (2.62g) and that showed outstanding 1000 seed weight and accessions IC22221 (39days), IC120167 (43days) and IC328860 (44days) were earlier in flowering as compared to checks. A significant phenotypic diversity observed in the accessions indicates a diverse gene pool that can be utilized effectively by breeders or researchers for the selection of diverse parents for breeding cultivars and the development of mapping populations.

Keywords: Genetic resources. Germplasm evaluation. Phenotypic diversity.

OP-4-21

Harnessing Wild Genetic Resources: Conservation, Characterisation and Utilisation of Wild Accessions for Broadening the Genetic Base and Climate-Resilient Agriculture in Rice

Divya Balakrishnan[1]*, P. Magudeeswari[1], G. Pranay[1], K. S. Naresh[1], Amurutharao[1], V. Santosh[1], V. Sandeep[1], T. Saketh[1], N. Nagamani[1], S. Suriya[1], P. Swetha[1], D. Saiprasanna[1], S. Michelle[1], T. Kishore[1], R. Priya[1], Y. G. Ravi[1], Y. Yogendra[1], N. Sarla[1], S. V. Sai Prasad[1] and M. Sreenivas Prasad[1]

[1]*ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad, Telangana, India*

*Corresponding author email: Divya.Balakrishnan@icar.org.in

ABSTRACT

Wild relatives harbour a wealth of novel alleles governing economically important traits, including tolerance to biotic and abiotic stresses, enhanced resource-use efficiency, and improved nutritional quality. These untapped genetic resources have become increasingly important for developing climate-resilient crop varieties capable of sustaining productivity under rapidly changing environmental conditions. Domestication has considerably narrowed the genetic base available to plant breeders by eliminating much of the diversity present in wild relatives and reducing the gene pool in most crop species. ICAR–Indian Institute of Rice Research (IIRR), Hyderabad, maintains one of the largest collections of wild Oryza germplasm in India, representing a valuable reservoir of novel genetic diversity for rice improvement. The collection comprises more than 400 accessions belonging to 23 wild Oryza species, conserved in two dedicated wild rice gardens. These accessions have been assembled through extensive collections from diverse agro-ecological regions of India and through international introductions from the International Rice Research Institute (IRRI). Comprehensive characterisation of the wild germplasm has been undertaken for agro-morphological traits, along with systematic phenotyping for key physiological and biotic stress-related traits and photosynthetic efficiency. The institute also serves rice researchers across the country by sharing the wild species and their derived pre-breeding materials for breeding programmes. To facilitate genomic characterization and allele mining, wild accessions have been genotyped using a 1K SNP marker platform as well as for major reported genes for yield, biotic stress, quality and. Interspecific hybridisation has been successfully accomplished using *Oryza nivara*, *O. rufipogon*, *O. glaberrima*, and *O. barthii* as donor species in the genetic backgrounds of popular cultivars. These efforts have resulted in the development of advanced backcross populations, chromosome segment substitution lines (CSSLs), and diverse mapping populations. These genetic resources are being extensively characterized and shared with the national and international research community for the discovery of novel genes and quantitative trait loci governing agronomically important traits, including yield, nutrient-use efficiency, resistance to biotic and abiotic stresses, and grain quality. This pre-breeding programme also resulted in the release of four high-yielding, nutrient-use-efficient varieties, DRRRdhan65, DRRdhan74, DRRdhan88 and DRRdhan99. The integration of wild genetic diversity into cultivated rice through pre-breeding provides a robust foundation for developing climate-resilient, high-yielding rice varieties to address future food security challenges.

Keywords: Wild Oryza; Wild rice germplasm; Genetic diversity; Pre-breeding; Allele mining; Climate resilience.

OP-4-23

Exploring Heterozygosity for Genetic Diversity and Trait Improvement in Grapes

Roshni R. Samarth*, Anuradha Upadhyay, Pushpa Aher,
Vidya Mane, Komal Thorat and Indu Sawant
ICAR-National Research Centre for Grapes, Pune
*Corresponding author email: sroshnir@gmail.com

ABSTRACT

Grape is a highly heterozygous perennial fruit crop, providing immense genetic variability for breeding. The grape breeding programme at ICAR–National Research Centre for Grapes was initiated to develop downy mildew-resistant cultivars possessing superior commercial traits. Since both disease resistance and fruit quality traits are quantitatively inherited, understanding the extent of genetic variability is essential for effective selection. A total of 125 F_1 hybrids were developed from the cross Seyve Villard-12375 × Thompson Seedless. The population exhibited a near-normal distribution for downy mildew reaction on the 1–9 UPOV rating scale, confirming the quantitative nature of resistance. Among the hybrids, 23 were classified as highly resistant or resistant, 58 as moderately resistant, and 44 as susceptible. The population was further evaluated for 19 commercially important bunch and berry traits. Moderate genotypic variability (GCV: 10–20%) coupled with high heritability (>60%) was observed for berry diameter, berry length, bunch length, must recovery, pedicel length, and peduncle length. High variability (GCV: >20%) together with high heritability (>60%) was recorded for bunch weight, bunch width, berry firmness, number of berries per bunch, acidity, berry weight, ramification length, and seed weight. The combination of high genetic variability and high heritability indicates that these traits are predominantly governed by genetic factors and can be effectively improved through phenotypic selection. The extensive genetic variability present in this segregating population enabled the simultaneous selection for downy mildew resistance and superior bunch and berry traits, leading to the identification of elite recombinants with high commercial potential. One such hybrid, Manjari Madhura, was identified as a dual-purpose grape variety for both table and raisin use. It combines moderate resistance to downy mildew with high yield, attractive coloured berries, and naturally bold berry size (>18 mm in length and diameter) without the need for gibberellic acid application for berry enlargement. The variety also possesses high pulp content and total soluble solids (TSS), resulting in superior raisin recovery (25–27%). The successful development of Manjari Madhura demonstrates the effective exploitation of heterozygosity and genetic variability to combine disease resistance with desirable fruit quality traits, underscoring the potential of targeted selection for developing high-yielding, climate-resilient grape cultivars with enhanced market value.

Keywords: Grape; *Vitis vinifera*; Downy mildew resistance; Genetic variability; Heritability; GCV; Quantitative resistance.

OP-4-24

Coconut Genetic Resources-Status and Prospects in Breeding for Climate Resilience and Industrial Applications

V. Niral[1]*, Y. Diwakar[2] and K. B. Hebbar[1]
[1]*ICAR-Central Plantation Crops Research Institute, Kasaragod, Kerala, India*
[2]*ICAR-CPCRI Research Centre, Kidu, Karnataka, India*
*Corresponding author email: niral.v@icar.org.in

ABSTRACT

Coconut productivity is increasingly constrained by climate change with prolonged droughts, rising temperatures, salinity, cyclones, and evolving pest and disease pressures, necessitating the development of cultivars with enhanced resilience and stable productivity. Further, increasing global recognition of coconut as a nutraceutical crop, necessitates the development of varieties suitable for industrial applications. As a perennial crop with long breeding cycle, coconut requires breeding strategies that combine adaptation, yield, resource-use efficiency and product quality. This necessitates a better understanding of physiological and biochemical mechanisms contributing to higher productivity, resource use efficiency, stress tolerance, and nutritional quality and screening germplasm resources to identify trait-based donor lines for development of climate resilient and processable varieties. India has established a robust crop improvement programme, exploiting indigenous and exotic germplasm through selection, hybridization and multi-location evaluation. ICAR- Central Plantation Crops Research Institute (ICAR-CPCRI) hosts the NAGS for plantation crops, and conserves a vast assemblage of coconut, cocoa and arecanut germplasm in field gene banks. The institute has a large repository of over 464 accessions, representing germplasm of major coconut growing regions across the world viz., South Asia, Southeast Asia, Africa, the Caribbean Islands, Indian Ocean Islands, and Pacific Ocean Islands. Further, the International Coconut Genebank for South Asia& Middle East (ICG-SAME), hosted by India is located at ICAR-CPCRI, Research Centre, Kidu, ICG-SAME conserves designated regenerated germplasm from India, germplasm from regional member countries as well as the Indian Ocean region and contributes to enhancing international cooperation in germplasm conservation for posterity. Characterization of the germplasm resources has resulted in development of descriptors and identification of trait-specific donor lines and release of 24 improved varieties suitable for diverse production systems and market needs. These include varieties with tolerance to drought, root (wilt) disease, eriophyid mite as well improved nitrogen-use efficiency. Integration of high throughput phenotyping of germplasm with multi- omics can help in better understanding of plant responses to climate stress, precise identification of adaptive traits and trait-specific donor lines and help accelerate development of climate resilient varieties, thereby strengthening sustainability and global competitiveness of the plantation crops sector.

Keywords: germplasm, abiotic/biotic stress tolerance, varietal development, product diversification, NAGS, ICG-SAME.

OP-4-25

Genetic Diversity Studies for Yield, Nutritional Quality and Powdery Mildew Resistance in Sunflower (*Helianthes annuus* L.)

N. Nagamani[1], D. Malarvizhi[2]*, R. Saraswathi[2], R. Sasikala[3] and S. Harish[3]
[1]*Centre for Plant Breeding & Genetics, TNAU, Coimbatore*
[2]*Department of Plant Genetic Resources, Tamil Nadu Agricultural University*
[3]*Department of Oilseeds, Tamil Nadu Agricultural University*
*Corresponding author email: dmalarvizhi@tnau.ac.in

ABSTRACT

Genetic improvement in sunflower genotypes for yield and its contributing characters is very essential to meet the growing demands. But sunflower production is highly affected by various biotic stresses, among which powdery mildew is of significant concern. In the present study, 100 sunflower germplasm along with five checks IR6, PM 81, COSF10B, COSF15B, CSFI 99 were evaluated during *rabi* 2024-25, using augmented block design, for 12 biometric traits and various morphological traits as per DUS descriptors. Hypocotyl anthocyanin pigmentation was strong in 58 genotypes. Except CB IHE 250-1 and CB EC 421078 -1 (lanceolate), other genotypes displayed cordate leaf shape and green leaves, with varying levels of blistering and serration. drooping leaf orientation, petiole pigmentation, stem pigmentation and disk florets with variation in stigma pigmentation. Pollen was yellow across all genotypes and bract shapes consistently rounded without pigmentation. Head shapes varied, with convex being the most common, with branching types positioned below the central head in 24 accessions. Seed coat colour ranged from grey to black, with stripes. Seed shapes were mostly ovoid, either wide or elongated. D^2 statistics grouped the sunflower germplasm into seven clusters with Cluster I having highest number of genotypes (61), followed by Clusters II and III. Seed yield per plant ranked first and contributed 21.54% to genetic divergence, followed by oil yield (18.98%) and leaf size (8.88%). Further the first four principal components accounted for 63% of the total variability, the first component primarily associated with the key traits, seed yield, head diameter, oil content and plant height, the second focused on phenological traits and the third component encompassed volume weight and 100-seed weight. Screening for powdery mildew under field and greenhouse conditions identified 19 resistant accessions CB-IHE 250-1, CB-EC 421078-1, CB-NO.179/6-1, CB-GMU 1032, CB-GP 85, CB-ACC 142-1, CSF1 5205, IR 6, PM81, CB-PS 1049-1, CB-CSF1 5095, CB-GP 118-1, CB-NO.88-8, CB-IHE 269-1, CB-IB 119, CB-GMU-386, CB-GMU-470, CB-GMU-451 and CB-GMU-401 with notable resistance (less than 25% disease incidence). High protein content (24.62%) and oil content (35.50%) was found in PM 81, while CB-IB-62 had the lowest protein (19.56%) but higher oil content (39.70 %). Notably, the results indicated that as the oil content increased, there was reduction in protein content. The study resulted in the identification of 14 accessions as trait specific germplasm for high yield (>35g/plant), five accessions for high oil content (40-43%) and 22 genotypes for high 100-seed weight (>6g). The accession PM 81 had high protein (24.62%) and oil content (35.50%), can be employed for developing protein rich, powdery mildew-resistant hybrids. Therefore, these promising accessions can serve as foundational material for the genetic improvement of sunflower.

Keywords: Sunflower germplasm- Genetic divergence-Yield traits-Nutritional traits- Powdery mildew resistance.

OP-4-26

Molecular Insights into Charantin and B-Carotene Biosynthesis in Bitter Gourd (*Momordica charantia* L.): Gene Expression Dynamics and Metabolite Profiling

Banoth Tharun[1], Gograj Singh Jat[1]*, Manisha Mangal[1], Vishal Sunartiya[1], Sachin Kumar[1], Rakesh Bhardwaj[2], Naveen Singh[1], Jeetendra Kumar Ranjan[1], Avinash Tomer[1], Deepak Singh[3] and Tusar Kanti Behera[4]

[1]*ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi 110012, India*

[2]*ICAR-National Bureau of Plant Genetic Resources, New Delhi 110012, India*

[3]*ICAR- Indian Agricultural Statistics Research Institute, New Delhi 110012, India*

[4]*ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, 560089, India*

*Corresponding author email: singhgograj@gmail.com

ABSTRACT

Bitter gourd is recognized for its anticancer and antidiabetic properties, largely attributed to charantin, and is also a rich source of carotenoids, including β-carotene. In this study, considerable variation was observed in both the accumulation and gene expression patterns associated with charantin and β-carotene biosynthesis across diverse genotypes. PVGy-201 exhibited the strongest gene expression profile, with the highest transcript levels for five key genes, including *McIDI* (~16,493-fold), *McPMK* (~694-fold), and *McSE* (~466-fold), which corresponded with the maximum charantin content (38.53 µg/g FW). Similarly, DBGS-2 showed elevated expression of *McHMGR1* (~271-fold) and *McMK* (~13-fold), supporting its high charantin accumulation (35.27 µg/g FW). The wild species *Momordica balsamina* demonstrated strong expression of *McHMGR2* and *McSE*, consistent with charantin content of 29.36 µg/g FW. For β-carotene, DBGS-21-06 recorded peak expression of *McPSY* (~17.2-fold), *McZDS* (~4.9-fold), and *McCHXB* (~2.8-fold), aligning with high carotenoid levels at both edible (18.46 µg/g FW) and ripening (52.31 µg/g FW) stages. Pusa Rasdar showed elevated expression of *McZEP* (~6.9-fold) and *McPDS* (~10.8-fold), correlating with maximum carotenoid content (19.49 µg/g FW at edible stage and 55.66 µg/g FW at ripening). DBGS-100-0 expressed *McLCYE1* (~2.9-fold) and *McLCYE2* (~3.1-fold), with high carotenoids (15.91 µg/g FW) at the edible stage. Collectively, PVGy-201 and DBGS-2 were identified as promising candidates for charantin enrichment, while DBGS-21-06 and Pusa Rasdar emerged as superior for β-carotene accumulation. These genotype-specific insights provide a molecular framework to support marker-assisted selection, transcriptome-based screening, and metabolic engineering for the development of nutritionally enhanced bitter gourd cultivars with stable metabolite profiles.

Keywords: Bitter gourd, gene expression, charantin, β-carotene, metabolites.

OP-4-27

Collection, Characterization, Evaluation and Utilization of Appemidi Mango Genotypes of Westren Ghat

M. Sankaran*, M. R. Dinesh, K. S. Shivashankara, K. V. Ravishankar, G. L. Veena, K. Abirami, K. Ranjitha, C. Vasugi, Nishita Raj, Dharampal Singh and D. C. Sunil Gowda
Division of Fruit Crops, ICAR-Indian Institute of Horticultural Research, Hesaraghatta Lake Post, Bengaluru - 560089, Karnataka.
*Corresponding author email: kmsankaran@gmail.com, m.sankaran@icar.org.in

ABSTRACT

Mango (*Mangifera indica* L.), a member of the family Anacardiaceae, is one of India's most important fruit crops, with immense cultural, socio-economic and religious significance. India harbours extensive mango diversity, particularly in the Western Ghats of Karnataka, where indigenous pickling types known as 'Appemidi' (midi meaning tender mango in Kannada) are traditionally conserved and used in Malnad cuisine. Appemidi mangoes are highly valued for their distinctive aroma and superior pickling quality, and the group has received Geographical Indication (GI) recognition. Fruits at different developmental stages are used for culinary purposes, with tender fruits being preferred for pickling. The Western Ghats region possesses considerable unexplored varietal diversity of Appemidi mangoes. However, genetic erosion caused by urbanization, deforestation, habitat fragmentation and indiscriminate harvesting threatens several indigenous types. Further, morphological similarities and variation in local names across regions create challenges in accurate identification and documentation. Therefore, systematic collection, characterization, conservation and utilization of these genetic resources are essential. ICAR-IIHR, Bengaluru, the National Active Germplasm Site (NAGS) for mango, conserves 808 accessions, including 792 in the field gene bank and 16 in the nursery. Of the field collections, 250 accessions represent Appemidi types. Based on Bioversity International descriptors, 80 accessions were characterized for 61 traits, while 115 were evaluated for fruit characteristics, including the traditional sap-burn test, an Indigenous Traditional Knowledge (ITK) used to assess pickling quality. The characteristic aroma of Appemidi is associated with volatile compounds, particularly terpenes such as terpinolene, 3-carene, caryophyllene and α-pinene. Eight polymorphic SSR markers were used to assess genetic diversity among 150 Appemidi genotypes. Eight genotypes were identified as promising for pickling, while five are being utilized in breeding programmes. Selected superior genotypes are also being multiplied and distributed to farmers through the IIHR Fruit Nursery. Conservation, characterization, documentation and sustainable promotion of Appemidi mangoes are vital for safeguarding this unique genetic resource, supporting custodian farmers and ensuring its long-term economic and cultural sustainability.

Key words: Appemidi, Western Ghats, Pickling, ITKs, NAGS, Genetic resources.

POSTER PRESENTATIONS

PP-4-01

Morphological Characterization and Fat Content Estimation of Different Avocado Accessions Collected from Kodagu Region of Karnataka

P. Laya*, Anuradha Sane, G. Karunakaran, B. M. Muralidhara and Roopendra Kumar
Indian Institute of Horticultural Sciences, Bengaluru
*Corresponding author email: layaprasanna05@gmail.com

ABSTRACT

Avocado is a nutritionally rich exotic fruit crop belonging to the Lauraceae family, originated from Mexico and Central America, possibly from more than one wild species. Over the past decade, the demand value for Avocado fruits has been quite high. This growing market highlights the need for systematic crop improvement programs aimed at developing high yielding varieties. As a prerequisite for any breeding program, characterization of germplasm is essential. Thus, morphological characterisation and fat content estimation of various avocado accessions maintained in the field gene bank of ICAR-IIHR, CHES, Chettalli were carried out. Ten accessions were evaluated for fruit, pulp, seed parameters, and the fat content to identify the one with higher fat percentage to incorporate in future breeding programs. These accessions exhibited wide variability in fruit colour (Light green, Green, Dark green, Yellow, Purple), fruit shape (obovate, pyriform, clavate, narrowly obovate, ellipsoid, rhomboidal) and degree of glossiness (low, medium, intermediate) assessed as per Bioversity's International descriptors for avocado. Accession PA064 recorded the highest fruit weight (611.8 g) and accession PA072 recorded better organoleptic properties. Fat analysis of the dried pulp revealed that accession PA031 had comparatively high fat content (17.67%). The superior accessions identified in this study will serve as a valuable genetic resource for future avocado breeding programmes aimed at improving yield and fruit quality.

Keywords: Avocado, *Persea americana*, Germplasm characterization, Morphological diversity, Fruit quality, Fat content, Field gene bank.

PP-4-06

Assessment of Watermelon Germplasm to Identify Lines with High Citrulline Content in Pulp of Fruit

S. Sreelekshmi*, E. Sreenivasa Rao and M. Arivalagan
ICAR-Indian Institute of Horticultural Research, Hesaraghatta, Bengaluru, Karnataka
*Corresponding author's email: Lekshmisree481@gmail.com

ABSTRACT

Watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakai (2n = 22)) is a cucurbitaceous vegetable crop grown for its crisp and juicy flesh which is usually consumed in fresh form. Mesocarp of mature watermelon fruits is a valuable source of antioxidants, minerals, and amino acids citrulline and arginine. Citrulline is a non-protein α-amino acid with around 80% bioavailability from pulp . It aids in metabolic functions, muscle development and vasodilation through enhanced nitric oxide synthesis. The amino acid citrulline found in watermelon is also present in several other cucurbit species including bitter melon, cucumber, muskmelon, pumpkin, bottle gourd, ridge gourd, and wax gourd but watermelon contains tenfold higher concentrations compared to other cucurbits. Hence, watermelon have the potential to be a natural and freshly consumable alternative to citrulline supplements. The present investigation was carried out with the objective of identifying lines with high citrulline content. In the present study, systematic screening of 160 watermelon germplasm lines was carried out to identify accessions with high citrulline content in the flesh. Initial screening enabled the selection of 40 high citrulline lines, which were subsequently re-evaluated during the following season for confirmation. The evaluated germplasm exhibited an average citrulline concentration of approximately 400 mg/100 g of pulp, whereas commercial checks recorded 160-200 mg/100 g across both seasons. Based on two season performance, six germplasm lines were identified as stable and superior sources of high citrulline content. The identified lines from this experiment are valuable genetic resources for further breeding programmes for developing bio-fortified watermelon hybrids.

Keywords: watermelon, citrulline, germplasm.

PP-4-09

Characterization of Morphological, Floral and Phytochemical Diversity in *Clitoria ternatea* L. Germplasm

Gajjala Vasavi Reddy*, Rohini M. R., K. M. Yuvaraj, Arivalagan M. and Pushpa Chethan Kumar
Dr. YSRHU, College of Horticulture, Anatharajupeta
Senior scientist, ICAR-IIOPR (RC), Palode
Principal Scientist & Head Dr. YSRHU, HRS, Anatharajupeta
Senior scientist, ICAR-IIHR, Bengaluru
Senior scientist, ICAR-IIHR, Bengaluru
*Corresponding author email: gajjalavasavireddy3@gmail.com

ABSTRACT

Clitoria ternatea L. (Shankhpushpi) is an important medicinal legume valued for its ornamental appeal and rich phytochemical composition. Systematic characterization of its germplasm is essential for effective conservation, genetic improvement and sustainable utilization of plant genetic resources. To characterize twenty-five *Clitoria ternatea* genotypes based on morphological, floral, yield and phytochemical traits. Considerable variability was observed for both qualitative and quantitative characters. Plant height ranged from 131.26 to 265.43 cm, while days to flowering varied from 27.66 to 67.33 days. Double-petalled genotypes exhibited vigorous vegetative growth and superior flower production, with genotype IIHR-CT-63 recording the highest fresh flower yield (43.21 g plant^{-1}). In contrast, single-petalled genotype IIHR-CT-36 produced the highest pod yield (247.16 g plant^{-1}) and seed yield (138.85 g plant^{-1}), indicating greater reproductive efficiency. High heritability coupled with high genetic advance was recorded for flower, pod and seed yield, suggesting the predominance of additive gene action and the effectiveness of direct selection. Cluster and principal component analyses clearly differentiated the genotypes based on floral type and identified flower longevity, leaf width and yield attributes as the major contributors to genetic diversity. Biochemical evaluation revealed significant variation in anthocyanins (0.31–7.77 mg C3GE g^{-1} DW), flavonoids (7.52–10.26 mg CE g^{-1} DW) and total phenols (14.23–26.97 mg GAE g^{-1} DW), with blue-flowered genotypes consistently recording higher concentrations than white-flowered types. The study identified IIHR-CT-63 and IIHR-CT-64 as promising genotypes for floral production, while IIHR-CT-36 and IIHR-CT-5 were superior for seed production. These findings provide valuable baseline information for germplasm conservation, selection of elite genotypes and future breeding programmes aimed at enhancing the medicinal and commercial value of *Clitoria ternatea*.

Keywords: Germplasm characterization, Morphological diversity, Floral traits, Sustainable utilization, Crop improvement.

PP-4-11

Honeycomb Design: A best method for plant architecture and ideotype development in okra {*Abelmoschus esculentus* (L) Moench}

M. Pitchaimuthu*, O. P. Dutta, Manjunatha Gowda, K. Padmini L. T. Chaithra, and G. V. Nagamani
[1]Division of Vegetable Crops, *ICAR-Indian Institute of Horticultural Research Hessaraghatta Lake Post, Bengaluru - 560 089 Karnataka, India*
*Corresponding author email: pitchaimth9@gmail.com

ABSTRACT

The honeycomb breeding design is an efficient selection approach for developing superior okra ideotypes by minimizing inter-plant competition and allowing each plant to express its maximum genetic potential. Its primary objective is to maximize genetic gain by reducing the effects of competition and spatial heterogeneity, thereby enabling precise selection of superior individual plant. The experiment was conducted during Kharif 2025 using a hexagonal honeycomb design with 2 m × 2 m spacing, providing equal growing space in all directions. This design minimized competition and allowed accurate evaluation of yield and plant architectural traits. Among the nine germplasm evaluated, IIHR-1779-1 (Silver Queen) recorded the highest fruit yield **(**1.98 kg per plant**),** followed by IIHR-1780-2 (1.18 kg per plant**)**. These accessions significantly outperformed the commercial checks Arka Anamika (480 g per plant) and Pusa Sawani (260 g per plant)**.** Under conventional spacing (30 × 60 cm), IIHR-1779-1 produced only 680 g per plant**,** under normal growing conditions. This accession also possessed shorter internodes, an important ideotype trait. Although not suitable for direct consumption, it is a valuable donor parent for improving yield potential. Another accession, IIHR-1777-1 (Heavy Hitter)**,** exhibited abundant primary, secondary, and tertiary productive branches with wider adaptability, making it a promising parent for improving plant architecture. IIHR-1780-2 showed a wider branch angle **(**9.33°**)** and a vigorous root spread, indicating its suitability for long-term ideotype breeding.The honeycomb design enhances the precision of selecting superior genotypes with desirable traits, including medium plant height, short internodes, optimum branching, erect growth habit, early flowering, high fruit set, dark green tender fruits, efficient resource use, and resistance to Yellow Vein Mosaic Virus (YVMV) and Enation Leaf Curl Virus (ELCV**)**. It is particularly effective in early segregating generations, where genetic variability is high. Based on these findings, a modified double-cross breeding programme is planned to combine the high yield of Silver Queen, superior branching of Heavy Hitter, and favourable plant architecture of IIHR-1780-2 into a single ideotype. This strategy is expected to accelerate the development of high-yielding, climate-resilient, disease-resistant okra cultivars for sustainable vegetable production.

Keywords: Okra, *Abelmoschus esculentus*, Honeycomb breeding, Ideotype breeding.

PP-4-12

Genetic Dissection of Grain Yield, Protein and Essential Micronutrients in Pearl Millet [*Pennisetum glaucum* (L.) R. Br.] Through Line × Tester Analysis and SSR Marker-Assisted Diversity Assessment

Ravi M. Jambukiya[1]* and Balvant C. Patel[2]

[1]*MSc., Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand Agricultural University, Anand (Gujarat), India - 388 110*

[2]*Principal and Unit Head, College of Agriculture, Anand Agricultural University, Vaso (Gujarat), India - 387 380*

*Corresponding author email: ravijambukiya359@gmail.com

ABSTRACT

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is an important climate-resilient cereal cultivated extensively in arid and semi-arid regions owing to its exceptional tolerance to drought, high temperature and poor soil fertility. Besides its adaptability, pearl millet is recognised as a nutrient-dense "Nutri-cereal" rich in protein and essential micronutrients, particularly iron (Fe), zinc (Zn), calcium (Ca), copper (Cu), potassium (K), phosphorus (P) and manganese (Mn), making it a promising crop for addressing global nutritional insecurity. Exploiting heterosis while simultaneously improving grain nutritional quality remains a major objective in pearl millet breeding. Therefore, this investigation was undertaken to estimate heterosis, combining ability, gene action and genetic diversity for grain yield, yield-attributing traits, protein and micronutrient content. The experimental material comprised seven cytoplasmic male sterile (CMS) lines, nine restorer lines and their 63 F_1 hybrids generated through a Line × Tester mating design. The hybrids, parents and a standard check (GHB 1129) were evaluated in a randomized complete block design with three replications during *Kharif* 2023 at the Regional Research Station, Anand Agricultural University, Anand. Nineteen traits, including phenological, morphological, yield, biochemical (protein) and micronutrient parameters (Fe, Zn, Ca, Cu, K, P and Mn), were recorded. Genetic diversity among parental lines was assessed using polymorphic SSR markers. Analysis of variance revealed highly significant genetic variability for all studied traits. Significant heterobeltiosis and standard heterosis were observed for grain yield and nutritional traits, with crosses ICMA 02444 × ICMR 17560 and ICMA 05444 × ICMR 17276 emerging as the most promising combinations. Hybrids also exhibited remarkable enhancement for micronutrients, with ICMA 05444 × ICMR 17305 recording the highest Fe content (122.47 ppm), ICMA 98444 × ICMR 17336 the highest Zn content (58.99 ppm), ICMA 04999 × ICMR 17444 the highest Ca content (375.42 ppm), ICMA 02444 × ICMR 17336 the highest Cu content (3.03 ppm), ICMA 04999 × ICMR 17560 the highest K content (2635.76 ppm), ICMA 785 × ICMR 17276 the highest P content (3671.43 ppm), ICMA 95333 × ICMR 17264 the highest Mn content (7.71 ppm), and ICMA 02444 × ICMR 17327 the highest protein content (18.54 %). Combining ability analysis indicated the predominance of non-additive gene action for grain yield, protein and all micronutrient traits, suggesting the effectiveness of heterosis breeding for simultaneous improvement of productivity and nutritional quality. SSR analysis further revealed substantial genetic diversity among parental lines, supporting their strategic utilization in hybrid breeding programmes. The identified superiour parents

and hybrids provide valuable genetic resources for developing high-yielding, nutrient-rich pearl millet hybrids to enhance food and nutritional security under climate-resilient agriculture.

Keywords: Pearl millet, Heterosis breeding, Combining ability, Micronutrient biofortification and SSR markers.

PP-4-13

Morpho-Biochemical Characterization of Half-Sib Pummelo Progenies for Fruit Quality Improvement

Bharti Thakur[1]*, M. Sankaran[1*], K. Abirami[1], B. R. Raghu[2], T. Sakthivel[1], K. S. Shivashankara[3], M. Arivalagan[3], P. Nandeesha[4], Bandi Navya[1] and P. S. Nitin[1]

[1]*Division of Fruit crops, ICAR- Indian Institute of Horticultural Research, Bengaluru - 560089, India*

[2]*Division of Vegetable Crops, ICAR- Indian Institute of Horticultural Research, Bengaluru - 560089, India*

[3]*Division of Basic Sciences, ICAR - Indian Institute of Horticultural Research, Bengaluru - 560089, India*

*Corresponding author email: bhthakur777@gmail.com

ABSTRACT

Pummelo (*Citrus grandis* (L.) Osbeck), the most primitive and genetically diverse cultivated citrus species, which exhibits wide variability in fruit traits and constitute a valuable genetic resource for citrus improvement. However, excessive seediness, bitterness and thick rind reduce consumer preference, emphasizing the need to develop genotypes with superior fruit quality. In the present study, 197 half-sib progenies derived from five maternal accessions (Acc. 18-4, Acc. 18-2, Acc. 6-1, Acc. 12-2 and Acc. 12-1) were evaluated for morphological and biochemical traits. Morphological traits included fruit weight, fruit diameter, fruit length, rind thickness, number of segments, fruit axis diameter, segment length and seed number, while biochemical traits comprised total soluble solids (TSS), titratable acidity, TSS:acid ratio, ascorbic acid, reducing sugars, total sugars, total phenols and total flavonoids. Substantial phenotypic variability was observed among the progenies, with fruit weight ranging from 0.30 to 2.42 kg, rind thickness from 0.98 to 3.20 cm, TSS from 6.46 to 11.70 °Brix, titratable acidity from 0.73 to 3.58%, total sugars from 2.83 to 10.85%, ascorbic acid from 10.0 to 63.3 mg/100 ml juice, total phenols from 25.18 to 158.56 mg GAE/100 ml, and total flavonoids from 1.16 to 24.95 mg catechin equivalents/100 g. Among the evaluated progenies, HS 42-6, HS 45-13, HS 46-10 and HS 48-12 exhibited higher TSS (>10 °Brix) with comparatively thinner rind, whereas HS 46-10 recorded the highest total sugars (10.85%), indicating its potential as a sweet-fruited genotype. The wide variability observed among the half-sib progenies reflects the rich genetic diversity present within the breeding population. The identified elite progenies constitute promising genetic resources for selection and utilization in pummelo breeding programmes aimed at enhancing fruit quality, sweetness and consumer acceptability.

Keywords: Pummelo, Half-sib progenies, Fruit quality, Morphological characterization, Biochemical traits.

PP-4-14

Genetic Variability, Heritability and Correlation Studies in Gerbera (*Gerbera jamesonii* Adlam) Varieties Grown under Protected Cultivation

Y. V. Bhavana, P. Naveen Kumar*, Rajiv Kumar, S. A. Safeena, R. T. Anuradha and Veeresh
ICAR- Indian Institute of Horticultural Research, Hesaraghatta, Bangalore, 560089, India
*Corresponding author email: naveeniari@gmail.com

ABSTRACT

Gerbera (*Gerbera jamesonii* Adlam) is one of the most important commercial cut flower because of its attractive blooms, diverse colour range, long flower stalks, and excellent vase life. The present investigation was undertaken to evaluate the extent of genetic variability, heritability, genetic advance, and character association among eleven commercial gerbera varieties grown under protected cultivation with the objective of identifying superior varieties and important selection criteria for crop improvement. Significant differences were observed among the varieties for all the vegetative, floral, yield, and post-harvest traits, indicating the existence of substantial genetic variability. Among the evaluated varieties, Haimi exhibited superior vegetative vigour with the longest leaves (32.93 cm), maximum leaf breadth (11.82 cm), highest number of suckers (3), thickest flower stalk (5.52 cm), and longest vase life (7.75 days). Livia recorded the maximum plant spread (50.84 cm) and flower diameter (2.8 cm), whereas Terra Kalina produced the longest flower stalk (55.68 cm) and Terra Snooki recorded the highest number of flowers per plant (3.85). The estimates of phenotypic coefficient of variation (PCV) were consistently higher than the corresponding genotypic coefficient of variation (GCV) for all the characters studied, indicating the influence of environmental factors on trait expression. High GCV and PCV values were observed for number of leaves, number of flowers, number of suckers and leaf breadth, suggesting greater scope for genetic improvement through selection. High heritability coupled with high genetic advance was recorded for number of flowers per plant, flower stalk length, and plant spread, indicating the predominance of additive gene action and the effectiveness of direct phenotypic selection for these traits. Correlation analysis revealed a strong positive association of number of leaves with number of flowers (r = 0.846), flower stalk diameter with flower stalk length (r = 0.841), and number of suckers with flower diameter (r = 0.746) and vase life (r = 0.722). Based on their overall performance, Haimi, Livia, Terra Kalina, and Terra Snooki can be recommended for further utilization in future breeding programmes, while number of leaves, plant spread, flower stalk diameter, flower stalk length, and number of suckers were identified as reliable selection criteria for improving flower yield, quality, and post-harvest longevity in gerbera.

Keywords: Gerbera, phenotypic and genotypic coefficients of variation, heritability, genetic advance and correlation.

PP-4-15

Assessment of Morphological Diversity in Ridge Gourd (*Luffa acutangula* Roxb.) Genotypes through DUS Characterization

V. Bhavitha[1*], L. Mukunda Lakshmi[2], Syed Sadarunnisa[3], M. Jayaprada[4] and T. Susila[5]
PG Scholar, Department of Vegetable Science,
Dr. Y.S.R. Horticultural University, College of Horticulture,
Anantharajupeta, Annamaya Dist. A.P.516105
*Corresponding author email: bhavitha3636@gmail.com

ABSTRACT

Thirty ridge gourd (*Luffa acutangula* Roxb.) genotypes were evaluated during February 2025 at the Research Farm, Department of Vegetable Science, College of Horticulture, Dr. Y.S.R. Horticultural University, Anantharajupeta, to assess morphological diversity using the Distinctiveness, Uniformity and Stability (DUS) descriptors prescribed by the Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA). A total of 17 morphological descriptors covering vine, leaf, flower and fruit characteristics were recorded and the genotypes were classified according to the descriptor states specified in the DUS guidelines. Considerable morphological variation was observed among the evaluated genotypes for several morphological traits. Based on plant growth habit, 24 genotypes were classified as medium viny, while 3 each were short viny and long viny. Leaf shape varied with 23 orbicular, 5 reniform and 2 ovate genotypes. The majority of the genotypes 25 exhibited five-lobed leaves, whereas 5 genotypes had more than five lobes. Fruit length was categorized as medium in 18 genotypes, short in 10 genotypes and long in 2 genotypes. Fruit shape exhibited considerable diversity, comprising 20 elongate, 6 elliptical, and 4 oblong genotypes. Similarly, fruit ridge shape was deep in 15 genotypes, medium in 12 genotypes and superficial in 3 genotypes. The substantial phenotypic variation observed across these descriptors indicates the existence of a broad genetic base among the ridge gourd genotypes. The study demonstrates the effectiveness of DUS descriptors in the characterization and discrimination of ridge gourd germplasm and provides valuable information for varietal identification, germplasm conservation, protection of plant varieties and the selection of genetically diverse parental lines in ridge gourd breeding programmes.

Keywords: Ridge gourd, DUS characterization, PPV&FRA, morphological descriptors and genetic diversity.

PP-4-16

Dissecting the Genomic Regions for Root Nodulation Traits in Chickpea Through Genome Wide Association Mapping

B. S. Chandana[1,2], Rohit Kumar Mahto[1], Rajesh Kumar Singh[1], Danakumar[1,3] and Rajendra Kumar[1]*
[1]*ICAR -Indian Institute of Rapeseed Mustard Research Institute, Bharatpur, Rajasthan - 321303*
[2]*ICAR-Indian Agricultural Research Institute, 110012*
[3]*ICAR- Indian Institute of Millet Research-RRS On Pearl millet, Gudamalani - 344031*
*Corresponding author email: chandanabs7254@gmail.com

ABSTRACT

Chickpea being an important food legume crop is able to fix the atmospheric nitrogen and form root nodules that support biological nitrogen fixation-a sustainable alternative for nitrogen supply to agriculture worldwide. In order to support findings on nodule formation in chickpeas, a diverse core set of 284 chickpea genotypes, including four checks, were evaluated for morphological and nodulation traits in four different environments in an augmented randomized block design. The genotypes exhibited significant trait variation, encompassing all traits under study. Significant genotypic correlations and direct positive effects were exhibited by a number of nodules and number of pods per plant on grain yield. Based on the D^2 statistics, the number of seeds per plant, number of pods per plant, shoot fresh weight and numbers of nodules have been identified as top-ranking yield contributing traits. The genotypes ICC7390, ICC15,ICC8348 and ICC2474were identified as high nodulating across the locations. Genome-wide association studies (GWAS) identified noteworthy and stable marker–trait associations (MTAs) linked to the traits of interest. For the traits number of nodules (NON) and nodule fresh weight (NFW), 65 and 109 significant MTAs were identified, respectively. In addition, two SNPs, Ca1pos289.52482.1 and 6_33340878, identified in our earlier studies were validated by independent population studies, which are crucial in evaluating the accuracy and reliability of the projections. Subsequent analysis revealed that a substantial proportion of these MTAs were situated within intergenic regions with the potential to modulate genes associated with the focal traits. The candidate genes identified could be converted to Kompetitive allele-specific PCR (KASP) markers and exploited in marker-assisted breeding, accentuating their impact on future chickpea breeding efforts.

Keywords: Nodulation, Marker, Mapping, core collection.

PP-4-17

Evaluation of Advanced Breeding Lines of Chilli (*Capsicum Annuum* L.) for Deficit Moisture Stress Tolerance

K. Bharath Chandra[1], R. H. Laxman[1], Naresh Ponnam[2]*, K. S. Shivashankara[1], M. D. Prathibha[1], Channappa Mahadevaiah[2], Ashwini Yadav[1] and Hema Malini[1]

[1]*Division of Basic Sciences, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, 560089, India*

[2]*Division of Vegetable Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, 560089, India*

*Corresponding author email: Ponnam.naresh@icar.org.in

ABSTRACT

Chilli (*Capsicum annuum* L.) is a high-value vegetable cum spice crop. Productivity of chilli is severely constrained by recurrent water deficit stress. Developing deficit moisture stress tolerant cultivars requires robust phenotypic evaluation. In the present study, twenty-one advanced breeding lines along with parental lines were evaluated for deficit moisture stress tolerance. These lines (F5) were developed through pedigree selection targeted at deficit moisture stress tolerance and quality in crosses of Devnur Deluxe (DD) x IHR4517, IHR 3448 x IHR4517 and Attigere Dabbi (AD) x IHR4517. Lines were evaluated under controlled conditions in a rain-out shelter. The genotypes were subjected to two soil moisture regimes: 100% Field Capacity (FC) as the control and 50% FC as water-deficit stress. Significant genotypic variation ($p < 0.05$) was observed for growth, physiological parameters, biomass retention, root traits and drought tolerance indices, revealing substantial diversity for water deficit adaptation. Water deficit stress tolerant lines such as AD x IHR4517 F5-D64, AD x IHR4517 F5-D67, IHR 3448 x IHR4517 F5-D80, IHR 3448 x IHR4517 F5-D82 and IHR 3448 x IHR4517 F5-D84 consistently outperformed other genotypes under 50% FC by maintaining higher relative water content, chlorophyll stability, membrane stability index, photosynthetic efficiency, coupled with lower malondialdehyde accumulation, indicative of enhanced cellular integrity and oxidative stress tolerance. These adaptive responses contributed to improved plant growth, greater root development, increased root to-shoot ratio, and superior biomass retention under 50% FC conditions. Whereas the lines DD x IHR4517 F5-D22, DD x IHR4517 F5-D23, DD x IHR4517 F5-D28, AD x IHR4517 F5-D45, AD x IHR4517 F5-D54,

AD x IHR4517 F5-D61 and IHR 3448 x IHR4517 F5-D77 displayed poor stress adaptation and were identified as highly susceptible lines. The identified stress tolerant advanced breeding lines in this study serve as valuable for enhancing yields under moisture stress.

Keywords: Deficit water stress tolerance, Advanced breeding lines, Oxidative stress, Biomass retention and Climate-resilient breeding.

PP-4-19

Genetic Analysis for Flower Yield and Quality Traits in Mutant Phenotypes of Royal Jasmine (*Jasminum grandiflorum* L.)

S. M. Soundarya[1], M. Ganga[2] and D. Malarvizhi[3]*
[1]*Department of Horticulture, Kumaraguru Institute of Agriculture, Erode - 638315*
[2]*Department of Floriculture and Landscape Architecture, TNAU, Coimbatore - 641003*
[3]*Department of Plant Genetic Resources, CPBG, TNAU, Coimbatore - 641003*
*Corresponding author email: dmalarvizhi@tnau.ac.in

ABSTRACT

Royal Jasmine (*Jasminum grandiflorum* L.), locally known as Pitchi, is a commercially vital flower crop prized for its exquisite fragrance, essential oil content, and traditional uses. However, the commercial cultivation of this crop faces challenges due to limited genetic variability, restricting the scope of conventional breeding for yield and quality improvement. To overcome this bottleneck, induction of mutation using physical (gamma rays) and chemical mutagens (ethyl methane sulfonate) serves as a potent tool for creating novel genetic variations and alter plant architecture. Further, understanding the character association and correlation between vegetative and reproductive traits is vital to maximize total flower yield. Therefore, the present investigation was undertaken at Tamil Nadu Agricultural University, Coimbatore during 2020–2023, to evaluate the genetic parameters and trait correlations in pink and white flower mutants of Royal Jasmine with the primary objective of identifying high-yielding, superior mutant phenotypes. The results revealed that the pink and white flower mutants had significantly higher values than the control for vegetative growth parameters (primary and secondary branches, internodal length, leaf number, leaf length, and leaf width) followed by flower quality parameters (days to flowering, number of flowering cymes/branch, length of flower bud, length of corolla tube, bud girth, flower diameter, and 100-flower bud weight). Based on high phenotypic coefficient of variation and genotypic coefficient of variation, selection can be effectively practiced for traits viz., flower yield, number of primary and secondary branches per plant, flowering cymes/branch, plant height, length of internode, stem girth, leaf length, leaf breadth, and hundred-bud weight. High heritability (> 60%) coupled with high genetic advance (> 20%) indicated that these traits are governed by additive gene effects, highly effective for progeny selection. Correlation analysis showed desirable positive directions for flowering cymes, plant height, and secondary branches toward enhancing total flower yield. For yield improvement, maximum selection preference should be given to the number of flowering cymes and 100-bud weight. This variation is attributed due to mutation that induced vigorous growth both morphological and reproductive traits. The mutant phenotypes expressing distinct variations were selected in comparison with the parental controls. Based on yield performance and contributing traits, four promising mutants of pink pitchi PPM 12, PPM 72 (EMS derived), PPM 96, and PPM 115 (gamma ray derived) and two EMS derived genotypes of white pitchi WPM 2 and WPM 25 were identified as superior, with enhanced flower quality for future commercial exploitation and cultivation.

Keywords: Royal Jasmine, pink and white pitchi, mutant phenotypes, genetic parameters, evaluation, association of flower yield traits.

PP-4-20

Harnessing Genetic Diversity in CMS-Based Cauliflower for Heterosis Breeding and Sustainable Crop Improvement

Mokkala Siva Prasad*, Khushwant Singh, Neha Jamwal, Ankush Sharma and Shivani
[1]*Department of Vegetable Science, Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh 173230, India*
*Corresponding author email: mokkalasivaprasad1@gmail.com

ABSTRACT

Efficient utilisation of genetic diversity is central to strengthening vegetable crop improvement and developing hybrids with stable productivity. This study was conducted during 2023-2025 at the Department of Vegetable Science, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan, to assess combining ability, gene action and heterosis in cytoplasmic male sterility (CMS)-based cauliflower. Seventy-five hybrids were developed by crossing fifteen CMS lines (CMS-15 to CMS-29) with five testers (White Heart, Snowball Super, Cambridge No. 5, PSBK-25 and Kt-18) using a Line × Tester mating design. The hybrids, parents and standard check Pusa Snowball Hybrid-1 were evaluated in a randomized complete block design with three replications for fifteen quantitative traits. Analysis of variance showed significant genotypic differences for most traits, indicating ample variability in the material. Significant line, tester and line × tester effects confirmed the importance of parental diversity and specific cross combinations. CMS-19 was superior for curd polar length, curd size index, gross plant weight, marketable curd weight and yield, whereas CMS-18 was promising for curd equatorial length, harvest index and dry matter content. Based on general combining ability and mean performance, CMS-19, CMS-18, CMS-27, Snowball Super, Kt-18 and PSBK-25 were identified as useful parents for yield improvement. The hybrids CMS-18 × Snowball Super, CMS-23 × PSBK-25 and CMS-19 × Snowball Super recorded superior performance for curd size index, marketable curd weight, yield, net curd weight and associated traits. For most characters, the additive to dominance variance ratio was below unity, indicating predominance of non-additive gene action and supporting heterosis breeding for late cauliflower. These promising CMS-based hybrids merit multi-location evaluation before consideration as alternatives to existing cauliflower hybrids.

Keywords: Cauliflower, CMS lines, combining ability, heterosis, Line × Tester, vegetable breeding.

PP-4-23

Assessment of Genetic Diversity in Barleria Genotypes using SSR Markers

S. Prerana, S. A. Safeena*, N. Chandrashekar, P. Naveen Kumar,
V. Sreenivasa, M. Arivalagan, and M. Chaithra
ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka - 560 089
*Corresponding author email: safeenaicar@gmail.com

ABSTRACT

Barleria (Acanthaceae) is a promising ornamental and medicinal genus whose Indian germplasm remains largely uncharacterised at the DNA level. Twenty-five Barleria genotypes maintained at ICAR–Indian Institute of Horticultural Research, Bengaluru, were characterised using SSR markers reported for the Acanthaceae, and the resulting groups were interpreted against the vegetative and floral characters recorded on the same collection. Of 59 SSR primers screened, 35 gave clear, reproducible and polymorphic amplification. These generated 88 alleles, all of them polymorphic, averaging 2.51 alleles per primer. Band frequency ranged from 0.038 to 0.962, and polymorphism information content ranged from 0.078 to 0.998. UPGMA clustering resolved the collection into two major clusters. Cluster I comprised five genotypes, namely IIHR BP-V-01, IIHR BP-T-03, IIHR BP-M-02, IIHR BU-T-01, and IIHR BP-V-07, while Cluster II contained the remaining twenty. The separation was largely corroborated by morphology. Cluster I was defined by the presence of thorns, absence of bracts, glabrous stems and yellow to yellow-orange flowers, together with smaller floral dimensions, late flowering and markedly lower flower yield. Cluster II, in contrast, comprised bracted, hairy-stemmed, broad-leaved types bearing larger and heavier flowers in shades of violet and purple and vigorous vegetative growth. Ward's clustering of 34 quantitative traits separated broadly almost same genotypes, confirming strong correspondence between molecular diversity and major morphological characteristics among the Barleria genotypes. These findings demonstrate the effectiveness of SSR markers in assessing genetic diversity in Barleria and provide a valuable foundation for germplasm conservation, parent selection, and future crop improvement.

Keywords: Barleria, Acanthaceae, Genetic diversity, Germplasm characterization, SSR markers.

PP-4-25

Integrative Assessment of Fruit Quality, Bioactive Compounds, and Genetic Diversity in Indian Coffee Plum [*Flacourtia jangomas* (Lour.) Raeusch.] from *Terai* Ecosystems of West Bengal

Prahlad Deb[1*], P. K. Mukherjee[1], P. Das[1], U. Tudu[1], P. Sutradhar[1], A. Majumdar[1], and N. Bhowmick[2]
[1]*Department of Horticulture and Postharvest technology, Institute of Agriculture, Visva-Bharati, Sriniketan, West Bengal*
[2]*Department of Pomology and Postharvest Technology, Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, West Bengal*
*Corresponding author email: debprld@yahoo.com

ABSTRACT

The present study aimed to elucidate the morpho-biochemical characteristics, bioactive potential, and genetic diversity of Indian coffee plum [*Flacourtia jangomas* (Lour.) Raeusch.] plants collected from the natural vegetation of the Terai region of West Bengal during 2022–23 and 2023–24. Substantial variability was observed in fruit morphological and quality attributes, including fruit length (14.7–22.4 cm), fruit diameter (17.1–23.7 cm), fruit weight (4.37–7.82 g), number of seeds per fruit (5.8–11.1), total soluble solids (6.2–10.9 ºBrix), acidity (0.40–0.52%), reducing sugars (4.02–5.80%), and ascorbic acid content (100.5–156.7 mg/100 g). The selected genotypes also exhibited considerable variation in bioactive constituents, with antioxidant activity ranging from 63.9 to 88.7% (DPPH inhibition), total phenols from 145.7 to 278.6 µg GAE/g, flavonoids from 85.1 to 163.9 mg QE/g, anthocyanins from 33.5 to 56.4 µg/100 g, and carotenoids from 1.135 to 1.6114 mg/100 g. Correlation analysis revealed significant positive associations among fruit size and key quality parameters such as TSS, acidity, and ascorbic acid. Notably, ascorbic acid content showed strong positive correlations with fruit size, total sugars, antioxidant activity, phenols, flavonoids, and carotenoids. In contrast, a pronounced negative correlation was observed between the number of fruits per cluster and the number of seeds per fruit with other evaluated traits. Cluster analysis grouped the population into three major clusters comprising 8, 3, and 9 genotypes, reflecting the underlying diversity across morphological, biochemical, and bioactive traits. Among the genotypes, ICPG-J5 emerged as the most suitable for the fresh fruit market due to its larger and heavier fruits, superior biochemical attributes, high ascorbic acid content, and strong antioxidant activity. ICPG-J7 was identified as ideal for processing owing to its maximum fruit size, highest weight, and desirable sweet–tangy balance. ICPG-J2 proved promising for functional food applications, being rich in flavonoids, anthocyanins, and exhibiting high antioxidant potential.

Keywords: Bioactive compounds, fruit morphology, genetic diversity, Indian coffee plum, quality parameters.

PP-4-27

Decoding Genetic Diversity on Agronomic, Nutritional Traits and Dry Root Rot Resistance in Sesame (*Sesamum indicum* L.) Germplasm

Ganesh Babu[1], S. R. V. N.[1], R. Saraswathi[2], A. Mahalingam[3], M. Paramasivan[4], D. Uma[5] and D. Malarvizhi[2]*

[1]*Centre for Plant Breeding & Genetics, TNAU, Coimbatore*

[2]*Department of Plant Genetic Resources, Tamil Nadu Agricultural University*

[3]*Department of Oilseeds, Tamil Nadu Agricultural University*

[4]*Regional Research Station, Vridhachalam, Tamil Nadu Agricultural University*

[5]*Department of Biochemistry, Tamil Nadu Agricultural University*

*Corresponding author email: dmalarvizhi@tnau.ac.in

ABSTRACT

From sesame germplasm conserved at Dr. K. Ramiah Gene Bank, 100 accessions along with four checks *viz.,* GT 10, VRI 4, VRI 5, and TMV 7 were evaluated during February 2024, in Alpha lattice design with three replications at the Regional Research Station, Vridhachalam, TNAU. Ten agronomic traits including single plant yield were recorded. The earliest germplasm to attain fifty percent flowering was GRT 83126-A in 27 days. Among the traits related to plant habit, the range of diversity was wide for plant height (71.80cm to 133.30cm) and number of primary branches (nil to 9.3). The genotypes namely Si 2008 (5.49), KMS 370 (5.37) were desirable for number of secondary branches. The extreme on the positive side for yield governing traits *viz.,* number of capsules per plant, capsule length, seeds per capsule and thousand seed weight were in the order 102.3, 4.2cm, 83.50 and 4.33g. The nutritional traits namely protein content of the meal in varied between 8.33% (DCB 1844) and 27.05% (KMR 42) and oil content in seeds ranged from as low as 11.33 % in PSR 3022 to as high as 56.21% in Swetha. Out of seven clusters delineated in Mahalanobis D^2 analysis, Cluster II was the largest (26), followed by Cluster I (23). The trait oil content contributed the most (43.7%) to the divergence. Significant genetic divergence was observed between the clusters VI and VII. The 18 genotypes in Cluster V exhibited early flowering, high number of primary (5.49) and secondary branches (3.24), number of capsules per plant (71.19), and single plant yield. The first two principal components explained 88.99% of the total variance in bi-plot analysis. KMS 370 ranked as the best genotype, followed by DCB 1844, TMV 7, Chandana and G 17. From GYT biplot, four superior early flowering genotypes namely KMS 370, DCB 1844, Si 2008 and NIC 8283 grouped in cluster V were identified for high single plant yield that was contributed through number of capsules per plant, seeds per capsule, primary and secondary branches. Screening for dry root rot resistance undertaken in a sick plot revealed adequate disease development, wherein the susceptible check recorded 72.2% disease incidence. Three genotypes namely Si 9641, ES 9, Si 1804 showed resistance to root rot (11-21%), while five exhibited moderate resistance (21-26%). The study highlighted promising accessions for use in breeding programs for yield, quality enhancement and disease resistance in sesame.

Keywords: Sesame, Germplasm evaluation, Genetic divergence, Dry root rot resistance, Nutritional traits.

PP-4-28

Characterization of Mutant Progenies of Pummelo (*Citrus grandis* (L.) Osbeck)

Bandi Navya[1]*, M. Sankaran[1], K. Abirami[1], T. Sakthivel[1], K. S. Shivashankara[2], P. Nandeesha[2], B. R. Raghu[3] and Bharti Thakur[1]

[1]*Division of Fruit Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru-560089, India*

[2]*Division of BasicSciences, ICAR-Indian Institute of Horticultural Research, Bengaluru, India*

[3]*Division of Vegetable Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru, India*

*Corresponding author email: bandinavya1211@gmail.com

ABSTRACT

Pummelo (*Citrus grandis* (L.) Osbeck), one of the three ancestral species of cultivated citrus, is an underutilized fruit crop possessing immense genetic diversity, high nutritional value, and considerable potential for citrus improvement. However, its commercial cultivation remains limited due to undesirable traits such as thick rind, high seed content, delayed bearing, and pronounced bitterness. Among the indigenous germplasm, the genotype 'Kallar' is distinguished by its attractive deep pink pulp, vigorous growth, and superior adaptability, but its high bitterness restricts consumer acceptance. Induced mutagenesis through gamma irradiation offers an effective approach to generate novel genetic variability for the improvement of such traits. The present investigation aimed to characterize gamma ray-induced putative mutant progenies of the pummelo genotype 'Kallar' using vegetative morphological descriptors. A total of 548 healthy putative mutant progenies were evaluated following the Bioversity International citrus descriptors. Observations were recorded on tree architecture, branching pattern, spine characteristics, shoot traits, vegetative growth cycle, leaf morphology, and petiole wing characteristics. Considerable phenotypic variation was observed among the progenies. Most progenies exhibited medium tree vigour with variable canopy architecture, branch density, branch angle, and spine characteristics. Leaf morphology showed substantial diversity, with lamina shape ranging from ovate to obovate and lanceolate, margins varying from crenate to entire, leaf apex from acute to obtuse, petiole wing shape from obcordate to obdeltoid and ovate, and leaf colour intensity from light, medium and dark green. Precocious flowering and fruiting were observed in seven progenies during 2025, while twenty-four progenies fruited during the 2026 season. These progenies exhibited considerable variation in fruit characteristics, including fruit shape (spheroid, pyriform, and obloid), pulp colour ranging from light to dark pink, and wide variation in seed number. The extensive morphological diversity observed among the putative mutant progenies demonstrates the effectiveness of gamma irradiation in generating novel genetic variability and provides valuable germplasm for the selection of superior pummelo genotypes and future citrus breeding programmes.

Keywords: Pummelo, PGR, Gamma-induced mutants, Bioversity descriptors, Morphological diversity.

PP-4-30

Exploiting Genetic Variability and Heritability for Quantitative and Qualitative Improvement in Mango (*Mangifera indica* L.)

Rachapally Prashanth[1*], Rajasekhar Marri[2], V. Suchitra[3], P. Saidaiah[4], P. Harikanth[5] and P. Gouthami[6]

[1]*Research Scholar, Department of Fruit Science, Sri Konda Laxman Telangana Horticultural University, Mulugu, Telangana,*

[2,3]*Professor, Department of Horticulture, Sri Konda Laxman Telangana Horticultural University, Mulugu, Telangana*

[4]*Professor, Department of Genetics and Plant Breeding, Sri Konda Laxman Telangana Horticultural University, Mulugu, Telangana*

[5]*Assistant Professor, Department of Fruit Science, Sri Konda Laxman Telangana Horticultural University, Mulugu, Telangana*

[6]*Assistant Professor, Department of Crop Physiology, Sri Konda Laxman Telangana Horticultural University, Mulugu, Telangana*

*Corresponding author email: prashanthswaero27@gmail.com

ABSTRACT

A study was conducted during 2024–25 at the Fruit Research Station, Sangareddy, to estimate the mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2), and genetic advance as a percent of mean (GAM) for 33 characters across 26 mango genotypes. Relatively high GCV and PCV were observed for several critical vegetative, reproductive, yield and quality attributes, notably leaf area (35.73% and 37.57%), number of hermaphrodite flowers (51.89% and 52.29%), yield (99.21% and 100.03%), fruit weight (70.42% and 71.26%), pulp weight (89.48% and 90.57%), titratable acidity (84.68% and 84.75%), ascorbic acid (77.62% and 78.28%), and β-carotene (59.62% and 60.08%). Broad-sense heritability estimates were high for almost all characters, ranging from 75.14% for peel thickness to 98.97% for the TSS: acidity ratio. Particularly high heritability values were recorded for yield (98.38%), number of hermaphrodite flowers (98.47%), fruit length (96.86%), fruit weight (97.65%), pulp weight (97.60%), total sugars (98.85%), total phenols (98.86%), and flavonoids (98.25%). Likewise, genetic advance as a percent of mean was substantial for several economically important traits, exceeding 100% for the number of hermaphrodite flowers (106.08%), fruit volume (106.16%), yield (202.71%), fruit weight (143.34%), pulp weight (182.11%), pulp: stone ratio (149.93%), titratable acidity (174.31%), TSS: acidity ratio (119.90%), ascorbic acid (158.54%), and β-carotene (121.87%). The results of high heritability and high genetic advance for these yield and quality traits indicate that additive gene action predominantly governs them, making direct selection highly effective for future mango crop improvement programs.

Keywords: Genetic variability, heritability, genetic advance, *GCV* and *PCV.*

PP-4-31

Morphological and Biochemical Characterization of Interspecific Hybrids of Guava

C. Vasugi[1*], T. Veera Nagasupriya[2] and M. Arivalagan[3]
[1]*Principal Scientist, Division of Fruit Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka - 560089*
[2]*PhD Scholar, Division of Fruit Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka - 560089*
[3]*Principal Scientist, Division of Basic Sciences, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka - 560089*
*Corresponding author email: vasugiperumal@gmail.com

ABSTRACT

Guava (*Psidium guajava* L.) is an economically important tropical fruit crop of India valued for its high nutritional quality and commercial importance. Interspecific hybrids were developed at ICAR-IIHR by crossing Arka Poorna and H12-5 with wild species *Psidium cattleianum* var. *cattleianum* and *P. cattleianum* var. *lucidum* with a view to incorporate resistance to biotic stress (nematode and wilt). Among the developed hybrids, ISHG-3 and ISHG-10 (Arka Poorna × *P. cattleianum* var. *lucidum*) and ISHG-12 (Arka Poorna × *P. cattleianum* var. *cattleianum*) exhibited combined resistance to root-knot nematode and Fusarium wilt. These resistant hybrids were characterized for their morphological and biochemical traits to assess their horticultural potential. Morphological characterization using DUS descriptors focusing fifteen vegetative and twenty fruit traits revealed distinct differences between the parental genotypes and considerable variability among the hybrids. The hybrids exhibited both intermediate and parent-specific traits, particularly in fruit shape at the stalk end (rounded), pulp colour (Yellow White 158), peel colour (Yellow Green 154) and medium outer pulp thickness (1.1-1.5), confirming successful introgression of desirable traits from the wild species. The fruits are round, medium in size, white and thick outer pulp with good total soluble solids (11-14^{0}Brix). Biochemical analysis of fruits harvested at the colour break stage revealed vitamin C content (150-220 mg 100 g^{-1} FW) on par with Arka Poorna with low titratable acidity (0.233–0.310%), high total phenols (100–250 mg GAE 100 g^{-1} FW), total flavonoids (15-50 mg CE 100 g^{-1} FW), total antioxidant activity (120–300 mg AEAC 100 g^{-1} FW; FRAP assay), and total sugars (2– 6 g 100 g^{-1} FW). The study revealed that the interspecific hybrids possess desirable fruit quality in addition to resistance to biotic stress.

Keywords: Morphological characterization, *Psidium guajava*, interspecific hybridization, biochemical analysis, wild species.

PP-4-32

Fruit Morpho-Biochemical Characterization of Some Tamarind (*Tamarindus indica* L.) Genotypes Under Sriniketan Block, Birbhum, West Bengal

Pradipto Kumar Mukherjee*, Biman Ghosh, Tanni Paul, Urmila Tudu and Prahlad Deb
Department of Horticulture and Postharvest Technology Institute of Agriculture,
Visva-Bharati, Sriniketan - 731236, West Bengal
*Corresponding author email: kumarpradipto123@gmail.com

ABSTRACT

Tamarind (*Tamarindus indica* L., Family: Fabaceae) is a multipurpose tropical tree crop with significant economic, nutritional and medicinal importance. The present investigation was undertaken to characterise twenty-five tamarind genotypes (T1–T25), collected from different localities under Sriniketan block, Birbhum, West Bengal, with respect to eleven morphological traits and biochemical parameters, and to identify elite genotypes through Pearson correlation analysis, Principal Component Analysis (PCA), biplot analysis and Ward's hierarchical cluster analysis. Morphological evaluation revealed significant genotypic variation. Pod length ranged from 6.64 cm to 11.96 cm , pod weight from 7.48 g to 16.08 g and pulping percentage from 24.89% to 52.50%. Biochemical characterisation showed that total soluble solids (TSS) ranged from 6.00°Brix to 11.40°Brix , ascorbic acid from 4.460 to 19.315 mg/100g , total phenol from 0.755 to 2.305 mg GAE/100g , flavonoid from 1057 to 1992 µg/g FW and DPPH scavenging activity from 35.60% to 63.47%. Pearson correlation analysis identified pod weight and pulp weight per pod as the most strongly associated trait pair ($r = +0.866$, $p<0.001$). DPPH scavenging was positively correlated with total phenol ($r = +0.544$, $p<0.05$), confirming phenolics as the primary antioxidant drivers. PCA condensed 19 traits into five principal components explaining 82.66% of cumulative variance. PC1 (30.10%) represented a fruit size and yield axis while PC2 (19.01%) represented a nutritional quality axis. Ward's hierarchical cluster analysis resolved the genotypes into three distinct clusters representing distinct agronomic ideotypes. Genotype T6 emerged as the overall elite amongst the twenty five tamarind genotypes, and the cross T6 × T10 can be recommended for variety improvement in future.

Keywords: *Tamarindus indica,* germplasm, morphological traits, biochemical traits, PCA, cluster analysis, antioxidant, elite genotype, Sriniketan.

PP-4-33

Integrative Assessment of Phenotypic Divergence and Molecular Diversity in Tomato (*Solanum lycopersicum* L.) Germplasm

B. H. Patel[1*], K. C. Patel[1] and Lalita Kumari[1]
[1]*Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand Agricultural University, Anand (Gujarat) - (388 110), India*
*Corresponding author email: barish3011@gmail.com

ABSTRACT

Genetic divergence is a fundamental prerequisite for the success of any crop improvement programme, as the magnitude and pattern of diversity among available germplasm determine the scope for selecting superior and genetically diverse parents for hybridization. In tomato (*Solanum lycopersicum* L.), a wide range of variation exists for yield, quality and adaptive traits; however, effective utilization of this variability requires a comprehensive assessment using both phenotypic and molecular approaches. Mahalanobis's D^2 statistics is one of the most reliable multivariate techniques for estimating genetic divergence based on multiple quantitative characters simultaneously. It classifies genotypes into distinct clusters according to their genetic distances, thereby facilitating the identification of diverse parental combinations capable of producing superior segregants and heterotic hybrids. Estimation of intra- and inter-cluster distances, cluster means and the relative contribution of different traits towards total divergence provides valuable information for parent selection and broadening the genetic base of breeding materials. Nevertheless, phenotypic divergence may not always accurately represent the actual genetic relationships because the expression of morphological traits is often influenced by environmental conditions and genotype × environment interactions. Therefore, assessment of genetic diversity using DNA-based molecular markers has emerged as a powerful complementary approach. Molecular markers detect polymorphism directly at the DNA level, are highly reproducible, unaffected by environmental influences and provide precise estimates of genetic relationships among genotypes. Among the available marker systems, Simple Sequence Repeat (SSR) markers are extensively employed in tomato due to their co-dominant inheritance, high polymorphism, genome-wide distribution, reproducibility and ease of detection. SSR-based analysis enables the estimation of allele frequency, polymorphic information content (PIC), genetic similarity or dissimilarity and clustering of genotypes through dendrogram construction, thereby revealing hidden genetic variation that may not be evident from morphological evaluation alone. Integration of Mahalanobis's D^2 analysis with SSR marker-based diversity assessment offers a comprehensive understanding of the genetic architecture of tomato germplasm by combining phenotypic performance with molecular variation. Comparative analysis of clustering patterns generated through both approaches further helps in validating genetic relationships and identifying truly divergent genotypes for breeding purposes. Such integrated characterization enhances the efficiency of germplasm conservation, parental selection and hybrid development while reducing the risk of narrowing the genetic base. Therefore, the present investigation was carried out to study the genetic divergence among tomato genotypes using Mahalanobis's D^2 statistics and to assess their genetic diversity using molecular markers, thereby generating reliable information for the effective utilization of diverse germplasm in future tomato improvement programmes.

Keywords: Tomato, Genetic divergence, Mahalanobis's D^2 statistics, Simple Sequence Repeat (SSR) markers, Molecular characterization, Germplasm evaluation.

PP-4-34

Genetic Architecture, Trait Association, and Diversity Assessment of China Aster [*Callistephus chinensis* (L.) Nees.] Genotypes using PCA and Cluster Analysis

N. R. Poojashree*, Rajiv Kumar, T. Usha Bharathi, M. R. Rohini,
C. Mahadevaiah, K. V. Ravishankar, R. Venugopalan and Sridhar Gutam
ICAR-Indian Institute of Horticultural Research, Hessaraghatta Lake Post,
Bengaluru - 560089, Karnataka, India
*Corresponding author email: ps376591@gmail.com

ABSTRACT

China aster belongs to the family Asteraceae and is a native of China. It is grown as annual flower for cut flower, loose flower, flower decoration, preparation of bouquets and garlands. For identification and selection of desirable traits for inter-varietal breeding programme, it is necessary to characterize and understand the genetic diversity and genetic relationships among the available germplasm. The present investigation was conducted to evaluate the genetic variability and trait association in China aster genotypes. A total of 54 genotypes, including four checks, were evaluated during *Kharif* and *Rabi* 2024 under an augmented block design, at ICAR-Indian Institute of Horticultural Research, Bengaluru, India. Significant differences were observed for all the quantitative traits, indicating the presence of substantial genetic variability. High GCV and PCV was estimated for traits such as plant height, plant spread, number of branches, leaves and seed yield/plant and flower yield (MT/acre). High heritability coupled with high genetic advance per cent mean was recorded for most of the traits, suggesting the predominance of additive gene action and the effectiveness of direct selection. Correlation analysis revealed that flower yield was significant positive association with plant height, flower stalk length, days to 50% flowering and number of flowers per plant. Principal component analysis explained 70.68% of the total variation in the first three principal components and PCA-biplot also confirm that the traits such as number of flowers/plant, vase life, days to 50% flowering and flower yield have close association. Cluster analysis grouped 54 genotypes into six distinct clusters, indicating considerable genetic divergence. Genotypes belonging to clusters IV (2 genotypes) and I (6 genotypes) exhibited maximum inter-cluster distance and can be utilized as potential parents in hybridization programmes. Superior genotypes identified for desirable traits included G13 for flower stalk length (50.47 cm), G18 for number of flowers per plant (55.72), G32 for flower weight per plant (188.87 g), G16 for early flowering (62.52 days to first flower opening), and AAC-1 (C2) for seed yield (7.51 g plant^{-1}). Importantly, phenological screening stratified the genotypes into early- (4 genotypes), mid- (18 genotypes), and late-flowering (32 genotypes) clusters. The investigation revealed substantial genetic diversity within the China aster germplasm and pinpointed elite parental lines well-suited for future breeding initiatives and commercial production.

Keywords: China aster, Heritability, Genetic advance, Correlation, Principal component analysis.

PP-4-39

Comparative Analysis of Diosgenin Accumulation in Fruit Tissues of Various Southern Indian Accessions of *Balanites roxburghii* Planch.

Guggalada Govardhana Yadav[1,2] and Hosakatte Niranjana Murthy[1,3]*
[1]*Department of Botany, Karnataka University, Dharwad - 580003, India*
[2]*Department of Botany, ADB College, Harapanahalli - 583131, India*
[3]*Department of Horticultural Science, Chungbuk National University, Cheongju - si 28644, Republic of Korea*
*Corresponding author email: hnmurthy60@gmail.com

ABSTRACT

Diosgenin is a highly sought-after steroidal sapogenin in the pharmaceutical industry. In this work, diosgenin levels in the epicarp, pulp, and seed kernels of nineteen *Balanites roxburghii* accessions from Southern India were assessed using high-performance liquid chromatography (HPLC). The accessions were divided into four groups, with greater diosgenin accumulation found in Clusters 1 and 4. Pulp and seed kernels had the highest diosgenin production. While Chennagiri (CHEN) and Chowdlapura-A (CHOW-A) produced the highest levels of seed kernels (16.11 and 14.57 mg/g DW, respectively), Shiruguppi (SHIR) and Jenukallupalya (JENU) produced the most pulp diosgenin (22.46 and 14.74 mg/g DW, respectively). The lowest amount of diosgenin (0.15 to 2.68 mg/g DW) was found in epicarp. A high-quality supply of raw materials for commercial synthesis is guaranteed by cultivating these superior genotypes. Additionally, commercial *B. roxburghii* cultivation offers two benefits: it reduces overexploitation of wild *Dioscorea deltoidea* and provides farmers in arid locations with a sustainable source of income.

Keywords: *Balanites roxburghii*, diosgenin, HPLC analysis, superior accessions, underutilized species.

PP-4-43

CRISPR/Cas9-Mediated Induction of Male Sterility for Use in Plant Breeding

A. Vijeth Gowda[1]* and B. R. Raghu[2]
[1]*M.Sc. scholar, ICAR-IIHR, Bengaluru*
[2]*Senior scientist, ICAR-IIHR Bengaluru*
*Corresponding author email: vijeth.atgc@gmail.com

ABSTRACT

Genome editing represents a transformative advancement in plant breeding, providing the ability to introduce precise and predictable genomic modifications. Unlike conventional breeding approaches, which are often slow and imprecise, genome editing technologies accelerate trait improvement with greatly enhanced accuracy. Among the available systems, CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) has emerged as the most versatile and widely adopted tool. The CRISPR/Cas9 system was originally identified in bacteria as an adaptive immune mechanism against invading phages and plasmids. In this system, fragments of foreign DNA are integrated into CRISPR arrays, transcribed into CRISPR RNAs (crRNAs), and paired with a trans-activating crRNA (tracrRNA) to guide the Cas9 nuclease to the complementary DNA target. Cas9 then introduces double-strand breaks, which are repaired by cellular pathways, resulting in targeted genetic modifications. This natural defense mechanism has been successfully repurposed for genome editing in plants and various other organisms. As a genome editing tool, CRISPR/Cas9 is efficient, cost-effective, and capable of multiplex editing, providing significant advantages over earlier technologies such as zinc finger nucleases (ZFNs) and TALENs. One promising application of this system is in understanding and inducing male sterility. The molecular mechanism of male sterility is associated with disruptions in key genes regulating pollen development, tapetal cell function, callose deposition, or mitochondrial gene expression. Such defects prevent the formation of viable pollen and thereby enforce cross-pollination. Through targeted disruption of fertility-related genes, CRISPR/Cas9 enables the precise and stable induction of male sterility, facilitating hybrid seed production. Successful examples include CRISPR/Cas9-mediated induction of complete male sterility in tomato, tobacco, bread wheat, and several other crops. This powerful tool can also be harnessed in under-utilized horticultural crops to accelerate their genetic improvement by enabling the efficient development of hybrids. In conclusion, CRISPR/Cas9-mediated male sterility offers a powerful strategy for enhancing hybrid breeding and contributing to global food security.

Keywords: Genome editing, CRISPR/-Cas systems, CRISPR Cas9, Male sterility and under-utilized horticultural crops.

PP-4-45

Heterosis, Combining Ability and Gene Action Studies for Yield, Quality Traits and TOLCD Resistance in Tomato (*Solanum lycopersicum* L.)

Raju Sarkar[1], Zakir Hussain[1]*, P. K. Singh[1], R. Selvakumar[1], Navinder Saini[2] and Alka Joshi[3]
[1]*Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India*
[2]*Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India*
[3]*Division of Food Science and Post Harvest Technology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India*
*Corresponding author email: drzakirhussain24@gmail.com

ABSTRACT

Tomato (*solanum lycopersicum* L.) is an important vegetable crop in world scenario. To exploit heterosis and study combining ability with inheritance, total 32 genotypes including seven lines, three testers, twenty-one hybrids and one standard check were evaluated in Line × Tester design. Observation were taken on total 16 traits including yield, quality and ToLCD incidence in tomato. Mean squares for treatments were highly significant for all characters. Mean square values of lines found significant for maximum traits except thickness of pericarp (mm), number of locules per fruit, titratable acidity (%), ascorbic acid (mg/100g), lycopene (mg/100g), beta carotene (mg/100g) and ToLCD incidence (%). Hybrids DTK-102 × Pusa Prasanskrit performed best for yield, firmness and β-carotene content. DTK-54 × Pusa Prasanskrit exhibited strong resistance to ToLCD. Pericarp thickness and fruit shape index showed marked differences, with DTK-103 and DTK-54 × DT-1023933 being outstanding. DTK-102 × DT-1023932 were showing desirable negative heterosis for days to flowering and fruiting. Yield related traits such as fruit number, yield per plant (kg) and 5 fruit weight (g) were enhanced in hybrid DTK-54 × DT-1023933. Hybrid DTK-102 × DT-1023933 was excelling in ascorbic acid, San Marzano × DT-1023932 in lycopene, and DTK-89 × DT-1023932 in β-carotene content. Processing attributes like viscosity and titratable acidity were good enough in DTK-54 × DT-1023933 and DTK-54 × Pusa Prasanskrit, respectively. Disease resistance was notable in DTK-54 × DT-1023933. DTK-102 emerged as effective general combiners for TSS (°B) and earliness, while Pusa Prasanskrit contributed positively to fruit number and lycopene content (mg/100g). Superior specific combining ability was observed in hybrids such as DTK-89 × Pusa Prasanskrit for fruit number. Gene action analysis showed that traits like pericarp thickness (mm), firmness (kg/cm2), weight of 5 fruits (g), yield per plant (kg), ToLCD incidence (%), ascorbic acid and β-carotene were predominantly controlled by non-additive effects, favouring heterosis breeding. Fruit number per plant, TSS (°B), days to 50% flowering and fruiting governed by additive gene action.

Keywords: Tomato, *Solanum lycopersicum*, Heterosis, Combining ability, Line × Tester analysis, General combining ability, Specific combining ability.

PP-4-46

Evaluation of Fertility Levels and Water-Soluble Fertilizers for Sustainable Utilization of Brinjal (*Solanum melongena* L.) var. GJLB-4

Sabhaya Nirali Bharatbhai[1]* and M. V. Patel[2]
[1]*Ph.D. Scholar, Department of Horticulture, B.A.C.A. Anand agricultural University, Anand*
[2]*Associate Professor, Department of Horticulture, C. P. College of Agriculture,*
S. D. Agricultural University, Sardarkrushinagar
*Corresponding author email: sabhayanirali26@gmail.com

ABSTRACT

Brinjal (*Solanum melongena* L.) is an economically important solanaceous vegetable crop widely grown across tropical and subtropical regions. Sustainable utilization of this crop demands efficient nutrient management strategies that optimize agronomic performance without compromising soil health and resource and nutrient use efficiency. In this context, the present investigation was conducted at the College Farm, College of Horticulture, S. D. Agricultural University, Jagudan, during Late *Kharif* 2022 to evaluate the effect of fertility levels and water-soluble fertilizers (WSF) on growth, yield, quality, and soil nutrient status of brinjal var. GJLB-4 for its sustainable utilization. The experiment was laid out in a Factorial Randomized Block Design with three replications, comprising twelve treatment combinations of two fertilizer levels f_1 (80% RDF) and f_2 (60% RDF) and six WSF treatments involving three concentrations (0.5%, 1.0%, and 1.5%) sprayed at 20 and 40 day intervals. Evaluation of agronomic performance revealed that f_1 (80% RDF) recorded significantly maximum plant height at 60 DAT and last harvest (63.91 cm and 70.50 cm), number of branches (4.82), number of fruits per plant (16.91), fruit yield per plant (1.80 kg) and fruit yield per hectare (289.43 q/ha). Post-harvest soil analysis under f_1 revealed maximum available nitrogen (174.37 kg/ha), phosphorus (33.54 kg/ha) and potassium (268.43 kg/ha), reflecting enhanced soil nutrient status and resource use efficiency. Among WSF treatments, s_3 (1.0% WSF at 20-day intervals) recorded maximum plant height (67.07 cm and 73.91 cm), branches per plant (5.43), fruit weight (93.64 g), number of fruits per plant (19.60) and fruit yield per hectare (308.12 q/ha). Maximum soil available nitrogen (175.26 kg/ha), phosphorus (34.47 kg/ha) and potassium (269.60 kg/ha) were recorded under s_5 (1.5% WSF at 20-day intervals). The interaction treatment f_1s_3 proved most effective, recording the highest plant height (68.79 cm and 76.43 cm), number of fruits per plant (23.27), fruit yield per plant (2.45 kg), fruit yield per hectare (346.61 q/ha) and benefit-cost ratio (2.86), demonstrating the potential of integrated nutrient management for sustainable and profitable brinjal production. It is concluded that 80% RDF combined with six foliar sprays of 1.0% water-soluble fertilizer (NPK 19:19:19) commencing 20 days after transplanting at 20-day intervals is superior for agronomic performance, soil nutrient status and sustainable utilization of brinjal var. GJLB-4.

Keywords: *Brinjal, Solanum melongena, nutrient use efficiency, water-soluble fertilizer, foliar spray, benefit-cost ratio, soil nutrient status.*

PP-4-49

Morphological, Biochemical, and Molecular Characterization of *Syzygium cumini* (L.) Skeels Collections from South India

Kirti Saini, Kanupriya Chaturvedi*, Karunakaran Ganesan,
Pritee Singh, Lakshmana Reddy, and Channappa Mahadevaiah
ICAR-Indian Institute of Horticultural Research (IIHR), Hessarghatta, Bangalore-560089
*Corresponding author email: kp.kanu@gmail.com

ABSTRACT

Jamun (*Syzygium cumini* Skeels) is a nutritionally rich fruit valued for its phenolics, anthocyanins, vitamin C, and antioxidant activity, making it a promising raw material for the food, pharmaceutical, and cosmetic industries. However, systematic genetic improvement of jamun remains limited. This study assessed the genetic diversity of twenty-three genotypes through morphological, biochemical, and molecular characterization to identify elite lines for breeding and value addition. The evaluation (2023–25) was conducted at ICAR-IIHR, Bengaluru, and ICAR-IIHR–CHES, Hirehalli. Morphological characterization followed DUS guidelines, while biochemical traits included fruit weight, pulp percentage, total soluble solids (TSS), titratable acidity, vitamin C, phenolics, anthocyanins, and antioxidant activity. Multivariate analysis was applied for clustering. Molecular diversity was estimated using 50 SSR markers. Significant variability was observed across genotypes for fruit and biochemical traits (fruit weight: 1.97–18.32 g; pulp: 66.50–92.26%; TSS: 10–18.2 °Brix; titratable acidity: 0.43–2.67%; vitamin C: 23.40–65.07 mg/100 g; phenolics: 120.78–936.26 mg GAE/100 g; antioxidant activity: 307.78–2493.91 mg AEAC/100 g; anthocyanins: 42.59–268.50 mg/100 g). Multivariate analysis grouped the genotypes into three clusters, identifying CHESHJ-XI/3, CHESHJ-V/1, and CHESHJ-Wd-1 as rich in nutraceutical compounds. SSR analysis revealed high polymorphism (mean PIC = 0.687), with CHESHJ-Wd-1 being the most divergent genotype. The results underscore jamun's potential as a functional food and industrial crop. Kaithnal and AJG-85 were superior for fresh fruit quality, CHESHJ-XI/3 and CHESHJ-V/1 for nutraceutical traits, CHESHJ-Wd-1 for antioxidant potential, and CHESHJ-Wt-1 for dwarf stature with high TSS. These findings provide a foundation for targeted breeding, germplasm conservation, and nutraceutical product development, reinforcing jamun's role in food security and health innovation.

Keywords:

PP-4-51

Phytochemical Profiling and Antioxidant Activity of *Jasminum* Species

V. Siva Teja[1]*, Anupama T. V.[2], Mini Sankar[3], Shajma Nafeesa Basheer[3], Parvathi M. Sreekumar[3] and Asish I. Edakkalathur[4]

[1]*Department of Floriculture and Landscaping, College of Agriculture, Thrissur, Kerala Agricultural University, Thrissur, Kerala - 680 656*

[2]*Fruits Crops Research Station, Kerala Agricultural University, Thrissur, Kerala - 680 656*

[3]*College of Agriculture, Kerala Agricultural University, Thrissur, Kerala - 680 656*

[4] *Cashew Research Station, Kerala Agricultural University, Madakkathara, Kerala - 680 656*

*Corresponding author email: sivatejaveera777@gmai.com

ABSTRACT

The Peninsular India, a landscape encompassing globally significant biodiversity hotspots including the Western Ghats, harbours a rich repository of aromatic and medicinal plant genetic resources, including diverse species of the genus *Jasminum* (family Oleaceae). Species such as *J. sambac*, *J. multiflorum*, *J. grandiflorum*, and *J. auriculatum* are traditionally valued for their fragrant flowers and therapeutic properties. To explore this traditional relevance in a scientific context and assess the phytochemical diversity and antioxidant potential of selected *Jasminum* species, eight *Jasminum* genotypes such as *J. sambac*, *J. multiflorum*, *J. grandiflorum*, *J. auriculatum*, *J. nitidum*, *J. fluminense*, *J. coarctatum* and *J. malabaricum* were collected from selected regions of Western Ghats and cultivation tracts of Kerala. These accessions were established and maintained in the Department of Floriculture and Landscaping, College of Agriculture, Vellanikkara, Thrissur. Qualitative phytochemical screening confirmed the presence of alkaloids, flavonoids, phenols, tannins, and saponins in all the genotypes. The highest phenol, flavonoid and tannin contents were recorded in *J. grandiflorum* (40.52 mgGAE/g), *J. multiflorum* (31.48 mgQE/g) and *J. malabaricum* (39.60 mgTAE/g) respectively, while *J. fluminense* (0.0205 g) showed the highest alkaloid and *J. nitidum* (0.1021 g) recorded the highest saponin content. Antioxidant activity assessed through DPPH and ABTS radical scavenging assays showed that *J. multiflorum* exhibited the lowest IC_{50} value of 28.394 µg/ml (DPPH) and 28.909 µg/ml (ABTS), indicating the strongest free radical scavenging potential among the genotypes. The observed genotype specific variability in metabolite profiles further emphasizes the value of these species as promising sources of bioactive compounds for future pharmacological exploration.

Keywords: *Jasminum*, Antioxidant activity, Western Ghats, Phytochemicals, Secondary metabolites.

PP-4-52

Integrated Multivariate Characterization and Multi-Trait Selection of Finger Millet Genotypes for Yield and Nutritional Improvement

Mihir A. Hansalia[1]*, Vikas Pali[2], Hemanthkumar Koorakula[1], Parth Patel[1] and Ahwan Sanket Pradhan[1]
[1]*Department of Genetics and Plant Breeding, N. M. College of Agriculture, Navsari Agricultural University, Navsari (Gujarat), 396 450, India*
[2]*ICAR Research Complex for NEH Region, Kolasib, Mizoram, 796 081, India*
*Corresponding author email: mihirhanssaliya@gmail.com

ABSTRACT

Finger millet (*Eleusine coracana* (L.) Gaertn.) is an important climate-resilient nutri-cereal with considerable potential for simultaneous improvement of productivity and nutritional quality. However, selection based on individual traits may be ineffective because yield and nutraceutical attributes are complex and interrelated. The present study therefore employed an integrated multivariate approach to identify promising finger millet genotypes based on 19 agro-morphological and nutraceutical traits evaluated in 50 genotypes during kharif 2023 under semi-arid conditions of Middle Gujarat. Principal Component Analysis (PCA), Exploratory Factor Analysis (EFA) and the Multi-trait Genotype Ideotype Distance Index (MGIDI) were used to characterize the multidimensional variation and identify genotypes with balanced multi-trait performance. The first seven principal components accounted for 74.00% of the total variation, with phenology, plant architecture, yield components and nutritional attributes contributing substantially to the observed diversity. EFA further organized the correlated traits into seven biologically meaningful factors, providing a simplified representation of the complex trait relationships. At a 16% selection intensity, MGIDI identified eight promising genotypes, namely PCGF-27, PCGF-42, FMA-54, FMA-5, FMA-36, FMA-33, FMA-17 and PCGF-9, as the closest to the defined multi-trait ideotype. The predicted selection response was particularly high for harvest index (27.3%), grain yield per plant (26.4%) and protein content (21.9%), indicating the potential for simultaneous improvement of productivity and nutritional quality. Factor contribution analysis further revealed genotype-specific strengths and weaknesses, providing a basis for identifying complementary parents for future hybridization. The integrated PCA-EFA-MGIDI approach therefore provides an efficient framework for translating complex phenotypic variation into practical multi-trait selection decisions and identifying promising genetic resources for the development of high-yielding and nutritionally improved finger millet cultivars.

Keywords: Finger millet, Multivariate analysis, PCA, Exploratory factor analysis, MGIDI, Multi-trait selection, Nutritional quality.

PP-4-54

Genome Analysis in Pre-Breeding Lines derived from Greengram × Ricebean Crosses

P. Venkatesh* and P. Jayamani
Department of Genetics and Plant Breeding, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India
*Corresponding author's email: venkateshagri29@gmail.com

ABSTRACT

Greengram (*Vigna radiata* (L.) Wilczek) possesses a narrow genetic base that restricts genetic improvement. Ricebean (*Vigna umbellata* (Thunb.) Ohwi & Ohashi), a tertiary gene pool species, represents a valuable source of novel alleles for broadening the genetic base of greengram. Three advanced (F_{11}) interspecific pre-breeding lines COGRISC 1 (CO 6 × RBL 35/1), COGRISC 2 (CO 6 × RBL 35/2), and COGRISC 3 (CO 7 × LRB 576) were developed from greengram × ricebean crosses. To identify parental polymorphism, the greengram parents (CO 6 and CO 7) and ricebean parents (RBL 35 and LRB 576) were screened using 155 adzuki bean-derived simple sequence repeat (SSR) markers. Of these, 148 (95.5 %) amplified successfully, including 124 (80.0 %) polymorphic, 18 monomorphic, and six multi-allelic markers. The polymorphic markers were subsequently used for genotyping the three pre-breeding lines along with parents. The allele size ranged from 110 to 280 bp. CEDG050 and CEDG141 differentiated the greengram parents, whereas CEDG010 and CEDG073 differentiated the ricebean parents. Ten markers namely, CEDG008, CEDG024, CEDG033, CEDG050, CEDG117, CEDG121, CEDG141, CEDG156, CEDG174 and CEDG196 differentiated the three pre-breeding lines. The studies on allelic composition revealed a predominance of ricebean-derived alleles, with COGRISC 1 and COGRISC 2 each possessing 25 greengram, 71 ricebean, and 28 hybrid alleles, whereas COGRISC 3 contained 30 greengram, 65 ricebean, and 29 hybrid alleles, indicating preferential retention of ricebean genomic segments. Graphical Genotype (GGT) analysis revealed mosaic introgression of parental genomic segments across all 11 linkage groups, and predominance of ricebean-derived alleles in the introgressed lines. UPGMA cluster analysis performed using DARwin software grouped the seven genotypes into two clusters. The greengram parents formed Cluster I, whereas the ricebean parents together with the three pre-breeding lines formed Cluster II. These findings validate ricebean genome introgression and demonstrate the utility of SSR markers for genome characterization and assessment of genetic relationships in interspecific pre-breeding lines. These introgressed lines represent valuable genetic resources for broadening the genetic base and accelerating greengram improvement.

Keywords: Greengram, Ricebean, Genome introgression, SSR markers, Pre-breeding lines.

PP-4-55

Screening Avocado (*Persea americana* Mill.) Accessions from Kodagu Region of Karnataka for Low-Browning Genotypes

P. Laya*, Anuradha Sane, G. Karunakaran, B. M. Muralidhara and Roopendra Kumar
Indian Institute of Horticultural Sciences, Bengaluru
*Corresponding author email: layaprasanna05@gmail.com

ABSTRACT

Avocado is a nutritionally rich exotic fruit crop belonging to the Lauraceae family, originating from Mexico and Central America, and is believed to have evolved from more than one wild species. Over the past decade, the demand for avocado fruits has increased considerably; however, one of the major post-harvest challenges faced by consumers is the rapid browning of the pulp after the fruit is cut open. The present study was undertaken to evaluate browning intensity among selected avocado genotypes, and a total of thirty genotypes were assessed for their browning response under ambient conditions following four hours of exposure to air. Browning intensity was evaluated through visual scoring, and several low-browning genotypes were identified during the study. Among the genotypes assessed, several exhibited low browning intensity, while genotypes PA026 (yellow fruit pulp), PA059 (desirable average fruit weight of 300-350 grams), and PA072 (better fruit size) showed reduced browning along with superior morphological characteristics. The study identified promising genotypes with reduced browning potential that can be utilized for fresh consumption and processing industries. These findings also provide a valuable basis for selection and breeding programmes aimed at improving post-harvest quality in avocado.

Keywords: Avocado, *Persea americana*, Germplasm evaluation, Post-harvest quality, Pulp browning, Browning intensity, Low-browning genotypes.

PP-4-56

Harnessing indigenous Finger millet (*Eleusine coracana* (L.) Gaertn.) germplasm through integrated genetic variability and diversity analysis for sustainable crop improvement

Koorakula Hemanth Kumar[1]*, Shweta[2], Mihir A. Hansalia[1] and Kalva Santhi Kumari[2]
[1]*Department of Genetics and Plant Breeding, Navsari Agricultural University, Navsari, Gujarat, India*
[2]*Department of Genetics and Plant Breeding, CSA University of Agriculture and Technology, Kanpur, Uttar Pradesh, India*
*Corresponding author email: hemanthkoorakula123@gmail.com

ABSTRACT

Indigenous plant genetic resources (PGR) represent an invaluable reservoir of novel alleles for strengthening crop resilience, productivity and nutritional security. Finger millet (*Eleusine coracana* (L.) Gaertn.), one of the most nutritious yet underutilized small millets, possesses substantial genetic diversity that remains insufficiently characterized for effective use in breeding programmes. The present investigation was undertaken to decipher the extent of genetic variability, identify key yield-determining traits and characterize genetic divergence among indigenous finger millet germplasm to facilitate strategic parent selection and sustainable utilization of these genetic resources. Fifty finger millet genotypes collected from Indian Institute of Millet Research (IIMR), Hyderabad, Telangana, were evaluated over two consecutive growing seasons for seventeen agro-morphological and yield-related traits using quantitative genetic and multivariate analytical approaches. Highly significant variation among genotypes for all evaluated traits demonstrated the existence of a broad genetic base within the germplasm. Culm thickness and biological yield per plant exhibited the highest phenotypic and genotypic coefficients of variation, indicating considerable opportunities for effective selection. Broad-sense heritability ranged from 67.2% to 98.4%, with traits including biological yield, culm thickness, finger length and flag leaf dimensions expressing high heritability coupled with substantial genetic advance, suggesting that additive genetic effects predominantly govern their inheritance. Grain yield exhibited strong positive associations with biological yield, ear head length, number of fingers per ear, number of leaves per plant, flag leaf blade length and days to maturity. Path coefficient analysis further established biological yield, harvest index, ear head length, number of fingers per ear, culm thickness, sheath width and finger length as the principal contributors exerting direct positive effects on grain yield, thereby identifying robust phenotypic selection criteria for yield enhancement. Multivariate analyses revealed extensive genetic divergence among the evaluated germplasm. The first six principal components accounted for 72.80% of the total phenotypic variability, indicating that variation was predominantly governed by yield-contributing and phenological attributes. Mahalanobis D^2 analysis resolved the germplasm into twelve distinct clusters, including six solitary clusters that represent genetically unique accessions with considerable breeding potential. Days to 50% flowering contributed the largest proportion (33.87%) to total genetic divergence, while the maximum inter-cluster divergence observed between Clusters IV and IX identified highly contrasting parental groups capable of generating broad variability and superior transgressive segregants. Collectively, the integration of variability, association and diversity analyses enabled the identification of genetically

distinct and agronomically valuable germplasm that can be effectively harnessed to broaden the breeding pool, accelerate genetic gain and promote the sustainable utilization of indigenous finger millet plant genetic resources.

Keywords: Finger millet; Germplasm; Variability; Correlation study; Diversity.

PP-4-57

Genetic Variability for Rind Citrulline Content and Yield Traits in Diverse Watermelon (*Citrullus lanatus* L.) Germplasm

M.S. Varshini[1]*, Eguru Sreenivasa Rao[2] and M. Arivalagan[3]

[1]*Ph.D. Scholar, Division of Vegetable Crops, ICAR–Indian Institute of Horticultural Research (IIHR), Bengaluru, Karnataka, India*

[2]*Principal Scientist, Division of Vegetable Crops, ICAR–Indian Institute of Horticultural Research (IIHR), Bengaluru, Karnataka, India*

[3]*Senior Scientist, Division of Biochemistry, ICAR–Indian Institute of Horticultural Research (IIHR), Bengaluru, Karnataka, India*

*Corresponding author email: varshinims18@gmail.com

ABSTRACT

Watermelon (*Citrullus lanatus* L.) is an economically important cucurbit crop with considerable potential for nutritional enhancement and value addition. The rind, constituting nearly one-third of the fruit biomass, is a rich natural source of L-citrulline, a non-protein amino acid recognized for its role as a precursor of L-arginine and nitric oxide, contributing to cardiovascular health, antioxidant activity, and immune regulation. Despite its nutritional significance, watermelon rind is largely discarded as processing waste. Exploration of genetic variability for rind biomass and citrulline content among diverse germplasm is therefore essential for the effective utilization of plant genetic resources and the development of value-added cultivars. The present investigation was carried out to evaluate the extent of genetic variability for rind yield traits and rind citrulline content in diverse watermelon germplasm over two consecutive seasons. A total of 87 genotypes were evaluated during Rabi 2025, while the germplasm set was expanded to 89 genotypes during Summer 2026 under field conditions. Observations were recorded for fruit weight, rind weight, rind thickness and rind L-citrulline content, which was quantified using High-Performance Liquid Chromatography (HPLC). Evaluation of the germplasm across two seasons revealed substantial phenotypic variability for rind yield traits and L-citrulline content, indicating the availability of exploitable genetic variation within the collection. During Rabi 2025, the highest fruit weight, rind weight and rind thickness recorded were 2.92 kg, 1.069 kg and 16.5 mm, respectively, while the corresponding maximum values during Summer 2026 were 6.44 kg, 3.246 kg and 18 mm. Rind L-citrulline concentration varied widely among the genotypes, with maximum values of 230 mg 100 g^{-1} in Rabi 2025 and 350 mg 100 g^{-1} in Summer 2026, whereas the check varieties consistently exhibited lower concentrations ranging from 32–79 mg 100 g^{-1} in Rabi 2025 and 150–200 mg 100 g^{-1} in Summer 2026. The observed variability across seasons highlights the potential of these germplasm resources for breeding watermelon cultivars

with enhanced rind biomass and improved nutraceutical quality. The superior genotypes identified in the present investigation constitute promising parental material for breeding programmes aimed at developing watermelon cultivars with enhanced nutraceutical value and improved rind biomass. The study further demonstrates the potential of harnessing watermelon genetic resources for rind valorization, thereby supporting sustainable utilization of plant genetic resources, reducing agro-industrial waste and promoting the development of functional food and nutraceutical products.

Keywords: Watermelon, germplasm, genetic variability, L-citrulline, rind biomass, HPLC, plant genetic resources, nutraceuticals.

PP-4-58

Multivariate Analysis of Morphological Diversity in Bitter Gourd (*Momordica charantia* L.) Germplasm

A. Adithya*, Tusar Kanti Behera, B. Varalakshmi, K. Hanumegowda, Vivek Hegde, and Mahadev Kivati
ICAR–Indian Institute of Horticultural Research (IIHR), Bengaluru, Karnataka, India
*Corresponding author email: adithyaanilkumar23@gmail.com

ABSTRACT

Genetic diversity assessment is essential for the effective utilization of germplasm in bitter gourd (*Momordica charantia* L.) breeding programmes. In the present study, 98 bitter gourd genotypes comprising breeding lines, germplasm accessions, released varieties, and advanced selections were evaluated for seven quantitative morphological traits to assess phenotypic diversity. Mahalanobis D^2 analysis grouped the genotypes into distinct clusters, indicating substantial genetic divergence among the evaluated materials. Principal component analysis (PCA) further characterized the pattern of variability, with the first three principal components explaining 80.0% of the total phenotypic variation. Among these, PC1, PC2, and PC3 accounted for 41.2%, 22.0%, and 16.8% of the variation, respectively. PC1 was predominantly associated with fruit weight (26.33%), yield per plant (19.72%), fruit circumference (17.44%), days to first female flower appearance (15.73%) and fruit length (14.95%), indicating that fruit size, yield, and earliness were the major contributors to genetic divergence. The PCA score plot revealed wide dispersion of genotypes, with IIHR-BTG-24-1, IIHR-BTG-IP-20-179, IIHR-BTG-29, IIHR-PMR-IP-24-11, IIHR-PMR-IP-24-9, IIHR-209, IIHR-203, IIHR-210, IIHR-BTG-IP-20-156 and IIHR-BTG-134 occupying extreme positions, indicating their high genetic divergence from the remaining germplasm. The PCA pattern complemented the clustering obtained through Mahalanobis D^2 analysis, confirming broad phenotypic diversity among the evaluated genotypes. These genetically divergent accessions represent valuable parental resources for hybridization and population development aimed at improving yield, earliness, and fruit quality in bitter gourd breeding programmes.

Keywords: *Momordica charantia* L.; Genetic diversity; Multivariate analysis; Mahalanobis D^2; Phenotypic diversity.

PP-4-59

Bridging Genetic Bottlenecks in Chickpea through Exploiting Wild *Cicer* Gene Pools for Sustainable Crop Improvement

Ramachandran Senthil[1*], Swapnil Baraskar[1,2], Ganesh Pawar[1],
Vetriventhan Mani[1], Ovais Peerzada[1] and Kuldeep Singh[1]
[1]*International Crops Research Institute for the Semi-Arid Tropics (ICRISAT),*
Patancheru - 502 324, Hyderabad, Telangana, India
[2]*Professor Jayashankar, Telangana Agricultural University (PJTAU), Hyderabad, India*
*Corresponding author email: senthil.ramachandran@icrisat.org

ABSTRACT

Chickpea (*Cicer arietinum*) is an important pulse crop that contributes to global food security. However, its yield is severely limited by biotic stresses [Ascochyta blight (AB) and Fusarium wilt (FW)] and abiotic stresses (drought and heat). The domestication of chickpea has narrowed its genetic base, thereby limiting its adaptive potential to cope with climatic variability and environmental stresses. Therefore, crop wild relatives (CWRs) of *Cicer* can serve as repositories of genetic diversity to broaden the genetic base and improve resilience to environmental stresses. The primary gene pool, consisting of cultivated chickpea (*C. arietinum*) and its wild progenitor (*C. reticulatum*), offers immediate breeding utility owing to cross-compatibility. Secondary (*C. echinospermum*) and tertiary (41 wild species) gene pools harbour valuable traits but are not widely used due to hybridization incompatibility and reduced fertility. The ICRISAT genebank conserves 20,838 chickpea accessions, including 478 wild relatives belonging to 12 species. Among them, *C. pinnatifidum* (ICC 17344), *C. bijugum* (ICC #20177, 17294, 20166, 20167), *C. echinospermum* (ICC 17334 and ICC 17335), and *C. yamashitae* (ICC 20203) were identified as resistant to *Ascochyta* blight, while *C. bijugum* (ICC# 17290, 17297, 17299, 17305, and 17307) and *C. reticulatum* (ICC 17270) were identified as resistant to *Fusarium* wilt. Furthermore, *C. bijugum* (ICC 20167) and *C. pinnatifidum* (ICC 20172) are the most valuable sources, exhibiting combined resistance to *Fusarium* wilt and *Ascochyta* blight. Wild Cicer constitute important sources for scouting genes offering resistance to AB and FW, but there are barriers to utilizing them in breeding programmes. Some of these barriers include pre- and post-zygotic crossing barriers, linkage drag, and limited evaluation of the wild Cicer germplasm. New genomics-assisted breeding methods and refined pre-breeding approaches may provide opportunities to resolve these constraints. Developing climate-resilient cultivars with stable productivity will require a targeted approach and more effective use of wild Cicer germplasm, particularly the underutilized wild gene pools.

Keywords: Chickpea, Germplasm, Wild, Gene pool, Pre-breeding, Sustainability.

PP-4-60

Harnessing Plant Genetic Resources for Hybrid Development in Bell Pepper (*Capsicum annuum* L.)

Pratibha Singh[1*], Devinder Kumar Mehta[1*], Ramesh Kumar Bhardwaj[2], Rajesh Kumar Dogra[3] and Meenu Gupta[4]

[1]*Department of Vegetable Science, College of Horticulture, Dr Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh-173 230, India*

[2]*Department of Vegetable Science, College of Horticulture and Forestry, Dr Yashwant Singh Parmar University of Horticulture and Forestry, Neri, Hamirpur, Himachal Pradesh-177001, India*

[3]*Department of Fruit Science, College of Horticulture, Dr Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh-173 230, India*

[4]*Department of Plant Pathology, College of Horticulture, Dr Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh-173 230, India*

*Corresponding author email: parul1799@gmail.com; devinder1971@gmail.com

ABSTRACT

Plant genetic resources provide the gene pool essential for developing high-yielding, nutritionally superior and climate-resilient cultivars. Bell pepper (*Capsicum annuum* L.) possesses considerable genetic diversity that can be effectively exploited through heterosis breeding. The present investigation was conducted during 2024–2025 at the Experimental Farm, Department of Vegetable Science, Dr Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India, to evaluate the heterotic potential and combining ability of diverse bell pepper germplasm. The experimental material comprised 15 genetically diverse lines and three testers, crossed in a Line × Tester mating design to generate 45 F_1 hybrids. The hybrids, along with 18 parents and one commercial check (F_1 Diamond Star), were evaluated in a Randomised Complete Block Design with three replications for yield, horticultural and quality traits. Analysis of variance revealed significant genetic variability among the genotypes for all the traits studied. Among the parental lines, UHF-CAP-132, UHF-CAP-131 and UHF-BP-5 were identified as superior general combiners, while California Wonder proved to be the most efficient tester. Specific combining ability analysis identified UHF-BP-4 × California Wonder, UHF-BP-3 × Solan Bharpur and UHF-BP-2 × Solan Shakti as the most promising hybrid combinations for fruit yield. Standard heterosis over the commercial check (F_1 Diamond Star) identified hybrids UHF-BP-4 × California Wonder and UHF-CAP-132 × California Wonder as the most promising for fruit yield per plant, while UHF-BP-5 × Solan Shakti and UHF-CAP-131 × California Wonder emerged as superior hybrids for number of fruits per plant. The study demonstrates that the effective utilisation of genetically diverse bell pepper germplasm can accelerate hybrid development through heterosis breeding. The superior parental lines and hybrid combinations identified in this study represent valuable plant genetic resources for developing high-yielding, nutritionally enriched bell pepper hybrids and warrant further evaluation through multilocation trials for sustainable crop improvement.

Keywords: Combining ability, *Capsicum annuum*, gene pool, heterotic potentail, line × tester, plant genetic resources.

PP-4-61

Estimation of Heterosis for Yield and Yield-Attributing Traits in Okra (*Abelmoschus esculentus* L. Moench)

Sristi Sharma[1]*, Happy Dev Sharma[1], Devinder Kumar Mehta[1],
Rajesh Kumar Dogra[2] and Vipin Sharma[3]
[1]*Department of Vegetable Science, Dr Yashwant Singh Parmar University of Horticulture and Forestry Nauni, Solan, Himachal Pradesh - 173 230, India*
[2]*Department of Fruit Science, Dr Yashwant Singh Parmar University of Horticulture and Forestry Nauni, Solan, Himachal Pradesh - 173 230, India*
[3]*Department of Environmental Science, Dr Yashwant Singh Parmar University of Horticulture and Forestry Nauni, Solan, Himachal Pradesh - 173 230, India*
*Corresponding author email: sristisharma519@gmail.com

ABSTRACT

Okra (*Abelmoschus esculentus* (L.) Moench) is an economically important vegetable crop valued for its nutritional, medicinal and commercial significance. Heterosis breeding offers considerable potential for developing high-yielding hybrids with superior traits. The present study estimated heterosis for yield and related attributes using nine genetically diverse open-pollinated parental genotypes and 36 F_1 hybrids generated using a half diallel mating design during *Kharif* season of 2024 at the Vegetable Research Farm, Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India. Significant variability among genotypes confirmed substantial genetic diversity. Among parents, Pusa Bhindi-5 performed best for earliness, fruit weight, fruit length and fruit yield per plant. The hybrid Perkins Long Green × Pusa Bhindi-5 was most promising, recording maximum yield per plant (388.99 g), number of fruits per plant (22.53), number of pickings (23.26) and crop duration (94.67 days). Pusa Bhindi-5 × Kashi Lalima excelled in fruit length (15.80 cm), fruit weight (19.16 g) and inter-nodal length (5.95 cm). Significant heterosis and heterobeltiosis were observed for several yield-contributing traits. Perkins Long Green × Pusa Bhindi-5 exhibited maximum positive heterobeltiosis (46.78%) and standard heterosis (68.44%) for yield per plant. Significant negative heterosis for earliness such as days to 50% flowering and first picking highlighted potential hybrids for early marketable yield. This study reveals trait associations; fruit number, fruit length and crop duration as key contributors to yield heterosis in okra. Diverse parental integration and superior hybrid identification provide novel resources for ideotype breeding, supporting hybrid development, molecular validation and multi-location testing for commercial improvement.

Keywords: Heterobeltiosis, Heterosis vigour, Okra, Standard Heterosis, Yield.

PP-4-62

Protocol Optimization of *In Vitro* Regeneration in Rice utilized for Genetic Transformation Studies in Rice Varieties Suited for Konkan Region

Tanmay B. Kamble[1]*, S. V. Sawardekar[2] and S. H. Sherkar[3]

[1]*M.Sc. Agri., Department of Agricultural Botany, College of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli - 415 712*

[2]*Incharge, Plant Biotechnology Centre, College of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli - 415 712*

[3]*Junior Research Assistant Plant Biotechnology Centre, College of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli - 415 712*

*Corresponding author email: kamble21tanmay@gmail.com

ABSTRACT

Rice (*Oryza sativa* L.) serves as the primary staple food for nearly one-half of the global population, particularly in East and Southeast Asia, with 95 % of the total yield consumed directly by humans. Given the continuous demographic growth and the shrinking availability of arable land due to urbanization, expanding cultivated areas is increasingly unfeasible. Consequently, the most viable solution to enhance productivity is the utilization of novel biotechnological tools. Genetic engineering is strongly dependent on genotype and availability of an efficient *in vitro* plant regeneration method. Numerous reports been published regarding the rice tissue culture, but genotype dependence remains a hurdle and regeneration in *indica* rice is still a difficult task. Owing to poor regeneration abilities, *indica* cultivars are recalcitrant to various biotechnological advances. The key steps in rice genetic improvement programme through application of biotechnology includes identification and screening of useful cultivars for embryogenic callus formation and subsequent *in vitro* plant regeneration with embryogenic calli obtained from mature seed embryos serving an efficient target in *indica* rice transformation. To address the above important aspects the investigation entitled "*In vitro* regeneration studies in rice (*Oryza sativa* L.)" was carried out in tissue culture laboratory at Plant Biotechnology Centre, College of Agriculture, Dapoli-Ratnagiri (M.H.). The research aimed to develop suitable *in vitro* regeneration protocol which can be utilized for genetic transformation studies in the three rice varieties, *viz.*, Ratnagiri-8, Karjat Shatabdi, Karjat-3. The callusing ability of the varieties was tested on 12 medium combinations consisting M.S. basal medium supplemented with different concentrations of 2,4-D and NAA, their combinations and one control treatment. The highest callus induction was recorded for medium combination T_2:M.S.+2,4-D(2.0mg/l)+NAA (0.5 mg/l) in Ratnagiri-8 (66.67 %) and Karjat Shatabdi (53.33 %) while Karjat-3 showed highest callus induction of 68.33 % for medium combination T_3: M.S. + 2,4-D (2.0 mg/l) + NAA (1.0 mg/l). Embryogenic, soft, friable callus with granular texture and yellowish white colour was obtained from all media combinations in all three varieties. The regeneration ability of the varieties was tested on 15 medium combinations with M.S basal medium supplemented with different concentrations of BAP and Kinetin, their combinations and one control treatment. The highest regeneration was observed for T_5: M.S. + BAP (2.5 mg/l) in Ratnagiri-8 and Karjat Shatabdi and for T_6: M.S. + BAP (3.0 mg/l) in Karjat-3.

Keywords: Genetic transformation, Callus induction, In vitro regeneration and Media.

PP-4-63

Reproductive Trait Characterisation of Annona Plant Genetic Resources: A Comparative Study of Pollen Germination, Pollen Viability and Stigma Receptivity

Madhumathi[1]*, T. Sakthivel[1], M. Sankaran[1], P. L. Anushma[1], G. Karunakaran[1], K. S. Shivashankara[2], D. C. Lakshmana Reddy[2] and C. Mahadevaiah[3]

[1]*Division of Fruit Crops, ICAR-Indian Institute of Horticultural Research, Hesaraghatta Lake Post, Bengaluru, Karnataka, India*

[2]*Division of Basic Sciences, ICAR-Indian Institute of Horticultural Research, Hesaraghatta Lake Post, Bengaluru, Karnataka, India*

[3]*Division of Vegetable Crops, ICAR-Indian Institute of Horticultural Research, Hesaraghatta Lake Post, Bengaluru, Karnataka, India*

*Corresponding author email: madhuvijayarengan@gmail.com

ABSTRACT

Annona species are valuable tropical fruit crops with immense potential for crop improvement, nutritional security, and sustainable horticulture. Peninsular India harbours diverse Annona genetic resources, including cultivated species, hybrids, and underutilised germplasm. However, breeding and genetic improvement in Annona are constrained by their unique reproductive biology. Although the flowers are hermaphroditic, they exhibit protogynous dichogamy, in which the stigma becomes receptive before pollen is released from the same flower, thereby limiting natural pollination and necessitating assisted pollination to improve fruit set and quality. Understanding pollen quality and stigma receptivity is therefore essential for efficient hybridisation and sustainable utilisation of Annona genetic resources. The present study evaluated pollen germination percentage, pollen viability, and stigma receptivity in seven Annona species, namely *Annona muricata, A. squamosa, A. reticulata, A. cherimola, A. × atemoya*, Arka Sahan (*A. atemoya × A. squamosa*), and *A. glabra*. Pollen collected during the male floral phase was assessed for *in vitro* germination and viability using standard protocols, while stigma receptivity was evaluated at different stages of floral development to determine the effective pollination period. Significant interspecific variation was observed in pollen germination and viability among the evaluated taxa. *Annona glabra* recorded the highest pollen germination (65%) and viability (92%), whereas *A. × atemoya* exhibited the lowest pollen germination (38%) and *A. reticulata* showed the lowest pollen viability (68%). The hybrid Arka Sahan recorded 10% pollen germination and 65% pollen viability, indicating distinct reproductive characteristics compared with the evaluated species. The findings provide baseline information on reproductive traits that will facilitate optimisation of assisted pollination, selection of suitable parents for hybridisation, and efficient utilisation of Annona germplasm. The study contributes to the characterisation of plant genetic resources and provides a foundation for future research on reproductive compatibility, pollen–pistil interactions, and the genetic improvement and conservation of Annona.

Keywords: Annona; plant genetic resources; pollen germination; pollen viability; stigma receptivity; assisted pollination; germplasm characterisation; sustainable utilisation.

PP-4-64

Characterization and Evaluation of Yellow Mangosteen (*Garcinia xanthochymus*) accessions for Morpho-Biochemical Traits

Akriti Tiwari*, Anuradha Sane, Roopendra Kumar and A. Vithiyalakshmi
ICAR-Indian Institute of Horticulture of Research, Hessaraghatta, Bengaluru - 560089
*Corresponding author email: akrititiwari1222@gmail.com

ABSTRACT

Garcinia xanthochymus, commonly known as yellow mangosteen, belongs to family Clusiaceae. It is native to Indian subcontinent, found widely distributed in the lower hills of eastern Himalayas and in the western ghats from Konkan to Keralam. It is valued for its health promoting properties showing strong anti-oxidant, antiobesity and antidiabetic activities. Since there is a lack of comprehensive research, the current study aimed at evaluation and characterization of morphological traits of 13 genotypes to understand the extent of variability present. The morphological traits of tree, leaf and fruits were recorded using IPGRI descriptors for Mangosteen. Tree height ranged from R1P1 (3.65m) to R8P2 (6.6m). The canopy diameter ranged from 2.5 m to 5.4m (E–W) and 2.7 m to 5.5m (N–S). The accessions exhibited a pyramidal crown shape with a spreading growth habit and dense branching. The number of primary branches ranged from 25 to 64, trunk diameter from 42 to 98 cm, and fruit yield from 200 to 1,220 fruits per tree. Fruit length varied between 6.34 and 7.70 cm, fruit breadth from 6.37 to 8.09 cm, and fruit weight from 132.26 to 241.76 g. Pulp weight ranged from 114.16 to 205.08 g, while total seed weight varied from 19.67 to 36.85 g, and pulp recovery of 83.99–87.52%. The number of seeds per fruit ranged from 2.1 to 3.4, total soluble solids (TSS) from 12.50 to 15.26 °Brix, and titratable acidity from 3.072 to 4.736%, indicating considerable phenotypic diversity among the accessions. The number of fruits per tree exhibited a significant positive correlation with north–south canopy spread (N–S) (r=0.579**). Fruit weight showed strong and significant positive correlations with pulp weight (r =0.998**), fruit breadth (r =0.985**), fruit length (r = 0.884**), and total seed weight (r =0.843**). Fruit weight is an important selection trait due to its strong positive association with fruit size and pulp weight, while canopy spread was associated with higher fruit production, indicating their potential as key selection criteria in breeding and germplasm improvement. Among the evaluated accessions, R2P1 was identified as a superior accession for fruit size, fruit weight, and total soluble solids (TSS), while R4P2 exhibited desirable traits including larger fruit size, higher fruit weight, and high TSS, indicating their potential for selection and crop improvement.

Keywords: *Garcinia xanthochymus,* Konkan, Keralam, antioxidants, variability.

PP-4-65

Character Association and Path Coefficient Analysis for Yield and its Components in Pigeonpea (*Cajanus cajan* L. Millsp.)

M. Jeya Varshini[1], D. Malarvizhi[2*], A. Thanga Hemavathy[3], D. Amirtham[4] and L. Karthiba[5]

[1]*Department of Pulses, Centre for Plant breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore - 641003, India*

[2]*Department of Plant Genetic Resources, Centre for Plant breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore - 641003, India*

[3]*Maize Research Station, Tamil Nadu Agricultural University, Vagarai - 624613, India*

[4]*Department of Plant Biotechnology, Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore - 641003, India*

[5]*Coconut Research Station, Tamil Nadu Agricultural University, Aliyar Nagar - 642101, India*

*Corresponding author email: dmalarvizhi@tnau.ac.in

ABSTRACT

Pigeonpea (*Cajanus cajan* L. Millsp.) is a vital protein-rich legume crop essential for food security and sustainable farming systems due to its nitrogen-fixing ability. However, breeding for higher seed yield is challenging because it is a complex polygenic trait heavily influenced by the environment. Direct selection is often inefficient, requiring breeders to target easily measurable agromorphological component traits. Investigating early segregating generations, such as the F_4 population, provides crucial insights into the genetic architecture and character interrelationships necessary to establish effective selection indices. Therefore, the present study was conducted to determine the character association and direct and indirect relationships between seed yield and its components. The field experiment was carried out during the *Kharif* 2025 season at the Department of Pulses, Tamil Nadu Agricultural University, Coimbatore. The experimental material comprised an F_4 segregating population derived from the bi-parental cross AL 882 × COR1. Phenotypic data were recorded on individual plants for eight quantitative traits: days to 50% flowering, days to maturity, plant height, number of branches per plant, total number of pods per plant, pod length, number of seeds per pod, and 100-seed weight. The mean phenotypic data gathered were subjected to statistical analysis to determine associations between seed yield and its component traits. Correlation analysis revealed that 100-seed weight exhibited a highly significant and strong positive association with total seed yield ($r = 0.614$, $P < 0.01$). In contrast, the other traits such as days to 50% flowering ($r = 0.057$), days to maturity ($r = 0.048$), and pod length ($r = 0.143$) showed weak positive correlations with seed yield. The results of path coefficient analysis partitioned the correlation coefficients into direct and indirect effects. The path analysis indicated that 100-seed weight exerted the highest positive direct effect on seed yield ($r = 0.693$), followed by pod length ($r = 0.221$) and days to 50% flowering ($r = 0.155$). These findings conclusively demonstrate that 100-seed weight and pod length are the most critical yield-determining components and should be prioritized as the primary selection indices for accelerating genetic gain and improving seed yield in early segregating populations of pigeonpea.

Keywords: F_4 population, Correlation, Path coefficient analysis, Seed yield, Yield components.

PP-4-66

Development and Genetic Evaluation of Anthocyanin-Rich Okra (*Abelmoschus esculentus* L.) Hybrids for Yield and Yield Attributes

B. N. Anjali[1]* and Prakash Kerure[2]
[1]*Department of Vegetable Science, College of Horticulture, Hiriyur - 577 598*
[2]*Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga*
*Corresponding author email: anjalibn@uahs.edu.in

ABSTRACT

The present investigation entitled "Development and Genetic Evaluation of Anthocyanin-Rich Okra (*Abelmoschus esculentus* L.) Hybrids for Yield and Yield Attributes" was conducted during 2025–26 at Department of Vegetable Science, College of Horticulture, Hiriyur. Six parental genotypes were crossed in half-diallel mating design to generate fifteen F_1 hybrids. The hybrids along with their parents and standard checks (Arka Nikita and Pusa Lal Bhindi-1) were evaluated in a Randomized Complete Block Design with three replications. Analysis of variance revealed significant differences among genotypes for most of the traits studied, indicating substantial genetic variability. Considerable standard heterosis was observed for several yield and quality traits. Positive and significant heterosis over standard check was recorded for plant height (11.34 %), fruit length (14.57 %), average fruit weight (35.55 %), number of fruits per plant (28.55 %), fruit yield per plot (48.71 %), estimated fruit yield per hectare (38.29 %) and anthocyanin content (446.51 %). Desirable negative heterosis was recorded for days taken for 50 per cent flowering (-10.97 %) and days to first fruit harvest (-10.04 %), indicating earliness in hybrids. Among the hybrids, Harihara Local × Kashi Lalima was identified as the most promising hybrid, recording highest estimated fruit yield per hectare (41.42 t/ha) and anthocyanin content (17.51 mg/100 g). Combining ability analysis revealed importance of both additive and non-additive gene actions for growth, yield and quality traits. Among the parents Kashi Lalima, Double Colour Okra and Harihara Local were identified as good general combiners, whereas hybrids Harihara Local × Kashi Lalima, Red Okra × Kashi Lalima and Kashi Lalima × CP-104-15-6 exhibited superior specific combining ability effects for yield and quality traits. The predominance of non-additive gene action indicated the importance of heterosis breeding for improvement of okra.

Keywords: Half-diallel, Earliness, Heterosis, Combining ability and Anthocyanin-Rich Hybrids.

PP-4-67

Decoding Rice Germplasm Diversity for biofortification and climate-resilient rice breeding: Integrating Phenotypic, Biochemical and Molecular Characterization

Shuvendu Shekhar Mohapatra[1,2], Torit Baran Bagchi[1], Shaswati Rout[1], C. Anilkumar[1], and Krishnendu Chattopadhyay[1]*

[1]*ICAR-Central Rice Research Institute, Cuttack - 753006, INDIA*

[2]*Department of Biotechnology, Berhampur University, Ganjam - 760007, INDIA*

*Corresponding author email: krishnenducrri@gmail.com

ABSTRACT

Genetic diversity within plant genetic resources (PGR) provides the foundation for sustainable crop improvement and climate-resilient agriculture. Decoding this diversity through integrated morphological, biochemical, and molecular characterization enables the identification of superior donor genotypes for genomics-assisted breeding and precision trait enhancement. In the present study, a diverse panel of 435 rice germplasm accessions, comprising traditional landraces, released cultivars, and advanced breeding lines, was systematically evaluated for agro-morphological and yield-related traits to identify genetically diverse and agronomically superior accessions. Principal component analysis (PCA) and Euclidean K-means clustering revealed distinct genetic groupings, reflecting broad phenotypic diversity and facilitating the selection of diverse parental combinations for maximizing genetic gain and transgressive segregation. Based on the diversity analysis, 150 representative genotypes were selected for detailed biochemical characterization of grain protein content and essential amino acid composition. To complement phenotypic evaluation, these accessions were genotyped using trait-linked single nucleotide polymorphism (SNP) markers associated with grain yield, nutritional quality, and stress tolerance. Marker profiling revealed substantial allelic variation, enabling the identification of favorable alleles at key loci, including Gn1a, GS3, and NAL1, which are associated with yield and grain quality improvement. Integration of phenotypic, biochemical, and molecular datasets enabled comprehensive decoding of functional diversity within the germplasm and facilitated the identification of elite donor genotypes carrying superior trait combinations. Among the evaluated accessions, Dhinkiasali, Salibahan, CR Dhan 313, and Ratna exhibited superior agronomic performance with high favorable allele loads, whereas Malabati, Jasmine, and CR Dhan 310 demonstrated enhanced grain protein content and desirable nutritional quality traits. These genetically diverse accessions represent valuable donor resources for biofortification and climate-resilient rice breeding. The study demonstrates how integrated characterization of PGR bridges the gap between diversity assessment and practical breeding applications, providing a translational framework for sustainable utilization of rice genetic resources. The identified donor panel will accelerate genomics-assisted breeding and precision improvement strategies aimed at simultaneously enhancing grain yield, nutritional quality, and resilience, thereby contributing to sustainable food and nutritional security.

Keywords:

PP-4-69

Heterosis, combining ability and gene action studies for yield, quality traits and ToLCD resistance in tomato (*Solanum lycopersicum* L.)

Raju Sarkar[1], Zakir Hussain[1]*, P. K. Singh[1], Selvakumar R.[1], Navinder Saini[2] and Alka Joshi[3]
[1]*Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India*
[2]*Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India*
[3]*Division of Food Science and Post Harvest Technology, ICAR-Indian Agricultural Research Institute, New Delhi – 110012, India*
*Corresponding author email: drzakirhussain24@gmail.com

ABSTRACT

Tomato (*solanum lycopersicum* L.) is an important vegetable crop in world scenario. To exploit heterosis and study combining ability with inheritance, total 32 genotypes including seven lines, three testers, twenty-one hybrids and one standard check were evaluated in Line × Tester design. Observation were taken on total 16 traits including yield, quality and ToLCD incidence in tomato. Mean squares for treatments were highly significant for all characters. Mean square values of lines found significant for maximum traits except thickness of pericarp (mm), number of locules per fruit, titratable acidity (%), ascorbic acid (mg/100g), lycopene (mg/100g), beta carotene (mg/100g) and ToLCD incidence (%). Hybrids DTK-102 × Pusa Prasanskrit performed best for yield, firmness and β-carotene content. DTK-54 × Pusa Prasanskrit exhibited strong resistance to ToLCD. Pericarp thickness and fruit shape index showed marked differences, with DTK-103 and DTK-54 × DT-1023933 being outstanding. DTK-102 × DT-1023932 were showing desirable negative heterosis for days to flowering and fruiting. Yield related traits such as fruit number, yield per plant (kg) and 5 fruit weight (g) were enhanced in hybrid DTK-54 × DT-1023933. Hybrid DTK-102 × DT-1023933 was excelling in ascorbic acid, San Marzano × DT-1023932 in lycopene, and DTK-89 × DT-1023932 in β-carotene content. Processing attributes like viscosity and titratable acidity were good enough in DTK-54 × DT-1023933 and DTK-54 × Pusa Prasanskrit, respectively. Disease resistance was notable in DTK-54 × DT-1023933. DTK-102 emerged as effective general combiners for TSS (°B) and earliness, while Pusa Prasanskrit contributed positively to fruit number and lycopene content (mg/100g). Superior specific combining ability was observed in hybrids such as DTK-89 × Pusa Prasanskrit for fruit number. Gene action analysis showed that traits like pericarp thickness (mm), firmness (kg/cm2), weight of 5 fruits (g), yield per plant (kg), ToLCD incidence (%), ascorbic acid and β-carotene were predominantly controlled by non-additive effects, favouring heterosis breeding. Fruit number per plant, TSS (°B), days to 50% flowering and fruiting governed by additive gene action.

Keywords: Tomato; *Solanum lycopersicum*; heterosis; combining ability; Line × Tester design; gene action; non-additive gene action; additive gene action; ToLCD resistance; yield; fruit quality; lycopene; β-carotene.

PP-4-70

Genetic Analysis of Heterosis, Combining Ability and Molecular Diversity in Gynoecious Parthenocarpic Cucumber (*Cucumis sativus* L.) under Protected Cultivation

Yamini Yadav[1*], S. S. Dey[2], K. K. Gangopadhyay[2], Shrawan Singh[2],
Prolay Kumar Bhowmick[3], Manjusha Verma[4] and Vikrant Tomar[2]
[1]*Division of Vegetable Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru - 560089.*
[2]*Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi - 110012*
[3]*Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi - 110012*
[4]*Division of Genomic Resources, ICAR-Indian Agricultural Research Institute, New Delhi - 110012*
*Corresponding author email: yaminiyadav1105@gmail.com

ABSTRACT

Hybrid breeding remains one of the most effective approaches for enhancing yield and fruit quality in cucumber, particularly under protected cultivation, where gynoecious parthenocarpic hybrids offer distinct advantages. The present study was conducted at the Division of Vegetable Science, ICAR–Indian Agricultural Research Institute, New Delhi, to elucidate the genetic basis of yield and quality traits in gynoecious parthenocarpic cucumber under protected cultivation. Eleven genetically diverse parental lines were crossed in a half-diallel mating design (excluding reciprocals) to generate 55 F_1 hybrids, which were evaluated in a randomized block design with three replications for 28 morpho-agronomic, biochemical, and mineral traits.

Analysis of variance revealed highly significant genotypic variation for most traits, indicating substantial genetic diversity among the parental lines and hybrids. Combining ability analysis showed significant general combining ability (GCA) and specific combining ability (SCA) effects for the majority of the traits, indicating the involvement of both additive and non-additive gene actions. DPaC-47, DPaC-44, and DG-8 emerged as superior general combiners for biochemical and nutritional traits, whereas DPaC-21 and DPaC-43-1 were identified as promising combiners for vegetative growth and yield-related attributes. The hybrids DG-8 × DPaC-43-1, DG-8 × DPaC-44, DPaC-6 × DPaC-9-3, and DPaC-45 × DPaC-48 exhibited superior SCA effects coupled with high heterotic performance for yield and quality traits. Among these, DG-8 × DPaC-43-1 and DG-8 × DPaC-44 recorded the highest heterotic advantage for fruit yield, number of fruits per vine, and shelf life. Gene action analysis revealed the predominance of non-additive effects for most yield and vegetative traits, whereas additive effects were relatively more important for fruit length and selected quality traits. The low narrow-sense heritability estimates further emphasized the importance of heterosis breeding for genetic improvement. SSR marker-based genetic distance and phenotypic distance analyses grouped the parental lines into distinct clusters consistent with their morphological diversity. Correlation analysis revealed weak associations of genetic and phenotypic distances with GCA and SCA, while genetic distance exhibited a modest, trait-dependent relationship with heterosis, suggesting that optimum heterotic expression is achieved at intermediate levels of genetic divergence. These findings provide

valuable insights into the genetic architecture of economically important traits and identify promising parental combinations for developing high-yielding, nutritionally superior cucumber hybrids suitable for protected cultivation.

Keywords: *Cucumis sativus* L., Gynoecious, Parthenocarpic, Heterosis, Combining ability, Diallel analysis, Protected cultivation.

PP-4-71

Exploring Gamma Ray-Induced Variability in Jackfruit CV. Tubagere through Multi-Level Characterization

S. Ambrish[1]*, Prakash Patil[2], Kundapura V. Ravishankar[3] and
Kodthalu Seetharamaiah Shivashankara[3]

[1]*College of Horticulture, University of Horticultural Sciences, Bagalkot, GKVK Post, Bengaluru - 560065, India*

[2]*Project Coordinator (Fruits), ICAR-Indian Institute of Horticultural Research, Hessaraghatta Lake Post, Bengaluru, Karnataka - 560089, India*

[3]*Division of Basic Sciences, ICAR-Indian Institute of Horticultural Research, Hessaraghatta Lake Post, Bengaluru, Karnataka-560089, India.*

*Corresponding author email: sambrishs1999@gmail.com

ABSTRACT

Jackfruit (*Artocarpus heterophyllus* Lam.) is a promising fruit crop with considerable potential for future cultivation; however, its genetic improvement is constrained by a prolonged juvenile phase and a narrow genetic base resulting from predominant vegetative propagation. Induced mutagenesis using gamma irradiation provides an effective approach for generating novel genetic variability, and comprehensive characterization of induced mutants is essential for identifying true mutants and assessing the extent of induced variation. The present study characterized a gamma ray-induced mutant population of jackfruit cv. Tubagere using morphological, biochemical, and whole-genome sequencing (WGS)-based single nucleotide polymorphism (SNP) analyses. Seeds of cv. Tubagere were irradiated with gamma rays at doses of 20, 40, and 60 Gy, along with an untreated control. The resulting M_1 population was established under field conditions, and 24 plants from each treatment were evaluated for key morphological traits (tree growth, canopy architecture, leaf, and fruit characteristics), biochemical attributes [total soluble solids (TSS), titratable acidity, ascorbic acid, carotenoids, and lycopene], and genome-wide SNP variation. Gamma irradiation significantly influenced vegetative growth, with mean tree height ranging from 4.38 to 6.58 m, trunk height from 0.41 to 0.59 m, trunk circumference from 39.11 to 44.80 cm, and plant spread from 3.13 to 4.57 m^2 in three-year-old trees. Leaf blade length, width, and petiole length varied from 15.13 to 19.71 cm, 7.65 to 9.17 cm, and 1.83 to 1.92 cm, respectively. Among the irradiation treatments, 40 Gy emerged as the optimum dose, maintaining vigorous vegetative growth while producing a balanced expression of morphological traits compared with 20 and 60 Gy. Fruit and biochemical characterization of selected mutants revealed substantial variability in fruit shape (ellipsoid, oblong, and spheroid), fruit

weight (4.8–10.5 kg), rind thickness (0.4–2.0 cm), flake number (64–106), and flake colour (light yellow to coppery red). Considerable variation was also observed for TSS (19.2–22.5 °Brix), titratable acidity (0.15–0.35%), ascorbic acid (4.4–13.0 mg/100 g), carotenoid content (1.1–7.9 mg/100 g), and lycopene content (0.14–1.21 mg/100 g). Mutants derived from the 40 Gy treatment exhibited superior fruit quality, including the highest TSS values. Genome-wide SNP analysis further demonstrated that the 40 Gy treatment generated the greatest genomic variation, with the highest SNP density (4,116 SNPs/Mb), followed by 20 Gy (3,858 SNPs/Mb), whereas 60 Gy (3,355 SNPs/Mb) was comparable to the untreated control (3,404 SNPs/Mb). The identified SNPs were distributed across all 28 chromosomes. Overall, the results demonstrate that 40 Gy is the optimum gamma irradiation dose for inducing useful genetic variability in jackfruit, as it combines favourable vegetative growth, superior fruit quality, and the highest level of genome-wide variation. The elite mutant lines identified in this study constitute valuable genetic resources for future jackfruit breeding and genetic improvement programmes.

Keywords: Jackfruit, Gamma irradiation, Morphological characterization, SNPs, Genetic variability.

PP-4-72

Collection, Conservation and Characterization of Jackfruit (*Artocarpus heterophyllus* Lam.) Germplasm in Peninsular India under AICRP on Fruits

S. Priya Devi[1]*, J. Monisha[1], Dicto Jose[2], S. Muthulakshmi[3], P. Ashok[4] and Prakash Patil[1]
[1]*ICAR-Indian Institute of Horticultural Research, Bengaluru*
[2]*Banana Research station, Kannara*
[3]*Horticultural College & Research Institute, Periyakulam*
[4]*Horticultural Research Station, Kovvur*
*Corresponding author email: spriyadevi99ars@gmail.com

ABSTRACT

The All India Coordinated Research Project on Fruits [AICRP(F)] has played a significant role in the collection, conservation, and characterization of jackfruit (*Artocarpus heterophyllus* Lam.) genetic resources in Peninsular India, a recognized secondary centre of diversity for the crop. Over the past 12 years, the ICAR-coordinated network has undertaken systematic exploration of jackfruit-growing regions across the Western Ghats, Eastern Ghats, Deccan Plateau, and coastal ecosystems. Extensive surveys conducted in Kerala, Andhra Pradesh, and Tamil Nadu resulted in the collection of 125 jackfruit accessions, of which 95 are being conserved in field gene banks established at Kannara, Kovvur, and Periyakulam, thereby strengthening the National Active Germplasm Site (NAGS) for jackfruit in Peninsular India. Comprehensive passport data were recorded, and 91 accessions were characterized using standardized IPGRI descriptors, leading to the development of a well-documented germplasm inventory. Fifty-three accessions were further evaluated for important horticultural traits, including earliness, extended cropping period, off-season bearing, fruit shape, size and weight, flake colour, sweetness, firmness, culinary suitability, soft-seededness, compact fruit size, prolonged tender stage,

low latex content, and value-addition potential. Based on multi-year evaluation, nine elite accessions exhibiting superior yield and fruit quality were identified for further utilization. These elite lines will be subjected to multi-location evaluation to assess their adaptability across diverse agro-climatic regions and will serve as valuable donor parents in future jackfruit improvement programmes. The coordinated efforts of AICRP on Fruits have significantly enhanced the conservation and utilization of jackfruit genetic resources by establishing a comprehensive germplasm repository and identifying promising breeding materials. This initiative provides a strong foundation for varietal development, genetic improvement, and sustainable cultivation, while contributing to enhanced productivity, conservation of genetic diversity, and improved livelihood opportunities for farming communities.

Keywords: Jackfruit-Genetic resources-AICRP on Fruits.

PP-4-73

Genetic Diversity Analysis of M_3 Mutant Lines of Mothbean (*Vigna aconitifolia* (Jacq. Marechal) for Yield and Yield Contributing Traits

A. Jaikeerthi[1]*, Bangaremma S. Wadyer[2], G. M. Sajjanar[3], Sidharam Patil[4] and N. Rekhamani[5]

[1]M.Sc. (Agri.), Department of Genetics and Plant Breeding, College of Agriculture, Vijayapur University of Agricultural Sciences, Dharwad - 580005, Karnataka, India

[2]Scientist (Plant Breeding), AICRP on Pearl Millet, RARS, Vijayapur, Karnataka - 586101

[3]Associate Director of Research, RARS, Vijayapur - 586101.

[4]Assistant Professor, Dept of Soil Science and Agril. Chemistry, College of Agriculture, Vijayapur - 586101.

[5]M.Sc. (Agri.), Department of Genetics and Plant Breeding, College of Agriculture, Vijayapur University of Agricultural Sciences, Dharwad - 580005, Karnataka, India

*Corresponding author email: jaikeerthi67@gmail.com

ABSTRACT

Mothbean is a drought-resilient pulse crop with immense potential for cultivation in arid and semi-arid regions. The present study aimed to assess the genetic diversity among 27 M_3 mutant lines to identify diverse and promising genotypes for future breeding programmes. The experiment was conducted during late *kharif* at the Regional Agricultural Research Station (RARS), Vijayapur, using 23 M_3 mutant lines along with three checks (KBMB-1, MBS-803, Lathur bold, Bijapur local) in a Randomized Block Design with three replications. Nine quantitative traits, viz., days to 50 per cent flowering, days to maturity, plant height, number of pods per plant, pod length, number of primary branches, number of seeds per pod, test weight and seed yield per plant were recorded. Genetic divergence was estimated using Mahalanobis D^2 statistics. The 27 genotypes were grouped into six distinct clusters, indicating the presence of substantial genetic diversity. Cluster I was the largest, comprising 17 genotypes, while Clusters II to VI each contained two genotypes. The maximum inter-cluster distance was observed between Clusters IV and V (D^2 = 254.75), followed by Clusters III and IV (253.01), suggesting the existence of highly divergent genotypes that could be exploited in hybridization programmes. The

highest intra-cluster distance was recorded in Cluster VI (89.39), indicating considerable variability among its constituent genotypes. Cluster IV exhibited the highest mean seed yield per plant (3.56 g) and number of pods per plant (33.14), whereas Cluster III recorded the maximum plant height (38.81 cm). Cluster II was identified as the earliest flowering group (50.00 days), while Cluster V exhibited the earliest maturity (108.17 days). Among the traits, test weight contributed the highest to total genetic divergence (23.36%), followed by days to 50 per cent flowering (14.81%), number of pods per plant (14.53%) and seed yield per plant (11.40%). The study revealed considerable genetic variability among the M_3 mutant lines, and the highly divergent clusters identified provide valuable parental material for developing high-yielding and early-maturing mothbean cultivars.

Keywords: Mothbean, M_3 mutant lines, Mahalanobis D^2, genetic divergence, cluster analysis, mutation breeding.

PP-4-75

Phenotypic Characterization and Multivariate Assessment of Diversity in Coconut (*Cocos nucifera* L.) Germplasm

Y. Diwakar[1]* and V. Niral[2]
[1]*ICAR-CPCRI Research Centre, Kidu*
[2]*ICAR-Central Plantation Crops Research Institute, Kasaragod*
*Corresponding author email: diwakar.y@icar.org.in

ABSTRACT

Coconut (*Cocos nucifera* L.) germplasm represents an important source of phenotypic diversity for crop improvement. The present study characterized 15 coconut accessions maintained at ICAR-CPCRI Research Centre, Kidu using quantitative traits related to mature fruit and tender coconut characteristics. Significant differences were observed among the accessions, demonstrating substantial phenotypic variability. Husked fruit weight ranged from 427.77 g in Sakhi Gopal Tall to 763.57 g in Borneo Tall, while tender coconut water quantity ranged from 257.50 to 444.92 ml. Borneo Tall recorded superior values for several important traits, including fruit weight, husked fruit weight (763.57 g) and tender coconut water (444.92 mL). Principal component analysis revealed substantial multivariate diversity, with PC1 and PC2 accounting for 53.44% and 17.32% of the total variation, respectively, and 70.76% cumulatively. Fruit size, husked fruit characteristics, cavity attributes and tender coconut traits contributed substantially to accession differentiation. Borneo Tall was distinctly positioned towards the positive side of PC1 and was characterized by high fruit weight, husked fruit weight, husked fruit dimensions, cavity volume and tender coconut water quantity. Hierarchical cluster analysis broadly corroborated the PCA results and grouped the accessions according to their overall phenotypic similarity. Closely associated groups included Zanzibar Tall–Karkar Tall–Fiji Rotuma Tall, Guam I Tall–Car Nicobar Tall, and West African Tall–Sakhigopal Tall, whereas Seychelles Tall and several other accessions exhibited greater differentiation. The combined application of ANOVA, PCA and cluster analysis effectively discriminated the coconut germplasm and identified accessions with contrasting

trait combinations. The observed diversity provides valuable opportunities for trait-specific selection, conservation and strategic utilization of genetically diverse parental material in coconut breeding programmes, particularly for mature-fruit characteristics and tender coconut production.

Keywords: Coconut, germplasm; phenotypic diversity; fruit traits; PCA.

PP-4-76

Assessment of Genetic Variability for Yield and Yield-Contributing Traits in Horse Gram [*Macrotyloma uniflorum* (Lam.) Verdc.] Germplasm

N. Rekhamani[1*], Bangaremma S. Wadyer[2], G. M. Sajjanar[3], Sidharam Patil[4] and A. Jaikeerthi[5]

[1]*M.Sc. (Agri.), Department of Genetics and Plant Breeding, College of Agriculture, Vijayapur University of Agricultural Sciences, Dharwad - 580005, Karnataka, India*

[2]*Scientist (Plant Breeding), AICRP on Pearl Millet, RARS, Vijayapur, Karnataka - 586101*

[3]*Associate Director of Research, RARS, Vijayapur - 586101*

[4]*Assistant Professor, Dept of Soil Science and Agril.Chemistry, College of Agriculture, Vijayapur - 586101*

[5]*M.Sc. (Agri.), Department of Genetics and Plant Breeding, College of Agriculture, Vijayapur University of Agricultural Sciences, Dharwad - 580005, Karnataka, India*

*Corresponding author email: rekhanagappa2000@gmail.com

ABSTRACT

Horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] is an underutilized climate-resilient pulse crop possessing immense potential for enhancing food and nutritional security in the rainfed ecosystems of Peninsular India. Effective utilization of its plant genetic resources requires a thorough understanding of the existing genetic variability. The present investigation was conducted to assess the extent of genetic variability, heritability and genetic advance for yield and yield-related traits in horse gram germplasm. A total of 62 genotypes, comprising 56 germplasm lines and six checks (GPM-6, CRIDA-18R, CRHG-4, Bailhongal local, AK-42 and ATPHG-11), were evaluated in an augmented design at the College of Agriculture, Vijayapura. Analysis of variance revealed highly significant differences among germplasm lines for all fourteen traits studied, indicating the presence of substantial genetic variability. Seed yield ranged from 520.83 to 1786.83 kg ha^{-1}, with a mean of 1024.96 kg ha^{-1}. High genotypic and phenotypic coefficients of variation were observed for biological yield (25.91% and 29.97%), number of pods per plant (22.88% and 24.11%), harvest index (22.39% and 23.26%) and dry matter content (19.97% and 21.09%), indicating considerable genetic diversity for these traits. High heritability coupled with high genetic advance as per cent of mean was recorded for biological yield (74.73%, 46.21%), number of pods per plant (90.06%, 44.79%), harvest index (92.63%, 44.45%), dry matter content (89.59%, 38.99%) and seed yield (90.37%, 34.53%), suggesting the effectiveness of selection for genetic improvement. The narrow differences between GCV and PCV for most traits indicated minimal environmental influence on trait expression. The diverse germplasm identified in this study constitutes a valuable reservoir of

plant genetic resources and provides promising parental material for developing high-yielding, climate-resilient horse gram cultivars suited to the agro-ecological conditions of Peninsular India.

Keywords: Horse gram, *Macrotyloma uniflorum*, plant genetic resources, germplasm, genetic variability, heritability, genetic advance, yield improvement.

PP-4-77

Identification of Stable Horse Gram [*Macrotyloma uniflorum* (Lam.) Verdc.] Germplasm Across Different Sowing Dates Using AMMI and GGE Biplot Analysis

N. Rekhamani[1]*, Bangaremma S. Wadyer[2], G. M. Sajjanar[3], Sidharam Patil[4] and A. Jaikeerthi[5]

[1]*M.Sc. (Agri.), Department of Genetics and Plant Breeding, College of Agriculture, Vijayapur University of Agricultural Sciences, Dharwad - 580005, Karnataka, India*

[2]*Scientist (Plant Breeding), AICRP on Pearl Millet, RARS, Vijayapur, Karnataka-586101*

[3]*Associate Director of Research, RARS, Vijayapur-586101*

[4]*Assistant Professor, Dept of Soil Science and Agril.Chemistry, College of Agriculture, Vijayapur-586101*

[5]*M.Sc. (Agri.), Department of Genetics and Plant Breeding, College of Agriculture, Vijayapur University of Agricultural Sciences, Dharwad - 580005, Karnataka, India*

*Corresponding author email: rekhanagappa2000@gmail.com

ABSTRACT

Horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] is an underutilized, climate-resilient pulse crop representing valuable plant genetic resources for improving productivity and resilience in the rainfed agro-ecosystems of Peninsular India. Identification of stable and widely adapted germplasm is essential for developing cultivars with consistent performance across diverse sowing environments. The present investigation was undertaken to evaluate the stability and adaptability of horse gram germplasm across different sowing dates using Additive Main Effects and Multiplicative Interaction (AMMI) and Genotype plus Genotype × Environment Interaction (GGE) biplot analyses. A total of 62 genotypes, comprising 56 germplasm lines and six checks (GPM-6, CRIDA-18R, CRHG-4, Bailhongal local, AK-42 and ATPHG-11), were evaluated in an augmented design under three sowing environments, namely early (second fortnight of July), recommended (second fortnight of August) and delayed (second fortnight of September) at the College of Agriculture, Vijayapura. Seed yield per plant was considered as the principal trait for stability assessment. The AMMI1 biplot identified TCR-1771 and GPM-19 as high-yielding and relatively stable genotypes, whereas GPM-6, CRIDA-18R and CRHG-4 exhibited broad adaptation with minimal genotype × environment interaction. The GGE biplot further identified TCR-1771 and GPM-19 as the most suitable genotypes for the early and recommended sowing environments, while AK-42 showed specific adaptation to the delayed sowing environment. Based on the ideal genotype view of the GGE biplot, TCR-1771, GPM-19, TRC-1488, GPM-6, GPM-17 and Bailhongal local were identified as desirable genotypes combining high mean performance with superior stability across environments. These stable and specifically adapted germplasm lines represent valuable plant genetic resources and can be effectively utilized as

parents in breeding programmes for developing high-yielding, climate-resilient horse gram cultivars with broad and specific adaptation to the diverse agro-ecological conditions of Peninsular India.

Keywords: Horse gram, *Macrotyloma uniflorum*, plant genetic resources, genotype × environment interaction, AMMI, GGE biplot, stability analysis, germplasm.

PP-4-78

Biochemical Characterization of Sugar Apple (*Annona squamosa* L.) Genotypes based on Fruit Traits for Crop Improvement

Shivam Kumar Rajpoot[1,4*], Mahesh Kumar Dhakar[2], Vishal Nath[3] and Chavlesh Kumar[4]
[1]*Division of Fruit Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka - 560089, India*
[2]*ICAR-Research Complex for Eastern Region, Farming System Research Centre for Hill and Plateau Region, Ranchi, Jharkhand - 834010*
[3]*ICAR-Indian Agricultural Research Institute, Hazaribagh, Jharkhand - 825405, India*
[4]*ICAR-Indian Agricultural Research Institute, New Delhi - 110012, India*
*Corresponding author email: skrajpoot7388@gmail.com

ABSTRACT

Sugar apple (*Annona squamosa* L.) is an important fruit crop of tropical and subtropical region of India. The family Annonaceae comprises 40–50 genera and 173 species, six of which are commercially important: *Annona squamosa, Annona cherimola, Annona reticulata, Annona muricata, Annona atemoya*, and *Annona glabara.* To characterize local germplasm, extensive survey and data collection were conducted in three districts of Jharkhand, *i.e*. Chaibasa (West Singhbhum), Khunti, and Ranchi. A total of 70 wild and semi-wild genotypes from the Eastern Plateau region were evaluated for biochemical traits. High variability was observed in the fruit's biochemical traits. Biochemical profiling showed considerable diversity in TSS (12.60- 29.37 °Brix), sugars (10.82-27.77%), titratable acidity (0.26- 0.67 %), ascorbic acid content (12.60-39.84 mg/100 g) and total phenols content (86-139.97 mg GAE/100 g), with antioxidant activity ranging from 72.53 to 164.36 mg AEAC/100 g among the sugar apple diversity in the region. The fraction of phenolics was studied using UHPLC, and the results showed that gallic acid was the dominant phenolic, followed by p-coumaric acid, vanillic acid, chlorogenic acid, protocatechuic acid, 4-hydroxybenzoic acid, ferulic acid, and syringic acid. The genotypes CCA04 (High TSS) and RCA14 (highest TAC) were found superior genotypes with their respective quantitative traits. These results highlight the rich genetic diversity present in sugar apple germplasm of the Eastern Plateau and provide a strong foundation for targeted breeding, conservation, and cultivar development programs aimed at enhancing productivity and quality.

Keywords: *Annona squamosa*, biochemical characterisation, total soluble solids, antioxidant activity, genotypes.

PP-4-79

Unlocking the Genetic Diversity of Shankhpushpi (*clitoria ternatea* L.) Genotypes: Insights into Morphological and Phytochemical traits

V. Sreenivasa*, M. R. Rohini, K. Hima Bindu, R. Gowthami,
C. S. Karthik, K. S. Divya, and Shivan and D. Ainapur
Division of Flower & Medicinal Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru
*Corresponding author email: v.sreenivasa@icar.org.in

ABSTRACT

Medicinal plants have been used for therapeutic, religious, cosmetic, nutritional, and beautification purposes since ancient times. *Clitoria ternatea* (CT) belong to family fabaceae and it's a perennial climber and commonly called as 'Butterfly pea'. It's grown as cover crop and as green manure crop, in South East Asia, its blue colour petals used as natural food colouring agent. In the Indian systems of medicine particularly in Ayurveda, the roots, seeds and leaves of CT have long been widely used as a brain tonic and is believed to promote memory and intelligence. The leaves and roots are used in the treatment of a number of ailments including body aches, especially infections, urinogenital disorders, and as an anthelmentic and antidote to animal stings. The root is used in the treatment of various diseases, like indigestion, constipation, fever, arthritis and eye ailments. The flower petals extract of CT contains flavonoids and anthocyanins, which play role in scavenging free radicals, and their activity. The present investigation was carried out at ICAR-IIHR, Bengaluru to study the amount of variability present among the germplasm lines evaluated for the listed morphological and phytochemical traits. The experiment was laid out in an Augmented Design with three checks and 74 test entries. All the characters showed narrow differences between phenotypic and genotypic coefficient of variation, indicating very low effect of environment and greater role of genetic factors in the expression of these traits and the estimates of heritability were found to be high. All the traits have recorded higher degree of GAM indicating the presence of higher variability for the traits under consideration and the probability of identifying better genotype from the lot.

Keywords:

PP-4-80

Integrative Morphological, Quantitative and Molecular Characterization of Contrasting Rice Genetic Resources and F_1 Hybrids reveals Breeding Potential for Marker-Assisted Improvement

T. J. Shree Bhavatharani[1]*, Rose Mary Francies[2], Jiji Joseph[3], E. R. Aneena[4], A. G. Kiran[5], and Jauhar Ali[6]

[1]*Ph.D. Scholar, Department of Genetics and Plant Breeding, Kerala Agricultural University*

[2]*Agricultural Research Station, Kerala Agricultural University, Mannuthy, Thrissur*

[3]*Department of Plant Breeding and Genetics, College of Agriculture, Kerala Agricultural University, Vellanikkara, Thrissur*

[4]*Department of Community Science, College of Agriculture, Kerala Agricultural University, Vellanikkara, Thrissur*

[5]*Department of Plant Biotechnology, College of Agriculture, Kerala Agricultural University, Vellanikkara, Thrissur*

[6]*Hybrid Rice Development Consortium (HRDC), Rice Breeding Innovation Department, International Rice Research Institute (IRRI), Los Baños, Laguna, Philippines*

*Corresponding author email: shreebhava1999@gmail.com

ABSTRACT

Rice (*Oryza sativa* L.) genetic resources represent an invaluable source of allelic diversity for the genetic improvement of grain quality and nutritional traits. Effective utilization of these resources requires comprehensive characterization of parental genotypes and validation of their hybrids prior to their deployment in breeding programmes. The present study aimed to characterize two contrasting rice accessions, the high-yielding, red-bold kernel cultivar Jyothi (PTB 39) and the low-glycemic-index (GI) donor line PSB Rc 86, and to validate their F_1 hybrids to facilitate marker-assisted breeding for the development of low-glycemic-index red rice. The parental genotypes were characterized using qualitative and quantitative morphological descriptors together with molecular marker analysis. Distinct variation in DUS descriptors, particularly anthocyanin pigmentation and grain characteristics, enabled clear discrimination between the two parents and facilitated the identification of putative F_1 hybrids. Hybrid authenticity was subsequently confirmed using polymorphic SSR markers, demonstrating the reliability of integrating morphological descriptors with molecular profiling for rapid and accurate hybrid validation. The validated F_1 hybrids exhibited the expected combination of parental morphological traits, confirming successful hybridization and providing reliable breeding material for subsequent marker-assisted backcross breeding. Quantitative characterization of the parental genotypes was carried out in a randomized block design with three replications. Analysis of variance revealed significant differences ($P \leq 0.05$) for plant height, productive tillers per plant, days to panicle emergence, 1000-grain weight, grain width, kernel length, kernel width, number of grains per panicle, and grain yield per plant, whereas duration, total tillers per plant, panicle length, and grain length did not differ significantly. PSB Rc 86 recorded significantly greater plant height (119.50 cm), productive tillers per plant (19.00), grains per panicle (130), and grain yield per plant (45.08 g), whereas Jyothi exhibited significantly higher 1000-grain weight (26.00 g), grain length (9.10 mm), grain width (3.50 mm), kernel length (6.70 mm), and kernel width (2.70 mm), while retaining the desirable red kernel trait. The observed phenotypic divergence

highlights the complementary genetic potential of these parental lines for targeted trait introgression. The integration of morphological characterization, statistical evaluation, and molecular validation highlighted the value of these rice genetic resources for parental selection, while successful validation of the F_1 hybrids established a reliable platform for marker-assisted introgression of low-glycemic-index traits into elite red rice backgrounds. These findings contribute to the effective conservation and utilization of rice genetic resources and provide a strong basis for developing nutritionally improved rice cultivars.

Keywords: Rice, DUS characterization, SSR markers, Quantitative traits, Marker-assisted breeding.

PP-4-81

Developing Bridge Species through Complementary Strategies to Overcome Ploidy Bottlenecks in Wild Germplasm

Madhvi Sharma, Srinivas Muluguri, Senthil Ramachandran, Kuldeep Singh and Manish K. Pandey*
Accelerated Crop Improvement & Center for Pre-Breeding Research (CPBR), International Crop Research Institute for the Semi- Arid Tropics, (ICRISAT), Hyderabad, India-502324
*Corresponding author email: manish.pandey@icrisat.org

ABSTRACT

Cultivated groundnut (*Arachis hypogaea* L.) possesses a narrow genetic base, limiting its adaptability to biotic and abiotic stresses and restricting the effective utilization of valuable alleles from wild *Arachis* species. Although diploid wild relatives represent an invaluable reservoir of genes for disease resistance and other agronomically important traits, their direct use in breeding is constrained by ploidy differences with cultivated tetraploid groundnut. Developing bridge species is therefore essential to facilitate gene introgression from wild species into cultivated backgrounds. This study employs two complementary strategies to develop novel bridge species. The first involves interspecific hybridization between *A. valida* (B genome) and *A. decora* (A genome) both possessing desirable resistance to Late Leaf Spot (LLS), to generate synthetic AB-genome hybrids. The second strategy focuses on the development of autotetraploids through in vivo chromosome doubling using colchicine treatment directly given to wilds. Two colchicine treatment methods were evaluated: (i) treatment of pre-germinated seeds following cotyledon excision and (ii) treatment of the shoot apical meristem using the cotton-swab method. Treated plants are being assessed for survival, morphological variation, stomatal characteristics, pollen viability and germination. Ploidy status is confirmed through flow cytometry, followed by cytological validation through chromosome counting that is in process. The successful development of stable tetraploid bridge species is expected to overcome ploidy barriers and enable efficient introgression of novel alleles governing disease resistance, abiotic stress tolerance, yield, and quality traits into cultivated groundnut. By integrating cytogenetics with pre-breeding approaches, this study aims to expand the global reservoir of synthetic groundnut species beyond the currently available ~25 amphidiploids, thereby providing valuable genetic resources for the development of climate-resilient and high-performing groundnut cultivars.

Keywords: Groundnut; bridge species; ploidy; chromosome doubling; flow cytometer.

PP-4-82

Agro-Morphological Characterization and Yield Evaluation of Parents and F_1 Hybrids Derived from Crosses between KAU Manuratna and Green Super Rice (GSR) Donor accessions in Rice (*Oryza sativa* L.)

P. Harshitha[1]*, Jiji Joseph[1], Rose Mary Francies[2] and Jauhar Ali[3]
[1]*Department of Plant Breeding and Genetics, College of Agriculture, Kerala Agricultural University, Thrissur*
[2]*Professor and Head, Agricultural Research Station, Mannuthy*
[3]*Hybrid Rice Development Consortium, Rice Breeding Innovation Department, IRRI, Phillipines*
*Corresponding author email: harshithapandiyan@gmail.com

ABSTRACT

Improving rice productivity under changing climatic conditions requires the development of climate-resilient varieties by introgression. Green Super Rice (GSR) donor lines have been developed to combine high yield potential with tolerance to multiple abiotic stresses and improved nutrient-use efficiency. Their effective utilization in breeding programmes requires comprehensive phenotypic characterization and evaluation of derived hybrid populations. In this study, four green super rice donor accessions (EC 123, EC 124, EC 126, and EC 128) were crossed with KAU Manuratna (recipient) to develop F1 hybrids. The parents and F1 hybrids were evaluated for yield-related traits and DUS (Distinctness, Uniformity, and Stability) descriptors in a randomized block design with three replications. Nine quantitative traits such as plant height, number of tillers, leaf area per plant, number of productive tillers, panicle length, grain weight per panicle, thousand-grain weight, number of grains per panicle, and grain yield were recorded for each replication. Analysis of variance revealed significant differences for all nine traits studied. Among the parents, the donor EC 124 recorded the highest mean grain yield (48.55 g), while the recipient parent Manuratna recorded the lowest (32.50 g). Among the F1 hybrids, Manuratna×EC 124 produced the highest grain yield (43.69 g), exceeding the recipient parent. Mean performance of traits such as panicle length, number of grains per panicle, grain weight per panicle were higher in donors compared to recipient parent. Further, Agro- morphological characterization using 53 DUS (Distinctness, Uniformity, and Stability) descriptors identified 26 traits as monomorphic, 23 as dimorphic, and 4 as polymorphic. Decorticated grain shape showed the largest variation, spanning five classes: short bold, medium slender, long slender, long bold, and basmati type. Variable morphological descriptors observed between parents such as length of leaf blade, leaf pubescence, stem thickness and panicle awn can be used for identifying the parents and its progenies in future breeding generations. Parental polymorphism survey using SSR (Simple Sequence Repeat) markers identified two markers: RM1, polymorphic between Manuratna and EC 123, EC 124, and EC 126; and RM202, polymorphic between Manuratna and EC 124 and EC 128. Manuratna × EC 124 F1 hybrid, with higher yield than KAU Manuratna, offers a promising line for advancing high-yielding, stress-tolerant rice. The superior yield performance of the GSR donors and F1 hybrids over Manuratna, variation observed in DUS characterization, indicates their potential of donors in diverse breeding programs.

Keywords: Hybridization, Green super rice, DUS characters.

PP-4-83

BLUP-Based Genotype-by-Yield*Trait Analysis for Identification of Groundnut Germplasm lines with In-situ Germination Tolerance and Superior Agronomic Performance

M. Jayanth[1*], B.N. Motagi[2*], Mahesh S. Hullur[1], B. Rajanna[1], Akshatha[3],
R. Gurumurty[3], Kiran Dasanal[3,4] and Ramesh S. Bhat[2]

[1]*Department of Genetics and Plant Breeding, University of Agricultural Sciences, Raichur, Karnataka, India*
[2]*Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India*
[3]*Department of Seed Science and Technology, University of Agricultural Sciences, Dharwad, Karnataka, India*
[4]*ICAR – Division of Germplasm Conservation, National Bureau of Plant Genetic Resources, New Delhi, India*
*Corresponding author email: motagibn@uasd.in; jayanthm15015@uasraichur.edu.in

ABSTRACT

Groundnut (*Arachis hypogaea* L.), also known as peanut, is an important food and oilseed crop widely used for human nutrition, cooking oil, confectionery products, and livestock feed. Climate change, characterized by rising temperatures, altered rainfall, drought, and increased pest and disease incidence, has posed severe threat to groundnut production. In situ germination of freshly matured seeds at harvest when coincide with rain is a major constraint affecting yield, seed quality, and market value. In India, groundnut is cultivated during *kharif, rabi,* and summer seasons. Therefore, early-maturing cultivars with 2–3 weeks of fresh seed dormancy are desirable to minimize in situ germination and ensure stable production and quality. This study was conducted across two seasons, *kharif* of 2023-24 and 2024-25 in two location *i.e* Dharwad and Raichur. Available 132 groundnut mini core germplasm accessions were evaluated for in situ germination tolerance and superior agronomic performance in an augmented design with Dh86 and TMV2 as in situ germination susceptible check while Dh8, TMV2NLM as tolerance check. Mixed model was employed considering year as fixed effect and genotypes, blocks and genotype x environment as random effect. Significant variation was observed between genotypes and revealed significant GXE interaction for in situ germination (IG) and yield attributing traits. Best linear unbiased prediction (BLUP) values were estimated for each genotypes for combined analysis across two season and these BLUP values were used assess trait association and principal component analysis (PCA) and genotype by yield trait (GYT) analysis. IG exhibited positive association with pod yield per plant (PYP) and kernel yield per plant (KYP), while negative association with days to maturity (DM) and days to fifty percent flowering (DFF). Such association was supported by PCA where PC1 explained 33.3% and PC2 explained 23% variation. The GYT analysis identified **ICG36, ICG721, ICG982, ICG875 and ICG101** as promising genotypes based on their favourable positioning across multiple yield–trait combinations. These genotypes combined higher grain yield with desirable secondary traits, particularly **reduced in-situ germination**, highlighting their potential for further evaluation and use in groundnut breeding programmes.

Keywords: Groundnut, Mini core, Mixed model, BLUP, genotype by yield trait analysis.

PP-4-84

Evaluation of Oriental Pickling Melon (*Cucumis melo* L. var *conomon*) Genotypes Growth and Yield Traits

Supriya Jaiswal and D. C. Manjunathagowda*
ICAR-Indian Institute of Horticultural Research,
Hessaraghatta Lake Post, Bengaluru, Karnataka, India, 560089
*Corresponding author email: dcmgowda@gmail.com

ABSTRACT

Oriental pickling melon (*Cucumis melo* L. subsp. *agrestis* var. *conomon*), an underutilized cucurbit predominantly cultivated in southern India, possesses considerable potential as a functional food due to its rich nutritional and phytochemical composition. Despite its economic and dietary importance, limited research has focused on its morphological, molecular, and nutritional diversity. The present investigation, entitled "Morpho-molecular and nutritional characterization of oriental pickling melon (*Cucumis melo* L. subsp. *agrestis* var. *conomon*)", was undertaken at ICAR–Indian Institute of Horticultural Research, Bengaluru during 2024–25 to assess variability, heritability, genetic advance, and trait associations in a diverse set of germplasm. Significant genetic variability was observed for most traits. High heritability coupled with high genetic advance as a percentage of mean was recorded for fruit weight (94.02%; 67.64%), fruit length (95.21%; 69.89%), fruit shape index (91.31%; 63.68%), and plot yield (99.53%; 77.73%), indicating strong additive gene action and high potential for genetic improvement through direct selection. IIHR-OPM 13 emerged as the best performer for yield traits (fruit weight: 1124.67 g; yield per hectare: 23.38 t/ha), while IIHR-E86 excelled in seed traits. Several checks, including Mudikode Local and KAU Vishal, were statistically comparable with the best genotypes. These finding aid in the selection of genotypes base the trait association useful in further breeding and improvement programmes of oriental pickling melons.

Keywords: Correlation, Oriental pickling melons, Path analysis, Yield.

PP-4-86

Characterization of root distribution and mineral profiling of the *Annona* Hybrid 'Arka Sahan' grafted onto different rootstocks

Roja H. S.*, J. Satisha, T. Sakthivel, S. Sujatha, Anuradha Sane,
K. V. Ramesh, D. Kalaivanan and Vasantha S. V.
Ph. D. Scholar, Indian Institute of Horticultural Research, Bengaluru, Karnataka – 560 089
*Corresponding author email: rojasrinivas10@gmail.com

ABSTRACT

The integration of root distribution pattern analysis and root mineral profiling into crop productivity studies has emerged as an important area of research, owing to their critical roles in resource acquisition, plant growth, and stress adaptation. In the present investigation, the root distribution pattern and root mineral profile of the Annona hybrid 'Arka Sahan' grafted onto different rootstocks were evaluated. The rootstocks included *Annona muricata* (Soursop), *Annona squamosa* cv. Balanagar, *Arka Sahan* (self-rootstock), *Annona glabra* (Pond apple), *Annona reticulata* (Ramphal), *Annona squamosa* cv. Washington, and *Annona cherimola* (Cherimoya). Root distribution was characterized using root fresh weight (g), root dry weight (g), root length (cm), root diameter (cm) and the number of primary, secondary, and tertiary roots, while root mineral profiling comprised the analysis of macro- and micronutrient concentrations. Significant differences in root distribution patterns were observed among the rootstock treatments, highlighting the substantial influence of rootstocks on the development and performance of the scion. The combined evaluation of root distribution patterns and root mineral profiles provides valuable insights for identifying superior rootstocks with enhanced resource acquisition efficiency, improved vegetative growth, greater productivity, and increased resilience to environmental stresses. These findings contribute to the development of efficient rootstock selection strategies and sustainable production systems for Annona cultivation.

Keywords: Root distribution pattern, mineral profiling, annona.

PP-4-88

Evaluation of Morpho-Physiological and Anatomical Adaptations in Coconut Genotypes for Climate Resilience

Rithika A.#, Niral V.*, U. K. Gayathri, K. M. Ashwitha, P. Ashitha, S. V. Ramesh, K. B. Hebbar
Division of Crop Improvement, ICAR-Central Plantation Crops Research Institute, Kasaragod, Kerala
*Corresponding author email: niral.v@icar.org.in

ABSTRACT

A morpho-physiological and anatomical study across 26 coconut accessions was undertaken to assess the adaptive capacity for abiotic stress tolerance and climate resilience. The micro-morphological and anatomical leaf parameters including- stomatal index, stomatal density, laminar thickness, cuticular thickness, epicuticular wax content (ECW) were measured, alongside the functional physiological indicators like stomatal resistance, chlorophyll index, quantum efficiency of photosystem II(F_v /F_m) and growth parameters were also studied to determine how effectively these accessions insulate their photosynthetic core while optimizing water-use efficiency under normal environmental conditions. The study revealed significant variation for all the parameters except for photosynthetic efficiency, which remained highly stable across genotypes, with a mean quantum yield (F_v /F_m) of 0.795±0.028. The stomatal density ranged from 221.82 mm^{-2} (TPT) to 374 mm^{-2} (PLNT), while stomatal index ranged from 5.372 mm^{-2} (LCOD) to 8.676 mm^{-2} (SNRT). Leaf laminar thickness ranged from 202.2 µm (MGD) to 284 µm (KS). The leaf ECW ranged from 69.222 $µg.cm^{-2}$ (CRD) to 126.96 $µg.cm^{-2}$ (SNRT). The stomatal resistance was higher in the genotypes viz., WCT01, LMT, AGT, SNRT indicating relatively stronger adaptive response towards climate resilience whereas, the genotypes viz., COD, MYD, GBGD indicated poor stomatal resistance. Futhermore, cuticular thickness ranged from 8.02 µm (JSBT) to 11.12 µm (KS) which emerged as a primary driver of climate resilience, showing positive correlation (r = 0.61) with stomatal resistance. This indicates that robust cuticle works in tandem with stomatal control to minimize non-stomatal water loss during periods of high evaporative demand. ECW was positively associated with stomatal resistance (r = 0.31) and quantum yield(r = 0.25), confirming the dual role of surface waxes in mitigating transpirational water loss and reflecting excessive solar radiation to prevent photo-inhibition. Cuticular thickness displayed a positive correlation with quantum yield(r = 0.36), proving that genotypes with thicker structural barriers can protect their photosynthetic machinery. The findings establish, superior growth performance under climate-stressed conditions is mediated by a coordinated strategy where increased cuticle thickness and ECW enhance stomatal resistance and shield photosynthetic function. Accessions like, SNRT optimize this balance, with high chlorophyll retention, stomatal resistance and robust growth. Such accessions that balance these traits can serve as parental lines in breeding programs seeking to engineer climate-smart crops varieties optimized for survival and high yield stability in the unpredictable future ecosystems.

Keywords: Climate Resilience; Epicuticular wax content; Cuticular thickness; Stomatal Resistance; Quantum Yield (F_v/F_m)

Technical Programme

National Symposium on Harnessing Plant Genetic Resources (PGR) of Peninsular India

September 17-19, 2026

ICAR-IIHR, Bengaluru

Technical Programme

DAY 1: September 17, 2026 (Thursday)

Welcome	
8.30 – 8.45	**Inauguration of Exhibition**
8.45 – 9.00	**Welcome and About the Symposium** **Dr. R. S. Paroda,** President, ISPGR **Dr. R. C. Agrawal,** Vice President, ISPGR **Dr. R. K. Tyagi,** Vice President, ISPGR, New Delhi **Dr. V. B. Patel,** ADG (HS), ICAR, New Delhi **Dr. Tusar Kanti Behera,** Director, ICAR-IIHR **Dr. Anuradha Agrawal,** Secretary, ISPGR

TECHNICAL SESSION I **Securing the Genetic Heritage of Peninsular India - from Exploration to Conservation** **Venue:** G S Randhawa Auditorium, ICAR-IIHR		
Co - Chairs	**R. C. Agrawal,** Vice President, ISPGR, New Delhi **J. C. Rana,** Senior Scientist and Country Representative for India, Alliance of Bioversity International and CIAT, New Delhi	
Convenors	**M. Sankaran**, Head, Div. of Fruit Crops, ICAR - IIHR, Bengaluru **Rohini M. R.,** Co-Organizing Secretary, NSPPI	
Rapporteurs	**Anuradha Sane**, Principal Scientist, Div. of Fruit Crops and **V. Sreenivasa,** Senior Scientist, Div. of Flower & Medicinal Crops, ICAR-IIHR, Bengaluru	
09:00 - 09:05	**Welcome**	**Convenor**
	Invited Lectures	
09:05 - 09:20	Plant Genetic Wealth of Peninsular India	**S. R. Yadav**, Professor of Botany (Retd.), Shivaji University, Kolhapur
09:20 - 09:35	Identifying Geographical and Taxonomic Gaps in PGR Exploration and Collection in Peninsular India	**K. Pradheep**, OIC, ICAR-NBPGR, Regional Station (RS), Thrissur
09:35 - 09:50	Role of Botanical Survey of India in Plant Diversity Documentation and Conservation	**Hameed S. S.,** Scientist F & Head, Botanical Survey of India, Southern Regional Centre, Coimbatore

09:50 - 10:05	Measuring Landscape Dynamics to Monitor Change in Flora	**T. V. Ramachandran**, Centre for Ecological Sciences, Indian Institute of Science, Bengaluru
10:05 - 10:20	Diversity, Distribution and Conservation Priorities of PGR in the Nicobar Islands	**Joseph John K.**, Former Head, ICAR-NBPGR, RS, Thrissur
10:20 - 10:35	Community - Centric Conservation of PGR: Lessons from Traditional Knowledge Systems	**Abdul Kareem**, The University of Trans - Disciplinary Health Sciences and Technology, Bengaluru
10:35 - 10:45	**Discussion and Co - Chairs' Remarks**	
10:45 - 11:00	**Tea/Coffee Break**	

TECHNICAL SESSION II **PGR Governance: From Biosecurity to Benefit Sharing** **Venue:** G S Randhawa Auditorium, ICAR-IIHR		
Co - Chairs	**R. R. Hanchinal,** Former Chairperson, PPV&FRA, New Delhi **Dhananjaya M. V.**, Vice Chancellor, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences (KSNUAHS), Shivamogga	
Convenors	**V. B. Patel,** ADG (Fruits and Plantation Crops), ICAR, New Delhi, and **S. Sriram**, Head, Div. of Plant Protection, ICAR-IIHR, Bengaluru	
Rapporteurs	**Anushma P. L.**, Scientist and **Linta Vincent**, Senior Scientist, Div. of Fruit Crops, ICAR-IIHR, Bengaluru	
11:00 - 11:05	**Welcome**	**Convenor**
	Invited Lectures	
11:05 - 11:20	Policy Frameworks and ABS: Aligning Global Commitments with Local Policy Needs	**D. K. Agrawal**, Registrar General, PPV&FRA, New Delhi
11:20 - 11:35	Understanding recent developments in the global policy instruments & ABS	**Sunil Archak**, OIC, Germplasm Exchange and Policy Unit, ICAR-NBPGR, New Delhi
11:35 - 11:50	Enhancing Adaptive Management of Crop Diversity for Resilient Agriculture and Rural Livelihoods	**J. C. Rana,** Senior Scientist and Country Representative for India, Alliance of Bioversity International and CIAT
11:50 - 12:05	Biosecurity and PGR: Safeguarding Against Emerging Threats	**Celia Chalam V.,** Head, Plant Quarantine Division**,** ICAR-NBPGR, New Delhi

12:05 - 12:20	Farmers' Rights and Community Participation in PGR Governance	**Dr. Vimal Kumar**, Principal Scientific Officer, Kerala State Biodiversity Board, Thiruvananthapuram
12:20 - 12:35	Geographical Indications (GIs) as tools for biodiversity valorization in Peninsular India	**C. R. Elsy,** Professor (Retd), Kerala Agricultural University, Thrissur
12:35 - 13:00	**Discussion and Co - Chairs' Remarks**	
13.00 – 14.05	**Lunch**	

TECHNICAL SESSION III **Innovation, Bioeconomy and Livelihood Enhancement** **Venue:** G S Randhawa Auditorium, ICAR-IIHR		
Co - Chairs	**D. K. Agrawal**, Registrar General, PPV&FRA, New Delhi **Srinivasulu,** IFS, Principal Secretary, Forest, Ecology and Environment, Govt of Karnataka **J. Dinakara Adiga**, Director, ICAR-Directorate of Cashew Research, Puttur, Karnataka	
Convenor	**G. Karunakaran**, Principal Scientist, ICAR-IIHR, Bengaluru & General Secretary, SPH	
Rapporteurs	**H. P. Sumangala**, Principal Scientist, ICAR-IIHR, Bengaluru and **V. Sankar**, Principal Scientist, ICAR-IIHR, Bengaluru	
14:15 - 14:20	**Welcome**	
	Invited Lectures	
14:20 - 14.35	Nurturing Innovations from the Grassroots	**Anil Gupta**, Founder, Honey Bee Network and SRISTI; Former Professor, IIM Ahmedabad
14:35 - 14:50	Reimagining the Apple Value Chain: From Genetics to Market Through Technology	**Aashish Barwale**, Director, Seven Star Fruits Pvt Ltd, MahycoGrow
	Panel Discussion	
14.50 - 15.20	**Custodian Farmers**	6 custodian farmers
15:20 - 15:35	**Discussion & Co - Chairs Remarks**	
15.55 - 16.00	**Tea/Coffee Break**	

Evening Lecture	
Co - Chairs	**R. S. Paroda**, President, ISPGR, New Delhi
	Bhag Mal, Secretary**,** TAAS, New Delhi

Convenor	**R. C. Agrawal**, Vice President, ISPGR, New Delhi	
Rapporteur	**T. R. Usha Rani**, Principal Scientist, ICAR - IIHR, Bengaluru	
17.30 - 17.40	**Introduction of Speaker**	**R. C. Agrawal**, Vice President, ISPGR, New Delhi
17.40 - 18.10	People, Plants, and Landscapes: A Holistic Approach to PGR Conservation in the Peninsular India	**Ramakant Venkataraman**, IFS (Retd.), Former Principal Chief Conservator of Forests; Chairman, Forests by Heartfulness, Heartfulness Institute, Hyderabad
18.10 - 18.20	**Co - Chairs' Remarks**	
18.20 - 18.25	**Vote of Thanks**	
18.25 - 19:00	**Comfort Break**	
19:00 - 20:00	**Cultural Program**	
20:00 onwards	**Welcome Dinner**	

DAY 2: September 18, 2026 (Friday)

Poster Session

09:00 – 10:15 AM

Poster Sessions: (Venue 1: Biotechnology building - Theme 1,2,3
Venue 2: Main lab building - Theme 4)

(Followed by Tea & Coffee Break; All to be seated in Auditorium by 10:30 AM for Inaugural Session)

INAUGURAL SESSION - September 18, 2026 (Friday)		
11.00 - 11.06	**Vandemataram and National Anthem**	
11.06 - 11.11	**Welcome**	**T. K. Behera**, Director, ICAR - IIHR, Bengaluru
11.11 - 11.16	**Remarks**	**D. K. Yadava,** DDG (Crop Sciences)
11.16 – 11.18	**Release of Publications**	
11.18 - 11.28	**Address by President, ISPGR**	**R. S. Paroda**, President, ISPGR & Chairman, TAAS, New Delhi
11.28 - 11.48	**Address by Chief Guest**	**Shri Thaawarchand Gehlot**, Hon'ble Governor, Karnataka
11.48 - 11.50	**Felicitation of Chief Guest**	

11.50 - 11.54	**Vote of Thanks**	**Anuradha Agrawal,** General Secretary, ISPGR, New Delhi
11.54 - 12.00	**Vandemataram and National Anthem**	
12.00 - 12.15	**Group Photo**	

TECHNICAL SESSION IV **Decoding Diversity for Sustainable Use** **Venue:** G S Randhawa Auditorium, ICAR-IIHR		
Co - Chairs	**D. K. Yadava,** DDG (Crop Science), ICAR and **S. V. Suresha,** Vice Chancellor, University of Agricultural Sciences, Bengaluru	
Convenors	**R. K. Gautam**, Head, Div of Germplasm Evaluation, ICAR-NBPGR, New Delhi and **H. C. Prasanna**, Head, Div. of Vegetable Crops, ICAR-IIHR, Bengaluru	
Rapporteurs	**T. Usha Bharathi,** Senior Scientist, Div. of Flower & Medicinal Crops, ICAR-IIHR, Bengaluru and **Manjunatha Gowda**, Senior Scientist, ICAR-IIHR, Bengaluru	
12:15 - 12:20	**Welcome**	**Convenor**
	Invited Lectures	
12:20 - 12:35	Tropical and Subtropical Fruit Genetic Resources of Peninsular India	**S. B. Dandin**, Liaison Officer, Bioversity International, Bengaluru and former VC, UHSB
12:35 - 12:50	Pulse Genetic Resources for Peninsular India	**Aditya Pratap,** PC, Kharif Pulses, IIPR, Kanpur
12:50 - 13:05	Utilization of PGR of Peninsular India Conserved in NGB.	**Rakesh Singh**, HoD, ICAR-NBPGR
13:05 - 14:00	**Lunch Break**	
	Session continues…	
14:00 - 14:15	Horticultural Genetic Resources: Status, Challenges and Future Prospects	**T. K. Behera,** Director, ICAR-IIHR, Bengaluru
14:15 - 14:30	Leveraging Genomics and Digital Tools for Characterization and Utilization of PGR	**Kuldeep Singh**, ICRISAT, Patancheru, Hyderabad
14:30 - 14:45	Millets for the Future: Unlocking Genetic Resources for Climate Resilience and Nutritional Security	**Tara Satyavathi,** Director, ICAR-IIMR, Hyderabad
14:45 - 15:00	**Discussion & Co - Chairs' Remarks**	
15:00 - 15:30	**Tea/coffee Break**	

Rapid Oral Presentations on PGR of Peninsular India (Session 1) - Theme 1 **Securing the Genetic Heritage of Peninsular India - from Exploration to Conservation** **Venue:** Committee Room, Main Administrative Building	
Co - Chairs	**R. K. Tyagi,** Vice President, ISPGR, New Delhi **R. Selvarajan,** Director, ICAR-NRC Banana
Convenor	**Sherry Rachel Jacob**, Organizing Secretary, NSPPI
Rapporteurs	**Rohini M. R.,** Co-Organizing Secretary, NSPPI **Vivek Hegde**, Scientist, ICAR-IIHR, Bengaluru
15:30 - 15:35	**Welcome - Convenor**
15:35 - 18:35	**Rapid Oral Presentations (27)-6 mins each**
18:35 - 18.50	**Discussion & Co - Chairs' Remarks**

Rapid Oral Presentations on PGR of Peninsular India (Session 2) - Themes 2 & 3 **PGR Governance: From Biosecurity to Benefit Sharing & Innovation, Bio economy and Livelihood Enhancement** **Venue:** Video Conferencing Room, Main Administrative Building	
Co - Chairs	**K. B. Hebbar,** Director, ICAR-CPCRI, Kasargod **Chandish R. Ballal,** Former Director, ICAR-NBAIR, Bengaluru
Convenor	**Sunil Archak**, OIC, GEPU, ICAR-NBPGR, New Delhi
Rapporteurs	**Rajendiran S.,** Senior Scientist, ICAR-IIHR, Bengaluru **Bhagyasree S. N.,** Scientist, ICAR-IIHR, Bengaluru
15:30 - 15:35	**Welcome - Convenor**
15:35 - 18:35	**Rapid Oral Presentations (27) - 6 mins each**
18:35 - 18.50	**Discussion & Co - Chairs' Remarks**

Rapid Oral Presentations on PGR of Peninsular India (Session 3) - Theme 4 **Decoding Diversity for Sustainable Use** **Venue:** G S Randhawa Auditorium	
Co - Chairs	**Kuldeep Singh,** Head, Genebank, ICRISAT, Hyderabad **Tara Satyavathi**, Director, IIMR, Hyderabad
Convenor	**Basavaprabhu Patil,** Head, ICAR-IIHR, Bengaluru
Rapporteurs	**Kuldeep Tripathi,** Senior Scientist, ICAR-NBPGR, New Delhi **Bhargavi H.A.,** Scientist, ICAR-IIHR, Bengaluru
15:30 - 15:35	**Welcome - Convenor**
15:35 - 18:35	**Rapid Oral Presentations (27)-6 mins each**
18:35 - 18.50	**Discussion & Co – Chairs' Remarks**

Evening Lecture		
Co - Chairs	**V. B. Patel,** ADG (Horticulture), ICAR, New Delhi	
	Anuradha Agrawal, PD, DKMA & General Secretary, ISPGR	
Convenor	**E. S. Rao,** OIC, PME, IIHR & Organizing Secretary, NSPPI	
Rapporteur	**Rajiv Kumar**, Principal Scientist, ICAR-IIHR, Bengaluru	
19.00 - 19.05	**Introduction of Speaker**	**E. S. Rao,** OIC, PME, ICAR-IIHR, Bengaluru
19.05 - 19.45	Corporate Stewardship of Plant Genetic Resources: BIAL's Landscape Conservation	**Prasanna Murthy Desai**, Vice President and Head of Landscape, Bangalore International Airport Ltd (BIAL)
19.45 - 19.55	**Co - Chairs' Remarks**	
19.55 - 20.00	**Vote of Thanks**	
DINNER (20:00 PM onwards)		

DAY 3: Sept 19, 2026 (Saturday)

Youth Forum on Genetic Resource Management **Venue:** G S Randhawa Auditorium, ICAR-IIHR		
Co - Chairs	**R. C. Agrawal,** Vice President, ISPGR, New Delhi **Anil Gupta**, Founder, Honey Bee Network and SRISTI; Former Professor, IIM Ahmedabad	
Convenors	**V. Celia Chalam**, Head, ICAR-NBPGR, New Delhi **Kuldeep Tripathi**, Treasurer, ISPGR, New Delhi	
Rapporteurs	**Smitha G. R.,** PS, ICAR-IIHR, Bengaluru and Co-Organizing Secretary, NSPPI and **Pushpa Chetan Kumar,** Senior Scientist, ICAR-IIHR, Bengaluru	
09:00 - 09:05	**Welcome**	**Convenor**
09:05 - 09:15	**Remarks**	**Co - Chairs**
09:15 - 11:15	**Selected Oral Presentations from Youth on New Innovations in PGR Management and Use (12)**	10 mins each
11:15 - 11.30	**Discussion & Co - Chair's Remarks**	
11:30 - 12:00	**Tea/Coffee Break**	

Valedictory Session & ISPGR Awards Function **Venue:** G S Randhawa Auditorium, ICAR-IIHR		
Co - Chairs	**R. S. Paroda**, President, ISPGR, New Delhi and **T. K. Behera**, Director, ICAR - IIHR, Bengaluru	
Convenors	**Prakash Patil**, PC (Fruits) and **Karunakaran G.**, General Secretary, SPH	
12:00 - 12:15	**Summary of Major Recommendations of NSPPI**	**R. K. Tyagi**, Vice President, ISPGR, New Delhi
12.15 - 12.45	**Distribution of Best Oral & Best Poster Awards**	
12.45 - 13.45	**ISPGR Award Function**	**Anuradha Agrawal**, General Secretary, ISPGR, New Delhi
13:45 - 14:00	**Remarks by Co - Chairs**	
14:00 - 14.15	**Vote of Thanks**	**E. S. Rao**, Organizing Secretary, NSPPI
14.15 - onwards	**Lunch**	



Venue:

ICAR - Indian Institute of Horticultural Research

Hesaraghatta Lake Post, Bengaluru - 560089

Published by:

Indian Society of Plant Genetic Resources (ISPGR)

Office Block A, 2nd Floor, National Agricultural Science Complex

Dev Prakash Shastri (DPS) Marg, New Delhi-110012, India