BOOK OF ABSTRACTS

National Conference
on
Managing Agro-Biodiversity
in North Eastern India
(From Biodiversity to Bio-Wealth)
(NCMAN-2024)
October 23-25, 2024

Venue: ICAR Research Complex for NEH Region, Umiam, Meghalaya

Supported by

National Conference
on
Managing Agro-Biodiversity in North Eastern India (From Biodiversity to Bio-Wealth)

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Indian Society of Plant Genetic Resources, New Delhi
ICAR Research Complex for North Eastern Hill Region, Umiam, Meghalaya
ICAR-National Bureau of Plant Genetic Resources, New Delhi

Co-organizers

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Alliance for Bioversity International and CIAT, New Delhi
Trust for Advancement of Agricultural Science, New Delhi
ICAR-Agricultural Technology Application Research Institute, Zone-VI, Guwahati, Assam
ICAR-Agricultural Technology Application Research Institute, Zone-VII, Umiam, Meghalaya
ICAR-National Research Centre on Orchids, Pakyong, Sikkim

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PREFACE

We are delighted to present the Book of Abstracts of the **National Conference on Managing Agro-Biodiversity in North Eastern India (NCMAN),** held during October 23-25, 2024. This event is projected to provide a roadmap for improving livelihood as well as food and nutrition security for better health through optimal, efficient and sustainable use of agro-biodiversity, which includes the animals and fisheries of northeastern India using innovations through interdisciplinary and inter-institutional scientific collaboration, as well as for ensuring enabling policies to conserve, use, benefit sharing and mainstream the agrobiodiversity of the region.

The national seminar comprises six Technical Sessions with >100 keynote/ invited lectures and oral presentations and >120 posters, one Plenary Session, an evening lecture and a Valedictory Session.

This publication contains abstracts related to agro-biodiversity, which includes animals and fisheries of north eastern India, their production potential, the current status of research related to genetic improvement, their conservation through use, nutritional and medicinal values, value chain options, socio-economic dimensions (women empowerment, consumption pattern, cost and affordability), and enabling policy support relating to their promotion as alternative sources of livelihood, food, nutrition and health security.

The abstracts and articles included in this publication give a comprehensive overview of the genetic resource management work being done in north-eastern India, as well as related crops and species in other regions of the country. The organizers duly acknowledge the contributors for submitting the articles and abstracts, as well as the editors for compiling the publication on time. It is hoped that this collation will be useful for policy makers, students, faculty, and researchers working in this area.

Core Organizing Committee

ACKNOWLEDGEMENTS

The National Conference on Managing Agro-Biodiversity in North Eastern India (NCMAN) is a great opportunity for us, as both organizers and participants, to share mutual experience in such an important field of management of agrobiodiversity including animal and fisheries of northeastern India.

The delegates (>250) 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 Center for Agricultural Research in the Dry Areas (ICARDA), International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Central and State Universities, Council for Scientific and Industrial Research (CSIR), Meghalaya Biodiversity Board, Directorate of Animal Husbandry & Veterinary, National Bank for Agriculture and Rural Development (NABARD) and other Agencies of Government of Meghalaya, Tea Research Institute, private stakeholders, progressive farmers and entrepreneurs etc.

We would like to express our sincere gratitude to Padma Bhushan Dr. R.S. Paroda, President, ISPGR, and Chairman TAAS, New Delhi for guidance and support to organize the event in northeastern India as well as extended discussions and valuable suggestions.

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Dr. P. L. Gautam, Chancellor, RPCAU, Bihar; Dr. Anupam Mishra, Vice-Chancellor, CAU, Imphal; Dr. Prabha Shankar Shukla, Vice Chancellor, NEHU, Shillong, Meghalaya and Dr. B. C. Deka, Vice Chancellor, AAU, Jorhat, Assam, Dr. S. K. Chaudhari, Deputy Director General, NRM, ICAR, New Delhi, Dr. G.P. Singh, Director, ICAR-NBPGR, New Delhi are profoundly thanked for the excellent technical and administrative support provided for organizing this Seminar. We also thank for the technical and administrative support by Dr. Vinay Kumar Mishra, Director, ICAR Research Complex for North eastern Hill Region, Umiam, Meghalaya.

We thank our co-organizers, Dr. A. K. Mohanty, Director, ICAR –ATARI, Umiam; Dr. G. Kadirvel, Director, ICAR-ATARI, Guwahati and Dr. S. P. Das, Director, ICAR-NRC, Orchid, Sikkim for their technical support and financial assistance in organizing the "Agrobidiversity Exhibition" during the conference.

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We duly acknowledge the financial support provided by ICAR, New Delhi; Alliance for Bioversity International and CIAT, New Delhi; PPV&FRA, New Delhi; ICARDA, New Delhi; ICRISAT, Hyderabad; NABARD and Meghalaya Biodiversity Board, Shillong, and Directorate of Animal Husbandry & Veterinary, Shillong, Meghalaya.

We place on record the assistance received from the Core Organizing Committee, Local Organizing Committee, Technical Session Co-Chairs, Conveners and Rapporteurs, Poster Session Convener and Co-convener, for the smooth conduct of the Conference.

We express our sincere appreciation to public and private sector partners for joining hands with us in this endeavour. We draw our strength from the support of colleagues from different participating institutes in this Seminar. A confluence of people involved in genetic resources management would not have been possible without the cooperation of many government and scientific institutions. We thank each one of them for their role in organizational steps.

October 23, 2024 **Editors**

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A **AGRICULTURE**

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OP1-01

On Farm Conservation of Fruit Diversity in North East India

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The on-farm conservation of fruit species in Northeast India is a critical component of sustaining the region's rich biodiversity and local livelihoods. Numerous factors, categorized into ecological, socio-economic, cultural, and policy-related aspects, influence this conservation effort, each significantly contributing to the sustainability of fruit diversity. Northeast India is widely referred to as a biodiversity hotspot ecologically, with its diverse topography and microclimates providing an ideal region for growing over a variety of fruit species. Many genera of fruit in the region are diverse, and numerous illustrative examples include *Citrus, Musa, Pyrus, Prunus, Garcinia, Artocarpus, Averrhoa, Annona, Passiflora, Emblica, Tamarindus, Morus, Ziziphus, Ficus* and *Rubus*. Apart from these major genera, North East India is enriched with numerous underrated fruit species, creating a discrete biodiversity profile of this region. Some of these minor fruits are *Prunus nepalensis, Elaeagnus latifolia, Baccaurea sapida, Haematocarpus validus, Aegle marmelos, Phyllanthus acidus, Docynia indica, Cyphomandra betacea, Malus baccata, etc*. A significant number of them have been domesticated traditionally in homegardens, horti-based farming and other integrated farming systems, thereby offering a diverse genetic resource base for these fruit species. Sergio points out that these systems are instrumental in the protection of biodiversity, but more than that, they become models for forest environments to provide habitats and resources at various levels to a number of other species, helping maintain the ecological equilibrium. The cultivation of these fruit plants holds significant socio-economic value for rural households in the region. Fruits are diverse in local diets, providing nutritional benefits as well as a source of income due to their potential in the local and regional markets. Tapping the economic potential of non-traditional fruit varieties such as *Prunus nepalensis, Aegle marmelos, Elaeagnus latifolia, Baccaurea sapida, Haematocarpus validus, etc.* can encourage the farmers to conserve diverse species in their farming area, thus promoting on-farm conservation. Provisions of market and value addition options such as processing, and packaging increase the economic worth of the fruit cultivation, thereby inducing farmers investment in conservation of their local biodiversity. In the local communities of Northeast India, traditional knowledge and practices connected with fruit cultivation are deeply rooted culturally. Minor fruits such as *Citrus indica, Pyrus pashia, Phyllanthus acidus* and *Docynia indica* are also of cultural importance that is closely related to the local rituals, festivals, and culinary practices in many fruit species. Protecting this traditional knowledge is critical to ensuring its recognition and respect, which in turn enable local communities to manage and conserve their biodiversity. By incorporating these practices into modern conservation strategies, the region can effectively preserve its fruit diversity. There are also policy related aspects that influence the on-farm conservation of fruit species. Thus, there is a need to implement related supportive policies that can recognize the significance of agroforestry systems in biodiversity conservation in order to avoid such system degradation. As sustainable agricultural practices on a large-scale are focused towards the farmers, whether we like it or not, giving them the power to be able to decide which direction they want their crops and life to go could bring a change that will pump purely animals into the ecosystem. We need collaborative work between local communities, researchers and policy makers to ensure that conservation efforts are done better, guided by the interests of local people. Indeed, the immense importance of on-farm conservation in maintaining fruit diversity (comprising major and minor fruits) in Northeastern India cannot be over emphasised. The region has a rich diversity of fruit species which are native to the area, having developed over centuries specifically to suit the environment and cultural factors. Conserving these endangered fruit trees on farms saves not only the genetic diversity of tree fruits but also the unique trait that exist in them that allow them to remain in a world changed by climate change, pests and diseases. In-situ strategy for conservation is emphasized because species continue to evolve in their natural habitats and are able to adapt themselves to changing ecological scenarios. On farm conservation has also been identified as a reliable option to guarantee that even species which may not fall under the formal domain of ex-situ conservation programs can be saved by way of securing biodiversity on a larger scale. The interaction among ecological, socio-economic, cultural and policy-related factors in on-farm conservation of fruit species in NE India emphasizes the need for a comprehensive approach. Facilitated by collaboration among stakeholders and the appreciation of traditional knowledge, it should be possible to protect this valuable biodiversity for posterity while bettering the lives and sustenance of local communities. Adoption of multipronged approaches encompasses not only environmental conservation but also heritage preservation and income generation. The protection of North East India's valuable resources will ensure a balance between development and ecology.

Keywords: Fruits, Biodiversity, Underutilized, Conservation

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OP1-02

Morphological Diversity in Orchids

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The present investigation was conducted using all vegetatively propagated species and hybrids of commercially grown orchid genera viz. *Cattleya* Lindl., *Cymbidium* Sw., *Dendrobium* Sw., *Mokara* (Arachnis X Ascocentrum X Vanda), *Oncidium* Sw., *Paphiopedilum* Pfitz, *Phalaenopsis* Blume and *Vanda* *J*ones ex R. Br. With the study of morphological diversity of 8 orchid genera, 53 descriptors in *Cattleya*, 62 descriptors in *Cymbidium*, 52 descriptors in *Dendrobium,* 61 descriptors in *Mokara*, 60 descriptors in *Oncidium*, 77 descriptors in *Paphiopedilum*, 58 descriptors in *Phalaenopsis* and 54 descriptors in *Vanda* were developed. Amongst different morphological descriptors of commercially grown orchid genera, diversity in pseudobulb shape, leaf shape, inflorescence variation, floral characteristics and their diversity were studied in detail. Morphological descriptors of 35 orchid species namely *Acampe*

rigida, *Acampe papillosa*, *Aerides rosea, Arachnis labrosa, Ascocentrum spp., Diplomeris hirsute, Paphilionanthe vandarum, Renanthera imschootinmacrophylla, Gastrochilusundina graminifolia, Phaius wallichii, Calanthe masuca, Coelogyne elata, Coelogyne flaccida, Coelogyne fuscescens, Coelogyne nitida, Coelogyne ovalis, Coelogyne suaveolens, Coelogyne orchracea, Coelogyne graminifolia, Coelogyne cristata, Coelogyne barbadense, Cleisocentron trichonum, Cottonia peduncularis, Eria bambusifolia, Eria coronaria, Eria flava, Eria suaveolens, Lycaste cruentus, Lycaste macrophylla, Gastrochilus bellinis, Thunia marshalliana, Epidendrum radicans, Epidendrum xanthium* and *Epidendrum secundatum* developed which could be useful for identification of unique germplasm for pot plants, medicinal orchids, breeding materials and preparation of value added products.

Keywords: Descriptors, Orchid, Species, Hybrids

* * *

OP1-03

Conservation of Maize Genetic Resources of North Eastern India-Status, Prospects and Challenges

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The North Eastern Himalayan (NEH) region of India is endowed with one of the richest indigenous diversity for maize, within the country. The landraces found in the various states of NEH region have been reported to have extensive diversity for plant, ear and tassel characteristics, along with tolerance against several biotic and abiotic stresses. These unique genotypes were systematically conserved over the years, by the local farmers of that region, owing to their social and cultural relevance. But the rampant introduction of hybrids in the last few decades has wiped out majority of these rich genetic resources from their respective adapted zones and this has been observed many NBPGR explorers in their various collection missions. The National Genebank at ICAR-National Bureau of Plant Genetic Resources (NBPGR) conserves one of the largest collections of maize germplasm, which comprises of indigenous maize diversity collected from throughout the country. A major collection is from the north eastern hill region (4290 accessions), from where exploration missions have added large number of landraces. It has been undisputedly proven that this native diversity is a gold-mine that holds the key to effective crop improvement since they have reservoirs of genes that have survived domestication, selection, cross breeding and climatic hazards. Sikkim Himalaya has been reported as the secondary centre of diversity of maize and its prominent landrace known as Sikkim primitive/ Murli makkai has been one of the most unique collection in the National Genebank (NGB). Other prominent landraces of North-east India available in NGB are *Kuchungdari, Bacherey, Kuchungtamar, Kukharey* (dwarf, high altitude); dent kernel-, *Gadbade*, *Seti, Chaptimakai* (soft opaque cap), *Pahenli* (light dent) and *Pahari makai* (adapted to mid-to high-altitude, cold hardy). All these accessions have been characterized using 30 descriptors, under CRP (AB) programme. Efforts have also been made to address the issue of redundancy in mimban maize collections from this region, using passport,

morphological and molecular characterization data. The analysis could identify redundant sets within genetic clusters, through integration of geographic, morphological and molecular data and from within 24 accessions, 16 accessions were marked for bulking, which would bring down the conservation size from 24 accessions to 14 accessions.

Keywords: Maize, Descriptors, Gene bank, Eastern Himalaya

OP1-4

Yield and Yield Components of Potato germplasm in Northern Plains

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This research study conducted at ICAR-Central Potato Research Institute, Regional Station, Modipuram, Meerut during the 2021-22 season aimed to evaluate the genetic diversity and performance of 37 potato (*Solanum tuberosum*) germplasm lines. Key parameters such as germination, plant vigour, foliage maturity, marketable and total tuber yield, and specific tuber traits were assessed to understand the potential for crop improvement and germplasm utilization. Results revealed that several genotypes, including CP3469, CP3048, CP3050, CP3437, CP3337, CP1748, CP1454, CP3464, CP3252, CP3438, CP3085, CP3334, CP3288, CP1631, CP3353, CP3365, CP3389, CP3421, CP3413, and CP3270, exhibited 100% germination. Early maturity (foliage maturity 1-5 scale, 1=very late , 5= very early) was observed in CP3469 (4.5), CP3361 and CP3326 (4), CP3048, CP3050, CP3395, CP3266, CP3437, CP3337, CP1748, CP1454, CP2094, CP3255, CP3360, CP1471, CP3464, CP3252 and CP3414 (3.5) Noteworthy plant vigour (1-5 scale, 1=very poor , 5= highly vigorous) was demonstrated by CP3048 (4.5), CP3050, CP3266, CP3355, CP3395, CP3438 and CP3465 (4). CP3421 emerged as the top performer in total tuber yield (953g/plant), followed by CP3464 (587g), CP2094 (529g), CP3326 (521g), CP3414 (514g), CP3437 (487g), CP1651 (480g), CP3438 (477g) CP3413 (462g), CP3085 (453g) and CP3337 (453g). CP3326 exhibited the highest marketable tuber yield (514g/plant) followed by CP3464 (420g), CP3438 (411g), CP3413 (409g), CP3085 (393g), CP3337 (387g), CP3255 (364g), CP3252 (363g), and CP3421 (353g). Regarding tuber number, CP3334 found to have the highest count (18), followed by CP3469 (12), CP3385 (12), CP1748 (11), CP1651 (11), CP1471 (11), CP3413 (10), CP3361 (9.62), CP3085 (10), CP3365 (9), CP3438 9), CP3247 (9) and CP3294 (9). Higher marketable tuber numbers were recorded in CP3334 (8) followed by CP3326 (7), CP3385 (7), CP3085 (7), CP3469 (6), CP1651 (6), CP3464 (6), CP3337 and CP1748 (6), CP3438 (6), and CP1471 (6). The study also recorded tuber traits, including colour, shape, eye depth, and flesh colour. Promising genotypes for overall performance in terms of total tuber yield and marketable tuber yield were identified as CP3421, CP3464, CP3326, and CP3438. This comprehensive evaluation provides valuable insights into the genetic diversity of potato germplasm, offering a foundation for crop improvement and effective germplasm utilization.

Keywords: Potato, Genetic Variability, Germplasm, Yield

OP1-05

Insights into Phenotypic Diversity of Yard Long Bean Germplasm Conserved in National Genebank of India

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The Yardlong bean (*Vigna unguiculata* ssp. *sesquipedalis*) is a promising leguminous vegetable cultivated in India, known for its elongated pods used as a vegetable. It is also a versatile legume in the Northeastern region of India. The present study, conducted during the kharif seasons of 2022 and 2023 at ICAR-NBPGR, New Delhi, aimed to fully characterize 187 accessions conserved in the National Genebank. These accessions included seven exotic collections from Australia, Nigeria, Italy, and the Philippines, along with 180 indigenous collections from 21 states and union territories of India. Approximately 30% of the studied collections were native to the NEH regions, with Arunachal Pradesh contributing the highest number of accessions, followed by Mizoram. The accessions were grown under protected conditions using an Augmented Block Design with three checks-Arka Mangala, Gitika, and Lola and characterized using 36 distinct agro-morphological descriptors, including 19 qualitative and 17 quantitative traits, recorded at appropriate stages of crop growth when fully expressed. In 2022, Days to 50% flowering ranged from 26.29 to 112.29 days, with an average of 53.15 days. The mean value of Terminal Leaflet Length and Terminal Leaflet Width was observed as 13.7 cm and 8.63cm respectively. Based on the mean performance for targeted traits, IC622563, IC546883, and IC630384 exhibited early flowering. EC738116 had the maximum pod length (80.2 cm) and the highest pod weight (38.77 g), while IC471939 (22) and IC630391 (21) had the highest number of seeds per pod. This study marks the first comprehensive effort to characterize the entire Yardlong bean accessions, tapping into the diversity available in the National Genebank. The superior accessions identified in this study can be used to improve existing cultivars or be introduced as new varieties.

Keywords: Characterization, Diversity, Germplasm, Evaluation, Utilization, Vegetable, Yardlong bean

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OP1-06

Development of Non-Psychoactive *Cannabis sativa* L. Genotypes in Half Sib Seed Progeny Segregation Generation through Diversity Analysis

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Cannabis sativa L. is a versatile crop with diverse applications, from industrial hemp to medicinal and recreational cannabis. Understanding the genetic factors controlling the accumulation of critical phytochemicals, such as cannabinoids and terpenes, is crucial for developing tailored variety (ies) for specific end-uses. The study comprehensively analyzed the morphological, cannabinoid, and terpene profiles of CIM-CS-64 and its 60 half-sib progenies. Cannabinoid analysis revealed significant variation in the studied accessions, with total Cannabidiol content (Total CBD) ranging from 0.06% to 2.756% and total tetrahydrocannabinol (Total THC) content between 0.04% and 1.920%. The half-sib progeny of CIM-CS-64 segregated into two distinct groups: hemp-type (< 0.3% total THC) and drug-type (> 0.3% total THC), suggesting the parental plant was likely heterozygous for the genetic factors controlling THC and CBD biosynthesis. CIM-CS-64 seed progenies were classified in to four distinct chemotypes, based on THC and CBD content. The cluster analysis of the morphological traits revealed that Cluster-5, the largest group comprising 23 seed progenies, had most individuals with less than 0.3% THC content and high CBD content, making them promising genetic resources. In contrast, Cluster-2 had only one seed progeny, CIM-CS-64-4, which exhibited the highest values for most morphological traits and had less than 0.3% total THC, high CBD, and notable terpene levels, making it the most promising accession. Principal component analysis and hierarchical clustering highlighted key traits contributing to the observed diversity. Notably, 27 elite half-sib seed progenies were identified with total THC content below the 0.3% legal threshold, providing a valuable resource for further research and breeding programs. The comprehensive analysis of morphological, cannabinoid, and terpene profiles offers insights for developing tailored non-psychoactive Cannabis genotype(s) for various applications while adhering to regulatory requirements.

Keywords: *Cannabis sativa*, Cannabinoids, Terpenes, Chemotypes, Genetic Diversity, Segregations

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OP1-7

Exploring the Nutritional Potential and Anti-Nutritional Components of Wild Edible Fruits of the Eastern Himalayas

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Wild edible fruits are an important source of nutritional supplementation for the tribal communities in the northeastern mountainous region of India. In this study, the nutrient and anti-nutrient composition of 44 wild edible fruit species from the northeastern India were investigated. Among the studied species, *Elaeagnus umbellata* showed high content of soluble solids (24.50±0.41ºBrix), free fatty acids (67.79±1.75 mg KOH g^{-1}) and vitamin A (136.22±1.44 mg 100 g^{-1}). *Terminalia chebula* was shown to be a good source of reducing sugars (8.38±0.07 %) and total favonoids (445.20±1.18 mg 100 g^{-1}) and *Spondias pinnata* with high total carbohydrate (12.51±0.22 %) and vitamin C (74.16±5.33 mg 100 g^{-1}) content. *Castanopsis hystrix* had the highest starch (1764.84±8.85 mg 100 g^{-1}) and cellulose (711.62±7.68 mg 100 g^{-1}) content and *Machilus edulis* with high fat content (36.44±1.23 %). Chlorophyll, carotenoid and anthocyanin contents were highest in *Phoebe cooperiana*, *Rhus semialata* and *Prunus nepalensis* respectively. *Artocarpus lakoocha* (84.58±2.38 %) and *Spondias pinnata* (84.09±0.62 %) were found to be good sources of antioxidants. Regarding anti-nutritive factors, *Canarium strictum* showed the highest phenols (902.00±5.72 mg 100 g^{-1}), highest tannins in *Terminalia chebula* (1059.33±17.46 mg 100 g^{-1}), alkaloids in *Streblus asper* (274.27±6.31 mg 100 g^{-1}), cyanogen in *Castanopsis hystrix* (31.04±1.28 mg 100 g^{-1}) and phytic acid in *Viburnum foetidum* (10.64±0.30 mg 100 g^{-1}). The results indicate that all studied fruit species possess nutritional and anti-nutritional properties and are considered promising for nutraceutical and pharmaceutical industries.

Keywords: Wild fruit, Nutrition, Anti-nutritional factors, Northeast India

* * *

OP1-08

Collection and Conservation of Wild Edible Fruits and Spices from Upper Assam Valley

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This study presents the findings of a collaborative field trip undertaken by ICAR-NBPGR, New Delhi, and ICAR-IISR, Kozhikode, to the Upper Assam Valley, encompassing the Dibrugarh, Tinsukia, and North Lakhimpur districts. The expedition aimed to collect and conserve genetic resources of indigenous

wild edible fruits and spices. Over 80 collections were gathered from various habitats, including forests, wastelands, home gardens, and farmers' fields, between June 7th and 17th, 2022. The collected specimens represent a diverse array of botanical families, such as Myrtaceae, Dilleniaceae, Rutaceae, Piperaceae, Zingiberaceae, and Clusiaceae including 25 collections of *Piper*, 26 of Zingiberacious spices, five of Cinnamon, 26 of *Garcinia* and one accession each of *Syzygium jambos, Aegle marmelos* and *Dillenia indica.* The ethnobotanical use of this diverse germplasm was recorded during the study. Most of these species are wild and native to the region; some are semi-domesticated and cultivated by local farmers. Accessions of *Dillenia indica* and *Aegle marmelos* were cryopreserved in the cryo-bank of ICAR-NBPGR. Additionally, the Crop Wild Relatives (CWR) of spices were propagated using techniques like grafting, cuttings, seed rhizomes and suckers and maintained in the Field Gene Bank for spices at ICAR-IISR, Kozhikode. A total of 28 accessions, conserved at ICAR-IISR, Kozhikode with affirmed species identity were submitted for allocation of the IC numbers. Six species among the conserved accessions *viz*; *Garcinia assamica*, *G. acuminata*, *G. sibeswarii*, *Piper betleoides*, *P. pedicellatum*, and *Globba multiflora* are new additions to the ICAR-NBPGR database. CWR belongs to Zingiberaceae family consists of 18 species under the genera *Amomum, Alpinia, Boesenbergia, Curcuma, Globba, Hedychium* and *Zingiber.* The Upper Assam valley is a potential area for collecting the CWR of tropical spices such as black pepper, cinnamon, ginger, turmeric and *Garcinia*. Fine grid survey and collection from unexplored areas must be prioritized for the conservation and sustainable utilization of the valuable genetic resources from the region.

Keywords: Wild edible fruits, Spices, Zingiberaceae, Northeastern India

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OP1-09

Nutritional Potential of *Perilla frutescens* (Linn.) Britt. in the Northeastern Hill (NEH) Region of India

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Perilla frutescens (Linn.) Britt. is an edible herb native to many countries in Asia including India. Its leaves and oil are used in cooking and as medicine. *Perilla*, abundant in oil and protein, holds significant cultural and culinary importance among the tribal communities of the Northeastern Hill (NEH) region. Present study is aimed to characterize 62 accessions of *Perilla* collected from the different parts of the NEH region of India. This study explores the traditional consumption and uses of *Perilla,* with its seeds and leaves integrated into the daily food habits of tribal peoples of NEH region. *Perilla* serves as a staple food item across the region through commonly prepared as chutneys and incorporated into various recipes, ranges from chutneys to mixed vegetable salads and cakes. The *Perilla* seeds are an integral part of many traditional recipes in Arunachal Pradesh, Manipur, Meghalaya, Mizoram,

Nagaland, and Sikkim. Additionally, the leaves are commonly cooked as vegetables in Nagaland and Manipur, while in Mizoram, they are used in dishes like *Changkha Bawl* and *Snail Curry*. Phenotypic variations observed for many traits in present set of germplasm. Among the studied material, five types of seed colors were observed (white, gray, light brown, brown, and dark brown). Of these, gray seeds are generally preferred by consumers due to their softer husk. *Perilla* seeds' biochemical analyses reveal substantial variation in fatty acid composition, with notable levels of polyunsaturated fatty acids (PUFAs), particularly linolenic acid (omega-3), contributing to their nutritional value. Significant variations in fatty acid composition and oil content were observed among the accessions. *Perilla* oil, rich in PUFAs like linolenic acid (omega-3), holds potential as a healthful dietary supplement. The principal component and cluster analyses revealed distinct biochemical profiles among accessions, highlighting the genetic diversity within *Perilla* germplasm. Promising accessions with high oil content (>50%), including IC524554, IC524504, IC52445, IC422885, IC275959, IC016443, IC006444, IC006442, and IC599246, were identified and deposited to the National Genebank, ICAR-National Bureau of Plant Genetic Resources, New Delhi, for posterity. This study underscores the importance of traditional knowledge and emphasizes the potential of *Perilla* as a valuable resource for food and nutritional security.

Keywords: Perilla, Oilseed, Potential crop, PUFA

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OP1-10

Morphological Evaluation of Khamti Lahi Rice Landraces of Arunachal Pradesh

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Rice is a staple food in the Eastern and North East India. India is a major producer and consumer of rice in the World. The Indian subcontinent was home to thousands of varieties of domesticated rice (*Oryza sativa* ssp. *indica*). Due to varied topography, altitude, rainfall and the cultural heritage of different ethnic tribes, they preserve the various rice diversities in their respective areas. Nomenclature of each landrace of rice variety is maintained by the particular ethnic group. Otherwise, the major local diversities of rice are maintained by the local farmers themselves. Green Revolution, which began in the late 1960, most of these landraces were replaced with a handful of high yielding varieties (HYVs) and F_1 hybrids, and are now extinct from farm fields. Most of the farmers of Arunachal Pradesh, particularly in the Namsai region, cultivate traditional and indigenous varieties of rice. However, numerous reports have shown indigenous cultivars having a wide diversity in physiological, ecological, and morphological characteristics. So, it is essential to evaluate the performance of improved indigenous and traditional rice varieties to identify and popularize the promising ones. The present study was performed with the aim to evaluate the performance of 10 landraces of *Khamti Lahi*, a traditional rice variety of Namsai district in Arunachal Pradesh. *Khamti lahi* is a type of sticky rice which is not consumed in every meal, and has a unique process of cooking to prepare *tupula*

vat by rolling inside *koupaat* (*Phyrinium sp*. L.) and then steamed. The Tai Khamti community cooks this special rice during festivals and special occasions. This Khamti Lahi is cultivated only once in a year, under rainfed and semi irrigated condition during the months July - Dec. The landrace *Khau Seng Khaao* was found to attain maximum plant height (161.2±34.53), total no. of grains/panicle (175.43± 52.37), no. of filled grains/panicle (132.73± 48.61). Whereas the same landraces had minimum no. of tillers/m^2 (145.83± 3.84), no. of productive tillers/m^2 (129.40± 11.90), total biomass (1142.66±607.60 kg/ha) and seed yield (212± 63.92 kg/ha). The land race *Khau Mukok* produced maximum no. of productive tillers/m^2 (170.07± 87.48), panicle length (28.03± 1.36 cm) and seed yield (312± 103.59 kg/ha). The yield of *Khau Mukok* landrace was more than the control variety Ranjit sub 1 (304.66± 55.73 kg/ha), which is a popular lowland paddy variety in the district. Thus, the study clearly showed that these indigenous rice varieties are not only traditionally important but also adapted to the local environmental condition so well to give more yield than improved varieties.

Keywords: Rice, Local Landrace, Grain Yield

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OP1-11

Genetic Richness of Cucumber (*Cucumis sativus* L.) from Northeastern India: Characterization for Biotic, Abiotic and Nutraceuticals Properties

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Cucumber (*Cucumis sativus* L., 2n=2x=14, Family Cucurbitaceae), known as Kheera or Kakdi in Hindi, is a significant summer salad vegetable crop that thrives in tropical, subtropical, and temperate regions. Cucumber cultivation is believed to have been domesticated in India for 3,000 years. India is considered the primary centre of origin for cucumber, where progenitor, wild and cultivated species (*Cucumis sativus var. hardwickii* and *Cucumis sativus var. sativus*) are abundantly available from the foothills of the Himalayan region. India is the 26th largest cucumber producer globally, with a production of 183,223 metric tonnes. Cucumber cultivation in India spans an area of 1.13 lakh hectares, yielding an annual production of 1.638 million tonnes (NHB 2021-22). Northeastern India, particularly the seven sister states, has a rich genetic diversity of cucumber. ICAR-CITH, RS, Dirang, Arunachal Pradesh, has actively participated in collecting approximately 150 cucumber genetic resources from Nagaland, Arunachal Pradesh, Mizoram, and Meghalaya, covering regions with extreme cold (Tawang) and moderately hotter climates (Nagaland). The collected materials possess

important morphological characteristics (gynoecious and monoecious), low cucurbitacin content, rich beta-carotenoids, and resistance to various biotic stresses (downy mildew, powdery mildew, Tomato Leaf Curl New Delhi Virus) and abiotic stresses (cold tolerance and heat tolerance). The germplasm was evaluated over two seasons (2024 summer and rainy season) and the characterization of the collected germplasm was conducted according to DUS guidelines at ICAR-CITH, RS Dirang. These collected germplasm resources are highly useful in pre-breeding, varietal/hybrid breeding, and marker-assisted breeding for resistance to various diseases and pests. Moreover, the current findings, along with the characterization and conservation of germplasm, will help strengthen our efforts to achieve the national goal of a developing India (Viksit Bharat) by 2047.

Keywords: Cucumis, Genetic resources, Northeastern Himalaya, India

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OP1-12

Habitat Distribution Mapping of *Hippophae* spp. in Rcp 4.5 Climate Scenarios in the Indian Himalayas

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Hippophae rhamnoides is a stress tolerant, drought hardy, and cold tolerant shrubby species of the cold deserts in the Himalayas. The species is not only climate resilient but also has good economic value for its nutritionally rich fruits. The fruit juice, commercially known as *Leh Berry* is commercially exploited supporting livelihood of farmers in the Himalayan Mountains. Passport data of 203 accessions of *Hippophae rhamnoides*, and 14 accessions of *H. salicifolia* from the Western Himalayas, and North-eastern hill Region (NEH) were extracted and curated for the study. The screened data points were geo-referenced, diversity distribution maps developed and GIS-based grid mapping was done to analyze species richness, assess variability and occurrence of trait-specific germplasm of crops in different parts of the study area. The predicted habitat suitability map was developed using 19 bioclimatic variables in *BioClim* model. Climate data were taken for a period of 50 years (1950-2000) in a climate grid of 2.5 km^2 and habitat map of likely distribution of the species in RCP 4.5 scenario (IPCC, 2014) was developed. Areas with high probability of occurrences are observed to be in the higher altitudes (nearly 3000 m) of Chamoli, Pithoragarh, Rudraprayag and Uttarkashi districts of Uttarakhand; Chamba, Kinnaur and Lahual & Spiti districts of Himachal Pradesh, and Leh and Ladakh region of Ladakh Union territory. A general habitat shift was observed and new niches were observed in the Dibang valley, Upper Siang, Anjaw, West Siang and Upper Subansiri of Arunachal Pradesh. On the other hand, habitat shrinkage was noticed in Leh, and Lahul & Spiti district of Himachal Pradesh.

Key words: *BioClim* model, Species richness, Niche modelling

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OP1-13

Espalier Systems: Evaluating the Performance and Conservation of Tree Fruit Crops and Varieties

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The espalier system, rooted in ancient Egypt and Rome, involves pruning and tying branches to grow plants flat against a support structure and has proven effective in conserving and evaluating germplasm at VNR Research Centre, Chhattisgarh. This method allows for minimal land utilization, maximum sunlight exposure, improved air circulation, and ease of harvesting. The geometry of the espalier system facilitates researchers in studying the performance of different species and genotypes within a confined area, thereby aiding in conservation efforts. Evaluating the performance of various fruit species and genotypes under espalier systems is crucial for optimizing land use, labour, yield, fruit quality, and overall plant health. Different species and genotypes respond uniquely to espalier training, affecting factors such as precocity in bearing, vegetative growth rate, pest and disease resistance, and adaptability. This study aims to evaluate the growth, yield, fruit quality, and pest resistance of different fruit crops and genotypes trained using espalier systems. The research seeks to identify the benefits and challenges associated with the espalier system in conserving and evaluating various germplasm. At VNR Research Centre, the study includes a diverse range of species and genotypes with specific spacing requirements. For instance, Guava (*Psidium guajava*) varieties, like with VNR Bihi, VNR Rubina, VNR Rajat, VNR Magenta, Hisar Surkha, Hisar Safeda, Punjab Kiran, Arka Rashmi, Dhawal, Aishwarya, and, Allahabad Surkha, is spaced at 12ft x 8ft, allowing for 1125 plants per hectare. Custard Apple (*Annona squamosa*) varieties such as VNR Madhur and VNR Uttam are spaced at 12ft x 6ft, resulting in 1512 plants per hectare. Mango (*Mangifera indica*) varieties, including VNR Mongra, VNR Parakh, VNR Umang, Pusa Lalima, Pusa Arunima, Amrapali, Arunika, Ambika, Dasheri, Najuk Badan, Himsagar, Kingstone Pride, Chinnarasam, Nileshan, Kalahapus, Mallika, Maya, Sindhu, Royal Special, Irvin Perple, Shah Jahan, Totapuri, Tommy Atkins, Baramasi, Bajrang, Madhuri, Arka Puneet, Alphonso, Banganpalli, Malda, Dudh Penda, Rampuri, Taiwan, Langra, Neel Kiran, Anarkali, and Kesar, are also spaced at 12ft x 8ft, accommodating 1125 plants per hectare. In conclusion, the espalier system offers a promising method for the conservation and evaluation of fruit crops and varieties. Its ability to optimize land use and improve various growth parameters makes it a valuable tool in horticultural research and practice. Future applications of espalier systems could extend beyond current species to include a broader range of crops, potentially enhancing sustainable agricultural practices and supporting food security. Further research could explore the long-term impacts of espalier training on plant health and productivity, as well as its adaptability to different climatic conditions and farming systems.

Keywords: Fruit crops, Varieties, Genetic Diversity, Conservation

OP1-14

North East Collections of Sugarcane Genetic Resources and their Utilization for Climate Resilience

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The success of pre-breeding in sugarcane was very- well demonstrated with the development of the first commercial variety Co 205 through the interspecific hybridisation between *Saccharum officinarum* and *S. spontaneum* in 1918. Several expeditions from 1912 to date hold about 6000 germplasm and are maintained at Coimbatore, kannur and Agali. Of which 938 clones were collected from North East India since 1982. Co canes were developed from some clones. In order to use the Northeast collections to enlarge the genetic base with climate resilience, three cytotypes of *S. spontaneum viz*., IND 82-319 (2n=56), IND 82-321 (2n=88) of Sikkim, IND 84-338 (2n=60) of Arunachal Pradesh have been utilized through hybridisation with Co cane (BO 102). The vigorous 36 hybrids selected from the seedling nursery were evaluated clonally for agronomic and cytological performance. The hybrids were intermediate of the parents. Among the 9 characters studied, variability was high for NMC (number of millable canes) with CV% from 28.27 to 33.32%. Improvement for NMC, plant height, internode length, leaf sheath length, leaf blade width over the female parent was noticed in all three crosses. Cytological studies indicated n+n chromosome transmission pattern with aneuploids. The chromosome number ranged from 2n=72-99. Chromosome loss varied from 1-15. The hybrid AS 04-1425 of the cytotype 2n=88 had 2n=85 with the elimination of 15 chromosomes. The hybrid 04-359 had shown the maximum loss of 12 chromosomes with 2n=72 in the cross of BO 102 (2n=108) x *S. spontaneum* (IND 84-338, 2n= 60). The two hybrids AS 04-1687 and AS 04-1689 of the cross BO 102 x IND 82-316 (2n=56) were tolerant for waterlogging and drought in AICRP trial. AS 04-1687 registered as genetic stock (IC0636675:INGR20110) for water logging and drought tolerance. Anatomical studies revealed higher frequency of root hairs, aerenchyma cells, hypodermal layer and silica cells. The full length gene of the Transcription factor MYB59 (R2R3-type) (Size 1.5 kb) involved in plant growth and stress responses has been cloned and characterized from AS 04-1687. This multi-tolerant hybrid is further backcrossed for varietal development to enable climate resilient varieties.

Keywords: Sugarcane, Genetic resources, Genotypes, Climate resilient

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PP1-01

Quinoa (*Chenopodium quinoa*): A Promising Underutilized Crop for Nutritional Security in Hill Agriculture

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Quinoa is an incredibly nutritious and healthy food that provides all amino acids essential in optimum quantities which is comparable to milk. It can be grown in wide range of agro-ecological conditions with variant altitudes. It is tolerance to drought, crop sturdiness, short duration, and resistance to pests and diseases. However, little has been known to the farmers about this prized underutilized crop. Keeping in view all these facts, varietal evaluation for adaptability trial was carried out for three seasons (2020-2022) in mid hill condition of Arunachal Pradesh, Basar. The genotypes include *viz*. IC-411824, IC-411825, EC-507738, EC-507739, EC-507740, EC-507741, EC-507742, EC-507743, EC-507744, EC-507746, EC-507747, EC-507748 and EC-507749. The study intended to identify stable genotypes with promising yield under local climatic conditions. The accessions varied significantly for various phenotypic traits and yield potential. Recorded days to fifty percent flowering varied from 59.33 to 70 days, days to maturity 98.33 to 114.33, Plant height (cm) 61.67 to 105 cm, Inflorescence length 15.33 to 25 cm, Inflorescence number 15.33 to 25 per plant, test weight of 10 ml seed weight 5.26 to 6.04g and grain yield per plant 4.92 to 14.87 q/ha respectively. Based on AMMI yield stability analysis, the following accessions viz. EC-507739, EC-507738, IC-411824 and EC-507748 exhibited excellent stability with higher mean performance. While MGIDI identified two genotypes viz., EC-507739 (9.75q/ha) and EC-507739 (12.94 q/ha) higher mean performance and stable for all the traits. Therefore, introducing and popularisation these promising accessions suited to local climatic conditions could supplement the food basket for nutritional security.

Keywords: Quinoa, Seed yield, Stability, Mid-hills Ecology

OP1-02

Exploring the *Allium* Species of Himalayan Regions for Food and Nutrition Security

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The *Allium* genus is the largest among petaloid monocotyledons, with over 920 species distributed worldwide. *Allium* species are valued for their flavor, aroma, nutritional and medicinal benefits. Their distinctive aroma results from organic sulfur compounds released through enzymatic breakdown by *allinase* and *lachrymatoryfactorsynthase (lfs)*. These compounds originate from flavor precursors, specifically S-alk(en)yl cysteine sulfoxides, found within their cells. The North Eastern region is home to several notable *Allium* vegetables, including *Allium hookeri* (Jaynaut or Hooker chives), *A. chinense* (Rakkyo or Scallion), and *A. tuberosum* (Chinese chives or Chinese leek). *A. hookeri and A. chinense* are highly sought-after leafy green and extensively cultivated in the NE regions, where it commands a premium price due to its popularity. In contrast, the North Western Himalayan region is rich in diverse *Allium* species, such as *A. carolinium*, *A. humile* (Dune), *A. sanguineum*, *A. semnovii*, *A. stracheyi* (Jambu or Faran), *A. wallichii* (Himalayan onion or Jimbur), *A. przewalsklanum* (Ladakh onion or Jimbo), *A. prattii*, *A. macronthum*, and *A. rubellum*, which are harvested from their natural habitats for culinary and medicinal purposes. Recent discoveries have expanded the region's Allium repertoire, with *Allium negianum* being the latest addition, prized as a leafy vegetable by local communities. These *Allium* species have a long history of safe consumption, integral to local culinary traditions and hold cultural significance, featuring prominently in traditional festive and ceremonial dishes. Beyond their culinary importance, *Allium* species significantly contribute to local economies and livelihoods. The allied species need to be explored for their adaptation under sub-humid and hot tropical condition to diversify the food basket. Besides they can be utilized for introgression of disease resistance traits in onion, which generally lack disease resistance. Under Delhi condition, five different *Allium* species, namely *A. fistulosum, A. altaicum*, A. *chinense*, *A. tuberosum* and *A. schoenoprassum* are being maintained under open field condition and *A. hookeri* was found susceptible to water logging condition. These diverse Allium species provide nutritional and medicinal benefits, support income generation, and help alleviate poverty while playing a crucial role in sustainable agricultural systems. However, to fully realize their potential, increased research and extension efforts are essential to develop improved production technologies and value-added products. Conserving and utilizing the biodiversity of *Allium* species in the Northeast and North West region is crucial for sustainable development. Addressing research gaps and promoting appropriate conservation and management practices can unlock the vast potential of these species, contributing to the region's economic growth and food security.

Keywords: *Alliums*, Adaptation, Food and Nutritional Value

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PP1-03

Indigenous Fruit Tree Domestication in North East India: Strategies, Status and Future

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North East India is a treasure house of many wild edible plant resources which are a source of food, nutrition, medicine, income and security during unfavorable times. There are innumerable reports on the diversity of these species and there are ongoing efforts to characterize the morphological, nutritional and medicinal properties of these resources. Concurrently growing evidence reveals the potential of these resources to alleviate the rural household economy as well. Hence there is a large scope for integrating the species as novel crops within existing farming systems. Drawing lessons from the activities of the World Agro-forestry Centre, Nairobi Kenya, where various Indigenous fruit trees have been domesticated and integrated in farmer's field, the paper highlights strategies adopted, status and future of indigenous fruit tree (IFT) domestication in the North East region in order to improve their productivity, quality and marketability. The outcome of a decade's work on two IFTs - *Phoebe cooperiana* and *Parkia timoriana* carried out in the state of Arunachal Pradesh, Manipur and Mizoram is presented.

Key words: Vegetables, Fruit, *Parkia*, *Phoebe*, Genetics

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PP1-04

Evaluation of Nigella (*Nigella sativa* L.) Genotypes for Yield Attributes, Yield and Quality

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Nigella (*Nigella sativa* L.) well known as black cumin belongs to the Ranunculaceae family and is an important seed spice crop grown in India. The genus *Nigella* comprises more than 116 species, the most popular of which is *Nigella sativa* L. Nigella is classified as a seed spice because its dried seeds are used as a spice. This crop is predominantly cultivated in various Indian states, including Rajasthan, Madhya Pradesh, Chhattisgarh, Bihar, Punjab and Assam. Beyond India, Nigella is extensively grown in countries such as Pakistan, Sri Lanka, Bangladesh, Nepal, Egypt, Turkey and Iraq. Recognized as one of the most widely utilized medicinal plants globally, Nigella's seeds contain essential oil with concentrations ranging from 0.5% to 1.4%.. The most active constituent of nigella is thymoquinone, representing 18.4% to 24% of the volatile oil. Nigella seeds have been used as an important ingredient of medicine since ancient times. The global demand for nigella seeds is driven by their use in culinary applications, traditional medicine, and natural remedies. The seeds are traded internationally, with major exporters including India and Turkey, while consumers worldwide appreciate their unique flavour and health benefits. Nigella seeds are known for their anti-inflammatory and antioxidant effects, which help reduce inflammation and combat oxidative stress. The trial was carried out at ICAR-NRCSS, Ajmer during 2021-22 and 2022–23 to select high yielding and adaptable genotypes for commercial production in India. Nine advanced nigella genotypes were evaluated with one standard check variety namely Ajmer Nigella-1. The genotypes were arranged in Randomized Block Design with three replications. All the recommended package of practices was followed to raise a healthy crop. The observations were recorded for plant height (cm), days to 75 % maturity, primary branches per plant, capsules per plant, seeds per capsule, seed yield (kg/ha) and total oil (%). The highest seed yield was recorded from AN-37 genotype (1522.17kg ha-1) followed by AN-10(1478.67 kg ha-1) and these genotypes had 27.30% and 25.16 % yield advantage over the check variety-Aden respectively. Moreover, the two genotypes were better in oleoresin content among others. Therefore, the genotypes were selected as potential candidate genotypes for CVT trial.

Keywords: Nigella, Seed spices, Yield, Quality

PP1-05

Fruit Biodiversity in Bundelkhand Region of India: Prospects and Challenges

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Geographically, Bundelkhand lies between the Indo-Gangetic Plain to the north and the Vindhya Range to the south. The region is a semi-arid plateau comprising thirteen districts – seven districts of UP (Jhansi, Jalaun, Lalitpur, Hamirpur, Mahoba, Banda, and Chitrakoot) and six districts of MP (Datia, Tikamgarh, Chhatarpur, Damoh, Sagar, and Panna). The region is marked by extremes of temperature (48 ° C to 1° C) with average annual rainfall of 800-900 mm. The soils are black, red laterite and mixture of both with pH ranged from 6.5 to 8.4. The dominant vegetation in the region primarily consists of aonla (*Emblica officinalis* Gaertn), bel (*Aegle marmelos* Corrêa), ber (*Z. mauritiana* Lam.), Jhar ber (*Ziziphus nummularia* (Burm.f.) Wight & Arn.), kath ber (*Ziziphus xylopyrus*), *jackal* jujube (*Ziziphus oenoplia* (L.) Mill.), chironji (*Buchanania lanzan* Spreng.), mahua (*Mahuca indica*), jamun (*Syzygium cumini* (L.) Skeels), karonda (*C. carandas* Lour.), wild karaunda (*Carissa spinarum* Bedd. Ex. Hook.f), khirni (*Manilkara hexandra Roxb*.), lasoda or labhera (*Cordia myxa* Roxb.), phalsa (*Grewia asiatica* L syn. *Grewia subinaequalis* DC.), jackfruit (*Artocarpus hetrophyllus* Lam.), wood apple (*Feronia limonia* Swingle), anjir (*Ficus carica Roxb*.), tamarind (*Tamarindus indica*), gular (*Ficus glomerata* Roxb.), tendu (*Diospyros melanoxylon* Roxb.*)*, and paniyala [*Flacourtia indica* (Burm. f.) Merr.]. Enormous diversity in Bundelkhand is available in these fruit crops with varied uniqueness. The mismanagement of environmental issues, industrialization, mining, construction of highways and land use in the past has led to the rapid genetic erosion of precious germplasm. Therefore, native fruit species distributed in Bundelkhand region need to be conserved on priority. Under PGR management strategies, Banda University of Agriculture and Technology, Banda took concerted efforts for survey, collection and conservation of diverse fruit spp. of chironji (74), mahua (80), bael (65), ber (24), wood apple (25),

jackfruit (42), tendu (8) and star fruit (22) through PG/PhD research and projects funded by UPCST and UPCAR, Lucknow and Alliance of Bioversity International & CIAT along with the establishment of regional fruit gene bank for chironji and mahua. The paper discusses fruit diversity available in Bundelkhand region with its potential and challenges.

Key words: Bundelkhand, Biodiversity, Conservation, Semi-arid, Genetic Erosion

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PP1-06

Morphological Screening of Indigenous Vegetable Cowpea Germplasm Lines for Yield Attributing Traits in Semi Arid Region

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Cowpea (*Vigna unguiculata* (L.) Walp.) is predominantly a pulse crop, but nowadays it's utilized as an underutilized greeny vegetable. Among the cultivated species, it is rustic, adaptable and packed with nutrients plant that is also widely variable in terms of its forms of usage and consumption. It is also a staple food that is readily available to people worldwide and a crucial part of production systems. The current study attempted to assess and evaluate the diversity of cowpea varieties and offer a resource for selecting cowpea varieties that are appropriate for vegetable purpose. This study was conducted at Centre for Vegetable Research, Department of Genetics and Plant Breeding, S. D. Agricultural University, Sardarkrushinagar (Gujarat) during the summer 2023 in randomized block design with 27 indigenous genotypes in 4 replications. The aim was to manoeuvre correlation, genetic diversity and principal components for the identification of suitable genotypes for the future breeding programme from the indigenous germplasm collection. Green pod yield is highly and significantly correlated with the pod length, pod girth and pod weight. From the D^2 analysis, total 4 clusters are formed among the 27 genotypes in which the green pod yield, number of cluster per plant, pod weight and plant height contributed 90.30 % of diversity. Different clusters like cluster 2, 3, 4 contained genotypes with wider diverse characteristics. Among the 13 components, PC1, PC2, PC3, PC4 are observed as a Principal Component, which contributes 79.15 % among of variations among the total components. Days to flowering & maturity, plant height, Pod length, pod girth, pod weight, number of pods per plant, number of clusters per plant, number of pods per cluster and green pod yield are the major contributors to the origination of variation. Overall experiment findings indicated that there was variation and diversity present among the cowpea genotypes assessed under summer.

Keywords: Cowpea, Genetic diversity, Pod yield, Cluster analysis

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PP1-07

Characterization and Evaluation of Banana (*Musa spp.*) Germplasm

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The present study, entitled "Characterization and evaluation of banana (*Musa spp.*) germplasm" was carried out at the experimental block of Fruit Research Station (ICAR-AICRP on Fruits) Navsari Agricultural University, Gandevi that falls under the hot and humid tropical zone of South Gujarat. Total 64 banana germplasm of different genome group were accessed during 2022-23. In this study observed that the highest pseudostem height (4.30 m) in Gopan (ABB), stem girth (85.00 cm) in Hanuman (AAA) and no. of leaves (28.00) was recorded in Karpuravalli (ABB), whereas, minimum plant height (1.63 m) was obtained in Adhapuri (AAA). Maximum leaf area (1.86m^2) was observed in Pisang Seribu (AAB) and Peyan (ABB). Moreover, the minimum days taken for shooting (188 days) in Parakuni (AAB) and harvesting days (301 days) was recorded in Hybrid 1 (AAB). Therefore, the maximum weight of the bunch (31.10 kg) was obtained in Gandevi Selection (AAA). The higher number of hands per bunch (12.00) and fingers per hand (216) were recorded in Hanuman (AAA). The TSS was recorded highest (31.30^{0}B) in Bhurkel (ABB). On an overall basis, Gandevi Selection (AAA) found a promising genotype in terms of yield character and Bhurkel (ABB) best genotype (small banana) in case of fruit quality.

Keywords: Characterization, Germplasm, Genome group

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PP1-08

Indigenous and Minor Vegetable Crops of Tripura

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Tripura, a north eastern state of India, falls under the Indo-Burma hot spot and has rich biodiversity. Climate is mild hot and humid tropical with defined summer and winter season. This region is rich in diversity of vegetables, especially cucurbits namely bottle gourd, pumpkin, ash gourd, sweety gourd, spine gourd, Chayote, pointed gourd, tuber crops namely taro, swamp taro, greater and lesser yams, elephant foot yams etc, solanaceous namely chilli and brinjal, leguminous namely hyacinth bean, velvet bean, and leafy vegetable like amaranthus. However, locally grown traditional vegetables and various wild-semi wild plants-based foods are the unique specialty of food habit of this region. Moreover, all these minor traditional vegetables are rich source of vitamins and minerals, and provide nutritional security for the small and marginal households as well as for the below poverty level populations. Many of these minor vegetables are also used as ethno-medicinal purposes by the local traditional healers. Tubers of some wild types of elephant foot yams (*Amorphophallus bulbifer*

(Roxb.) Blume and *A. sylvaticus* (Roxb. (Kunrth.) are extremely acrid. Aerial yam (*Dioscorea bulifera* L.) is another commonly found yam along with few local types of lesser yams namely *D. hamiltonii* Hook. F and *D. pentaphylla* L. etc. Variability in both eddoe and bunda type taro has been recorded. Giant taro (*Alocasia fornicata* (Roxb.) Schott) is locally known as Bish kochu and big rooted taro or elephant ear (*Alocasia macrorrhizos* (L.) G. Don, Schott.), locally known as Man Kochu or Fen Kochu. Six types of swamp taro (*Colocasia esculenta* var. *stolonifera* (L). Schott) locally known as Jal kochu in Bengali and tuini Khema in Kokborok has been characterized. All these traditional crops are climate resilient with high food value.

Keywords: Vegetables, Tuber crops, Yam, Aroids

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PP1-09

Botanical Exploration of Plant Diversity and Analysis of Life Forms With their Biological Spectrum in the Kainengkol Grassland Ecosystem of the Koubru Hill Range, Kangpokpi District

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This study presents a botanical exploration of plant diversity and an analysis of life forms with their biological spectrum in the Kainengkol grassland ecosystem, situated in the high-altitude Koubru Hill Range of Kangpokpi District. Our research identifies a notable prevalence of species belonging to the Poaceae and Asteraceae families, each represented by seven distinct species. The Cyperaceae and Asteraceae families follow with two species each, while other plant families are represented by a single species each. In terms of life form, therophytic plants dominate the grassland with twelve species, followed by hemicryptophytes with seven species, geophytes with four species, and chaemophytes with the lowest representation at four species. The biological spectrum observed in this grassland does not conform to the typical Raunkiaer classification, highlighting a unique distribution of life forms in this ecosystem. This study underscores the importance of the Kainengkol grassland as a reservoir of botanical diversity and provides critical insights into the adaptive strategies of plant species in high-altitude environments. Our findings contribute to a deeper understanding of plant ecology in the Koubru Hill Range and offer a foundation for further ecological and conservation research.

Keywords: Exploration, Prevalence, Dominate, Raunkier Classification, Conservation

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PP1-10

Floristic Diversity and Conservation Status of Plants in Homegardens at Garo Hills, Meghalaya, India

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Homegardens are traditional farming systems, presumably the oldest land use system which allow its owner to produce a wide variety of products and ecosystem services. The present study was conducted to analyse the floristic diversity of homegardens in South Garo Hills Meghalaya. Purposive, multi-stage and random sampling procedures were followed in the present study. Total sampled area was 26.96 ha (average 0.27 ha) and 15,528 individuals were counted from the homegarden (N = 100) that harboured a diverse layer of useful plants species. The present study documented 214 species belonging to 78 families and 174 genera (Confirm the family and genus after species change) and plant species richness ranged from 07-64 with average 16.6 (±.86). Trees were the dominating life form (87 species, 36 families, 71 genera) followed by herbs ((62 species, 32 families, 51 genera), shrub (38 species, 22 families, 34 genera), climbers (17 species, 11 families, 16 genera), palm (seven species, one family, six genera), bamboo (two species, one family, one genus and fern (one species, one family, one genus. Homegardens exhibit complex structure, both vertically and horizontally having five vertical stratum, in ground stratum 82 species comprising herb, vine and climbers; 29 species in 2nd stratum mainly shrub species; on third strata with 43 species mainly associated with small tree and large size shrub of fruits and ornamental species; on 4th strata 33 species were associated, predominantly fruit, timber, fuel wood and multipurpose species; 28 species recorded on 5th strata predominantly trees were represented. In sampled homegardens 78% homegarden were recorded with animal component. There were two species of plant categorized as Critically endangered, three species Endangered, one species Vulnerable. Frequency estimated was 1-75 %, density was 0.01-103.6, species abundance was 1.0-138.13%and IVI was 0.19-87.28. The species diversity index or Menhinick's index, Concentration of dominance or Simpson's index, Shannon-Wiener diversity index and Species evenness of the studied homegardens was 1.72, 0.45, 2.00 and 0.21 respectively. Homegarden age and size was significantly and directly correlated. Homegardens of South Garo Hills are a useful tool for preserving genetic resources and promoting economic well-being.

Keywords: Homegarden, Species diversity, Structure, Utilization

PP1-11

Genetic Diversity of Cucumber Landraces in North East India

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Immature fruits of *Cucumis sativus* L. (2n=14) are utilised for salad preparation and pickling. In contemporary times, it has become an essential element in elegant meals. It is abundant in bioactive compounds, minerals, and dietary fibre. Its health-promoting effects include antibacterial capabilities, hydration and detoxification, aid in digestion and weight loss, and prevent cancer and other bones disorders. This study assessed the morphological traits of thirty cucumber land races originating from North East India. The morphological traits include include fruit weight, fruit length, fruit diameter, pericarp thickness, leaf morphology, and the fresh colour of the fruit, terminal lobe apex shape and transverse section of the fruit. RC Cucumber 23 reported the highest fruit weight at 1769.44g, followed by RC Cucumber 31 (1533.33g) and RC Cucumber 11 (1497.50 g). The maximum fruit length was recorded in RC Cucumber (19 37.17 cm), followed by RC Cucumber 23 (35.86 cm) and RC Cucumber 11 (29.51 cm). The maximum fruit diameter was recored in RC Cucumber 10(104 cm) followed by RC Cucumber 12 (101.11cm) and RC Cucumber 13 (96.8cm). Cultivar 31 had the greatest mesocarp thickness (2.55cm), followed by RC Cucumber 11(2.25 cm), RC Cucumber 17 (2.25 cm), RC Cucumber 29 (2.25cm), and RC Cucumber 32 (2.21 cm). Three distinct forms of terminal lobe apex shapes were identified in the collected genotypes, with the most common genotypes exhibiting an obtuse shape of the terminal lobe. A majority of the genotypes exhibited a round shape in the transverse section of the fruit.

Keywords: Cucumber, Genetic Variability, Yield, Local Landraces

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PP1-12

Biodiversity and Significance of Wild Berries in the Temperate Regions of West Kameng, Arunachal Pradesh

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The West Kameng district of Arunachal Pradesh, located in the Eastern Himalayas, is home to a rich diversity of wild berries, which play a crucial role in the region's ecology and the livelihood of its indigenous communities. This study explores the variety, distribution, and significance of wild berries

in temperate regions of West Kameng. The survey was conducted during the year 2023-24. Field surveys and interviews with local inhabitants reveal the presence of multiple berry species, including *Rubus ellipticus* (Golden Himalayan Raspberry), *Gaultheria fragrantissima* (Indian Wintergreen), *Rubus microphyllus*, *Elaeagnus umbellatea* (Autumn olive), *Rubus niveus* (Ceylon Raspberry), Wild strawberry, *Actinidia strigosa*, *Diospyros lotus* (Date plum) and some unknown species of wild berries. These berries are not only consumed as food but also have traditional medicinal uses, providing a natural source of vitamins and antioxidants. The findings underscore the importance of conserving these wild resources in the face of environmental changes and highlight their potential for sustainable economic development through eco-tourism and agroforestry initiatives. In addition, these berries can be used in future for the breeding of some varieties suitable for the region. The research contributes to the broader understanding of biodiversity in the Eastern Himalayas and collection, conservation and multiplication of wild plant species in Arunachal Pradesh.

Keywords: Blue berries, Genetic diversity, Eastern Himalaya, Arunachal Pradesh

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PP1-13

Screening for Resistance against Yellow Mosaic Disease (YMD) in Wild *Vigna* Germplasm

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Yellow Mosaic Disease (YMD) is a major threat to *Vigna* production worldwide; causing significant yield losses primarily caused by the mungbean yellow mosaic virus (MYMV) and Mungbean Yellow Mosaic India Virus (MYMIV). The Northeastern region of India has a rich genetic diversity of both wild and cultivated *Vigna* species. Wild *Vigna* species represent a valuable source of genetic diversity that could be harnessed to develop YMD-resistant cultivars. This study aimed to screen a diverse collection of wild *Vigna* germplasm for resistance to YMD. A panel of 601 diverse sets of accessions belonging to 36 different wild *Vigna* species from the National Gene Bank was evaluated for YMD resistance under field-hotspot conditions at New Delhi for two consecutive years, *Kharif* 2022 & 2023. The Percent Disease Incidence (PDI) was in the range of 0–100%. Among these, 39 accessions belonging to 10 different wild *Vigna* species exhibited resistance to YMD, as they showed no symptoms during field screenings. Of the 36 wild *Vigna* species screened, *Vigna stipulacea* exhibited the highest number of resistant accessions with 23%. The resistant wild *Vigna* germplasm was further evaluated under hotspot conditions at the University of Agricultural Sciences – Bengaluru, Chamrajnagar in the summer of 2024. Subsequently, these 39 resistant accessions were subjected to further validation of MYMV resistance through whitefly-mediated screening. The virus identification is confirmed by DNA isolation and PCR amplification using MYMV DNA-A primer pairs. PCR-based molecular detection yielded amplicons of approximately 770 bp. The amplified PCR products were subjected

to sequencing and blast analysis. All the isolated sequences were found to be related to MYMV & MYMIV. This study identified promising sources of YMD-resistant germplasm that can be utilized in developing YMD-resistant *Vigna* varieties.

Keywords: Yellow Mosaic Disease, CWR, *Vigna*, Germplasm, Resistance, Breeding, Food security.

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PP1-14

Evaluation and Identification of Potential Germplasm for Agro-Morphological Traits in Hexaploid Wheat (*Triticum aestivum* L.) Landraces

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Genetic erosion and narrowing of genetic base are the major challenges being faced by the Indian wheat breeding program in the post Green Revolution era. Fertilizer responsive, dwarf high yielding wheat varieties which were derived from the breeding programs utilizing CIMMYT materials as donors replaced the Indian landraces finally leading to a yield plateau. To restore the genetic diversity, the displaced wheat landraces were repatriated from overseas breeding centers by ICAR- National Bureau of Plant Genetic Resources (NBPGR) to characterize and evaluate them under the changing climate scenario. A set of 2632 genotypes containing 1138 accessions repatriated from Australia, 420 from John Innes centre UK, 1074 preserved at the National Genebank were evaluated at NBPGR, Pusa Farm during *Rabi* 2022-23 for 34 agro-morphological descriptors including qualitative and quantitative traits. The crop was grown in augmented design and standard agricultural practices were followed to raise the crop. The genotypes showed a wide range of variability for studied traits, for example 104 to 169 days for days to maturity, 4.73 to 22.83 cm for spike length (SL), 13 to 127 grains for grain number per spike (GS), and 7.08 to 67.08 grams for thousand-grain weight (TGW). The potential genotypes for early maturity were IC0113224, IC543356, IC416156, IC111845, and IC0028755, which were superior (18.90-22.83%) to best-performing check HD2733 (116 days). Similarly, genotypes VIR 30608, IC539315, VIR 33701, IC0145952, and W170 had 53.53-96.95% longer spike length with respect to best check PBW343. KOPERGAON BAXI, IC539315, SINGH'S WHEAT, IC445524, and IC416198 had the higher GS, than the best check HD2932. Similarly, INDIA 92, IC0111655, PUSA 106, IC539315, IC0112035 and AUS 10110 had 30.06-49.48% higher TGW with respect to best performing check PBW752 (44.85g). These genetic resources can offer unique traits for yield, nutritional quality, biotic and abiotic stresses and may be integrated into wheat improvement programs for the development of improved cultivars.

Keyword: Wheat, Repatriation, Landraces, Germplasm, Genetic resources

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PP1-15

Genetic Divergence Studies on Morphological and Biochemical Traits in Tomato (*Solanum lycopersicum* L.)

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Tomato (*Solanum lycopersicum* L. $2n = 2X = 24$, Solanaceae). Tomato is believed to be originated from South America. The present investigation entitled "Genetic divergence studies on morphological and biochemical traits in tomato (*Solanum lycopersicum* L.)," was carried out at the Vegetable Research Centre, GBPUAT, Pantnagar. The experiment was comprised of 34 genotypes and with four checks, were sown in Augmented-II design with five blocks during Rabi season, 2021 to study sixteen morphological and biochemical parameters, namely, days to first flowering, days to 50% flowering, days to first fruit set, days to first picking, plant height (cm), number of fruits per plant, average fruit weight (g), yield per plant (kg), number of locules, pericarp thickness, TSS (^{0} Brix), acidity, ascorbic acid (mg/ 100 g fruit weight), total carotenoids (mg/ 100 g fruit weight), lycopene content (mg/ 100 g fruit weight) and total phenol (mg/ 100 g fruit weight) content. Molecular characterization was carried out by using lycopene specific SSR molecular marker to check polymorphism in genetic level among the thirty-four genotypes. The pooled data were subjected to statistical analysis for analysis of variance (ANOVA), estimation of genetic variability, heritability h^2(b), genetic advance, correlation studies, path coefficient analysis and genetic divergence analysis (D^2 statistics) were studied. The traits, such as, number of fruits per plant, lycopene content (mg/ 100 g fruit weight), and total phenol content (mg/ 100 g fruit weight), high phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) along with higher heritability was reported. Average fruit weight and number of fruits /plant is found to be positively correlated with yield per plant and also has a high direct positive effect on yield. Polymorphic information content (PIC) value of all the primers was laid between 0.469 to 0.614, symbolizes medium range of polymorphism between the genotypes. The genotypes grouped under major cluster A and cluster B are more diverse in nature with having 60% of similarity which symbolizes maximum divergence clusters. Based on the results of the study, it was revealed that the genotypes varied widely, indicating that there was opportunity for selection-based improvement of the tomato genotypes.

Keywords: Tomato, Genetic Diversity, Yield, Quality, SSR Markers

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PP1-16

Assessment of Genetic Variability for Various Yield and Its Contributing Traits in Rice (*Oryza sativa* L.) Genotypes

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A field experiment was conducted on Rice (*Oryza sativa* L.) genotypes at Crop Research Centre, SVPUAT, Meerut during the Kharif season in 2022-23. The study was based on a total of thirty diverse genotypes of Rice in a Randomized block design having three replications. The objective of the experiment is to assess the Genetic variability of 30 genotypes for various morpho-quantitative traits viz., days to 50% flowering, days to maturity, plant height, number of effective tillers per plant, panicle length, grains per panicle, internode length, grain length/width ratio, test weight, biological yield per plant, grain yield per plant and harvest index. After a detailed study of these genotypes for various variability parameters, it was found that a sufficient amount of variability was noticed among treatments. The genetic variability estimates like range, heritability, genetic advance, GCV, PCV, etc suggested ample variability among the undertaken genotypes. Higher GCV and PCV were found in traits viz., grains per panicle, internode length, number of effective tillers per plant, days to 50% flowering, grain/ width ratio, test weight, days to maturity, plant height, panicle length, grain yield per plant, biological yield and harvest index. Higher heritability with high GAM was recorded in the traits viz., plant height, number of effective tillers per plant, Number of grains per panicle, test weight, BYP, GYP and harvest index. So, It was finally concluded that higher values of PCV and GCV could reveal that such traits could be advanced or improved through an effective selection. Higher heritability with high GAM in the recoded traits discloses the presence of additive genes. Because of this reason, the selection in such traits may be rewarding.

Keywords: Variability, Randomized, Tillers, Panicle, GCV, PCV, Heritability

PP1-17

Assessment of Genetic Variability for Various Morpho-qualitative Traits in Field Pea *(Pisum sativum* L. var. *arvense)* Genotypes

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A field experiment was conducted on Field Pea genotypes at PG Research Farm of BUAT, Banda, during *Rabi* season in 2023-24. The study was based on a total of thirty diverse genotypes of Field Pea in Alpha-Lattice design having two replications which each replication comprised of three blocks. The objective of the experiment is to assess the genetic variability of these genotypes for various morpho-qualitative traits viz., days to 50% flowering, days to maturity, plant height, number of pods per plant, number of effective pods per plant, pod length, number of seeds per pod, 100-seed weight, biological yield per plant, seed yield per plant, harvest index, protein content, total sugar, reducing sugar, non-reducing sugar and trypsin inhibitor activity. After a thorough investigation of all the genotypes upon considering the variability parameters, it was noted that a sufficient amount of variability was noticed among treatments. The genetic variability estimates like range, heritability, genetic advance, GCV, PCV; etc suggested the presence of ample amount of variability among the undertaken genotypes. Higher GCV and PCV were found in traits viz., plant height, number of pods per plant, number of effective pods number, number of seeds per pod, BYP, SYP, non-reducing sugar, reducing sugar, total sugar, and Trypsin inhibitor activity. Higher heritability with high GAM recorded in plant height, number of pods, effective pods per plant, Pod length, Number of seeds per pod, 100 seed weight, BYP, SYP, harvest index, reducing sugar, total sugar and trypsin inhibitor activity. It was concluded that higher values of PCV and GCV could reveal the advancement of such traits through selection. Higher heritability with high GAM in the recoded traits reveal the presence of additive genes due to which selection in such traits may prove to be rewarding, if done effectively.

Keywords: Diverse, Alpha-lattice, Genetic variability, GCV, PCV, Heritability, Selection**.**

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PP1-18

Biodiversity, Conservation and Sustainable Use of Medicinal Plants

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With 2.4% of the world's area and 8% of the world's biodiversity, India is one of the world's 12 mega diversity countries. Four of the 35 global biodiversity hotspots (GBH) in the world—the Himalayas, Indo-Burma, Sundaland, and Western Ghats—are located inside the geopolitical boundaries of India. Given the vast abundance of therapeutic plants that nature has bestowed upon India, the nation is frequently referred to as the "Medicinal Garden" or the "Botanical Garden" of the world. Out of the 48,655 plant species documented (including viruses, bacteria, algae, fungi, and lichens), 9,500 are important from an ethnobotanical standpoint, and 7,500 are used in medicine, both in traditional medicine and in contemporary systems. India possesses a wealth of experience with herbal medicines and has made significant contributions to the field of pharmacological research and modern drug discovery, in addition to Ayurveda and Siddha. According to the BSI (Botanical Survey of India), India is home to more than 8,000 species of medicinal plants. It is estimated that there are roughly 1052 Red-listed species in India, including hundreds of medicinal plants. Of these, 77 plant species are classified as critically endangered, and eight species have already gone extinct. According to estimates from the World Health Organisation, up to 80% of people still primarily get their medications from traditional sources like herbs. Approximately 25 % of prescribed medicines contains plant extracts or active ingredients obtained from plant materials. Aspirin (from Willow tree), Digitalis (from Foxglove), Quinine (from Cinchona), Vinblastine and Vincristine (from Periwinkle) and Artemisinin (from Artemisia) are some of the examples of the many contemporary medications that are derived indirectly from medicinal plants. Since medicinal plants are disappearing at a rapid pace, it is imperative that concrete steps be taken to ensure their conservation and incessant production. For the sustainable use of medicinal plant resources, conservation strategies (such as in situ and ex situ conservation and cultivation practices) and resource management (such as good agricultural practices and sustainable use solutions) should be sufficiently taken into consideration. To increase yield and alter the potency of medicinal plants, we advise applying biotechnical techniques (such as tissue culture, micropropagation, synthetic seed technology, and molecular marker-based approaches).

Keywords: Biodiversity, Conservation, Medicinal plants, Sustainable, Endangered, Extinct.

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PP1-19

Survey, Collection and Physico-Chemical Evaluation of Carambola (*Averrhoa carambola* L.) Genotypes

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The present investigation entitled as "Survey, Collection and Physico-chemical Evaluation of Carambola fruits" was carried out in different districts of Uttar Pradesh. The physico-chemical analysis was done in the Department of Fruit Science, College of Horticulture, Banda University of Agriculture and Technology, Banda (U.P.) during the year 2023-2024. The variation was recorded among different genotypes for fruit length (5.59-12.92 cm), fruit width (3.62 to 8.75 cm), fruit weight (46.97-238.43 g), fruit volume (40.67 cc to 245 cc), specific gravity (0.58 to 1.20 g/cc), number of seeds (9-10 seeds/fruit), seed length (6.63 mm to 9.77 mm), seed width (3.27 mm to 5.73 mm) and seed weight (0.49g to 0.76g). The chemical parameters also showed wide range of variation recorded in TSS (3.50 ^{0}Brix to 8.17 ^{0}Brix), acidity (0.45% to 0.93%), ascorbic acid (9.80 - 20.77 mg/100g), total sugar (3.18% to 5.43%), reducing sugar (2.98% to 5.20%), TSS: acid ratio (3.79 to 18.56), protein (0.45% to 0.97%), pectin (0.60% to 1.12%) and antioxidant (41% to 45%). The non-reducing sugar ranged from 0.11% to 0.25% but was non-significant. The significant correlation noted between the physical and chemical parameters. Fruit length showed significant positive correlation with fruit width, weight, volume, TSS, total sugar, reducing sugar and negative but significant correlation noted with antioxidant. Seed length showed significantly positive correlation with seed width and seed weight. TSS showed highly significant positive correlation with total sugar, reducing sugar, protein and TSS: acid ratio, while negatively significant with acidity, antioxidant and pectin. Protein showed highly significant negative correlation with antioxidants. On the basis of the results obtained, genotypes BUAT-K-5, BUAT-K-20, BUAT-K-6 and BUAT-K-3 were screened as promising genotypes and can be recommended for commercial multiplication, growing at farmer's field and conservation in the field gene bank for further evaluation and release of cultivar in future.

Keywords: Carambola, Correlation, Survey and Collection

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PP1-20

Characterization of Jackfruit (*Artocarpus heterophyllus* Lam.) Germplasm

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Jackfruit is an economically important tree that is widely cultivated in India for its fruit. Tree is evergreen and found at 450 – 1200 m altitude. India is the second largest producer of jackfruit in the world. In India trees are distributed in states of West Bengal, Tamil Nadu, Karnataka, Orissa, Kerala, Assam, Bihar, Tripura and Uttar Pradesh. Apart from its economic importance there is little knowledge about the genetic diversity in the country. The jackfruit trees are cross-pollinated and mostly propagated by seeds. Due to this, enormous range of variability in physico-chemical attributes are available in the nature. Because of the selective growing the genetic resource base is at risk. Farmers select and grow fruits on the basis of market demand. So far, there are no well-defined varieties, few local varieties like Champa, Gulabi, Rudrakshi, Hazari etc. are popular having based on their variability in yield, fruit weight, fruit shape, peel colour, flake colour, number of flakes, texture of flakes. Hence, there is an urgent need to identify the superior types for its improvement. Enormous variability in jackfruit found in evergreen forests of Western Ghats. The survey conducted during 2023-24 in different geographical locations of Uttar Pradesh particularly in Banda, Fatehpur, Lalganj, Pratapgarh, Ayodhya, Sultanpur, Varanasi, Ghazipur districts to select promising jackfruit genotypes. Morphological characterization carried out as per standard guidelines developed by IPGRI (International Plant Genetic Resources Institute, Rome, Italy). Considerable variation observed between all the collected genotypes. Variation was recorded in tree form, bark pattern, leaf shape, fruit shape, rind colour, stalk attachment, spine shape, spine density and latex exudation. A vast range of variation 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 ^{o}Brix).

Keywords: Jackfruit, Germplasm, Variability, Diversity, Characterization

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PP1-21

Characterization of Chironji (*Buchanania lanzan* Spreng.) Germplasm

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Chironji (*Buchanania lanzan* Spreng.), belongs to the family Anacardiaceae, is an important dryland fruit crop. It is widely distributed in South East Asia, Australia and Pacific Islands. Mostly, it is found in plateau regions of India, Burma and Indo-China. In India, trees are distributed in the states of Madhya Pradesh, Bihar, Orissa, Andhra Pradesh, Chhattisgarh, Jharkhand, Gujarat, Rajasthan, Maharashtra and Uttar Pradesh. The Survey conducted during 2022-23 and 2023-24 in the different geographical locations in Uttar Pradesh, Madhya Pradesh, Bihar and Gujarat particularly in the districts of Chitrakoot, Lalitpur, Satna, Katni, Burhanpur, West Champaran, Rohtas, Dahod and Panchmahal to select promising chironji genotypes. Morphological and molecular characterization carried out as per standard procedure developed by ICAR-NBPGR, New Delhi and PPV&FRA. Marked variation observed in between different genotypes but the range of variability in fruit/ kernel size and fruit quality parameters are less. Among all 74 chironji genotypes, 47 genotypes were of spreading type, 24 upright type, and 3 semi-spreading. Variability recorded for tree height (5.00–11.20m), tree spread E-W (3.30-6.20m), tree spread N-S (3.19-6.16m), tree girth (43.25-80.90cm), average no. of flower/inflorescence (1954.06-3650.10), average fruit yield kg/tree (12.76-30.50 Kg per tree), average fruit weight (0.89-1.20g.), average pulp weight (494-821mg), average kernel weight (46-95mg), kernel percent (12.45-25.07%). Fruit yield recorded maximum with BUAT-C-35, followed by BUAT-C-45, BUAT-C-46, BUAT-C-54, and BUAT-C-56 with spreading growth habit. Molecular diversity was worked out for 9 representative locations using 21 SCoT (Start Codon Targeted) markers. 17 chironji genotypes (BUAT-C-3, BUAT-C-4, BUAT-C-16, BUAT-C-23, BUAT-C-26, BUAT-C-35, BUAT-C-39, BUAT-C-42, BUAT-C-43, BUAT-C-45, BUAT-C-53, BUAT-C-54, BUAT-C-56, BUAT-C-64, BUAT-C-71, BUAT-C-72 and BUAT-C-73), two genotypes from each location were selected for study. The average number of alleles (4.0 to 18.0), average allele frequency (0.588 - 0.912), average gene diversity (0.157 to 0.480) and average PIC (Polymorphism Information Content) value noted as 0.142 to 0.365. The SCoT-9, SCoT-1, SCoT-22 and SCoT-18 were found to be informative and able to detect polymorphism among the studied genotypes due to its high PIC value.

Keywords: Chironji (*Buchanania lanzan* Spreng.), Germplasm, Molecular markers, Characterization.

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PP1-22

Differential Expression of Polyembryony in Certain Mango (*Mangifera indica* L.) Genotypes

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Mango (*Mangifera indica* L) is an important fruit crop, having both monoembryonic cultivars with single zygotic embryo and polyembryonic cultivars with more than one embryo, of which one can be zygotic and the rest adventitious of nucellar origin that are genetically similar to the mother plant. An attempt was made to study the expression of polyembryony in 21 polyembryonic genotypes of *M. indica* and two related species namely *M. zeylanica* and *M. odorata*. The results revealed that there were significant variations in number of segments per kernel, number of seedlings arising from a kernel and vegetative growth of the seedlings. The Chengavarikai genotype (9.25) had the highest number of segments in kernel followed by Turpentine (7.33) while the least (2) were recorded in Kitchener. Maximum number of seedlings emerged per kernel in Moreh (2.86) followed by Moovandan (2.82) whereas M. odorata (1.20) recorded the least followed by Vattam (1.27) and Kitchener (1.29). All season (29.41) was fastest in germination followed by Moovandan (30.25); on the other hand, Carabao needed the maximum number of days (45.12) for germination. Highest germination was was recorded in All season (94.29) followed by Moovandan (88.89) whereas the lowest was in *M. zeylanica* (6.90) followed by Starch and Prior (10.00). No variation in colour of emerging leaf was observed among the progeny of each genotype. Plant height, rate of leaf emergence, seedling girth and vigour index were more in Moovandan, Bappakai, All season and Gomavu while Peach, Prior, Corabao, *M. zeylanica*, and Vellaikolumban were less vigorous. The earlier emerging seedlings were more vigorous than later emerging ones within each genotype. No xenic effect was observed on expression of polyembryony in controlled pollination studies involving monoembryonic genotypes as male and vice versa.

Keywords: Mango, Polyembryony, Zygotic Embryo, Xenia

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PP1-23

Underutilized Fruits - Uncovering the Hidden Treasure

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India is home to the mega-biodiversity hotspots in the world, rich in many plant species which are underutilized, underexploited and endemic in nature. These plant species consist of number of underutilized and neglected plants like fruit crops, flowers, vegetables, millets, cereals and forest tree crops which are not well documented and still need to be explored and conserved properly. The potential use of these underutilized vast genetic resources to address issues of food and nutritional security for increasing population demand, climate change issues and income generation for the people.

As India aims to be a developed nation by 2047, the Government of India has also been taking various steps and measures by various schemes and projects being launched by educational and national institutes working under Ministry of Agriculture & Farmers Welfare. A wide gap is observed between cultivated plant species and natural plant resources like underutilized crops. The crops, which are neither grown commercially on large scale nor traded widely, may be termed as underutilized crops. These plants are cultivated, traded and consumed locally by tribals and have many advantages such as hardy growth, easy growing and production in adverse climatic situations and tolerant to biotic and abiotic stresses. So, exploration of underutilized crops like fruit crops may become a key solution for unemployment, food and nutritional security and for climate change issues. Underutilized fruits are rich sources of nutrients, vitamins, minerals, alkaloids and also used as medicines. These fruit crops may become helpful for income generation for small and marginal farmers by production, marketing and value addition, which may ultimately secure better Indian economy at global level and raise the standard of Indian people. So, conservation of natural biodiversity by people of India may conserve traditional knowledge and upcoming issues of human livelihood.

Keywords: Underutilized plants, Biodiversity, Food security, Climate change, Fruits, Genetic resources

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PP1-24

Collection, Characterization and Conservation of Indigenous Germplasm of Vegetable Crops

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Indigenous germplasm in context of vegetable crops is now referred to as plant genetic resource (PGR) which comprises landraces, traditional varieties, wild, weedy and other related species constituting primary (GP_1), secondary (GP_2) and tertiary gene pools (GP_3). Wild and indigenous relatives of vegetables crops are reservoirs of many important genes that are resistant to many biotic and abiotic stresses. Indian subcontinent being one of the Vavilovian centres of origin of crop plants possesses a lot of diversity in several important vegetable crops. Collection of local and land races varieties from different places through a trip of scientist. Characterization essentially means the recording of the observations on highly heritable traits, can be observed and expressed across the environments. Besides morphological characterization, germplasm is also characterized for biochemical (Protein/Isozyme) and molecular (DNA) markers. In vegetable crops, species of interest for *in situ* conservation, includes perennial types which do not set seed including wild relatives. The land races of vegetable crops have specific environments for their proper genotypic expression e.g. root development of radish (in Jaunpur), aroma and quality development in water melon (in Nagpur) and musk melon (in Tonk) need attention. *Ex situ* conservation includes field gene bank, seed gene bank, *in vitro* bank and Cryo bank preservation.

Keywords: PGR, DNA Markers, Cryo conservation, GP1, GP_2, GP_3

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PP1-25

Varietal Wealth of Guava

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Guava (*Psidium guajava* L.) belongs to the family Myrtaceae and is an important fruit crop of tropical and sub-tropical region of the country. Due to its high nutritive value, wide adaptability in adverse agro-climatic condition, early and prolific bearing with a good return, the crop has been gaining popularity as a commercial crop in Northern India. Guava plants are hardy and produce good yield. The fruit is a rich source a vitamin C, calcium, iron and pectin. Guava fruits are grown for their excellent health benefits and they can be consumed as fresh fruits or used in beverages, jams, candies, purees, jelly, ice cream, frozen pulp, fruit bars, yoghourts, and desserts. Many nutritionists refer to guava as a "MARVELOUS FRUIT" because of its abundance, ease of growing, and long list of health advantages. The traditional medical system is also aware of the beneficial effects of guava fruit, leaves, and other plant parts. In subtropical climates, there are three unique stages of growth and fruiting: Ambe bahar, Mrig bahar, and Hast bahar. Varietal characteristics in guava are not as distinct as found in majority of fruits. The variation is observed in plant growth, yield and physio-chemical composition among the different guava cultivars. Cultivars varied according to shape, colour, size and smoothness of skin as well as origin, bushy or erect tree, acidic nature, blooming, fruiting and fruit quality. Large number of cultivars are grown successfully in different parts of India. Some of the well-known selections from India are Allahabad Safeda, Allahabad Surkha, Pant Red, Lalit, Sardar, Bihi, Shwetha, Arka Mridula and the hybrids Safed Jam, Kohir Safeda, Arka Amulya and Arka Kiran. The western part of India, which receives reasonable amounts of rainfall, has enormous potential for growing guava.

Keywords: Guava, Varieites, Bahar, Growth

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PP1-26

Unlocking the Potential of Underutilized Traditional Vegetables Diversity in Bundelkhand Region

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The Bundelkhand region, characterized by its arid climate and resource constraints, faces challenges related to food and nutritional security and socioeconomic growth. This explores the potential of underutilized traditional vegetables (UTVs) in addressing these challenges. UTVs are indigenous to the region, resilient to harsh environmental conditions, and possess high nutritional value. However, they remain largely overlooked in mainstream agriculture and dietary practices. This study employs a multidisciplinary approach, combining agricultural, nutritional, and socioeconomic perspectives. It investigates the diversity, nutritional composition, cultivation practices, and market potential of UTVs like; Poi (*Basella alba* L*)*, Bathua (*Chenopodium album* L*)*, Chench *(Corchorus olitorius* L*)*, Kachri (*Cucumis callosus)*, Ratalu *(Dioscorea alata)*, Padora (*Momordica dioca)*, Kamalkakdi (*Nelumbo nucifera)*, Naribhaji (*Ipomoea eqatica)*, Chaulai *(Amaranth sp.)*, Malmala (*Portulaca oleracea)* and Suran *(Amorphophallus paeoniifolius)* in Bundelkhand. Additionally, it evaluates the socioeconomic implications of promoting UTVs, including income generation, employment opportunities, and women's empowerment. The findings reveal that UTVs offer a sustainable solution to enhance food and nutritional security in Bundelkhand. They are rich sources of essential nutrients including vitamins, minerals, and antioxidants, which can mitigate malnutrition and diet-related diseases prevalent in the region. Furthermore, promoting UTV cultivation can diversify income sources for farmers, reduce dependency on traditional crops vulnerable to climate change, and strengthen local food systems. Additionally, raising awareness among consumers about the nutritional benefits and culinary versatility of UTVs is essential to stimulate demand and foster a culture of dietary diversity.

Keywords: Underutilized, Traditional vegetable, Bundelkhand, Diversity, Nutritional value, Indigenous.

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PP1-27

Genetic Variability in Important Legume Vegetable Crops Of North-Eastern India

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French bean, lablab bean, and cowpea are the three most important legume vegetable crops after the garden pea, grown widely in the entire north-eastern states of India. To study the genetic variability in these legume vegetables, a total of 124 (French bean), 125 (lablab bean), and 30 genotypes of the cowpea collected earlier from north-eastern India were evaluated during the years 2022–24 for the growth and yield attributes. A wider variability was observed among the collections of all three crops. Out of 124 genotypes of the French bean, genotype MNFB-9 was identified as the earliest genotype for days to 50% flowering (32.3) and harvesting (47.0), followed by NFBC-16 and Collection-1, both for days to first flowering (32.33) and harvesting (50.0). HFBC-11 (20.33 cm), MZFBC-3 (19.56 cm), and RCFBS-5 (19.23 cm) exhibited the longest pod lengths. However, the maximum average pod weight was observed in NWFBC-5 (16.33 g), RCFB-78 (15.83 g), and MZFBC-13 (15.66 g). Moreover, RCFB-61 (657.33 g), RCFB-18 (486.67 g), and MNFB-9 (580.0 g) were identified as high-yielding. Similarly in lab bean, days to first flowering ranged from 51.67-101.67 days, raceme length (9.00-45.5 cm), leaf length (9.30-21.30 cm), pod weight (4.80-21.36 g), no of seeds per pod (3.0-7.0), 100 seed weight (42.0-102.0 g), yield per hill (0.26-1.37 kg). The high-yielding accessions were identified as ASDBC-17 (1.37 kg/plant), TRDBC-6 (0.98 kg/plant), and TRDBC-34 (0.78 kg /plant) under pole

type, and Sel-1 (175 g/plant) under bush type. Likewise, in cowpeas, the days to first flowering ranged from 29.66 to 75.0 days, days to first harvesting (47.66-98.0 days), pod length (18.4-50.93 cm), pod weight (4.5-22.16 g), number of seeds per pod (10.0-20.0), and seed weight (7.20-19.06 g). Among cowpea genotypes, the highest yield per plant was recorded from RCCPS-1 (785.3 g), followed by RCCPS-3 (750.5 g) and RCCPS-16 (663.6 g). These high-yielding genotypes can be further evaluated under multi-location testing to identify stable genotypes for commercial production and use in further crop improvement.

Keywords: French bean, Cowpea, Lablab bean, Genetic variability, Northeastern India

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PP1-28

A Review on Traditional Knowledge of Millets Practices in Nagaland

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Millets have played a central and an immense role in the agrarian system in many parts of civilizations, while introspecting the traditional Indian agriculture system millets had been the mainstay in terms of cultivation and production for country like India extensively dependant on agriculture for consumption, livestock and promotion of economy and for general usages. Millets are one of the important cereal crops in Nagaland and have long been cultivated on jhum land, terrace fields and as a millet-based bio-diverse farming system to provide a self-sustaining and climate-resilient system. The tribes of Nagaland conventionally followed animism with most social and cultural practices revolving around agriculture. And as such, millets were among the first crops to be domesticated, they have variety of traditional significance to the people mainly associated with it. Millets are climate-resilient crops, blended with a diverse range of nutrient-rich value, and are immensely linked with cultural heritage, beliefs, rituals, festivals, and folklores. The indigenous communities of India are incredibly diverse in terms of social, cultural, religious, food-habit, and culinary practices. The pattern of millet consumption and uses varies across north east states and has remained similar or reduced over time. This review aims to provide an outlook on the traditional knowledge such as that of cultural, nutritional significance, medicinal and biodiversity knowledge of millets practices in various parts of Nagaland. It plays a crucial role in ensuring food security in regions with unpredictable weather conditions and also on unreliable water sources depending on its climatic conditions as well as the topography. In the context of modern concerns, it is an ideal crop favouring climate change, environmental sustainability, and health-conscious diets. The practice of millet cultivation significantly promoted community and ecology-oriented approaches while placing co-creation and sharing of knowledge and collective governance centrally. The indigenous traditional knowledge of millets is essential in reviving, conserving and understanding their potential as means to sustainable, food security and bio-diverse farming system for the present and future generation and thereby, contributing towards adverse climate change.

Keywords: Millets, Traditional knowledge, Cultural, Nutritional, Medicinal, Biodiversity.

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PP1-29

Variability Studies in Bael *(Aegle marmelos* Corr.)

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Surveys were conducted in the districts Kushinagar, Gorakhpur, Khalilabad, Ayodhya and Sultanpur, of Uttar Pradesh during the year 2023-2024. A total of 30 genotypes having desirable traits were collected and morphological characterization of fruits carried out. Genotypes showed considerable variation for fruit morphological traits. The number of fruits per tree varied from (110 -315), fruit weight (0.212-1.670 kg) among the different genotypes collected. Variability recorded for fruit parameters, *viz.*, fruit length (7.70-17.5 cm), fruit width (4.46-13.02 cm), number of seeds per fruit (33-147), number of seed sack per fruit (9-17), shell weight per fruit (0.10-0.73 kg), shell thickness (2.0-5.80 mm), seed weight per fruit (2.8-15.8 g), pulp percentage (50.77-73.03) and shell percentage (17.15-32.31). Therefore, based on morphological and quantitative attributes, six genotypes (BUAT-B-1, BUAT-B-13, BUAT-B-19, BUAT-B-25, and BUAT-B-27) were screened as promising genotypes. These promising genotypes can be recommended for commercial multiplication, growing at farmer's fields, and conservation in the field gene bank for further evaluation and crop improvement.

Keywords: Genotypes, Morphological, Fruits, Uttar Pradesh.

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PP1-30

Enhancing Wheat Resilience: Genetic and Phenotypic Analysis of F_1 Hybrids for Heat and Drought Stress

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Wheat is a crucial and staple cereal crop globally. Despite numerous advancements in wheat improvement, climate variability and abiotic stress, particularly high temperatures and drought stress during the reproductive stage, significantly impact wheat production potential and quality. These stresses reduce spikelet fertility, grain number, grain weight, grain filling percentage, and duration. To address these challenges, crosses were attempted during the Rabi 2023-24 season at Main Experimental Station (MES), ANDUA&T, Kumarganj, Ayodhya. The experimental material comprised 10 lines (NW 1012, NW 1014, NW 1067, NW 1076, NW 2036, NW 4018, NW 5054, NW 6046, NW 7008, Sonalika, DDW 47) and 3 testers (RW-5, DTW 119, DWAP 1608). The lines are popular released varieties from Narendra Deva University, with two sourced from other regions. All testers exhibit heat and drought tolerance. Crosses were made in a Line x Tester design, resulting in 30 combinations and yielding a total of 150 F_1 progenies. In the subsequent Rabi 2024-25 season, the

F_1 progenies will be sown. Hybridity testing will be conducted using Simple Sequence Repeat (SSR) markers to identify true hybrids, optimizing resource use and efficiency. Phenotypic characterization of the true F_1 hybrids will be followed to estimate heritability to quantify the proportion of phenotypic variance attributable to genetic factors, thereby elucidating the genetic contribution to observed traits in the F_1 generation. Correlation and regression analyses will be performed to assess the strength and direction of relationships between various traits. Path analysis will investigate the direct and indirect effects of different variables, providing insights into causal relationships among traits. Principal Component Analysis (PCA) will be employed to reduce data dimensionality and identify key components explaining the variation. Cluster analysis will group individuals based on phenotypic similarities, identifying clusters of F_1 hybrids with analogous traits. These analyses will provide insights into the genetic and environmental factors influencing F_1 plant traits, facilitating the selection and breeding of superior wheat varieties. Additionally, this study will contribute to developing strategies to mitigate the adverse effects of abiotic stresses on wheat, thereby enhancing wheat resilience and productivity under changing climatic conditions.

Keywords: Heat tolerance, Climate resilience, Genotypic, Phenotypic analysis

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PP1-31

Unleashing the Power of Underutilized Vegetables

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Underutilized vegetable crops are being used increasingly frequently and successfully to combat hunger, impoverishment, and economic development. They are crucial biological resources for poor rural communities and can help millions of tribal people live more comfortably. Additionally, underutilized vegetables are resilient to a variety of biotic and abiotic stresses, and their yields can help nourish hungry people by supplying the nutritional requirements of vulnerable populations. They can help maintain the health of agro ecosystems since they are adapted to vulnerable conditions, especially in semi-arid and arid plains, hills, steppes, and tropical forests. They provide a wide range of crops to increase output, ensure the world's food supply, and fulfil new market demands the underutilized crops possess dense nutrients with higher micronutrients, rich in dietary fibre, resistant starch, and protein and bioactive with low glycemic index properties, while being highly adapted to agro-climate niches. Their ignorance has led to the erosion of genetic diversity and unique gene pools from cultivation areas. The government of India has been taking some steps to do research on underutilized crops like MIDH (Mission for Integrated Development of Horticulture), MEIS (Merchandize Export from India Scheme) and a national coordinated project has been also launched by Ministry of Agriculture. Basically, these underutilized vegetable crops have great potential for food security, income generation and environmental services and ultimately it makes Indian economy sounder.

Keywords: Food security, Nutritional security, Neglected crops, Underutilized plants, Wild food crops

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PP1-32

Morpho-Physiological and Bio-Chemical Characterization of (*Baccaurea sapida* (Roxb.) Muell.-Arg) – A Lesser Known Minor Fruit

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Baccaurea sapida (Roxb.) Muell.-Arg popularly known as 'Leteku' a minor fruit of Assam found growing in the wild and semi-domesticated conditions under less care and attention by local peoples. The fruits are being harvested for consumption and traditional medicinal uses. Very less systematic work has been carried our for morpho-physiological and biochemical characters of this fruit. The present study documented its tree morphology, flowering and fruiting traits. Biochemical profiling revealed the presence of crude fat (0.62±0.015 per cent), crude fibre (2.93±0.0.049 per cent), crude protein (4.88±0.016 per cent), total carbohydrate (89.06±0.073 per cent), energy content (381.39±0.261 Kcal/100 g). TSS (12.65±0.351 °B), total soluble sugar (11.85±0.238 per cent), reducing sugar (8.02 ± 0.060 per cent), riboflavin (92.31 µg/100 g) and thiamine (29.13 µg/100 g). The fruits exhibited considerable antioxidant activities due to the presence of ascorbic acid and phenol. Significant amount potassium and calcium was recorded in the fruit samples.

Keywords: Minor fruits, Biochemical traits, Antioxidant properties.

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PP1-33

Identification of Stable Genotypes for Development of Improved Variety/Hybrid in India's Hottest Chilli 'King Chilli' (*Capsicum chinense* Jacq.)

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King chilli (*Capsicum chinense* Jacq.), is one of the hottest Capsicum species in the world. This chilli species is endemic to the North Eastern Region of India and there is a wide diversity of the species in the region. This species of chilli has an ethnic, traditional and economic importance in the life of tribal people of North Eastern Region. It is not only high in pungency with palatable aroma but also rich nutritional quality. Despite of its being highly economical and potential crop there is no released variety or hybrid of this chilli species till now in the entire country. For development of any improved variety or hybrid systematic pre-breeding work is of utmost importance. Keeping in view the aforesaid points a study on evaluation, characterization and identification of stable genotypes of king chilli was conducted at ICAR Research Complex for NEH Region, Umiam, Meghalaya. The result of genetic parameter study revealed that environmental factors significantly affect the expression of growth behaviour such as no of branches and plant spread as depicted by wider difference between the PCV and GCV. High PCV accompanied with high GCV was observed in plant height (28.18%, 25.65%, respectively) no. of fruits per plant (25.36%, 20.75%, respectively), no. of seeds per fruit (26.93%, 23.30%, respectively) and ascorbic acid content (23.9%, 22.48%, respectively) indicating the presence of wide genetic variability for these traits in studied genotypes. High heritability (>60%) coupled with high GA (>20%) was recorded in plant height (82.90%, 48.11%, respectively), stem diameter (72.11%, 28.87%, respectively), plant spread (61.10%, 28.64%, respectively), no. of fruits per plant (66.90%, 34.97%, respectively), no. of seeds per fruit (74.90%, 41.53%); average fruit weight (65.70%, 29.15%, respectively), fruit length (64.20%, 29.61%, respectively); fruit diameter (64.60%, 22.81, respectively); fruit yield per plant (62.40%, 25.34%, respectively); ascorbic acid content (88.40%, 43.54%, respectively), total flavonoids (78.9%, 27.48%, respectively) and capsaicin content (60.30%, 21.95%, respectively). This indicates the prevalent of additive gene and hence selection of these traits would be effective for further improvement in *Capsicum chinense* Jacq. Stability analysis of the pooled data reveals that the accession RCNL1 was stable across environment for fruit yield per plant and no. of fruits per plant as depicted by its higher mean value greater than population mean, regression coefficient near to unity and non-significant deviation from linear regression. For quality traits none of the accessions was found to be stable across environments.

Key words: *Capsicum chinense* Jacq., Stability analysis, PCV, GCV

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PP1-34

Ethnobotanical Documentation and Conservation of Medicinal Plants Utilised by the Phom Tribe in Longleng District, Nagaland.

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This study presents a comprehensive documentation of medicinal plants used by the Phom tribe in Longleng district, Nagaland, India. Conducted between June and July 2024, the research aimed to preserve and highlight the indigenous knowledge of medicinal plants integral to the tribe's healthcare practices. Longleng district, situated between 94°-95° East Longitude and 26°-27° North Latitude, encompasses 885 square kilometres of rich biodiversity. Through extensive fieldwork, including in-depth consultations with local villagers and traditional healers, 95 medicinal plant species were identified and documented. Each plant's profile includes its scientific name, common name, local name, family, growth habit, parts used, and therapeutic applications. Key findings include *Calotropis gigantea* L. (Crown Flower, "Holojiph"): Utilized for fever and cough treatment; *Canna indica* L. (Indian Shot, "Choupha Cheu"): Known for its diuretic properties; *Caryota urens* Linn. (Jaggery Palm, "Mi"): Employed for seminal weakness and urinary disorders; *Clerodendrum colebrookianum* (East Indian Glory Bower, "Kainam"): Used as an antiseptic, tonic, and for bronchitis; Colocasia esculenta Linn. (Elephant Ear, "Yau Tou"): Applied for insect stings, cuts, and burns. The documentation reveals the vital role of these plants in addressing ailments ranging from toothaches and fevers to rheumatism and gastrointestinal issues. However, the study also underscores significant conservation concerns due to unsustainable harvesting practices and habitat destruction. Furthermore, the encroachment of modern pharmaceuticals threatens the transmission of traditional knowledge, risking the erosion of valuable ethnobotanical heritage. To address these challenges, the study advocates for immediate conservation efforts and the promotion of sustainable harvesting practices. By raising awareness about the importance of these medicinal plants, the research aims to foster more sustainable use and preserve the cultural and medicinal significance of the region's biodiversity. This study not only enriches our understanding of the Phom tribe's traditional practices but also calls for further research to explore integrating traditional remedies into contemporary healthcare practices. In conclusion, it serves as a crucial record of North-East India's rich ethnobotanical heritage, emphasising the need to preserve both plant species and the traditional knowledge associated with them for future generations.

Keywords: Ethnobotany, Medicinal Plants, Phom Tribe, Traditional Medicine, Indigenous Knowledge.

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PP1-35

Assessment of Genetic Diversity of Local Mango Collections in the North Eastern State of Tripura, India

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Mango (*Mangifera indica* L.), belonging to the Anacardiaceae family, is an important fruit crop that originated in the Indo-Burma region and knowledge related to genetic diversity is essential for any crop improvement activity. The northeastern region of the country shows a wide diversity of mango, though limited documented. Exploration of local and wild mangoes of the northeastern state of Tripura was undertaken to assess the morphological and qualitative diversity. For any crop improvement studies, morphological characterization is the initial step towards utilizing the germplasm. A total of 51 mango accessions of Tripura were assessed for 20 qualitative and 7 quantitative traits. The frequency distribution and co-efficient of variation of the qualitative characters were calculated. The analysis of variance for the traits studied showed significant differences among the 51 mango genotypes. Accession TM 48 recorded the maximum fruit weight (475g) and fruit length (13.9 cm), accession TM27 recorded the maximum TSS (26.2°Brix) and TM 50 recorded the minimum stone weight (3.7g). The principal component analysis showed the eigenvalues of the principal component axis, percent of total variation and cumulative variation among the genotypes. Based on the Eigen values of the 7 quantitative traits studied, the first four components were identified as major ones and showed 56.69% of the total variation studied. The correlation analysis showed the genotypes influenced multiple quantitative and qualitative traits. The adherence of fruit skin to pulp is significantly correlated with pulp texture, attractiveness, skin waxiness and pulp juiciness. Fruit weight is positively correlated with stone weight, length and stone width. The present work emphasized the need for the conservation of the diverse mango genotypes in the northeastern region and their utilization in future mango breeding approaches. Further, the characterization of the local mango germplasm and the development of a fruit catalogue would increase the awareness and interest of the custodian farmers about the available diversity, explore the commercial potential of these types and be helpful in linking the biodiversity with livelihood.

Keywords: Mango, Genetic Diversity, Quality, Correlation

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PP1-36

Performance of Varieties/Hybrids of Sapota against Bud Borer, *Anarsia achrasella* Bradley

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Sapota is one of the important and delicious fruits of humid tropical and sub-tropical regions in India. Its buds and fruits are available almost throughout the year in South Gujarat agro-ecological zone. Among insect pest fauna, bud borer, *Anarsia achrasella* Bradley is major pest harbor on bud, flower and cause significant yield loss. In South Gujarat, monoculture of Kalipatti is dominant, but in the recent past, there has been local collection as well as few varieties/hybrids from South India were come under screening purpose. Considering the significance of this pest, the damage intensity of bud borer in different 23 varieties/hybrids of sapota was evaluated at germplasm plot of AICRP on Fruits, FRS, NAU, Gandevi. The observations on per cent bud damage during the flowering phase (summer and winter) were recorded from 2018-19 to 2022-23. The pooled data of varietal evaluation revealed that the yearly average bud damage due to bud borer was higher in Kalipatti (9.50%), CO-2 (8.65%), Kirthibharti (8.26%), CO-1 (8.17%) and DHS-1 (7.60%). However, the lowest pooled infestation was reported in Chala Collection-3 (4.59%), PKM-1 (4.99%), Chala Collection-1 (5.18%) Pilipatti (5.39%) and Chala Collection-2 (5.40%). The maximum average infestation was observed from April to June at the peak flowering phase of sapota in Kalipatti (13.73-15.20%), CO-2 (13.69-14.77%), Kirthibharti (11.96-13.30%), DHS-1 (9.74-12.33%) and Cricket ball (10.45-12.45%). The bud infestation level was doubled during March-June (summer) period over Oct.-Jan. (winter) period. Many other varieties showed peak infestation levels below 10% during April to June. In susceptibility response of bud borer, CO-2, Kirthibharti, CO-1 and DHS-1 had nearer vulnerability reaction between 8.91 to 19.96% with standard check Kalipatti. Whereas, Chala Collection-3, PKM-1, Chala Collection-1, Pilipatti and Chala Collection-2 were 43.17 to 51.67% less susceptible than Kalipatti. The maximum infestation due to bud borer was found in May in maximum varieties/hybrids and June in few varieties/hybrids. In May, a maximum of 19 varieties/hybrids had higher damage by bud borer as well as four in June month. There was a non-significant correlation noted between bud length and diameter of different varieties/hybrids and bud damage by bud borer. As well, a non-significant correlation was observed between eight biochemical content of bud *viz*., crude protein, total carbohydrate, reducing sugar, non-reducing sugar, total soluble sugar, crude fiber, total phenol and lipid noted of different varieties/hybrids and bud damage, which indicate the pest population influenced by ecological factors.

Keywords: Sapota, Varieites, Bud borer, Varietal evaluation

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PP1-37

Evaluation of Taro (*Colocasia esculenta* L.) Genotypes for Growth, Yield and Quality Attributes Under Mid-hill Condition

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Although taro (*Colocasia esculenta* L. Schott.) is one of the most commonly consumed tuber crops by the ethnic tribes of north eastern region, limited literature is available with regards to growth, yield and quality attributes under mid-hill conditions. To study the growth, yield and quality attributes of taro, an experiment was conducted at ICAR Research Complex for North Eastern Hill Region, Umiam. Results revealed that significant variations were observed among the genotypes for all the parameters studied. Growth parameters such as plant height ranged 55.60±5.62 cm to 134.97±5.93 cm, number of side shoots ranged from 0 to 2, number of leaves 3±0.0 to 5.67±0.58 per plant, leaf size 407.80±8.93 to 2018.89±5.77 cm^2 and leaf sheath length, 8.97±1.05 to 45.23±5.45 cm. Yield parameters comprising weight of corm ranged 80±16.09 g to 641.67±18.77 g, weight of cormel ranges 19.53±4.32 g to 151.67±12.58 g, number of cormels/plant ranged 2.67±0.16 to 6.93±0.16, corm yield from 5.86±1.79 t/ha to 21.02±4.23, cormel yield 6.50±3.57 t/ha to 20.19±2.91 t/ha and total yield 18.97±7.45 t/ha to 35.77±0.90 t/ha with Tamitin recorded maximum value for most of the parameters. The biochemical parameters such as dry matter content ranges 20±3.39 % to 36.93±3.83 %, starch 15.16±3.00% to 35.49±4.20 % and total oxalate, 70.82±5.99 mg/100g dw to 208.54±5.21 mg/100g dw. Among the characters studied, genotypes *viz.,* Tamatim, Tamachongkham, Khweng-2 and Rengama were found promising and may have potential for utilization in future improvement programmes.

Keywords: Taro, Colocasia, Genotypes, Growth, Yield, Biochemical Parameters.

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PP1-38

Phenotypic Variability of Different Genotypes in Wood Apple (*Feronia limonia* L.) Germplasm in Bundelkhand Region of Uttar Pradesh, India

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Bundelkhand region is rich in wood apple biodiversity but less harnessed. The agro-climatic conditions of Bundelkhand have great potential for its commercial cultivation. Keeping these points in view, twenty-five genotypes of wood apple, fruit samples with shoot were collected from diverse areas of

the Bundelkhand region of Uttar Pradesh and analysed for various physico-chemical attributes and results of the study a revealed wide range of variability in morphological quantitative and qualitative etc. The quantitative variability of different genotypes in wood apple viz for the diameter of fruit (4.73cm to 7.75cm), seed weight (24.01g to 30.71g) and number of seed per fruit (103 to 657.50). Therefore, based on morphological quantitative and bio-chemical quality attributes, genotypes FS/WA-3, FS/WA-4, FS/WA-5, FS/WA-6, FS/WA-8, FS/WA-10, and FS/WA-25 were screened as promising genotypes. These promising genotypes can be recommended for commercial multiplication, growing at farmer's fields, and conservation in the field gene bank for further evaluation and crop improvement.

Key words: Wood apple, Germplasm, Characterization, Variability, Bundelkhand

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PP1-39

Study of Morphological Diversity in Traditional Rice Landraces of Tamil Nadu (*Oryza sativa*. L)

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A study was conducted to characterize 97 rice (*Oryza sativa* L.) landraces for 24 different morphological traits using DUS (Distinctiveness, Uniformity, Stability) characters. A total of three characters viz., leaf ligules, leaf auricles, and leaf shape of ligule were found to be monomorphic. The traits namely leaf anthocyanin colouration, leaf sheath anthocyanin colouration, panicle awns, panicle distribution of awns and leaf pubescence of blade surface were recorded as dimorphic. Seven qualitative traits including coleoptile colour, leaf intensity of green colour, ligule colour, leaf anthocyanin colouration of auricles, panicle exertion, leaf length of the blade and leaf width of the blade were trimorphic. Five traits including basal leaf sheath colour, culm attitude, flag leaf attitude of the blade (early and late observation), and panicle curvature of the main axis were recorded in four states of expression. The traits like spikelet colour of stigma, stem length, days to 50% flowering and time to maturity showed five states of expression. The DUS characterization of these qualitative characters will act as a tool for rice breeders to restore superior genes and they can be utilised in crop improvement programmes**.** The presence of uniform purple colour in the whole plant including ligules and auricles was observed in purple puttu and chitan samba. These traits can be used as morphological markers. The landraces namely Ayyan samba and red sirumani were observed to be the early maturity types. The short stem length and erect culms were observed in senthooram and seevan samba; these genotypes can withstand lodging. Therefore, these landraces would be used as donors for the development of short-duration and lodging-resistant rice in crop improvement programmes.

***Keywords**:* Rice, Landraces, Diversity, DUS characterization, Morphology

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PP1-40

Survey and Selection of Naturally Occurring Wild Kiwifruit (*Actinidia strigosa*) from Northeast India

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The present study, conducted from August 2021 to March 2023 in the state of Sikkim, Northeast India, focuses on *Actinidia strigosa* Hook. f. & Thomson (Theki Phal/ wild kiwifruit), a temperate, climbing shrubby plant species. It is distributed across the Eastern Himalayas, particularly in the West, South, and East districts of Sikkim, the Darjeeling hills of West Bengal, and parts of eastern Nepal, at altitudes ranging from 2100 to 2600 meters above msl. It plays a vital role in the daily lives of local communities and serves multiple economic purposes. It is used as a fresh fruit for consumption, fodder for livestock, traditional medicine, and in the production of fruit wine, offering potential for value-added products. *A. strigosa* exhibits promise in the kiwifruit breeding industry as a valuable genetic resource for enhancing cold tolerance of *A. deliciosa*. This characteristic may help expand kiwifruit cultivation to higher altitudes in the Himalayan regions, thus broadening the scope of kiwifruit production in areas with colder climates. During the period 2021 to 2023, a comprehensive survey and selection encompassing several morphological, biochemical, and sensory evaluations of fruit samples from 107 healthy and bearing female wild kiwifruit vines from the West, South and East Sikkim districts of Sikkim was carried out. The present study was aimed to assess the nature and magnitude of variability in wild kiwifruit vines growing in wild state in the forest of Sikkim. Extensive phenotypic variation was observed among the 107 wild kiwifruit female vines existing in natural condition in West, South and East district of Sikkim. As a result of the present study, eight wild kiwifruit selections viz. SKWHLY- 10, SKWHLY-12, SKWHLY-27, SKWBHR-09, SKWRBD-02, SKWRBD-04, SKEZK-03, SKEZK-06 were obtained which demonstrated exceptional performance across multiple horticulturally significant traits of commercial potential. The exploration and selection of wild kiwifruit in its natural habitat has yielded valuable germplasm that could be used in future breeding programs to develop cold-hardy cultivars. This study enables researchers, in collaboration with local farmers, to expand kiwifruit cultivation to higher altitudes (2000–3000 m) in the Northeast Himalayan hill states of India. Integrating these accessions into breeding efforts could significantly broaden kiwifruit production in these regions.

Keywords: Cold-hardy, Northeast, Selections, Sikkim, Variation**,** Wild-kiwi (*Actinidia strigosa*)

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PP1-41

Evaluation of *Capsicum annum* L. Genotypes of Northeastern India for the Yield Attributes in the Mid-Hills of Meghalaya

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The northeast region of India is known for its rich genetic diversity of *Capsicum* species, particularly *Capsicum annum* L., which is widely cultivated for its pungent fruits. This study aimed to evaluate the 68 genotypes of *Capsicum annum* of northeastern India for yield and its contributing characters. A total of 68 genotypes were collected from the northeastern states of India and evaluated for various morpho-agronomic traits over two consecutive years in a randomized complete block design with three replications. In this experiment, we recorded some yield and yield attributing characters like days to first flowering, days to first harvest, number of flowers per plant, number of branches, fruit weight, fruit length, fruit width, number of fruits per plant, red ripe fruit yield per plant, leaf length, leaf width, plant height, and plant spread. The study revealed significant variation among the genotypes and the results showed that days to first flowering ranged from 34 to 86 days, days to first harvest from 68 to 116 days, number of flowers per plant from 2 to 129, number of branches from 2 to 5, fruit weight from 2 to 9.5 g, fruit length from 3.6 to 13.6 cm, fruit width from 0.83 to 1.73 cm, number of fruits per plant from 5.33 to 115.33, red ripe fruit yield per plant from 24 to 363.66 g, leaf length from 4.36 to 11.7 cm, leaf width from 2 to 4.86 cm, plant height from 30.56 to 94.83 cm, and plant spread from 22.16 to 56.76 cm. The study highlights the rich genetic diversity of *Capsicum annum* in Northeast India and its potential for chilli crop improvement through selective breeding and genetic enhancement programs.

Keywords: *Capsicum*, yield, Evaluation, Germplasm, Genotypes.

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PP1-42

Collection, Evaluation and Maintenance of Wild Spine Gourd (*Momordica dioica* Roxb. ex Willd.) Germplasm for Crop Improvement in Telangana

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Spine gourd (*Momordica dioica* Roxb. ex Willd.) is a minor dioecious cucurbit, native to Asia. It is a perennial vegetable crop traditionally grown in the wild and gaining popularity for cultivation due to its high nutritional value and medicinal benefits, which contribute to a healthy diet. However, significant crop improvement is required to identify and exploit new traits for developing high-yielding varieties. Germplasm collection plays a crucial role in breeding programs aimed at enhancing specific traits and conducting agronomical and propagation studies. The present investigation was conducted during 2022-23 at the Horticultural Research Station, Aswaraopet on “Collection, Evaluation and Maintenance of wild Spine Gourd (*Momordica dioica* Roxb. ex Willd.) Germplasm for Crop Improvement in Telangana”. A total of 48 accessions were collected, out of which 43 were flowered, resulting in the identification of 26 female and 17 male lines. Among the female lines, 21 were produced fruits. Key findings include the longest vine length was recorded in accession SGR_1P_2 (2.50 m) followed by SGR_2P_4 (2.10 m). Accession SGR_4P_4 yielded the maximum number of fruits per plant (21) followed by $SGR_{10}P_1$ (18). The maximum average fruit weight (15.00 g) was recorded in SGR_2P_2 followed by $SGR8P_1$ (14.20 g). The highest fruit yield per plant (202.00 g) was observed in $SGR_{10}P_1$ followed by SGR_8P_4 (129.00 g). Additionally, $SGR_{10}P_1$ exhibited the longest fruiting duration (67 days) and followed by SGR_8P_4 (52 days). The results demonstrated a positive correlation among yield-attributing traits, fruiting duration and vine length emphasizing potential accessions for breeding high-yielding varieties. This study provides valuable insights into the genetic potential of spine gourd germplasm, paving the way for future breeding and crop improvement initiatives.

Key words: Spine gourd, *Momordica dioica*, Germplasm, Crop improvement, Telangana.

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PP1-43

Collection, Characterization of Upland Rice Germplasm: A Treasure of North East Hill Ecosystem

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Upland rice cultivation includes growing rice by direct seeding, in slopping, unbunded fields with no standing water. In India, upland rice is grown in about 4.8 million hectares accounting for 11 % of the total rice area of the country and located mainly in eastern India including North East Hill Region. In North Eastern Hill region of India, upland rice is predominantly grown in steep slopes with slash and burn system and on level bench dry terraces mainly occupied by landraces. In the present study, an attempt was made to collect fifty-four upland rice landraces under cultivation from three hill districts of Manipur with preliminary varietal details and morphologically characterised under direct seeded terraced upland condition at Langol research farm, ICAR Manipur centre during kharif 2020 and 2021. Wide variability was observed for agronomic traits of economic importance. The stem length varied from 60.0 cm to 184.2 cm. Panicle length ranged from 20.2 to 34.4 cm. The palea and lemma colour varied widely from straw to black. The distinct landraces were submitted for conservation at National Gene Bank, New Delhi and obtained IC number numbers. As reservoirs of significant quality,

biotic, and abiotic stresses, the germplasm collection from the hill region of northeast is anticipated to be of rice breeding relevance for the upland ecology.

Keywords: Rice, Landrace, Northeastern India

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PP1-44

Sunflower Genetic Resources Management in India

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Sunflower crop is introduced in India during early 1970's with commercial hybrids, parental lines and germplasm accessions received from USA and erstwhile USSR. As of now, 3126 sunflower accessions are kept in the medium term storage of the Indian Institute of Oilseeds Research (IIOR) under the Germplasm Multiplication Unit (GMU). The ICAR-IIOR collection consists of the following: backcross converted lines (15), prebred lines, inbreds augmented from USDA, USA (360), genetic stocks (105), inbreds (350), populations (DRSF 5), exotic collection (350), genetic stocks (105), inbreds (350), and gene pools (GP) for high oil, yield, and autogamy (340). 2719 sunflower accessions, including EC (Exotic), IC (Indigenous), wild, weedy, landrace/traditional cultivar, breeding line/research material, genetic stocks, and registered germplasm, are maintained at ICAR-National Bureau of Plant Genetic Resources (NBPGR). In 2018, a catalogue of germplasm containing 3126 accessions was released, offering details on the accessibility of sunflower accessions that are conserved at ICAR-IIOR, Hyderabad and ICAR-NBPGR, New Delhi. Breeders of sunflowers will find the descriptive material useful in identifying accessions, selecting novel materials for a variety of uses, and identifying potential parents to use in breeding. Enhancement of trait-specific germplasm, use of promising cultivar germplasm and wild *Helianthus* species in inbred development, development of maintainer/restorer gene pools, parental line improvement, and resistance breeding programs are the current areas of interest. Regarding the enhancement, multiplication, conservation, and use of sunflower genetic resources in the Indian breeding program, there are a number of concerns. One of the biggest obstacles to expanding sunflower germplasm is getting access to international gene banks outside of the USDA and the USA. The multiplication of sunflower accessions is labour intensive; another problem is the non-viability of the seed due to prolonged storage under normal conditions where viability is reduced upto 20 to 30% within one year of storage. To keep the germplasm intact, accessions with viability lower than 50% are regularly rejuvenated and multiplied. The insufficiency of large-scale multilocation evaluation limits the ability to identify and subsequently utilize potential accessions. Major barriers to genetic improvement through interspecific hybridization are differences in ploidy. It is urgently necessary to identify duplicates using specialized instruments and methods. The present paper discusses about the various activities carried out with regards to conservation, multiplication, evaluation, issues and challenges in the utilization of sunflower germplasm during past two decades.

Keywords: Genetic resources, Sunflower, Utilization, Issues, India

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PP1-45

Diversity of Minor Fruits in Garo Hills, Meghalaya

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Minor fruits or underutilized fruits are generally those fruits which are collected directly from plants growing naturally in the forests or marginal lands of rural areas but not under commercial cultivation. These fruits are an integral part in the life of people in both urban and rural areas. These fruits are usually consumed as snacks or as an accompaniment to main meals. Besides being cheap, these fruits are also important sources of quality nutrition and medicine making them potential candidates for providing quality nutritional and economic security to the local farmers. However, due to lack of awareness of their potential, lack of proper cultivation practices and documentation, these fruits are gradually getting replaced by commercially cultivated fruits. Rapid habitat destruction and urbanization have also resulted in population shrinkage of these minor fruits from their natural habitats. Therefore, exploration, collection and documentation of potential minor fruits in selected districts of Meghalaya was undertaken to understand the diversity of minor fruits available in the region. Thirty-seven accessions of minor fruits belonging to 11 different families across 11 genera were collected. The collected fruits include *Hematocarpus validus*, *Baccaurea ramiflora, Willughbeia edulis, Artocarpus chama*, *Garcinia* spp., *Passiflora edulis*, *Averrhoa carambola*, *Aegle marmelos*, *Musa spp.*, *Syzygium cumini* and *Eriobotrya angustissima*. Morphological diversity was observed within the same species of fruit collected from different areas. Among the seven accessions of *B. ramiflora*, variations in morphological characters *viz*. fruit length, fruit width and fruit weight were observed. Fruits collected from Dobe dare, Asiragre, East Garo Hills and Nilwa adinggre, South Garo Hills were larger in size with fruit length 2.71±0.05cm, 2.85±0.26cm and 2.91±0.41cm; fruit width 2.90±0.15cm, 2.80±0.22cm and 2.96±0.11cm; and weight of individual fruit 11.01±1.63g, 12.26±3.17g and 11.90±1.67. In *W. edulis* maximum fruit length (8.92±0.07cm) and maximum fruit width (7.72±0.19cm) was observed in fruits collected from Dawachipitgre, East Garo Hills. Whereas, highest weight of individual fruit (180.20±2.02g) was recorded in fruits collected from Songmagre, West Garo Hills. While, in *G. cowa* var. *kydia*, fruits collected from Songmagre, West Garo Hills were smaller in size with fruit length 3.60±0.1cm, fruit width 3.23±0.20cm and individual fruit weight (15±2.0g) having 5-6 seeds per fruit. Whereas, the fruits collected from Reserve Gittim and Nilwa Adinggre, South Garo hills were larger in size with fruit length 3.93±0.11cm and fruit width 3.40±0.17cm having 6 to 7 seeds per fruit; and fruit length 5.10±0.17cm and fruit width 4.43±0.11cm having 5 to 6 seeds, respectively. Maximum individual fruit weight was recorded highest in fruits collected from Nilwa Adinggre (43.43±0.94g).

Key words: Minor fruits, Garo hills, Meghalaya

PP1-46

Evaluation of Grass Pea (*Lathyrus sativus* L.) Landraces for Genetic Variability and Character Association for Growth, Yield and Quality Attributes

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Grasspea has immense potential as a dual-purpose pulse-cum-forage crop in areas prone to adverse climatic conditions. To study the genetic variability and character association for yield and quality traits of seeds and forage of grass peas, a field experiment was conducted during Rabi 2021–22 using local collections from Assam. Except for pod length and pod width, significant variations were observed for all the growth, yield, and quality traits. Wider variability was observed for important traits such as green forage yield (41.27–20.67 g/plant), seed yield (3.09–5.67 g/plant), β-N-oxalyl-L-α, β-diaminopropionic acid (β-ODAP) and protein content in seeds (0.08–0.44% and 23.6-28.8%) and forage (0.07–0.37% and 13.3-20.1%), respectively. High GCV and PCV were observed for β-ODAP content in leaf and seed and dry matter yield per plant. High heritability coupled with high genetic advance was observed for leaf width, green forage yield, dry matter yield, crude protein content in leaves, and β-ODAP content in leaf and seed. Under principal component analysis (PCA), the first five principal components explained 81.98% of the total variance, and the first PC accounted for 29.53 percent of the total variations, which were contributed by growth and yield-related traits. Based on the mean performances, JCL-21-N-1, JCL-21-N-5, and JCL-10-4 were found promising for green fodder yield, and JCL-21-N-1, JCL-21-N-4, and JCL-10-4 for higher yield with low β-ODAP and high crude protein content. The only genotype with a combination of low β-ODAP content, high fodder, and high grain yield was JCL-21-N-1. Correlation and path analysis revealed the importance of number of leaves per plant, primary branches per plant, secondary branches per plant and dry matter yield per plant for improvement of green forage yield. On the other hand, the number of pods per plant and number of effective pods per plant were observed to be the most important traits for improving seed yield. β-ODAP content in leaf exhibited a significantly negative correlation with green forage yield per plant, dry matter yield per plant, and primary branches per plant, while β-ODAP content in seed showed a significant negative correlation with primary branches per plant, green forage yield per plant, and 100 seed weight. Therefore, selection for improvement in these traits would result in the isolation of genotypes with low β-ODAP content.

Key words: Grass pea, β-ODAP, Genetic Variability, Correlation, Path

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PP1-47

Evaluation of Gerbera Genotypes for Vegetative and Flowering Attributes under Shade Net and Open Field Conditions in the Mid-Hill Ecosystem of Meghalaya

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During the period from 2023 to 2024, five gerbera cultivars Glorious Purple, Olympic, Intense, Stanza, and Fundy were evaluated alongside a widely recognized cultivar, Alsmera. The evaluations were conducted under two distinct growing environments: low-cost polyhouse (LCP) and open field conditions (OFC) at the Horticulture Research Farm, ICAR RC NEHR, located in Umiam. Throughout the study, all gerbera cultivars exhibited superior performance under the polyhouse conditions compared to those grown in the open field, across all parameters assessed. Among the cultivars, Glorious Purple demonstrated outstanding traits, recording the highest number of leaves (12.7 under LCP and 11.0 under OFC), as well as the longest leaf length (22.8 cm under LCP and 21.7 cm under OFC) and greatest leaf width (11.5 cm under LCP and 10.5 cm under OFC). Additionally, it achieved the longest vase life, lasting 11.0 days in LCP and 10.0 days in OFC. When examining flowering attributes, the cultivar Intense stood out with the longest stalk length, measuring 39.5 cm in LCP and 34.3 cm in OFC, along with the largest flower stalk diameter (0.67 cm in LCP and 0.65 cm in OFC). Fundy, on the other hand, produced the largest flower diameter, measuring 12.5 cm under LCP and 11.8 cm under OFC. In terms of yield and quality traits, Olympic proved to be the most efficient, requiring the fewest days to bud formation (73.4 days in LCP and 77.2 days in OFC), bud burst (83.2 days in LCP and 87.3 days in OFC), and first flower opening (88.2 days in LCP and 93.8 days in OFC). Olympic also achieved the highest counts for flowers per plant (12.6 in LCP and 11.0 in OFC) and suckers per plant (14.5 in LCP and 13.3 in OFC). Notably, the gerbera varieties showed varying susceptibilities to pests. Glorious Purple and Olympic were identified as suitable for pot cultivation, whereas Intense and Fundy were found to be ideal for cut flower production.

Keywords: Gerbera, Open field, Shade net, Genotypes,

PP1-48

Characterization and Genetic Diversity in Groundnut Genotypes (*Arachis hypogaea* L)

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This study was conducted to analyze the genetic diversity and relationship among 50 groundnut genotypes of which belong to subsp. *hypogaea* (*Arachis hypogaea* L.) The collection was evaluated for 10 quantitative and nine qualitative traits during two consecutive years under Agriculture College and Research Institute, Eachangkottai, Thanjavur condition Coefficient of variation (CV) significantly differed among the genotypes for all the studied quantitative traits ranged from 9.0 to 19.5 while the highest CV was recorded for seed yield. Principal component analyses showed that the first three principal components accounted for 65.12% variation for quantitative traits. Major traits that accounted for the variation by the three principal components (PCs) include days to the first flowering, days to 50% flowering, number of pods per plant and shelling percentage. The groundnut collection also offers wide seed coat color diversity which affects the crop marketability. The information on variations in quantitative and qualitative traitsidentified in the present investigation provided useful genotypes which would be serving parents. These parental genotypes can be used in groundnut breeding programs to develop desirable cultivars in AC and RI, TNAU, Eachangkottai.

Keywords: Ground nut, Genetic variability, Principal Component Analysis

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PP1-49

Diversity of Maize in Northeast Hill (NEH) Region of India

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Maize is the one of the most important cereal crops in the world. The maize crop has importance as a model system of biological research, exhibiting tremendous genetic diversity and allowing exploration of genetic phenomena such as heterosis and gene transposition. In India, the Northeastern Hill (NEH) Region, a recognized Asiatic center of maize diversity, is home to various races of maize. Secondary centers of crop diversity have emerged globally in different agroclimatic zones, generating even higher levels of variability, especially in the form of maize landraces. The pigmented landraces are particularly important from a nutritional perspective. Pigmented kernels get their color from the synthesis of secondary metabolites such as anthocyanin. Kernels with anthocyanin deposition in the pericarp and/or aleurone layers have high antioxidant and antiradical properties and the health benefits include anti-mutagenic, anti-carcinogenic and oestrogenic effects. Additionally, since the majority of anthocyanins found in maize kernels are acylated, they are more stable as natural food colorants. When characterizing local germplasm besides phenotyping of visible morphological differences, molecular studies provide insights into the underlying genetic variation and associations of the material study. In plant breeding, because of their codominant behavior, SSR markers have been commonly used for both model and distance-based population structure studies. In India, the National Bureau of Plant Genetic Resources (NBPGR) is responsible for germplasm conservation of crop plants. It has around 9000 maize germplasm of both indigenous and exotic origin; about 60% of the collection are landraces. However, most of the landraces are found in the remote regions of India, including the North Eastern Hill Region (NEHR), and have yet to be included in this collection.

Keywords: Maize, Genetic Diversity, North-eastern India

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OP1-01

Indigenous Cattle Biodiversity in North East India: A Step towards Characterization and Documentation

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The cattle population of India is 192.52 million, which includes 142.11 million indigenous cattle distributed around the whole country and the cattle population in NE region is 13.31 million out of which 12.27 million cattle are indigenous (BAHS, 2019). These indigenous cattle reared by farmers are to be explored; characterized and documented that is present in these states and note any similarities or differences with current populations. The current study was carried out in different regions of Northeast India *i.e*. Arunachal Pradesh -Mechuka (Si yomi), Manipur-Churachandpur, Imphal West, Imphal East, Senapati, Meghalaya-South West Khasi Hills and Jaintia Hills, Mizoram-Area-Champhai, Sikkim- Sikkim North, Tripura-West Tripura, Gomati, South Tripura and Dhalai. This study aimed to differentiate and characterize indigenous cattle diversity in Northeast India using phenotypic morphological traits. Morphometric characteristics included height at withers, tail length without switch, face length, ear length, horn length, heart girth, and paunch girth. Phenotypic variations such as colours of coat, muzzle, horn, hoof, eyelids, and tail switch were recorded. The majority of cattle population varied in different colours like brown, light brown and black. The body length in adult male and female animals (Age ≥ 36 months) ranged from 101.06 ± 0.38 - 138.40 ± 0.79 and 97.67 ± 0.96 - 109.73±1.65 cm, respectively. Similarly, The height at wither in adult male and female animals varied from 104.01±0.46 - 138.98 ± 0.22 and 99.73±0.32-122.29 ± 0.14 cm, respectively. The age at first calving ranged between 37.54±1.91 to 51.50±0.81 months, whereas, average calving interval was 15-16 months. The average milk yield per day varied between 1.10±0.67 - 2.25±0.5 L and peak milk yield ranged from 1.31±0.51 - 3.25±0.75 L. The Lactation length (days) ranged between 145.89 ± 9.32 – 239 ± 23. The phenotypic characterization of indigenous cattle diversity is essential for managing animal genetic resources at nationwide and regional levels. This study enumerates the unique features of cattle population present Northeast India and provides baseline information for different stakeholders for breed characterization.

Keywords: Cattle, Native breeds, Variability, Northeastern India

OP1-02

Alternative Protein Sources from North East India's Snail Diversity: Addressing Food Safety Concerns

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The North East Hill region with tropical climate, dense forest, and freshwater bodies is home to a diverse range of snail species, including both terrestrial and freshwater snails. Snails are high in protein, low in fat, and rich in essential amino acids, vitamins (like B12), and minerals (such as iron and calcium). This makes them a valuable food source. There is a cultural acceptance in the tribal part of the region with major consumption in states like Manipur and Nagaland. Consuming snails can be nutritious, but it is crucial to address food safety issues to prevent health risks. We analyzed 34 pooled snail samples from different market of mostly belonging to the *Ballamya bengalensis, Pila globosa, Brotia spp, Cipangopaludina lecythis* etc during 2023-24 for bacterial isolation for five food borne pathogens associated with snails *viz.*, *Salmonella*, *Staphylococcus aureus*, *Listeria monocytogenes*, *Bacillus cereus*, *Aeromonas hydrophila*. There were presence of *Bacillus cereus* (6/34), *Aeromonas hydrophila* (22/34) and *Staphylococcus aureus* (5/34) in the fresh raw samples which suggests that food safety angle should be also looked on to use the snail as human food. We also performed aerobic plate count for raw samples and salt water washing to calculate the reduction of bacterial count which showed that the traditional salt washing practice is effective to reduce the burden of microbial population of snails with average 1.6 log reduction with one wash and 3.57 with three time wash. The freshwater snails used for food consumption are analyzed for bacterial load showed the presence of food borne pathogens and the traditional way of salt water washing of raw snails reduces substantially the bacterial load.

Keywords: Snail, Bacteria, North East India, Alternate protein

OP1-03

Traditional Animal Husbandry Practices among the Mising Tribal Population of Dhemaji District, Assam: A Case Study on Livestock and Poultry Management

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Present study was done in No-3, 4 Dirpai Chpori, Ukkhamati and Moniurikachari villages of Dhemaji District, Assam, to note the traditional animal husbandry practices of the Mising tribal people. Dhemaji, district has around 50% of its rural inhabitants belonging to scheduled tribes. The Mising people, originally from the Abor and Mishimi hills of Arunachal Pradesh, migrated to the plains of Assam, settling near the Brahmaputra and Subansiri rivers. Known for their preparation of *Apong* (a rice alcoholic beverage), the waste from this process is traditionally used as feed for pigs. A total of 30, Mising tribal families from four selected villages of Dhemaji district were interviewed to gather data on their animal husbandry practices. Descriptive statistics revealed that 96.7% of the farmers cultivate paddy, while 83.3% rear cattle, 46.7% keep goats, 83.3% rear pigs, 86.7% keep chickens and 40% keep ducks. Notably, all cattle were indigenous with an ox-to-cow ratio of 0.589. The average number of cattle, goats and pigs per family was found to be 2.96, 1.2 and 2.7, respectively. Cattle were primarily reared under an extensive system, with 72% of farmers tying them below paddy or paddy straw stores for night shelter, while 16% constructed separate shelters using bamboo and tin. Goats were also reared extensively, with 50% housed under paddy stores and 35% below homes during night time. About 80% of pig keepers used tethering methods and 96% offered rice husk, kitchen waste, and local rice wine waste and sometimes cooked leaves of *Colocasia sp*. and Banana stem as feed. Only, 11.53 % farmers offered commercial feed and out of them only one offered commercial feed solely. All chickens and ducks were reared extensively, 96% provided them temporary night shelter made up bamboo, wooden planks, tin and net. The study highlights a significant opportunity for scientific interventions in their traditional livestock and poultry feeding, housing and breeding system with spreading awareness regarding fodder cultivation, promotion of high milk yielding dairy animals and technology adoption for effective utilization of resources.

Keywords: Traditional, Livestock, Poultry, Production, Northeastern India

OP1-04

Balang: An Indigenous Cattle Germplasm in Eastern Himalaya of Arunachal Pradesh

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Livestock plays an integral part in the community in Arunachal Pradesh among which cattle is considered as one of the important animals among the communities near the Indo-China border which usually belong to Memba community of Arunachal Pradesh. The study was done in Shi Yomi district of Arunachal Pradesh located N 280.37'27"2, E940 6'30" with an average altitude of 1030 msl. A pretested questionnaire was developed and data was collected from 60 household. The socio-economic profile of the farmers showed that, majority (62.9 %) of the farmers belong to middle age group (36-57yrs old). Around 57.12 per cent studied up to secondary level .85.1 per cent had joint family with 5-8 family members. In terms of management of cattle cent per cent of the farmers reared on free range system grazing from 7:00 am to 3:00 P.M. Only 15.1 per cent provided flour meal along with millet for cows. Cent per cent of the farmers constructed houses with roof made from bamboo, wall from pinewood kuccha floor they used dried fern leaves as bedding material. None of the farmers did Dehorning of cattle. The majority (78.7%) of farmers reported milking during morning hours only 21.3 per cent twice i.e. morning and evening. 75.5 per cent of respondents reported average milk production of around 1-1.5 ltrs/day/cow. The majority (91%) of the respondents reported FMD, external and internal parasite infestation, diarrhoea and leech infestation. The indigenous cattle (Balang) are small size, stout body colour varied from black (62%), brown (23.8%) and light black (14.2%). The horn orientation (66.7%) curved upward. Horn colour was (71.4%) black and the remaining was brown colour. Cent per cent ear orientation was horizontal. Muzzle was black in colour (62.0 %) and followed by brown colour. The head was straight (80.9%) and convex. Hump and dewlap were small with small penis sheath. The udder was bowl in shape and small size. Around 62.5 per cent of the teats were funnel shaped with rounded tip. Milk vein was non-prominent. Hoof color varied from black (47.6%), black & white (33.3%) and brown (19.1%). The tail was up to the hock with switch colour was predominantly black (52.3%) followed by brown (38.1%) and white 9.5 per cent. The average body length, heart girth, height at wither, horn length, ear length, face length and tail length, neck length of Balang Bull were 101.06±0.38 cm, 135.29±0.44 cm, 104.01±0.46 cm, 12.11±0.20 cm, 18.90±0.11, 38.34±0.17 and 90.39±0.32 cm respectively. The average daily milk yield, peak yield, lactation length were 1.10±0.67 L, 1.31±0.51 L and 170.24± 9.32 days respectively. Milk fat % and SNF % were 4.52± 0.48 and 8.27±0.54 respectively

Key words: Balang, Breeds, Indigeneous cattle, Northeastern India

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OP1-05

Assessing Growth Performance, Economic Viability, and Adaptability of Black Bengal Goats in Mid-Hill Environments of Meghalaya

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Black Bengal goats, an indigenous dwarf breed valued for their high prolificacy and superior meat quality, play a crucial role in the livelihoods of resource-poor farmers. This study aimed to assess the growth performance, economic viability, and adaptability of Black Bengal goats in the mid-hill environments of Meghalaya at the College of Agriculture, CAU(I), Kyrdemkulai. The goats were reared under a semi-intensive system with slatted floor housing and received regular deworming and vaccinations to maintain their health. Body weights of 30 kids born between January 2022 and August 2023 were recorded from birth up to 4 months of age. The average body weights recorded were 1.03±0.04 kg at birth, 1.34±0.18 kg at 1 month, 2.78±0.17 kg at 2 months, 3.41±0.13 kg at 3 months, and 4.15±0.14 kg at 4 months. The average daily weight gain from birth to the weaning age of 90 days was 28 g/day. The average litter size was 1.33±0.14, with the percentages of singles, twins, and triplets being 64%, 47%, and 3.5%, respectively. Analysis indicated that seasonal variations did not significantly affect body weight. The average body weight of adult male and female goats at 12 months of age was 22±0.27 kg and 15±0.35 kg, respectively. The average age at first kidding and kidding interval were 10-11 months and 7-10 months, respectively. The goats were fed 150-200 g of concentrate per day and grazed for 5-6 hours on forest forages. The mortality rate recorded in kids was 13.3%. The results suggest that Black Bengal goats demonstrate good adaptability to the mid-hill environments of Meghalaya. This adaptability, combined with their growth performance, underscores the potential of Black Bengal goat farming as a viable option for improving livelihoods and fostering entrepreneurial activity. From a unit of 30 goats, the net profit generated from the sale of kids, manure, and adult goats was Rs. 1.03 lakhs, with a cost-benefit ratio of 2.1:1, highlighting their role in enhancing economic security for resource-poor farmers. Around 50 elite kids were distributed to tribal farmers, and they are performing well under village conditions in Meghalaya. The Black Bengal goat unit at CoA, CAU (I), Kyrdemkulai, not only serves as a centre for conserving indigenous germplasm but also plays a pivotal role in promoting scientific goat farming. Through training programs and the distribution of elite kids, the unit supports sustainable agricultural practices and contributes to the effective conservation of this valuable breed.

Keywords: Goat, Genetic characterization, Yield and Economics

OP1-06

Phenotypic Characterization of Goats of West Champaran, Bihar using Principal Component Analysis with Orthogonal and Non-orthogonal Rotations

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This study focuses on the indigenous goat population of West Champaran district in Bihar, India, emphasizing its importance in the livelihood security of the poor people and its significant contribution to the state's agriculture. This goat population attracts attention for conservation and genetic improvement to enhance farmer's income. The objectives of study were for estimation of various parameters of phenotypic characterization and to study the structural relationships among various body traits. The research conducted a survey covering 220 farmers' households in West Champaran district and measured over 646 adult goats to record body weight and various biometric traits. Statistical analyses were performed to assess correlations and principal components with orthogonal and non-orthogonal rotations using various packages of R statistics software. This population of goats of Champaran region are medium sized animals reared under semi-extensive production system for chevon production purposes by small and marginal farmers with average flock size of 5.6. The goats of Champaran region presents salient characteristics such as medium legged animals, lustrous hair, beard in aged animals, slightly convex nose line, prominent distance between two eyes innercanthus, resistant to heat and cold stress, disease tolerance and famous for high quality chevon production. The body weight of Champaran goat estimated for male in range of 2.51± 0.28 Kg to 31.82 ± 6.94 Kg and female in range of 2.44 ± 0.48 Kg to 22.65 ± 5.52 Kg between first month of age to adult age. The various reproductive performances of Champaran goats such as age at first mating in males (days), age at first oestrus (days), oestrous cycle duration (days), age at first mating in females (days), age at first kidding (days), kidding interval (days), service period (days), litter size and lifetime number of kidding were estimated to 328.91 ± 15.24, 242.44 ± 13.29, 1.99 ± 0.04, 341.40 ± 14.62, 390.75 ± 12.35, 296.27 ± 21.67, 73.57 ± 12.75, 2.78 ± 0.09 and 6.5 ± 0.86, respectively.

The least-squares mean of biometric traits (cm) of goats of West Champaran region such as body weight (BW), body length (BL), withers height (HW), chest girth (CG), paunch girth (PG), face length (FL), face width (FW), ear length (EL), horn length (HL), tail length (TL), leg length (LL), cannon bone circumference (CC), chest width (CW) and chest depth (CGF) were estimated to be 22.4 ± 0.33 Kg, 50.06 ± 0.27 cm, 53.72 ± 0.27 cm, 61.55 ± 0.31 cm, 70.3 ± 0.38 cm, 18.59 ± 0.17 cm, 11.33 ± 0.07 cm, 14.46 ± 0.07 cm, 7.59 ± 0.17 cm, 13.87 ± 0.10 cm, 32.49 ± 0.17 cm, 7.35 ± 0.21 cm, 15.95 ± 0.13 cm and 27.66 ± 0.18 cm, respectively. The effect of non-genetic factors sex and location on different biometric and body indices traits of body dimensions were found non-significant. The correlation between biometric traits were found in range of 0.75 (BW and CG) to 0.05 (CC and EL), respectively. Barlett test of sphericity and KMO measure of sampling adequacy (MSA) was found significant and revealed the proportion of the variance in different biometric and body indices traits caused by the underlying components. The R^2 statistics of different regression models for biometric traits and un-rotated and rotated components principal components scores varied between 0.58 to 0.14 and 0.73 to .003, respectively. The extracted principal components score of biometric traits and body indices

can be used in selection programme of animals instead of large numbers of traits. The grouped traits in PC1 such as FL, WH, CW, FW, CD, BL, FH, BW and CG of biometric traits may be used in selection programme of animals instead of large numbers of traits. Prediction of adult body weight using principal components score as predictor was found to have more accuracy than original biometric traits as estimators.

Keywords: Bihar, Goat, Non-orthogonal, Orthogonal, Principal Component Analysis, Rotation, West Champaran

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OP1-07

Fisheries and Aquaculture in Northeast India: Status, Issues, and Sustainable Development Opportunities

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Northeast India is a landlocked region surrounded by the Himalayan Mountain range in the north, the plain of Bangladesh to the south, the Burmese hills in the east, and the hills and the mountain in the west. The region features a different array of topography ranging from the plains of Brahmaputra and Barak to the Imphal valleys and highlands. This unique geography has fostered a rich aquatic biodiversity of the region, making it a global hotspot for freshwater fish diversity and a repository of extensive fisheries resources, including rivers, coldwater streams, floodplain wetlands, reservoirs, lakes, ponds, paddy fields, and mini-barrages. The Northeastern region of India is home to over 45% of the freshwater fish species reported in the country. About 130 new species were reported from the Northeastern region in the last 14 years. Few exotic fish species have been reported from the water bodies of the region bodies, raising alarms due to their significant ecological threat. Despite these vast fisheries resources, the region remains deficient in fish production, contributing merely 4.5% to the national inland fish production and the pond productivity at about half of the national productivity. About 97% of the populations in the region are fish eaters and a per capita fish consumption of about 10.9 kg. The escalating demand for quality, fresh, and locally sourced fish and fishery products driven by population growth, rising incomes, urbanization, dietary shifts, and health awareness underscores the immense potential for fisheries and aquaculture development. The region can meet its requirements and address the production gap by harnessing these resources sustainably and adopting scientific management and new culture technologies.

Keywords: Fishes, Availability, Status, Production

OP1-08

A Review of Aquatic Fish Biodiversity in Northeast India: Current Status, Conservation Challenges and Future Strategies

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Northeast India, comprising the eight states of Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram, Nagaland, Sikkim, and Tripura, is celebrated as one of the world's most significant biodiversity hotspots. This comprehensive review examines the current status of fish biodiversity in the region, highlighting key species, ecological roles, and conservation challenges. A systematic literature review was conducted, synthesizing data from more than 100 sources spanning 2000 to 2024. The research reveals that Northeast India harbors 162 to 422 fish species, with several endemic to the region. Notably, Assam hosts the highest diversity with 216 species, followed by Arunachal Pradesh (167 species) and Meghalaya (165 species). The Cyprinidae family emerges as the most diverse, with 154 species. Approximately 33% of the evaluated species are endemic to the region, with 33.85% primarily used as food fish and 28.44% having ornamental value. However, anthropogenic activities, climate change, and invasive species pose significant threats to this rich biodiversity. For instance, the invasion of African catfish (*Clarias gariepinus*) and the introduction of common carp have led to the near eradication of native and iconic mahseer populations in some water bodies. Conservation efforts, including habitat protection, captive breeding programs, and community-based management, show promise but face implementation challenges. The study concludes with recommendations for sustainable management and future research directions, emphasizing the need for comprehensive species inventories, ecological studies, impact assessments, and socio-economic research. This review provides a holistic view of the region's ichthyofaunal diversity and the efforts being made to preserve it, contributing to both regional and global biodiversity conservation efforts.

Keywords: Fish diversity, Northeast India, Conservation, Aquatic ecosystems, Biodiversity hotspot, SWOT analysis

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OP1-09

Ecological Study of Water Quality and Fish Species in Kyrdemkulai Reservoir, Meghalaya

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The Kyrdemkulai reservoir is a Stage III reservoir of the Umiam-Umtru hydroelectric project in Ri-Bhoi District, Meghalaya, commissioned in 1979 (Sugunan, 1995). A study conducted from January 2018 to December 2020 examined the reservoir's physicochemical characteristics and fish diversity. Water levels fluctuate between 675.0 and 683.4 m above mean sea level (MSL), varying between the post-monsoon and monsoon seasons. The average water temperature ranges from 17.0 to 26.9 ºC. Key water quality parameters include a mean pH of 7.6, dissolved oxygen of 7.9 ppm, total hardness of 19.8 ppm, free carbon dioxide at 1.7 ppm, total dissolved solids at 29.9 ppm, transparency at 228.76 cm, electrical conductivity of 59.8 µS/cm, chloride at 3.3 ppm, nitrite at 0.32 ppm, and phosphate at 0.07 ppm. The study recorded 25 fish species from 20 genera, 19 families, and 7 orders. Cypriniformes dominated the catch composition, contributing 48%, followed by Perciformes (20%), with Osteoglossiformes and Synbranchiformes contributing the least at 4%. The common carp was the most abundant species, comprising 75% of the catch. According to the IUCN, three species are classified as endangered (EN), three as vulnerable (VU), and two as near-threatened (NT). Gill nets are the most widely used fishing gear, along with hooks, lines, and locally made traps. Immediate conservation efforts are necessary to protect endangered species such as *Tor putitora* and *Pillaia indica*.

Keywords: Fishes, Genetic diversity, Water quality

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OP1-10

Fruit Fly (Diptera: Tephritidae) Fauna of Northeast India: A Profile

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Fruit flies belonging to the family Tephritidae in the Order Diptera is one of the most speciose taxon with 5000 described species from the world and nearly 300 species from India. Surveys conducted during the past decade in Assam, Arunachal Pradesh, Sikkim, Meghalaya, Tripura, Nagaland, Mizoram, Manipur to document the fauna of fruit flies revealed the presence of 68 species in 29 genera and five subfamilies which includes several undescribed species too. Collection methods employed were sweep netting, parapheromone (methyl eugenol, cue lure and Zingerone) traps, rearing of adults from infested host plant/part and luring flies to chopped tender shoots of bamboo (for the collection of bamboo-shoot fruit flies). Major genera encountered during the study are *Bactrocera* Macquart, *Zeugodacus* Hendel, *Dacus* Fabricius in tribe Dacini, which are predominantly frugivorous; *Acroceratitis* Hendel, *Acrotaeniostola* Hendel of tribe Gastrozonini infesting various species of bamboos; *Campiglossa* Rondani, *Actinoptera* Rondani, *Platensina* Enderlein in subfamily Tephritinae mainly associated with flowers of weed plants belonging to Asteraceae, Acanthaceae, Goodeniaceae etc; saprophytic *Ptilona* Wulp, *Rioxoptilona* Hendel, *Felderimyia* Hendel in Phytalmiinae often encountered in bamboo ecosystem; *Callistomyia* Bezzi, *Dimeringophrys* Enderlein, *Euphranta* Loew and *Acidoxantha* Bezzi of subfamily Trypetinae. A new genus *Dacimita* David & Hancock from Meghalaya and eight new species were described from northeast India during the course of study viz., *Campiglossa ialong* David, Salini and Hancock, *Platensina rabbani* David & Hancock, *Dacus nagarathnae* Abhishek & David, *Z. nasivittatus* David & Abhishek, *Z. umiam* David & Kennedy from Meghalaya, *Campiglossa shaktii* from Sikkim, *Zeugodacus momordicae* David & Ajaykumara infesting male flower buds of spiny gourd in Arunachal Pradesh, *Rhabdochaeta nigroapicalis* David, Hancock and Sachin infesting flower buds of *Ageratina* sp. from Assam. New records include *Ortalotrypeta isshikii*

(Matsumura), *Acroceratitis incompleta* Hardy, *Bactrocera abbreviata* Hardy, *Dacus vijaysegarani* Drew & Hancock, *Elaphromyia yunnanensis* Wang. Major pestiferous species collected include *Bactrocera minax* (Enderlein) infesting khasi mandarins, *Bactrocera dorsalis* (Hendel) on various fruit crops, *Zeugodacus cucurbitae* (Coquillett), *Zeugodacus tau* (Walker), *Zeugodacus scutellaris* (Bezzi) on cucurbitaceous vegetables. Aforementioned data unveils the enormous diversity of northeast India, which is a clear indication that several taxa await discovery from northeast India, one of major biodiversity hotspots in the world.

Keywords: Fruit fly, Diversity, Northeast India

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OP1-11

Stink Bugs (Hemiptera: Heteroptera: Pentatomidae) Diversity of Meghalaya: What We Know and What We Need To Understand

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Northeastern states, a part of Indo-Burma biodiversity hot spots, are rich in diversity of stink bugs (Hemiptera: Heteroptera: Pentatomidae), which accounts for more than one-third of the known stinkbug diversity for the country. Among these states, Meghalaya was recorded with 67 species belonging to 51 genera in four subfamilies of Pentatomidae by past researchers (Distant, 1902; Paiva, 1919; Mathew, 1986; Chakraborty and Ghosh, 1999). Several stink bugs affect economically important crop plants, but a few are predatory and are important as biological control agents. They play a major role in the food chain, serve as food sources for various predators or even for human beings. In spite of the economic importance and state's rich diversity, a recent holistic treatment of the stink bug fauna for the region is lacking. Therefore, an intensive study of this fauna, from various northeastern states (Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram, Nagaland, Tripura and Sikkim) was undertaken during the period 2020-2023. This revealed the presence of potential species belonging to several genera, *Axiagastus*, *Cahara*, *Cappaea*, *Dalpada*, *Erthesina*, *Halyomorpha*, *Placosternum* and *Tolumnia*. Besides, around five genera and five species are recorded for the first time from Meghalaya, along with a new species for *Dunnius*. Therefore, a total number of 72 species belonging to 56 genera in four subfamilies were recorded from Meghalaya. It comprises more than one fourth of the total stinkbug fauna recorded from the north eastern states. As most of the species of Pentatomidae were documented only based on external colouration or at most with a few morphological characters, by the various past researchers, the present illustration and documentation of post abdominal structures of several stink bug species are new to science. Most of the identified species were confirmed by the examination of types deposited at NHMUK. Hence the present collection, characterization and documentation of stink bug fauna from Meghalaya help us to take stock of the existing biodiversity apart from harnessing its benefits for the management of pestiferous species or for their utilization either as biological control agents or as edible species.

Keywords: Sting bug, Diversity, Meghalaya, Northeast India

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OP1-12

Genetic Characterization of *Hermetia illucens* (Black Soldier Fly) and Its Potential Use as An Alternative Protein Source in Poultry Farming for the North East Hill Region.

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Hermetia illucens, commonly known as the black soldier fly (BSF), is increasingly gaining attention for its use as an alternative protein source in poultry farming, in different parts of world specially in Asian and European countries, because of its rich nutritional profile and environmentally sustainable production process. With the above context, to explore India, this experiment was carried out in the College of Veterinary Science, Khanapara, Guwahati, AAU, to study molecular identification of Assam origin, wild black soldier fly and proximate analysis of black soldier fly larvae meal (BSFLM), to optimize the potential use, as an alternative protein source in poultry farming for northeast hilly region. The genetic sequencing result and phylogenetic analysis's of BSF showed 99-100% similarity with *Hermetia illucens* from Gene Bank and current strain is closely related with Austro-Asiatic strain. The proximate composition of BSFLM was 9.88%, 40.34%, 30.11%, 8.25% and 7.89% for moisture, crude protein, crude fat, crude fibre and total ash respectively on dry matter basis. The crude protein content is under comparable range, with soyabean meal (SBM) 46.3% and ground nut cake (GNC) 45%, making them a viable substitute for conventional protein sources. In reference to environmentally sustainable point of view, BSF farming requires significantly less land and water compared to traditional production of protein sources (SBM & GNC). Unlike specific inputs required for insect farming as a protein source, BSF larvae can be raised on any organic Municipal, Restaurant and kitchen waste, thereby helping in organic waste disposal, reducing environmental pollution and turning organic waste into valuable feed ingredients. The climate of the North East hill region is well-suited for BSF farming, since they thrive best in warm (25–35°C) and humid environments (60-70%), making them ideal for rearing in Assam, Tripura and different parts of Arunachal, Nagaland, Meghalaya, Mizoram and Manipur. Therefore, BSFLM can be incorporated as alternative protein source, into poultry farming practices in the North East hill region to reduce reliance on imported feed ingredients, reduce feed costs, and promote local circular economies with less carbon footprint.

Keywords: Hermetia, Illucence, BSFLM, Genetic, Sequence, Assam, Origin, Alternative, protein

OP1-13

Diversity of Syrphid Flies in Mid-Altitude Hills of Meghalaya

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Syrphid flies commonly called hoverflies; flower flies; drone flies or simply syrphids are dipteran insects that belong to the family Syrphidae and insect order Diptera. As their common name suggests, the adult flies are often seen hovering or nectaring at flowers; nectar and pollens of flowers are fed upon by the adults, while the larvae (maggots) eat a wide range of foods including insects like aphids, thrips and other soft-bodied insects. The larvae are thus potential biocontrol agents while the adults are considered as pollinators second only to wild bees. The diversity of Syrphid flies visiting various flowering plants and trees including wild plants have been collected and documented from Ri-Bhoi region of Meghalaya. The adult syrphid flies were collected using sweep nets by visual observations. The adults collected were identified through Integrative taxonomy using both conventional and modern taxonomy methods. Relative abundance, species richness and diversity index were also worked out. About 14 species of syrphid flies belonging to 9 genera have been identified from this region. The genera include *Episyrphus, Eristalinu*s, *Eristalix, Eupodes*, *Melanostoma, Scaeva, Simosyrphus*, *Sphaerophoria and Syrphus.*

Keywords: Abundance, Diversity, Species, Syrphid flies, Taxonomy

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OP1-14

Taxonomic Insights: A Study of Meghalaya's Bee Diversity

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Order Hymenoptera is a species rich diverse group of insects in terms of structure, size, numbers, habits and food preferences. The Superfamily Apoidea encompasses a diverse array of bees, ranging from solitary ground-dwellers to highly social species like honeybees. They possess distinct morphological features, including specialized mouthparts, wing venation, legs and branched body hairs for pollen and nectar collection. Explorations were conducted during 2019-2023 and this study evaluates the bee diversity in Meghalaya, India, where bees were investigated and observed across diverse ecosystems in different districts of Meghalaya. Specimens were collected using sweep nets, yellow pan traps and Malaise traps, and they were brought to the laboratory, processed, pinned and mounted for detailed study. A total of 42 bee species were collected and studied falling under 5 families viz., Apidae, Megachilidae, Colletidae, Andrenidae and Halictidae, all together comprising 7 subfamilies, 12 tribes, 19 genera and 25 subgenera. Diagnostic keys for species identification of all the bee species were compiled, establishing 9 new country records for India and 24 for Meghalaya. An updated checklist comprising of 108 species that includes valid names, synonyms and distribution

records has been compiled from the present study as well as from various available literature. This research study has significantly expanded the knowledge of bee fauna in Meghalaya, increasing the documented species count on record from 84 to 108. The morphological characteristics of these species are illustrated with 44 coloured plates featuring around 370 photographs. Furthermore, the study recorded host associations of bees with 76 plant species. These findings greatly enhance the understanding of bee diversity in Meghalaya and establish a solid foundation for future conservation initiatives in the region. Such efforts are essential for the preservation of both domesticated and wild bee-pollinated populations, which are crucial for maintaining the genetic diversity needed to enhance cultivated strains.

Keywords: Hymenoptera, Bee, Taxonomy, Diversity, Meghalaya

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Theme-II:

Innovations and Modern Tools for *Ex Situ* Conservation and Utilization

(Biotechnology tools for trait discovery, *ex situ* conservation, geo-informatics, digital sequence information, information and communication technology)

OP2-01

Developing Seedless Bhimkol: A Strategy to Combat Hidden Hunger through Advanced Breeding Techniques

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Banana, with its BB genome, is a highly nutritious, seeded variety native to Assam and parts of Northeast India. Valued for its resistance to various biotic and abiotic stresses, it is utilized in breeding programs. However, despite its many advantages, the Bhimkol banana has not been widely cultivated due to its seeded nature, which makes pulp extraction for baby food production challenging. To expand its cultivation across India and combat hidden hunger, it is essential to develop a seedless variety of Bhimkol. This can be achieved by creating a triploid Bhimkol through breeding strategies that involve crossing tetraploid and diploid plants. The first step in the triploid breeding program is developing Bhimkol tetraploid, which can be achieved by chromosome doubling. An embryogenic cell suspension culture has been developed from immature male buds of Bhimkol. The concentration of the anti-mitotic agent was standardized based on the LD_{50} value, and plantlets were obtained from treated cells. The ploidy level of these plants was confirmed using a flow cytometer, and the tetraploid plants were planted in the field. Variations were observed in their morphological traits, and these tetraploid plants will be used as female or male parents in hybridization with diploid Bhimkol to develop stress-resistant, seedless triploid Bhimkol.

Keywords: Banana, Polyploidy, Seedless, Crop improvement

OP2-02

Genome Wide Association Study (GWAS) to Identify Novel Genomic Region for Fusarium Head Blight (FHB) Resistance in Indian Durum Wheat (*Triticum durum* L.) Germplasm

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Fusarium Head Blight (FHB), primarily caused by *Fusarium graminearum* and related species, is a severe fungal disease affecting wheat globally. It can lead to substantial yield losses, sometimes exceeding 50% in severe outbreaks. FHB also contaminates grains with mycotoxins, particularly trichothecenes like deoxynivalenol (DON), compromising grain quality and posing health risks to humans and animals. This disease affects both durum wheat and bread wheat, presenting a significant challenge for breeders worldwide. Climate change has exacerbated FHB's impact on durum wheat in Central and Peninsular India. The complex nature of the pathogen makes disease control difficult; highlighting the need to identify resistance genes or QTLs for developing resilient varieties. Despite some progress, integrating resistance QTLs from non-adapted sources into commercial durum cultivars has faced obstacles such as linkage drag, and resistance suppression in durum backgrounds. Consequently, leveraging existing FHB resistance within durum cultivars has become a preferred strategy for rapidly introducing improved resistant varieties. To address this, the evaluation of 285 diverse durum wheat accessions, including Indian wheat landraces for resistance to FHB was conducted under controlled conditions at New Delhi, and natural field conditions at Wellington (Tamil Nadu). Simultaneously, genotyping using 90K SNP assay was performed on durum wheat accessions. Association analysis using three multi-locus GWAS models identified 17 significant SNPs, mainly distributed across chromosomes, 2A, 2B, 3A, 5B, 7A, and 7B. Four SNPs were consistently detected across most models and environments. Ontology analysis of the associated genomic regions identified potential candidate genes and discovered some highly favorable alleles. Insights gained from this study will be valuable for enhancing FHB resistance in wheat cultivars through marker-assisted selection.

Keywords: Wheat, Genomics, Association analysis, Fusarium Head Blight

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OP2-03

Diverse Entomopathogenic Fungi in Manipur Soil: Isolation, Characterization, and Biodiversity Assessment

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Entomopathogenic fungi (EPF) hold great promise for the biological control of insect pests. Effective isolation of EPF can be achieved by sampling soil, where these fungi naturally thrive. In this study, soil samples were collected from ten districts across Manipur, totalling 100 samples from both cultivated and forested areas. The fungi were isolated using a soil baiting method with Galleria mellonella larvae. Out of the 100 samples, 73 fungal isolates were obtained, 54 of which were identified as entomopathogenic fungi. The most frequently isolated genus was *Aspergillus*, followed by *Beauveria, Clonostachys, Talaromyces, Trichoderma, Fusarium, Candida*, and *Meyerozyma*. Twenty-two of these isolates underwent both morphological and molecular characterization. All isolates exhibited a scattered growth pattern. Specifically, all *Beauveria bassiana* isolates were white on the front side and either white or pale yellow on the reverse side. *Clonostachys rosea* initially appeared white on the front but turned dirty green upon sporulation, remaining white on the reverse. *Talaromyces purpureogenus* was white on both sides, while *Talaromyces muroii* had a pinkish-yellow front and a yellow reverse. *Trichoderma* species were white on the front and pale to light yellow on the reverse. Fusarium species had white or creamy-white fronts and creamy or pale white reverses. *Aspergillus flavus* appeared creamy on the front and brown on the reverse, while *Aspergillus tamarii* showed a white front and brown reverse. *Aspergillus oryzae* was white on both sides. Diversity analysis revealed variations in fungal types and proportions across different regions of Manipur. The average isolation rate for fungi was 73%, with entomopathogenic fungi representing 54%. Senapati District had the highest isolation rates, with 130% for fungi and 110% for entomopathogenic fungi, while Churachandpur and Kakching had 100%, 90%, and 70% for fungi and entomopathogenic fungi, respectively. The Shannon-Weiner Index (SWI) indicated that Ukhrul had the highest fungal diversity with an SWI of 1.79, while Senapati, Churachandpur, Imphal West, and Kakching had SWIs of 1.64, 1.58, 1.33, and 1.27, respectively. Kakching also had the highest Simpson Index value of 0.19, reflecting good fungal diversity, whereas Kamjong, Ukhrul, and Chandel had a Simpson Index of 0, indicating lower diversity. Species richness was highest in Ukhrul, followed by Senapati, with Imphal East having the lowest. Pathogenicity tests confirmed the effectiveness of the isolated entomopathogenic fungi, with 14 Beauveria bassiana isolates and two Talaromyces purpureogenus isolates achieving 100% mortality in test insects. These findings suggest the potential of these fungi for large-scale production and use in pest management.

Keywords: Entomopathogenic fungi, *Beauveria, Trichoderma*

OP2-04

Collection and *Ex Situ* Conservation of the Diversity in *Garcinia* From Upper Assam

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Garcinia L., the largest genus of the family Clusiaceae, is a group of evergreen trees or shrubs with immense economic potential as the source of edible fruit, spice, medicine, natural dye, natural fat and timber. The genus comprises more than 260 species distributed throughout the world's tropics. Out of the 40 indigenous taxa occurring in India, North-East India hosts 15 species and 3 varieties, including 5 endemic taxa. Despite its tremendous potential, germplasm collection, *ex situ* conservation and utilization are inadequate owing to various challenges such as niche specificity, polygamous nature, and taxonomic ambiguity. The main challenge faced by the researchers working on *Garcinia* is the high taxonomic ambiguity. The taxonomic revisions of Indian Garcinia, specifically from Andaman and Nicobar Islands and North East India, are mostly based on literature and herbarium specimens and lack in-depth studies on live samples, resulting in repeated mistakes in the previous works. Lack of access to the species located in remote areas and difficulty in the seasonal collection of flowers and fruits are the major constraints for study of the live specimen. An *ex-situ* conservatory representing all indigenous species is the need of the hour to address these challenges. From this perspective, an exploration was conducted in Dibrugarh, Tinsukia and North Lakhimpur districts of Assam in June 2022 and collected 26 accessions of *Garcinia,* comprising 8 species: *G. acuminata*, *G. assamica, G. dulcis, G. lanceifolia, G. pedunculata, G. sibeswarii*, *G. xanthochymus* and an unidentified species. The accessions were established in the Field Gene Bank at the ICAR-IISR Experimental Farm, Peruvannamuzhi, Kozhikode, Kerala. The accessions collected from the forests and households were propagated and established through seeds, seedlings, and scions. The interspecific grafting technique was developed for conservation of five species collected during the exploration on the rootstocks of commonly occurring species of *Garcinia* in South India. *G. acuminata, G. assamica,* and *G. lanceifolia* were found to be compatible with the rootstocks of *G. gummi-gutta* and *G. indica,* whereas *G. sibeswarii* could be successfully established on *G. mangostana* and *G. celebica. G. xanthochymus* was found to be a suitable rootstock for *G. dulcis*. Above 85% survival was recorded in all the above combinations. Interspecific grafting was found to be an effective tool for conservation as it facilitates germplasm collection irrespective of the season, fast flowering and fruiting, and helps to establish male and female forms within a short period. Among the collected species, *G. acuminata*, *G. assamica, G. dulcis, G. lanceifolia, G. pedunculata* and G. *xanthochymus* are utilised as spices and medicines by the local people. G. sibeswari*i,* a species that is morphologically allied to *G. mangostana,* is found to be a potential rootstock for grafting mangosteen.

Keywords: *Garcinia*, Species, Diversity, Northeastern India

OP2-05

Comparative Metagenome Analysis of Rhizoshperic Soil Associated with Different Banana (*Musa* spp.) Genome Groups

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Northeast region (NER) of India harbours a high diversity of banana (*Musa* spp.) both in wild as well in the cultivated stands. Being located in the South East Asian region where banana originated, several unique and novel genetic resources are abundantly found such as the bananas belonging to different genome groups such as AA, BB, AB, AAA, AAB and ABB. It is also known that plant roots influence the soil microbiota via physical interaction, secretion, and plant immunity. Thus, the present study reports the comparative rhizospheric soil microbiome composition at various taxa levels associated with the different banana genome groups. Soil metagenome DNA from each sample were end-repaired separately and native barcodes were attached to each DNA sample. Metagenome sequencing was performed on MinION Mk1b (Oxford Nanopore Technologies, Oxford, UK) using SpotON flow cell on MinKNOW 1.1.21. The standard workflow for the microbiome analysis was carried out using the metagenome analyses pipeline and the composition of the microbial communities was studied generating diverse communities of microbes and their abundance associating with the different banana genome groups.

Keywords: Banana, Rhizosphere, Microbime, Metagenomics

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OP2-06

Near Infrared Reflectance Spectroscopy Coupled Artificial Intelligence-based Approaches for Predicting Protein Content in Potential Crops of NEH Region of India: A Rapid Mining Tool for Screening Large Germplasm

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The rich biodiversity of the North Eastern Hill (NEH) region of India offers a plethora of potential underutilized crops with significant nutritional potential, including Perilla (*Perilla frutescens* L.), Rice bean (*Vigna umbellata* L.), and Lablab bean (*Lablab purpureus* L.). Accurately predicting the protein content in these crops is crucial for optimizing their use in food and feed, thereby supporting sustainable agricultural practices. Traditional methods for protein content determination are labor-intensive and costly, necessitating the development of rapid, precise, and non-destructive alternatives. Our research area explores the application of Near-Infrared Reflectance Spectroscopy (NIRS) coupled with advanced Artificial Intelligence (AI) models to predict protein content in the aforementioned crops. For Perilla seed meal, a hybrid 1D CNN-LSTM-Inception derivative 1 model achieved superior predictive performance with an excellent Residual Prediction Deviation (RPD) of 8.0 and RSQexternal of 0.98, outperforming both the Modified Partial Least Squares (MPLS) and CNN models. In Ricebean, a 1D CNN model integrated with Competitive Adaptive Reweighted Sampling (CARS) for wavelength selection showed an 18% improvement in RPD compared to MPLS, achieving an RPD of 2.28 and an RSQ of 0.84. Meanwhile, in Lablab bean, a deep learning-based model exhibited exceptional predictive accuracy, with an RPD of 13.92 and an RSQ of 0.977, surpassing CNN and MPLS models by 22.86% and 32.21% in RPD, respectively. These results highlight the efficacy of NIRS coupled with advanced AI models as a rapid screening tool for large germplasm collections, thus enabling early-phase breeding and quality assessment of potential crops from the NEH region of India. The integration of these models can significantly accelerate the identification and selection of nutritionally superior genotypes, thereby supporting the region’s food and nutrition security initiatives.

Keywords: Potential crops, Lablab bean, Protein, Artificial intelligence

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OP2-07

Genetic Resources and Variability of Buckwheat for Physio-morphological and Phosphorus Solubilisation in Acid soils of Meghalaya

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To increase crop productivity under low pH soil induced phosphorus (P) inadequacies in challenging mountain agro-ecologies of Eastern Himalayan Region (EHR), identification and diversification of cropping systems having higher adaptability would be paramount. Field evaluation of 192 buckwheat genotypes showed significant genetic variability for various morpho-physiological and yield traits like total dry matter (TDM), R/S ratio, root length and number of leaves with a range of 0.19-5.22g/plant, 0.04-0.34, 5.33-23.3cm/plant and 6.0-43.3/plant respectively. Plant height, crop duration and seed yield varied significantly with range of 15.0-85.0cm, 85-113days, 26.9-2066kg/ha. Around 65.8% genotypes have leaf number between 12.0-24.0/plant and ≈79.7% genotypes had SPAD chlorophyll meter reading (SCMR) between 29.0-37.9. More number of genotypes (57.3%) shown duration between 95-104days and 36.4% genotypes have seed yield of 325.0 to 625.0 kg/ha. Higher chlorophyll exhibited by IC26592 (40.7SCMR) and IC107961 (40.0SCMR) and plant height was highest in IC13143 (60.3cm) and IC26592 (63.3cm). Seed yield was positively correlated to leaf number and TDM (r^2 value of 0.186 and 0.296) and the positive correlation between plant height and TDM was 0.145. Principal Component Analysis (PCA) employed for data dimension reduction explained cumulatively up to 53.51% of the total variance, thereby extracting three dominant PCs

with eigenvalues equal or greater than unity viz. PC1 (23.81%), PC2 (17.88%) and PC3 (11.82%), respectively. High-yielding buckwheat types (HYBT) like IC26592 and IC26589 have yielded 58.0% and 44.7% higher than local check (Himapriya) and IC26585, IC26589, IC26592 have yielded 4.42 times higher than low yielding buckwheat types (LYBT). The total root length, root surface area and root volume of HYBT were 32.0, 14.7 and 123.0% higher than LYBT. HYBT have 65.7% higher P solubilization capacity (37.32µg/plant) compared to LYBT (22.53µg/plant). Genotypes like IC17371, IC26586, IC37269, IC 37283, 37285, 107807, 107961 with rhizopsheric P solubilisation of 425.0, 403.14, 428.62, 429.72, 439.38, 435.89, 436.69kg available P/ha had higher leaf P of 0.8%, 0.95%, 0.85%, 0.83%, 0.89%, 0.86%, 0.89%. Genotypes like IC19191, IC26591, IC37299, IC26593, IC26592 showing lesser available P of 267.9, 322.9, 286.04, 324.6, 330.5kg/ha had higher leaf P of 0.83%, 0.97%, 1.19%, 1.37%, and 0.82% respectively. Available P content in rhizopsheric soil of MYBT (IC107961) and LYBT (IC37283) was 436.7kg/ha and 429.7kg/ha compared to HYBT (IC26592) with 322.8kg/ha. Root malate and citrate content of HYBT was 2.576µM/gFW and 0.781µM/gFW. Identified HYBT useful for novel crop improvement for increasing the buckwheat cultivation and enrichment of P under low pH soils of hill ecosystems of EHR

Keywords: Acid soils, P Solubilisation, Root morphology, Root exudation, Stress, physiological traits

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OP2-08

SRAP and TRAP Molecular Markers Based Fingerprinting Decodes High Genetic Diversity in Rice Germplasm of Northeast India

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The northeast region of India harbours the richest genetic diversity reservoir for agricultural crops, being a part of the Indo-Burma biodiversity hotspot. The region is not only a center of origin of rice but also a critical area where conservation of genetic diversity in crops are required. The present study was carried out in a collection of 197 landrace/germplasm. A better understanding of its extent of genetic variability is essential for translating these genetic diversity into breeding program. Our analyses, using phenotypic, genotypic, and combined genotypic/phenotypic distances, revealed an ample genetic variation in the collections and has a potential that can be explored for rice improvement in the region. Multivariate analysis for phenotypic variability indicated that 11

out of 13 phenotypic traits assessed were useful in discriminating the collections. Cluster analysis based on phenotypic data distinguished three significant clusters, while a corresponding analysis with SRAP and TRAP markers indicated four groups. Also the combined analysis for the phenotypic and genotypic data provided 4 distinct clusters providing valuable information about the diversity and variation in economically important agronomic traits. Our study partitioned the collections into distinct heterotic groups thereby, making it possible for parental selection and hybridization to maximize genetic diversity in the rice breeding program. Moreover, two combinations of SRAP, SRAP5 (ME01 & EM10) and SRAP6 (ME01 & EM07) with four TRAP combinations, TRAP1 (Auxr1 & FT14), TRAP2 (Auxr1 & T03), TRAP3 (Auxr1 & FT14) and TRAP5 (Auxr1 & T13) with highly informative PIC score greater than 0.70 could effectively discriminate the current collections/genotypes for a robust fingerprint system.

Keywords: Rice, DNA markers, Genetic diversity, Landraces

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OP2-09

Genetic Diversity and Trait-Marker Associations in Rice Bean (*Vigna umbellata*) For Yield and Yield Related Traits

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A panel of 94 ricebean (*Vigna umbellata* (Thunb.) Ohwi and Ohashi) genotypes was analyzed to assess molecular diversity and trait-marker associations. To evaluate the genetic diversity, 115 simple sequence repeats (SSRs) were used, of which 69 markers were polymorphic and capable of distinguishing between individuals. The average number of effective alleles per polymorphic marker was 1.48 and expected heterozygosity (He) ranged from 0.07 (cG27522c1) to 0.55 (Cg18775c0), with a mean of 0.3. The Shannon's information index (I), which measures genetic diversity, showed maximum diversity for Cg18775c0 (0.89) and minimum diversity for cG27522c1 (0.17), with an average diversity of 0.46. The fixation index, that indicates population differentiation due to genetic structure, ranged from 0.7 to 1, with a mean of 0.54. Marker-trait associations for seed yield analysed using the GLM model in TASSLE5 software, showed significant correlations at $p<0.001$ and $p<0.05$ with markers cG26585c1, CEDG118, c23448.graph_c0, c26585.graph_c1, cG25883c0, cG21640c0, cG30385c0, c18545.graph_c1, VUGA25, cp02271, and CEDG002. These markers had r^2 values between 4% and 12%, with marker CEDG118 showing the highest contribution (r^2 = 12%) towards total phenotypic variations (PVs). These markers hold potential for marker-assisted breeding programs to improve rice bean cultivation.

Keywords: Rice bean, Molecular marker, Yield related traits, Association analysis

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OP2-10

Characterization of Banana Cultivars from North Eastern India for Higher and Individual Functional Bioactives of Nutraceutical and Immunomodulatory Uses

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Flavonoids, fructans and anthocyanins are unique phytochemicals with high antioxidative and immunomodulatory activities preventing an array of diseases. Banana fruit peel and pulp and flower bracts are rich sources of these functional bioactives respectively. Here, 21 bananas grown in North Eastern states (Assam and Meghalaya) of the country were characterised for total and individual flavonoids and fructans in fruits and anthocyanins in flower bracts. Individual bioactives were estimated by using RP-High Performance Liquid Chromatography and a great variability were observed in the bananas evaluated. Generally, the 'B' (*Musa balbisiana*) genome cultivars possessed higher quantity of flavonoids and fructans than 'A' (*Musa acuminata*) genome bananas. Fruit peel of Attikol (BB), Bhimkol (BB), Beejikela (BB), *Musa balbisiana* (BB) and Katchkela (ABB) possessed more than 350 mg of total flavonoids and pulp of *Musa balbisiana* contained highest quantity of flavonoids with 270 mg. Three main flavonoids found are epigallocatechin, epicatechin and catechin with predominance of first one, particularly in 'B' genome bananas. Antioxidant activities of peel and pulp extracts of North Eastern banana cultivars measured by TEAC and ORAC assays showed Attikol, Bhimkol, *M. balbisiana* and Beejikela exhibiting greatest antioxidant potential in the range of 80-120 µmol TE/100 g. Epigallocatechin as individual flavonoid metabolite exhibited similar level of antioxidant activity. The fruit pulp contained relatively higher quantity of fructans than peel. In banana varieties of NER, the fructans content ranged between 35 and 558 mg/100 g in pulp with Attikol (BB), Bhimkol (BB), Beejikela (BB), *Musa balbisiana* (BB) containing highest quantity. Fructans contents in peel were in the range of 8-179 mg/100 g with again Attikol containing highest fructans content. The predominant fructan component detected in 'B' genome banana fruit pulp is inulin-type fructan with highest immunomodulatory activity. Total anthocyanins content in flower bracts of NE states ranged between 15 and 65 mg/ 100 g and the main anthocyanins identified and identified were cyanidin 3-*O*-rutinoside (Cy-3-rut) and cyaniding 3-*O*-rhamnoside (Cy-3-rham) among six major anthocyanidins with cyanidin constituting more than 90% in 'B' genome bananas. The antioxidant activities measured by TEAC and ORAC assays were around 600 µmol TE/100 g FW 'B' genome bananas. *In vitro* assays showed anthocyanins from Bhimkol (BB) effectively inhibited colon and cervical cancer cells (HT-29 and HeLa). The research findings showed that fruits and flower of 'B' genome bananas like with Attikol (BB), Bhimkol (BB), Beejikela (BB) and *Musa balbisiana* (BB) are potential sources of nutraceuticals and immunomodulatory molecules.

Keywords: Banana, Genotypes, Antioxidants, Secondary metabolites

OP2-11

Unraveling the Selection Criteria for *Capsicum chinense* with High Capsaicin Content

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Capsicum chinense Jacq. (ghost pepper), commonly known as ghost chilly is one of the hottest chilly in the world. Owing to its high capsaicin content the chilly finds immense demand in the food and beverage, pharmaceutical and allied industries due to which the economically important traits are of paramount significance. The present study was therefore aimed at deciphering traits which induce the high capsaicin content. A total of 153 genotypes with more than 0.8% capsaicin content (on dry weight basis) collected from across seven states of northeast India were subjected to variability, correlation and heritability studies. The phenotypic and genotypic coefficient of variation was found to be highest for the number of fruits per plant followed by capsaicin content and fruit yield per plant. The maximum direct contribution towards fruit yield per plant trait was attributed to a number of fruits per plant and the trait fruit yield per plant towards capsaicin content in the correlation study. High heritability with high genetic advance was observed for fruit yield per plant, number of fruits per plant, capsaicin content, fruit length and fruit girth. The study provides an insight into the selection criteria for elite germplasm of *C. chinense*.

Keywords: Capcaisin, *Capsicum chinense*, Correlation

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OP2-12

Georeferencing Biochemical Diversity for Prioritising Conservation Sites in Fruit Trees: A Case Study in Jackfruit (*Artocarpus heterophyllus* Lam.)

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A total of eighty Jack genotypes collected from eastern India evaluated for biochemical traits including total soluble sugar (10-25.1ºBrix), acidity (0.17-0.67%), total soluble sugar: Acidity ratio (17.69 – 132.50), total sugar (4.50-12.20%), reducing sugar (2.24-7.69%), non-reducing sugar (0.07- 7.23%), phenol (29.81- 152.51 mg GA eq/100 g) and anti-oxidant activities (FRAP: 30.93-167.88 mg AEAC/100g; DPPH: 36.02-146.95 mg AEAC/100g). Wide range of CV (15.97% - 38.37%) and high heritability (0.72 to 0.96) highlighted realised variations with high breeding values. Trait specific naturalised geographical grid analysis identified Simdega districts and adjoining regions of Jharkhand as a promising habitat for naturalising genotypes with high total soluble sugar, total sugar,

reducing sugar, phenol and anti-oxidant activities. The finding supplement time tested market value of Simdega Jack (Bano Jack) particularly for vegetable purpose. Hierarchical clustering based on biochemical traits and their mean performance identified fruit purpose 17 Jack genotypes (grouped in Cluster-III) having higher mean total soluble sugar (18.98 ºBrix), total sugar (8.86%), reducing sugar (5.16%), non-reducing sugar (3.51%), phenol (73.33 mg GA eq/100 g) and antioxidant activities (DPPH: 95.26 and FRAP: 94.05 mg AEAC/100g). While rest are of intermediate end use type. The phenomena underscored influence of human preferences over plant domestication. Employed genic SSRs explained morphological variations better than biochemical traits particularly pulp weight (65.9%), number of fruits/tree (56.7%) and fruit weight (56.4%). Nevertheless, variations in biochemical traits like total soluble sugar (54.3%), antioxidant activity (both based on DAPP: 49.9% and based on FRAP: 45.2%) and acidity (49.4%) comparably explained by the marker system. Over all, present study set a tone for utilising these naturalised resources for enhanced diversified end use.

Keywords: TSS, Reducing Sugar, Non-reducing sugar, Phenol, Antioxidant, DPPH, FRAP

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OP2-13

Microsatellite Marker Assisted Molecular Diversity and Population Structure Analysis of *Kaempferia galanga* Linn. Germplasm Collected from Different Parts of India

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Kaempferia galanga Linn. is an endangered medicinal and aromatic crop with a wide range of importance in the field of pharmaceutical industries. The current study is sought to examine the molecular variance and population diversity for the first time within the core collection of *K. galanga* germplasm. For this study, a total of 132 accessions of *K. galanga* were collected from various states of India and all the germplasm has been maintained *ex-situ* at the experimental farm of CSIR-NEIST, Jorhat. Initially, 58 simple sequence repeats (SSR) markers were tested among them 48 markers that were the most efficient, sensitive, with positive predictive and polymorphism were used in the study. The population structure analysis of *K. galanga* showed nine clusters based on the Bayesian model. The estimated population heterozygosity ranged from 0.117 to 0.250. According to the Analysis of molecular variance study (AMOVA), the variation within the population (68%) was more than among the population (32%). The genetic diversity among the population (Fst) was in the range of 0.28-0.60. The accessions under study demonstrated a high amount of polymorphism with a 99.4% polymorphism observed in molecular investigation. The outcome of the study would help in the identification of the genetic variance for unique germplasm which would be of great aid in the breeding program of *K. galanga.*

Keywords: *Kaempferia galanga,* Genetic diversity, Molecular markers

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POSTER PRESENTATION

PP2-01

Identification of Resistance Sources for Combating Wilt Diseases in Brinjal (*Solanum melongena* L.)

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Brinjal (*Solanum melongena* L.), a year-round crop grown under irrigated conditions, faces significant threats from multiple insect pests and diseases, including the soil-borne wilt-causing pathogens, leading to severe economic losses by reducing yield and market value. The study aimed to identify brinjal genotypes resistant to wilt diseases caused by fungus (*Fusarium oxysporum* f. sp. *melongenae*, and *Sclerotium rolfsii) and* bacteria (*Ralstonia solanacearum)*, to enhance breeding programs. The experiment, conducted in pots at ICAR-IIVR, Varanasi during the *Kharif* season of 2023-24, involved 25 genotypes, 4 checks and 57 $F1_s$ along with 7 related wild species (*S. incanum*, *S. gilo*, *S.microcarpon*, *S. torvum, S.virginianum*, *S. sisymbriifolium*, and *S. lacinatum*) under controlled conditions using a root-dip inoculation method. Data from hierarchical clustering revealed varying levels of resistance for *Ralstonia solanacearum*, 4 genotypes were resistant, while 10 were moderately resistant; for *Sclerotium rolfsii*, 6 genotypes showed resistance; and for *Fusarium oxysporum* f. sp. *melongenae*, 7 genotypes were resistant in the year 2023. Selected resistant lines were identified for further breeding, using them as male (6) and female (19) parents in a line × tester design. In subsequent trials, 2024: 25 genotypes, 4 checks and the newly developed 57 F_1 hybrids along with 7 wild accessions were evaluated for their performance against wilt-causing pathogens. Two hybrids (IVBHL-23W-21 and IVBHL-23W-23) exhibited resistance to all three pathogens, while Kashi Modak (IVBSR-1), Selection-10, PR-5, IVBL-25, Kashi Taru along with four hybrids (IVBHL-23W-12, IVBHL-23W-28, IVBHL-23W-6, IVBHL-23W-24) and other genotypes demonstrated resistance to *Ralstonia solanacearum* and *Fusarium oxysporum* f. sp. *melongenae*. Further, IVBHL23W-9 and IVBHL23W-29 showed resistance to both *Ralstonia solanacearum* and *Sclerotium rolfsii*. All seven wild accessions were found to be resistant for all three wilt-causing pathogens, which establishes their suitability for usage as rootstocks in preparing grafted plants for cultivation in the pathogen-affected soil. Further, the resistant hybrids and advance lines identified can be evaluated in multi-location trials to confirm their resistance levels and would also serve as valuable parental lines for wilt-resistance breeding program in brinjal.

Keywords*:* Bacterial wilt, Brinjal, *Fusarium oxysporum* f. sp. *melongenae*, Germplasm screening, *Ralstonia solanacearum* and *Sclerotium rolfsii*, Related wild species

PP2-02

Evaluating Tea Germplasms for Climate Resilience: Deep Learning and Computer Vision Approaches to Predict Drought Tolerance, Yield, and Quality

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The development of climate-resilient tea (*Camellia sinensis* (L.) O. Kuntze) cultivars with improved drought tolerance, yield, and quality is essential for sustainable tea production. North East India is home to a vast diversity of tea germplasms. Tocklai Tea Research Institute, the oldest and largest tea research facility globally, holds a collection of over 1,600 active tea germplasms which holds significant potential for exploration. Mature tea leaves display considerable variability in shape, size and color. These morphological traits are closely associated with key agronomic characteristics like drought tolerance, yield and quality. Traditional methods for evaluating these traits are expensive, time consuming and rely heavily on specialized human expertise. This study applies deep learning and computer vision techniques to automate the evaluation of tea germplasms, aiming to reduce reliance on manual labor and expert judgment. Mature leaves from widely planted tea cultivars, including the Tocklai Vegetative (TV) clones, TRA garden series, and other popular quality clones, were manually scanned to create extensive image datasets, 2100 leaf images from cultivar of known drought tolerance level and 1800 leaf images from cultivar of known yield and quality potential. The agronomic performances of these cultivars, particularly in terms of drought tolerance, yield, and quality, were previously well-documented through field trials and are widely acknowledged by tea growers. Two multilayer Convolutional Neural Network (CNN) classifiers were developed using these datasets and were trained for 60 epochs. The first classifier, designed to predict drought response, achieved training and validation accuracy of 93% and 95%respectively. The second classifier, focused on predicting yield and quality potential, attained training and validation accuracy of 92% and 93% respectively. These results highlight the potential of CNNs in automating tea germplasm evaluation based on mature leaf morphology. The high validation accuracy of both models suggests that unknown germplasms could be evaluated by presenting their mature leaf images to the trained classifiers, enabling predictions of their drought tolerance, yield, and quality potential. This approach offers tea breeders a means to accelerate the germplasm evaluation process, allowing for initial assessments prior to field level assessments. Eventually, this methodology enhances the precision and efficiency of selecting and breeding tea cultivars with desirable traits, contributing to more resilient tea production amidst changing climate conditions.

Keywords*:* *Camellia sinensis*, Artificial intelligence, Drought tolerance

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PP2-03

AI-Driven Decision Support: Revolutionizing Crop Improvement through Conserved Genetic Resources

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AI-assisted decision support systems for selecting and utilizing conserved genetic resources in crop improvement programs represent a cutting-edge approach to enhancing agricultural productivity and sustainability. These systems leverage the power of artificial intelligence to analyze vast amounts of data related to plant genetic resources, environmental conditions, and breeding objectives. By doing so, they provide plant breeders and researchers with valuable insights and recommendations for optimizing the use of conserved germplasm in crop improvement efforts. The foundation of these systems lies in the integration of diverse datasets, including genetic information (such as DNA sequences and molecular markers), phenotypic data (like yield, disease resistance, and quality traits), and environmental data (including climate patterns, soil conditions, and pest prevalence). Machine learning algorithms, particularly deep learning neural networks, are employed to process and analyze these complex, multi-dimensional datasets. These algorithms can identify intricate patterns and relationships that might be overlooked by traditional analysis methods. One of the key functionalities of AI-assisted decision support systems is their ability to predict the potential performance of different genetic combinations. By analyzing the genetic makeup of conserved accessions and comparing them with desired traits, these systems can suggest which germplasm sources are most likely to contribute beneficial characteristics to breeding programs. This capability is particularly valuable in the context of North-eastern India, where the rich agrobiodiversity holds untapped potential for crop improvement.

Furthermore, these systems can take into account the specific environmental conditions of target regions. For instance, in North-eastern India, where diverse microclimates exist, the AI can recommend genetic resources that are likely to perform well in particular locations, considering factors such as rainfall patterns, temperature ranges, and soil types. This targeted approach helps in developing crops that are not only high-yielding but also well-adapted to local conditions, contributing to sustainable agriculture. Another critical aspect of these AI systems is their capacity to optimize breeding strategies. By simulating different crossing scenarios and predicting outcomes, they can suggest the most efficient breeding plans to achieve desired traits. This capability can significantly reduce the time and resources required in traditional breeding programs, accelerating the development of improved crop varieties. Moreover, AI-assisted decision support systems can continually learn and improve their predictions as new data becomes available. As breeders use the system and provide feedback on actual outcomes, the AI algorithms refine their models, leading to increasingly accurate and valuable recommendations over time. In the context of addressing challenges like climate change, pest resistance, and nutritional enhancement – all of which are relevant to North-eastern India as mentioned in the provided text – these AI systems can be invaluable. They can quickly identify genetic resources with traits for drought tolerance, pest resistance, or enhanced nutritional profiles, facilitating the development of resilient and nutritious crop varieties. In conclusion, AI-assisted decision support systems represent a powerful tool for maximizing the value of conserved

genetic resources in crop improvement programs. By harnessing the power of artificial intelligence to analyze complex datasets and provide data-driven recommendations, these systems can significantly enhance the efficiency and effectiveness of breeding efforts, ultimately contributing to improved food security and sustainable agriculture in regions like North-eastern India.

Keywords: Artifical intelligence, Genetic resources, Management, Crop improvement

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PP2-04

NIR Spectroscopy and Machine Learning for Evaluating Nutritional Traits in Diverse Vegetable Pea (*Pisum sativum* L.) Germplasm

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In the North Eastern (NE) hills of India, vegetable pea is the predominant legume vegetable followed by the French and Dolichos beans. Vegetable pea is cultivated in all the NE regions, whereas field pea is commonly cultivated in Assam, Manipur, and Tripura. It is a cool season crop, valued for its nutritional composition including high-quality protein-carbohydrate complex, essential amino acids, starch, dietary fiber, vitamins, phytochemicals, and antioxidants. Near-infrared spectroscopy (NIRS) is a rapid, precise, and non-destructive method to determine biochemical traits in large-scale of germplasm, offering a significant advantage over conventional methods that are often laborious, costly, time-consuming, and require technical expertise. NIRS calibration models were developed employing various mathematical treatments and the best treatment "2,6,4,1", "2,4,6,1", "2,4,4,1", and "3,10,4,1" were finalized for protein, starch, total dietary fiber (TDF), and total soluble sugar (TSS), respectively in a diverse set of vegetable pea accessions. NIRS prediction models through modified partial least square regression method with the highest coefficient of determination $RSQ_{external}$ values for TDF (0.932), followed by protein (0.931), TSS (0.918), and starch (0.814). The ratio of performance to deviation values was>2, low bias, and slope values near 1 were obtained in all the models developed confirming the model's robustness and accuracy. These NIRS prediction models facilitate breeders in selecting desirable chemotypes, food industries and inspection agencies to control the quality of peas and identify adulterants accurately and economically.

Keywords: Near-Infrared spectroscopy modified partial least square, Coefficient of determination, Ratio of performance to deviation.

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PP2-05

Assessment of Genetic Diversity of Adlay (*Coix lacryma*-Jobi) Landraces of Manipur using ISSR Markers

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Job's tears *Coix lacryma-jobi* L are a minor cereal and an important food item in some parts of Asia. It has also been used in traditional medicine to relieve various ailments; therefore, it plays an important role in our lives. The lack of excellent new varieties hinders the development of coix as a sustainable crop, and it is urgent to provide new cultivars with excellent traits in the Indian Coix industry. Three ISSR markers (UBC-880, UBC-884, and UBC-885) were used to assess the genetic diversity of 7 landraces of Job's tears of Manipur (MC-1, MC-2, MC-3, SU-1, SU-2, SU-3, and BZ). The PCR amplification produced 130 bands ranging from 500 to 1700 bp, of which 28 were polymorphic. The genetic relationship was calculated using a similarity matrix. The highest similarity was obtained between SU-2 and SU-3, with a genetic distance value of 0.9615, followed by the closeness between MC-1 and SU-1. The lowest genetic distance of 0.5769 in the similarity matrix was obtained between BZ and MC-2. The results of UPGMA cluster analysis that investigated genetic diversity among the populations were consistent with the genetic distance results. Moreover, according to a cluster analysis based on the UPGMA for individuals of Job's tears, accessions were divided into two major clusters. In one cluster, MC-1, SU-1, SU-2, SU-3, MC-2, and MC-3 were included, and in the other cluster, BZ was included. This study provides us with valuable information pertaining to genetic improvement, and systematic utilization of Job's tears.

Keywords: Job's tears, DNA marker, Genetic diversity

PP2-06

Assessment of Genetic Diversity of Aromatic Rice (*Oryza sativa* L.) Landraces of Manipur using ISSR Markers

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Molecular markers provide valuable tools for distinguishing between different rice landracesand clarifying their relationships with other groups within *Oryza sativa*. We have evaluated the genetic diversity and patterns of relationships among the six aromatic rice (*Oryza sativa L.*) landraces of Manipur using the ISSR markers. A total of 5 ISSR primers, bands ranging from 1500-200 bp, producing 193 bands, of which73 polymorphic bands and which demonstrated significant genetic variation among the landraces. The genetic relationship was calculated from similarity matrix, with the highest similarity observed between ChakhaoKhongnembi and WairiChakhao (0.9048), as well as between Napnang and MagumaChakhao, generated using NTSYS-pc software version 2.02. The similarity matrix was supported by the dendogram obtained from the analysis of PCR amplification profile for the six rice landraces and PCoA analysis with Eigenvalue 11.826. Our findings emphasize the utility of ISSR markers in evaluating the genetic diversity of aromatic rice landraces and offer valuable information for their conservation, improvement, and sustainable use in breeding efforts aimed at preserving these culturally important varieties.

Keywords: *Oryza sativa L.*, ISSR, PCR

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PP2-07

Genetic Diversity Evaluation of Core Collection Gene Bank Using Simple Sequence Repeat Marker of *Acorus calamus* L.: An Important Aromatic Species

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Acorus calamus L. is an important aromatic plant having economic and medicinal properties. In this study, molecular diversity analysis was performed using 138 *Acorus calamus* accessions collected from Northeast India and planted in the experimental farm of CSIR NEIST, Jorhat. A molecular diversity study was conducted by employing 30 screened primers from which an average of 99.58% polymorphism was exhibited with a total of 186 polymorphic alleles. An analysis of molecular variance

(AMOVA) was performed among *A. calamus* accessions where genetic diversity among the population was found to be 28% and genetic variations of 72% was observed within the population. Genetic variations within and among populations were found significant with *P* value of 0.001. The analysis of population based genetic diversity parameters revealed an average value of 1.84 for observed number of alleles (Na), 1.48 for effective number of alleles (Ne), 0.28 for Nei's genetic diversity index (h), and 0.42 for Shannons information index in four grouped populations. Cluster analysis revealed three clusters based on unweighted pair group method with arithmetic mean (UPGMA) analysis. Principal component analysis (PCoA) was further performed. Moreover, three genetically diverse populations were also detected through structure harvester software. Until now, there are no such reports on the analysis of the genetic diversity of this industrially important crop using SSR markers. So, it can be considered as the first report on the molecular diversity of *A. calamus* which will be helpful for the crop improvement, conservation and identification of the elite genotypes.

Keywords: *Acorus calamus*, Aromatic plant, Genetic diversity, Molecular markers

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PP2-08

Genetic Diversity and Population Structure Analysis of *Homalomena aromatica* Schott. : An Industrially Significance Medicinal Species

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Homalomena aromatica Schott is a valuable medicinal plant of Araceae family. Currently, genetic diversity of *H. aromatica* was assessed on 119 samples collected from five states of northeast India using simple sequence repeat marker. Samples collected were planted in the year 2022 at the experimental farm of CSIR-NEIST, Jorhat, India. DNA was extracted using CTAB method and further proceeds for PCR run. A total of 44 SSR markers were selected based on polymorphic nature of markers. Total 208 numbers of polymorphic bands were produced by 44 numbers of primers where highest polymorphic information content (PIC) was exhibited by JHA27 with a value of 0.98. The JHA03 marker showed highest number of polymorphic bands with marker index (MI) value of 7.04 whereas, primer JHA21 showed the resolving power (Rp) of 2.74. Population-based genetic diversity analysis across five grouped populations revealed average values of 1.50572 for effective number of alleles (Ne), 0.44986 for Shannon's index (I), 1.88366 for observed number of alleles (Na), and 0.2986 for Nei's diversity index (h). A dendrogram clustering was performed using UPGMA analyzer where three clusters were formed and was confirmed by principal component analysis (PCA). From structure analysis, three genetically diverse populations were observed which was further confirmatory of the UPGMA and PCA results. From the Analysis of Molecular Variance (AMOVA) the genetic diversity among the populations was found to be 6% with genetic variation accounting for 82% as well as 12% was observed for within and among the individuals respectively. To the best of

our knowledge this is first report on *H. aromatica* molecular diversity analysis which highlights the novelty of the study. The present study will aid in the identification of elite lines, conservation of gene pool and development of breeding programmes.

Keywords: *Homalomena aromatica Schott.,* Medicinal plant, Genetic diversity, Molecular markers

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PP2-09

Molecular Characterization of *Citrus* Rootstocks through SCot Marker

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Citrus (*Citrus spp.)* is a subtropical evergreen plant that belongs to the family Rutaceae. The majority of Citrus species are indigenous to tropical and subtropical climates in Southeast Asia, particularly India, and China. The molecular characterization of 17 citrus rootstocks was carried out in molecular laboratory of Deptt. of GPB, BUAT, Banda during 2022-2023 as per the standard procedure developed by Collard & Mackill (2009). Characterization was carried out for seventeen Citrus rootstock genotypes *viz.,* NRCC-1 (Rough Lemon × Troyer Citrange), NRCC-2 (Rough lemon × Troyer citrange), NRCC-3 (Rough lemon × Troyer citrange), NRCC-4 (Rough lemon × Trifoliate Orange), NRCC-5 (Rough lemon × Troyer citrange), NRCC-6 (Rough lemon × Troyer citrange), SFS (Smooth Flat Sevelle), Volkamariana (*Citrus volkameriana*), Rough lemon (*Citrus jambhiri*), Rangpur lime (*Citrus limonia*), Calamondin (*Citrus madurensis*), Cleopatra mandarin (*Citrus reshni*), Sour orange (*Citrus aurentium*), Karna Khatta (*Citrus. karna*), Troyer citrange (*C. sinensis × P. trifoliata*), CRH-47, and Carrizo (*P. trifoliata × C. paradisi*) using 21 SCoT (Start Codon Targeted) markers namely SCoT-1, SCoT-2, SCoT-3, SCoT-4, SCoT-5, SCoT-6, SCoT-8, SCoT-9, SCoT-11, SCoT-12, SCoT-13, SCoT-14, SCoT-15, SCoT-16, SCoT-17, SCoT-18, SCoT-19, SCoT-20, SCoT-21, SCoT-22, SCoT-23, and SCoT-24. Out of twenty-one primers, two primers *i.e.,* SCoT-5 and SCoT 19 were found monomorphic and rest primers were polymorphic. The amplified product ranged between 200bp to 4000bp, and the range of the alleles varied from 2 to 8. The frequency of the major alleles ranged from 0.88 to 0.54. The value of gene diversity varied from 0.78 to 0.21, and the PIC (Polymorphism Information Content) value ranged from 0.18 to 0.42. The SCoT-23, SCoT-14, SCoT-4, SCoT-1, and SCoT-2, were found to be informative and able to detect polymorphism among the studied genotypes due to their high PIC value.

Keywords: *Citrus spp*., Germplasm, Molecular characterization, SCoT marker.

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PP2-10

Characterization of Ricebean Genotypes through Morphological and Molecular Analysis

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Rice bean (*Vigna umbellata*), formerly classified as *Phaseolus calcaratus*, is an underutilized tropical legume predominantly grown in small areas of North eastern hilly areas. Despite the region's vast genetic diversity, the full potential of indigenous germplasms remains untapped. Harnessing this genetic richness is essential for improving the crop's yield potential and identifying suitable parent plants for various breeding programs. So, this study was conducted with the aim of thoroughly characterizing rice bean germplasms. The research focuses on assessing both morphological traits and molecular profiles to better understand and utilize the genetic resources available. 92 rice bean accessions were collected from several north eastern regions (Manipur, Mizoram and Meghalaya) and ICAR-NBPGR, Shimla for evaluation at experimental plant breeding farm, ICAR-RC NEH. It was observed that Number of clusters per plant (CPP), number of pods per plant (PPP), number of pods per cluster (PPC) had high genotypic coefficient of variation (GCV) (>20%). Traits like number of pods per plant (PPP), pod length (PL), pod width (PW) and 100 seed weight (HSW) showed positive correlation with seed yield per plant as well as positive direct effect on it. Therefore, morphological traits that demonstrate a positive correlation with seed yield per plant, along with a direct positive impact on yield, should be prioritized as key selection criteria for enhancing rice bean productivity. Molecular characterization of the genotypes was conducted using 44 SSR markers, of which 14 were identified as polymorphic. The marker CG8775c0 exhibited the highest genetic diversity and PIC value, while cG25883c0 demonstrated the greatest heterozygosity among the genotypes. Analysis of molecular variance revealed that the majority of genetic variation occurred within populations at the individual level. Population structure analysis further categorized the accessions into two distinct clusters (K=2). Additionally, polymorphic markers with high PIC values will be instrumental in more accurately differentiating individuals at the molecular level, further aiding in targeted genetic improvement.

Key words: Rice bean, Characterization, Morphological, Molecular, SSR markers

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PP2-11

Evaluation of Wheat Genotypes for Heat Tolerance Based on Developing Green Grain Photosynthetic Pigments Characterization

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Photosynthetic pigments play an important role in the photoprotection of photosynthetic machinery under heat stress. Developing green grains of wheat have photosynthetic pigments. Thus, they actively take part in photosynthesis; contribute to yield formation and heat tolerance. Therefore, present investigation was carried out with an objective to evaluate 32 wheat genotypes for heat tolerance based on developing green grain photosynthetic pigments characterization. Heat stress was imposed by delaying the sowing date *i.e.*, normal (December 2, 2021) and over one month late sowing (January 10, 2022). All observations on photosynthetic pigments (chlorophylls and carotenoids), Fv/Fm ratio, Y (II), qp, NPQ were recorded at 7, 14, 21 and 28 days after anthesis and yield & its associated parameters were recorded at harvest. All the parameters were decreased under late sown heat stress condition except NPQ and exhibited huge genotypic variations under both normal and heat stress conditions. Identification of promising genotypes for different traits was done based on their performance above the average under normal and late sown heat stress conditions. The hierarchical clustering of genotypes was done based on photosynthetic pigments, Fv/Fm ratio, NPQ, yield, harvest index, and heat tolerance and thus four groups were formed and one group was named tolerant group as it was consisting only 5 tolerant genotypes namely PET 1239, PBW 555, Raj 3765, HD 3086, and HD 2851. These genotypes emerged out promising and proved to be heat tolerant. Present findings provide valuable insight on heat tolerance in wheat based on developing green grain characterization and open a new way for the development of resilient cultivars in the future.

Keywords: Wheat, Heat tolerance, Photosynthetic pigments.

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PP2-12

A Successful Tissue Culture Protocol for Conservation of Intergeneric Hybrid Papaya

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Biodiversity is the biological diversity which includes the variety of the whole species present on earth. The increase in population, industrialization and urbanization results in rapid loss of biodiversity. It can be preserved either *in situ* or *ex situ*. In case of *in situ*, it requires large area and extensive care and there is a possibility of loss of the valuable diversity due to natural disasters. So, as an alternative

method, the *in vitro* culture technique coupled with molecular tools can be productively employed for conservation, micropropagation, biotic and abiotic stress tolerance, provided there is a regeneration protocol for tissue culture technique. Work carried out in this direction at ICAR-IIHR, Bengaluru has resulted in the development of tissue culture protocol for intergeneric hybrids of papaya using shoot tip of seedling plants and found suitable for conservation of cultures *in vitro* without any genetic changes. Molecular markers (W11&T12) were employed for sex identification at seedling stage (with > 98 accuracy) and *in vitro* cultures before transplanting in the field. The standardized tissue culture protocol for regeneration coupled with markers for sex identification will be a suitable alternative conservation method for the intergeneric hybrids of papaya.

Key words: Biodiversity, Conservation, *in-situ*, *ex situ*, *in vitro*

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PP2-13

Ex-situ Conservation Leveraging *In-vitro* Asymbiotic Seed Germination and Micro Propagation of *Dendrobium nobile* var. *alba* - A Rare Threatened Orchids of Northeast India

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Dendrobium nobile var. *alba* is an endangered and rare threatened epiphytic medicinal orchid of North East India. The present study aimed to establish an *ex-situ* conservation strategy by leveraging in vitro regeneration. The six months matured pods of *Dendrobium nobile* var. *alba* were collected from the ICAR- NRC for Orchids, Pakyong, polyhouse and inoculated for seed culture under 8 treatments with 3 replication each. Asymbiotic *in vitro* seed germination was most successful on Nitsch media supplemented with 2.0 mg/l NAA for early seed germination (11.02 weeks) as well as for development of protocorm (14.12 weeks) and seedling (22.47 week) from days to *in-vitro* culture (DAC). Nitsch basal media in combination with equal amount of NAA and BAP (1.0 mg/l) produced tallest shoots (5.01 cm) and maximum number of leaves per shoot (8.01). However, maximum number of roots per shoots (4.44) observed with 1.0 mg/l NAA, 1.0 mg/l IBA and 1.5 mg/l BAP. The plantlets were subsequently acclimatized and hardened on pots containing cocopeat resulting in survival rate of 58.76%. This study represents a comprehensive protocol of mass multiplication through tissue culture technique which may be adopted for conservation of this endangered species.

Keywords: *In-vitro*, Asymbiotic seed germination, *Dendrobium nobile* var *alba*, Protocorm.

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PP2-14

Assessing Pollen Viability of Wild *Lathyrus* Species: A Foundation for Enhanced Grasspea (*Lathyrus sativus* L.) Hybridization and Crop Improvement

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Grasspea (*Lathyrus sativus* L.), also known as chickling pea, khesari, teora, or kesari, is a hardy pulse crop that requires minimal care and is highly valued for its nutritional content, particularly its protein level. Grasspea, with its exceptional resilience to both drought and flooding, is regarded as a promising legume crop that holds potential for cultivation on rice fallow land in the North Eastern region, contributing to enhanced global food security. However, its underutilization is largely due to the presence of the neurotoxin, β-N-Oxalyl-l-α,β-diaminopropionic Acid (β-ODAP) in its seeds, which can lead to neurolathyrism when consumed over extended periods. Despite this, many wild relatives of grasspea, known for their lower β-ODAP content and resilience to various stresses such as drought, powdery mildew, rust, and crenate broomrape, present valuable genetic resources for crop improvement. A significant challenge in grasspea breeding is the lack of flowering synchrony across different species, which results in limited pollen availability and reduces the number of successful crosses during hybridization programs. To address this, understanding and assessing pollen viability in these species is crucial for optimizing breeding strategies and conserving grasspea genetic resources. However, there has been no prior study on pollen viability in the wild relatives of grasspea. This study was therefore conducted to estimate the percentage of viable pollen of different wild grasspea species using the acetocarmine staining method. The results revealed that species such as *L. amphicarpos, L. ochrus, L. pseudocicera, L. cicera and L. tingitanus* exhibited high pollen viability, ranging from 90.90% to 100.00%. Notably, variability in pollen viability was observed among different accessions within the same species. These findings provide a valuable foundation for initiating wide hybridization programs aimed at developing superior hybrids, leveraging the genetic potential of these wild relatives.

Key words: Grasspea, β-ODAP, Wild relatives, Pollen, viability, Acetocarmine, Hybridization

PP2-15

Uncovering the Diversity of Microalgae and Cyanobacteria with Emphasis on their Antioxidant and Antimicrobial Activity

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In the present investigation, the diversity of microalgae and cyanobacteria from East Khasi Hills, West Khasi Hill, Jaintia Hills and Ri-Bhoi areas of Meghalaya were studied. Based on the morphology and phylogenetic analysis, microalgae dominate this region as 11 isolates were identified in comparison to only 6 cyanobacteria isolates. All isolates were screened for their phytochemical contents antioxidant and antimicrobial activity. The result showed that *Anabeana* sp NC-K1., *Parachlorella kessleri* NC-DW (K3) and *Synechococcus* sp. NC-DW (K3C2) exhibited strong antioxidant properties based on three radical scavenging assays ABTS, FRAP and DPPH. The highest carotenoid content was reported in *Anabeana* sp*.* with 7.442 mg L^{-1} while the highest phenolic and flavonoid content was reported in *Parachlorella kessleri* NC-DW (K3) (2.22 ± 0.25 mg GAE g^{-1}) and *Chlamydomonas reinhardtii* NC-DW (URF1)(10.03 ± 0.34 mg QE g^{-}1) respectively. All isolates were also evaluated for their antimicrobial potency against pathogenic strains *Pseudomonas aeruginosa*, *Escherichia coli* and *Klebsiella pneumoniae*. Disk diffusion assay demonstrated significant inhibitory effects of Neowestiellopsis sp. NC-DW (S1) showing very high inhibition zones against all tested bacterial strains. Minimum Inhibitory Concentration (MIC) assays further confirmed the antimicrobial potential of all the isolates with 2.5 mg/mL as the lowest MIC value. All isolates were also evaluated for their fatty acid composition. The analysis revealed the presence of various saturated, monounsaturated, and polyunsaturated fatty acids across the species.

Keywords: Microalgae, Cynobacteria, Phytochemicals, Antioxidants, Antimicrobial properties.

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PP2-16

Unfolding the Floral Nutraceutical Potential of *Arundina graminifolia* (D.Don) Hocr.–An endangered Orchid Species from the North Eastern Himalayan Region

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Arundina graminifolia (D. Don) Hocr. is an endangered perennial terrestrial medicinal orchid species having beautiful pink flowers grown in the reserve forests areas of North Eastern Himalaya states like Sikkim, Meghalaya, Arunachal Pradesh and Assam. The plant is widely recognized in the remote areas of NE region of India, due to its traditional herbal medicinal application for the treatment of diabetes, fever, heavy menstruation, fever, eye inflammation, hypertension, carve-depression and abdominal pain. In the present study, *A. graminifolia* orchid flowers have been aimed to explore for their nutraceutical potential. The *in-vitro* antioxidant scavenging activity such as total antioxidant activity, DPPH, ABTS, CUPRAC, FRAP, metal chelating activity including total anthocyanins, phenols, flavonoids with colour value (L*, a*, b*) of *A. graminifolia* flower has studied through UV-vis spectrophotometer and colour analyzer to explore their medicinal potential. The bioactive compounds such as phenolics, anthocyanins, vitamin E and amino acids through LC-MS/MS, micro-minerals composition through ICP-MS, and non-targeted bioactive compounds were profiled through LC-HRMS. The present study has reported bioactive phenolics such as caffeic acid, p-coumaric acid, trans-cinnamic acid, quercetin, anthocyanins like delphinidin, malvidin, and petunidin was reported. The quantification of amino acids showed the presence of essential amino acids such as lysine and other few essential amino acids in the flowers. The analysis of a total 11 minerals through ICP-MS has the presence of essential minerals such as calcium, magnesium, Iron, Zinc etc. The study of non-target compounds through LC-HRMS, has reported a total more than 70 major bio-active compounds of phenolics, flavonoids derivatives. The presence of potentially bioactive metabolites, namely phenolics, anthocyanins with antioxidant potential suggests its suitability as potential functional or nutraceutical food ingredients. Therefore, our study revealed that the flowers of the *A. graminifolia* orchid species showed significant nutraceutical potential and these findings highlight the importance of collecting, conserving, and promoting the use of these medicinal orchids among local farmers for sustainable commercial purposes.

Keywords: *Arundina graminifolia* flowers, Phenolics, LCMS/MS, Antioxidant, Medicinal Orchids

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PP2-17

AMPK Activation Potential of the Anti-Diabetic Herb *Centella asiatica*: An *In Vitro* Study

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Indian pennywort or *Centella asiatica* is a herb belonging to the family Apiaceae. In addition to its anti-diabetic property, *C asiatica* also possess anti-inflammatory, anti-carcinogenic, neuroprotective properties etc. As a traditional medicinal herb, this plant has been used in different places of the world in the treatment of skin diseases, ulcers, cardiovascular diseases and many other diseases, and mitigate ailments such as stomachache, arthritis and wounds etc. *C asiatica* also called 'Khlieng syiar' by the *Khasis* of Meghalaya, is also used as a culinary item and is consumed raw or as health drink by the local inhabitants of the state. The antioxidant activity of *Centella asiatica* extract (CAE) have been reported to show a beneficial role in metabolic diseases such as diabetes. In a diabetic condition, glucose dispensation to various organs of the body is compromised due to insulin resistance. As a result, blood glucose levels are relatively high whereas cells are relatively receiving less glucose leading to shortfall in ATP production. Therefore, maintenance of energy homeostasis is extremely crucial. 5' adenosine monophosphate kinase (AMPK) is a master regulator of energy homeostasis. This kinase enzyme phosphorylates and activates or inhibit downstream target proteins in metabolism. Plant extracts can activate AMPK and this activation can beneficially regulate energy homeostasis. The aim of the study is to investigate and hence validate the AMPK activation potential of *Centella asiatica* extract in a diabetic state in cellular system. An activated AMPK facilitates the uptake of glucose via signaling pathways regulating membrane translocation of glucose transporters (GLUTs). Therefore, to evaluate AMPK activation potential of *Centella asiatica* extract, the crude extract was screened for its glucose uptake effect after a preliminary phytochemical screening test of the extract and cell viability determination on L6 rat skeletal muscle cells. The result of the study showed (a) crude methanolic extract of *C asiatica* was found positive for phytochemicals viz., alkaloids, carbohydrates, phytosterols, tannins, saponins and phenol (b) cell viability determination in rat skeletal muscle cells (L6) was found non cytotoxic within the range of 50µg/ml to 1200µg/ml (c) glucose uptake assay showed *Centella asiatica* extract facilitates uptake of 2-NBDG, a fluorescent glucose analogue, however in presence of the AMPK inhibitor dorsomorphin (compound C), a reduced uptake was observed.

Keywords: *Centella asiatica*, Antidiabetic, AMPK inhibitor, Cell lines

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PP2-18

Unveiling the Nutritional Diversity in Wild *Vigna* Species

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Pulses are a rich and affordable source of vegetable protein, and the genus *Vigna* encompasses several agronomically significant species with substantial economic and environmental importance, including cowpea, urdbean, mungbean, mothbean, adzuki bean, and rice bean. However, challenges such as climate change, new pests and diseases, and changing cultivation practices have impacted the production and productivity of these crops. The wild *Vigna* species are known for their nutritious pods, grains and easily digestible proteins. Consequently, it is essential to evaluate wild species for nutritional traits to identify promising accessions leading to their future domestication and utilization. This study involved the evaluation of 71 different accessions of 12 species of wild *Vigna* for nutritional traits. Biochemical parameters for analysis included protein, sugar, starch, phenols, moisture, ash, iron, and zinc. The results demonstrated that wild species are nutritionally rich and have the potential to combat malnutrition, hidden hunger, and support nutritional security. The highest protein content was found in *V. oblongifolia* [EC1170492 (31.13%)], *V. trilobata* [IC305193 (30.56%)], and *V. vexillata* [EC1170508 (30.63%), EC550058 (30.8%) and EC529042 (30.74%)]. The highest iron content was recorded in *V. stipulacea* [IC647555 (110 ppm)], *V. oblongifolia* [EC1170496 (137.6 ppm)], *V. angularis* var. *nipponensis* [IC625714 (99 ppm)], and *V. unguiculata* ssp. *stenophylla* [EC1170517 (82.64 ppm)]. The highest zinc content was observed in *V. unguiculata* ssp*. dekindtiana* [EC1170526 (74.25 ppm)] and *V. vexillata* [EC1170508 (74.47 ppm)]. These elite accessions can serve as potential donors to improve cultivated *Vigna* species for various nutritional traits.

Keywords: Biochemical, Evaluation, Nutritional traits, Vegetable, Wild *Vigna* species

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PP2-19

Characterization and Genetic Improvement in Groundnut Genotypes (*Arachis hypogaea* L)

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Groundnut (*Arachis hypogaea* L.) is an important oilseed crop cultivated worldwide mainly for its edible oil. The experiment was carried out with seventy-five genotypes derived from different hybridization programmes involving different parent materials (56 cross combinations) having various desirable traits for improvement of plant characteristics. Seed materials were available at Regional Research Station Vridhachalam, Tamil Nadu Agricultural University, used as lines (Female parents) and received materials from ICRISAT (International crops research institute for the semi-arid tropics) for testers (Male parents). Exploiting genetic variations for desirable traits is essential to meet the demands of groundnut farmers. The analysis of variance (ANOVA) revealed a significant difference in the mean sum of squares for genotypes across all the traits studied. Additionally, the ANOVA for combining ability using L × T analysis showed considerable variation among all the traits investigated. In all ten traits the specific combining ability (SCA) variance outweighed the general combining ability (GCA) variance. This indicated that specific combinations of parent plants have a significant impact on the performance of groundnut hybrids for those traits emphasizing their crucial role in contributing to the hybrid's characteristics. Based on *per se* performance and *gca* effects, VRI 7, GG 7 CO 7, ICGV 15427 and ICGV 15402 were identified as the best combiners for yield traits. These research findings offer valuable insights for groundnut breeding programmes. Based on the analysis of mean performance, sca effects and standard heterosis, the cross combinations *viz*., VRI 7 × ICGV 15426, VRI 8 × ICGV 15402, VRI 8 ×ICGV 15427, CO 7 × ICGV 15426 and VRI 10 × ICGV 15388 were recommended for pod yield and oil content. The magnitude of SCA variances was much greater than those of general combining ability variances indicating the preponderance of non-additive gene action for all the characters. Among the six crosses studied for sixteen traits including yield and oil quality traits in F_2 Populations, the cross III demonstrated superior performance in several traits including number of primary branches per plant, number of mature pods per plant, shelling percentage, pod yield per plant, Kernel yield per plant, stearic acid and palmitic acid. On the other hand, cross I displayed a high mean in the plant height, number of primary branches per plant, oil content and oleic acid. Similarly, cross VI demonstrated a high mean in hundred pod weight and hundred kernel weight. In a correlation study of the F_2 generation, pod yield per plant showed significant positive correlations with traits like primary and secondary branches, mature pods, shelling percentage and various fatty acids across all crosses. Additionally, in crosses III and II pod yield correlated significantly with hundred kernel weight and hundred pod weights, highlighting their pivotal role in yield determination. This study provides valuable insights into groundnut breeding, facilitating the development of cultivars with enhanced yield and oil quality traits to meet the evolving needs of groundnut farmers.

Keywords: Groundnut, Genetic diversity, Combining ability, Crop imrpvement

PP2-20

Mango's Covert Identity

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Mangos are widely recognized for their high content of phenolic compounds, vitamin C, ß-carotene, and dietary fiber. Several studies have been conducted regarding the potential health and nutritional advantages of mangoes. Mango peel and seed have also been reported to have strong antioxidant properties. Therefore, mango types should be investigated to determine their viability for use. For this experiment, different portions of fruit were used, notably the pulp, peel, and seed kernel of fully ripe mangos. A study on "Phytochemical screening and determination of antioxidant activity of different mango cultivars" was laid out in CRD comprising of five varieties as treatments *viz*. Alphonso, Sonpari, Dashehari, Amrapali and Langra during the year 2021-2022 at ACH, NAU, Navsari. The treatments were repeated for five times. The result revealed that total polyphenol content (mg/100 g FW) reported maximum in pulp and peel of Langra and Dashehari kernel. Total flavonoid (mg rutin equivalent (QR Equiv)/g FW) observed maximum in Alphonso pulp and Langra peel and Dashehari kernel. Whereas Ascorbic acid (mg/100 mL) reported maximum in pulp and peel of Langra and kernel of Alphonso. DPPH scavenging activity (%) and ABTS scavenging activity (%) in pulp, peel and kernel of Langra. While, the Ferric-reducing capability (µg/g) observed maximum in pulp and peel of Langra and kernel of Sonpari. In case of phenolic acid, 4-hydroxy benzoic acid was only detected in pulp of Sonpari and Amrapalli. In peel, it was found maximum in Amrapalli cultivar and It was not detected in in kernel of any selected cultivar. In case of Vanilic acid, it was reported maximum in Alphonso pulp, Sonpari peel and Langra kernel. Gallic acid found maximum in pulp and kernel of Langra and peel of Sonpari. Whereas, Syringic acid recorded maximum in Alphonso pulp, Langra peel and Kesar kernel. Cafeic acid reported maximum in pulp, peel and kernel of Langra. Of the chosen cultivars, it was discovered that the Langra variety possessed a greater potential for antioxidants. For the nutraceutical qualities, peel and kernel waste from processing businesses can also be used.

Keywords: Mango, Varities, Quality, Antioxidants.

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PP2-21

Relevance of Plant-Microbe Interactions for Crop Improvement

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Due to constantly changing climatic conditions and global warming, crop yield and production has been severely affected. Therefore the plant production system should be optimized for higher yield in the limited fertile land. To increase crop yield and production, microbial/biological exploitation is the better solution and will play an important role in disease dissemination and control. Mainly the plant-microbe interaction research has been focused on three aspects, the oldest symbiosis between plants and mycorrhizae, nitrogen fixation in plants and pathogenesis. These systems are now well characterized and provide insights into common and diverged signalling network mechanisms in plant-microbe interactions. Resistant crop breeding which uses the molecular breeding and genetic engineering approach to transfer the resistance genes or QTLs against pathogens is one of the better and most effective and environmentally friendly approaches to counter microbial diseases as against the use of pesticides. The exploitation of the biotic and abiotic situation of plants is another environment-friendly approach to developing sustainable disease management strategies. However, the biotic approach requires a superior comprehension of how plants and microorganisms intimately interact with each other in a great degree of complex environment and how these interactions result in physiological changes in plants. Moreover, information is required on how plants organize their needs like utilizing energy and resources for their protection and resistance against the pathogens at the cost of their growth and development.

Keywords: Plant-Microbe Interactions, Symbiosis, Nitrogen fixation, Pathogenesis.

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PP2-22

Trichoderma Diversity and Potential Antagonism in the Mid-Hills of Meghalaya

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The North East a biodiversity hotspot region is home to many phytopathogenic as well as beneficial microbes. The demand for organically produced food and functional food has increased in the last decades and this has been recognized as an important consumer trend worldwide. One area of progress is in the field of plant disease management where a promising path has been arrived at through combining organic bioinputs and reduced use of chemicals. *Trichoderma* spp. (Pers.) are ubiquitous soil-borne, avirulent opportunistic plant symbionts. It is low cost, effective against pathogen, induces plant resistance to pathogens, production of anti-microbial metabolites, promotes absorption of nutrient and fertilizer use efficiency, improves developmental processes and yields. Amongst the various biocontrol agents *Trichoderma* species clearly dominate as biofungicides owing to its parasitizing ability on diverse group of phytopathogens. Ten (10) *Trichoderma* isolates were identified based on morphology, microscopic and molecular characterization. *In vitro,* evaluation of the isolates showed growth rate of 4.422 mm/h (TML-7) and 3.870 mm/h (TML-6), with correlated biomass production of 7.013 g/100ml (TML-7) and 6.597 g/100ml (TML-6). Similarly, screening of the ten isolates revealed high Zn solubilizing ability of TML-7 (95.14%) and TML6 (87.05%) and PO_4 solubilizing ability TML-7 (42.71%) and TML-6 (47.81%). All the isolates exhibited more than 50 percent inhibition of the fungi *S. sclerotiorum*. Maximum inhibition of 100% was shown by TML-7 (*T. viride*), followed by 90.37% inhibition by TML-6 (*T. asperellum*) against the test pathogen. The

combined efficacy of best potential *Trichoderma* isolates [TML-7 (*T. viride*) and TML-6 (*T. asperellum*)] and ecofriendly inputs (neem oil cake 0.1% and essential oil-citronella 25 µl/ml) were further tested in pot experiment with 14 treatments. The results showed the treatment combination of neem oil cake (0.1%) +TML-7 (*T. viride) +* citronella oil (25 µl/ml) (T-11) could completely reduce the white mold disease incidence of broccoli which was at par with the treatment (T7) with fungicide [Amistar Top (Syngenta)]. Accordingly, the maximum yield was for the treatments T-11 and T-12 which were 4.46 kg and 4.42 kg respectively and at par statistically.

Keywords: *Trichoderma*, Diversity, Antimicrobial properties.

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PP2-23

Exploring the Diversity of Tea Plant Microbiome in Assam

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The tea plant (*Camellia sinensis* var. *assamica*) is a species intrinsically linked to its specific climate and ecological environment. Central to this ecological niche is the plant's microbiome, which significantly influences nutrient acquisition and overall growth. Beneficial microorganisms, including certain bacteria and fungi, enhance the plant's resilience by improving nutrient uptake, providing disease resistance, and increasing stress tolerance. Conversely, pathogenic microorganisms can detrimentally impact the plant's health, yield, and longevity. This interplay encompasses both rhizosphere and endophytic microorganisms, underscoring the necessity of investigating microbial diversity associated with the tea plant to optimize its cultivation and ensure sustainability. A comparative study was conducted to investigate the microbiome of the tea plant, specifically focusing on the cultivar TV9, recognized for its fast-growing characteristics. Stems and rhizosphere soil samples were sourced from the National Active Germplasm Site at Tocklai in Jorhat, Assam, aimed at elucidating the diversity within the microbial population. Total genomic DNA was extracted from both the stem tissues and soil samples, followed by library preparation utilizing NEB Illumina Kits. Shotgun metagenomic sequencing of the 16S rRNA and Internal Transcribed Spacer (ITS) regions was performed on the Illumina NovaSeq 6000 system, generating paired-end 150bp reads. The resulting microbial composition and abundance were analyzed using Kaiju v1.7.3. The tea plant microbiome exhibits significant diversity, with a notable distinction between endophytes and the rhizosphere, as evidenced by 35.8 million reads in endophytes compared to 24.5 million in the rhizosphere. A total of 204,613 unique bacterial strains were identified in endophytes, predominantly belonging to Actinobacteria (98.3%), while the rhizosphere harbored 84,357 strains, primarily from Proteobacteria (60.1%) and Actinobacteria (27.1%). Among the endophytic bacteria, notable genera include plant growth-promoting species of *Bacillus*, *Rhizobium*, and *Sphingomonas*, whereas the rhizosphere featured nitrogen-fixing genera like *Bradyrhizobium* and *Pseudomonas*, forming symbiotic relationships with leguminous shade trees. Fungal diversity was less pronounced in endophytes, comprising 55 species mainly from Ascomycota (72.7%), in contrast to the rhizosphere, which contained 200 species, predominantly Ascomycota (78%). The high abundance of the genera *Fusarium*, *Thielavia*, *Thermothelomyces*, *Colletotrichum*, *Botrytis*, and *Magnaporthe* reflects their

ecological adaptability and the critical roles they play in decomposition and plant pathology. Despite the presence of pathogens within the core microbiome, several beneficial species offer promising potential for sustainable tea crop production. Understanding the dynamics of these genera is essential for advancing agricultural practices and managing plant diseases effectively.

Keywords: Tea, Rhizosphere, Plant microbiome intercaction, Endophyte

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PP2-24

Molecular Detection and Resistance Profiling of Mungbean Yellow Mosaic Virus in Diverse Mungbean Germplasm

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Mungbean [*Vigna radiata* (L.) Wilczek], a member of the Fabaceae family, is a nutritionally valuable crop. Despite India's leading global production, its average yield remains low due to various pests and diseases. Mungbean Yellow Mosaic Disease (MYMD), caused by the Mungbean Yellow Mosaic Virus (MYMV) of the *Begomovirus* genus in the *Geminiviridae* family, is particularly devastating, causing yield losses of 85-100 %. The lack of MYMV resistant mungbean varieties significantly impacts crop yields. To address this issue, we conducted an experiment at the College of Agriculture, Kyrdemkulai Research Farm in Meghalaya, India, from March to June 2024. Twenty mungbean germplasms were screened using a randomized block design with the infector row method under field conditions. Most germplasms tested were found to be moderately to highly susceptible to MYMV. However, three germplasms namely, IC32006, IC39373, and IC329079 showed moderate resistance to the disease. The moderately resistant lines discovered in this screening offer a promising foundation for future breeding efforts aimed at developing MYMVresistant mungbean varieties. Such varieties could significantly enhance mungbean production and contribute to food security in regions where MYMD poses a significant threat to crop yields. We confirmed the presence of the virus in collected samples using Polymerase Chain Reaction (PCR) with specific primers NM1 and NM2, which amplify the coat protein region (AV1 gene). The resulting amplicon of ~1000 bp indicated the presence of the MYMIV strain in the collected sample.

Keywords: Mung bean, Genotypes, MYMD, Begmovirus, Resistance

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PP2-25

Identification of Seed Physical Factors for Bruchid [*Callosobruchus maculatus* (Fabricius)] Resistance in Cowpea [*Vigna unguiculata* (L.)]

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Vigna unguiculata L. Walp is known by many different names *viz.*, Lobia, Boda, cowpea, Cuba bean and asparagus bean and it has pan India distribution including north-eastern India. It has complex uses in agriculture, as a green vegetable, *dal*, green manure and animal feed. It is believed that the yield potential of cowpea is not achieved due to several obstacles in production and storage like insect-pests, diseases etc. Among insect-pests in storage, majorly pulse beetle causes both quantitative and qualitative losses. Adverse effects of pesticides necessitate the need for ecofriendly approaches of pest control including host plant resistance. Hence, different cowpea accessions were analysed for evaluation of differential reaction to *C. maculatus* to identify the sources of resistance. Four hundred twenty five Cowpea core collection (425 acc.) were evaluated for their reaction to pulse beetles under no choice artificial infestation conditions. Significant variations among the accessions were observed for various parameters *viz*., oviposition, development period, adult emergence, number of emergence holes, weight loss and growth index (GI). Growth Index determines the appropriateness of the accessions for development andis the crucial consideration in growth and development of insect. The GI ranged from 0 to 6.83, and based on GI, accessions were categorized 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), highly susceptible (11 accessions, GI=5.464-6.830) to attack of *C. maculatus.*

Keywords*:* Bruchid, Cowpea, Growth Index (GI), Resistance

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PP2-26

Spray-Induced Gene Silencing for the Management of Fall Armyworm (FAW) in Maize: An Innovative and Eco-Friendly Approach

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The Fall Armyworm *Spodoptera frugiperda* (Lepidoptera: Noctuidae) is a widespread and most destructive insect affecting maize, particularly in regions with humid climates and temperatures ranging from 11 to 30°C, with an ideal temperature of 28°C. First instar caterpillars of FAW are gregarious and feed superficially on one side of leaf (or inside whorls) and spread to new host plant through ballooning mechanism. Initial sign of infestation is papery windows on leaf & defoliation. Second instar caterpillars feed gregariously in initial phase and make small leaf holes/shot holes while the third, fourth and fifth instar caterpillars often feed solitarily inside the whorls and cause large holes accompanied by larval droppings (excreta). Owing to increasing infestation of the pest and the limitations of current conventional methods for its management, there is a dire need for discovering advanced pest management approaches. To address these challenges, researchers are exploring for innovative strategies for effective and sustainable management of FAW. An alternative and promising approach could be Spray-Induced Gene Silencing (SIGS). SIGS involves the topical application of double-stranded RNA (dsRNA) or small RNA (sRNA) molecules to the plants. These molecules specifically target and silence virulence-related genes in the insect. When the insect comes into contact with or ingests these dsRNAs, its life cycle is disrupted, resulting in reduced infestation severity. SIGS offers a high degree of specificity, targeting only the insect's critical genes, thereby minimizing off-target effects and reducing environmental impact. Furthermore, SIGS can be seamlessly integrated into existing pests management practices, providing a sustainable and eco-friendly alternative to chemical treatments. This approach not only aligns with integrated pests management principles but also represents a significant advancement in pest management. By ensuring high specificity and minimal environmental impact, SIGS holds the potential to revolutionize the control of FAW in maize, offering a practical and sustainable solution to one of agriculture's persistent challenges.

Keywords: Maize, Fall Armyworm, Gene silencing

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PP2-27

Elevating Horticultural Standards: VNR Nursery's Contributions to Clean Plant Material

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As of December 2023, VNR Nursery has produced an impressive 8 million disease-free and virus-free fruit plants, significantly enhancing the quality and productivity of fruit crops across 325 districts in 24 states of India. This monumental achievement addresses the long-standing issue of inadequate

quality planting material, which has plagued the horticultural industry. VNR Nursery's journey began in 2012 with the establishment of healthy mother blocks of multiple fruit varieties and the implementation of necessary infrastructure to produce clean plants. These plants are cultivated in sanitized, protected structures and are subjected to rigorous pathogen testing and virus indexing, ensuring zero pathogen transfer to farmers' fields. This meticulous process guarantees the production of high-quality, disease-free planting materials. The availability of quality planting material is crucial for fruit crop production. Historically, farmers have relied on both organized and unorganized nurseries, which often lack the modern infrastructure required to produce healthy, disease-free plants. Existing nurseries in India frequently sell plant materials of unknown pedigree and poor quality due to the absence of greenhouses, mist chambers, and efficient nursery tools. Additionally, the use of inferior quality seeds, non-standardized rootstocks, outdated tools, and diseased scion woods further compromise the productivity and quality of fruit crops. To overcome these challenges, VNR Nursery adopted state-of-the-art infrastructure, equipment, and best practices recommended by horticultural experts. Their efforts included visits to ICAR institutions, SAUs, KVKs, and consultations with scientists and technologists to enhance their production capacity and infrastructure. VNR Nursery's commitment to quality has been recognized with a 3-star accreditation by the NHB since 2019. VNR Nursery operates with 13 hectares of modern nursery infrastructure and 65 hectares of mother blocks, producing over 2.5 million clean planting materials annually across more than 76 varieties of 20 fruits. This initiative not only ensures the availability of disease-free planting material but also significantly improves the productivity and quality of fruit crops, thereby contributing to the overall advancement of horticulture in India.

Keywords: Nursery management, Virus indexing, Quality planting materials

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PP2-28

Speed Breeding - A Robust Technique for Accelerating Crop Research and Breeding More Crops in Less Time''

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As the world's population rises and the climate shifts, global food security has become a serious concern. Several important crops are not improving at a rate that will meet future demand. The lengthy generation periods of agricultural plants, which have been shortened by various techniques including shuttle breeding, doubled haploid technology, genomic selection, and speed breeding, may be partially to blame for this sluggish rate of advancement. A technology created by NASA, speed breeding significantly shortens the generation time and accelerates global plant breeding and research initiatives. By quickly progressing generations, speed breeding shortens the breeding cycle and expedites agricultural research. Several methods for speed breeding include shortening the generation time, extending the amount of time that plants are exposed to light each day, combining early seed harvest, and cycling rapidly from seed to seed. Six generations of spring wheat, durum wheat, barley, chickpeas, and peas may be produced annually as opposed to two to three generations

under typical glasshouse conditions, and four generations of canola (*Brassica napus*) can be produced annually. Speed breeding offers a quick generation cycle through single-seed descent (SSD), shortens the generation period, and allows for responsiveness to broader agricultural development initiatives. In addition to optimizing the transgenic pipeline, gene stacking, genomic selection, and express editing for crop growth, speed breeding may be utilized to study a range of physiological factors. Speed breeding has several drawbacks, such as the inability to be used with plants that need vernalization or short days. In contrast to the fields where crop production typically occurs, the artificial environment surrounded by certain buildings is where the provided speed breeding operations are conducted. Over the past century, the rise of the human population has been made possible by the high-yielding crops that plant breeding has developed. The need for population growth will be satisfied in the upcoming decades via rapid breeding to create next-generation types.

Keywords: Breeding cycle, Controlled environment, Single-seed descent (SSD), Photoperiod.

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PP2-29

Meta-QTL Analysis and Gene Identification for Enhancing Aluminum Toxicity Tolerance in Rice

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Rice exhibits notable tolerance to elevated aluminum (Al) levels in the soil, yet the underlying genetic and physiological mechanisms remain incompletely understood. Recent studies have identified several candidate genes (CGs) and quantitative trait loci (QTLs) linked to Al toxicity tolerance in rice, though many remain to be accurately mapped. To address this, we conducted a meta-QTL (M-QTL) analysis by integrating data from 12 independent mapping studies and five Genome-Wide Association Studies (GWAS). This analysis identified 53 M-QTLs from 157 projected QTLs, which were further refined to 28 M-QTLs based on overlapping regions on a consensus map. A batch gene retrieval from the RAP database within these 28 M-QTL regions yielded 2,765 non-redundant genes. Cross-referencing M-QTL candidate genes with six expression datasets related to Al toxicity tolerance in rice identified 219 CGs showing significant differential expression, with 34 common CGs emerging across at least two studies. Further downstream analysis of these CGs revealed the presence of cis-regulatory promoter elements, transcription factors, and transporter proteins implicated in Al toxicity tolerance. The expression patterns of four key CGs—NRT2.3, ALMT4, MT1, and MTP11—were analyzed, revealing significant upregulation in the Al toxicity-tolerant rice genotype Anjali. In contrast, in the sensitive genotype Swarna, only NRT2.3 showed upregulation, while ALMT4, MT1, and MTP11 were downregulated. Understanding these meta-regions and the associated CGs offers significant potential for developing rice genotypes with enhanced Al toxicity tolerance in acidic soils.

Keywords: Rice, Aluminium toxicity tolerance, Meta-QTL analysis, Gene mapping, Crop breeding

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PP2-30

Biophysical and Biochemical Basis of Host Plant Resistance in Chickpea Genotypes against *Helicoverpa armigera* (Hübner) in Mid Hills of Meghalaya

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Chickpea (*Cicer arietinum* L.) is the third most significant legume crop cultivated globally. Chickpea is infested by an average of about 60 insect pests, of which gram pod borer, *Helicoverpa armigera* (Hübner) (Lepidoptera: Noctuidae) is identified as the major pest. The migratory nature, polyphagous, short life cycle, multivoltine and resistance to insecticides makes *H. armigera* very difficult to control. In order to develop the resistance in chickpea genotypes against *H. armigera*, it is very important to understand the interrelation between the chickpea biochemical constituents and their effect on insect growth and development. Hence, the research has been undertaken where nine chickpea genotypes including both susceptible and resistant check, ICC-3137 and ICCL-86111 respectively were screened against pod borer, Helicoverpa armigera. All the genotypes in the varietal screening showed notable differences in terms of eggs and larval population, percentage of pod damage, and level of pest resistance The mean least eggs population was observed on ICC-17160 (0.726 eggs/ 5 plants) which was at par with GL-13001(0.862 eggs/5 plants). The minimum larval population was recorded in genotypes GL-13001(2.271 larvae/5 plants). The levels of resistance against *H. armigera* on different cultivars are also investigated by adopting Detached Leaf assay. In leaf detached assay, significantly minimum and maximum weight gain as 2.39 mg and 4.65 mg recorded was respectively for ICC-17160 and JG-24. The egg and larval population, larval weight, larval survival, percent pod damage demonstrated an inverse relationship with the density and length of non-glandular trichomes on leaves as well as on the pods and also with pod wall thickness but exhibited a direct relationship with pod length and pod width. Different biochemical constituents viz., total soluble sugar (TSS), proteins, total phenols, flavanols, tannins, superoxide dismutase (SOD) and polyphenol oxidase (PPO) in chickpea genotypes were estimated from both leaves as well as pods at 48 and 96 hours after feeding of *H. armigera*. In the biochemical constituents, the highest total phenol, superoxide dismutase (SOD) and tannins content were observed in genotype ICC-17160 whereas the highest protein and total soluble sugar (TSS) content was recorded in the genotype JG-24. The flavanols and polyphenol oxidase (PPO) content was found highest in GL-13001 which was statistically par with the genotype ICC-17160. The correlation analysis at 5% significance level between the average populations of *H. armigera* and pod damage, with respect to biochemical constituents in various chickpea genotypes, revealed that total phenols, flavanols, tannins, superoxide dismutase, and polyphenol oxidase content were inversely correlated with the *H. armigera* population on chickpea genotypes. Whereas, total soluble sugar and protein content exhibited a positive association with the *H. armigera* population, leading to increased pod damage in chickpea genotypes. Among all the inter specific test genotypes, ICC-17160 showed best performance both biophysically and biochemically in contrast to the check varieties.

Keywords: Biochemical, Chickpea, Detached Leaf assay, Genotypes, *Helicoverpa armigera*

PP2-31

Characterisation of Soil Microbial Community of Scented Rice under Different Nitrogen Application and Soil Moisture Regimes

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Plant-microbe interactions at rhizosphere interface plays significant roles on plants nutrition and such interactions may be under tremendous influence by applied doses of inorganic nitrogenous fertilizers and availability of soil moisture. This study assessed whether applied low and high doses of inorganic N fertilizer under aerobic and submerged conditions alter the core microbiota community in the rhizosphere of scented rice. A control experiment was conducted under aerobic and submerged condition with four different treatments each viz., Control (no application), Biofertilizer (CAU Bioenhancer), Low N (25 kg ha^{-1}) and High N (125 kg ha^{-1}) with five replications. Rhizospheric soil were collected at flowering stage and their bacterial community composition was analysed based on sequencing of the V3-V4 region of the 16S rRNA gene. Values of soil pH, organic carbon and availability of N, P and K, and readily soluble Al were significantly varied between treatment combinations. Growth and yield attributes such as plant height, number of effective tillers and grain and straw yield of rice were also greatly influenced by different soil moisture regimes. The diversity parameters of bacterial community among the treatments varied significantly. The diversity parameters of bacterial community among the treatments varied significantly. A total of 1059 OTUs were identified commonly under aerobic and submerged condition by 16S rRNA sequencing profiling, using a 97% of similarity against the database. 221 OTUs and 400 OTUs were obtained from aerobic and submerged conditions, respectively. Different treatments under submerged condition showed higher indices of richness and diversity estimators (Sobs, Chao, ACE, Shannon, Simpson, and Fisher). Of the core bacterial genera, the order of most abundant genera under aerobic low N and high N were *Schlegelella*> *Thermomonas*> *Salinibacterium*> *Dyadobacter*> *Chitinophaga* and *Thermomonas*> *Salinibacterium*> *Mucilaginibacter*> *Aeromicrobium*> *Dyadobacter respectively.* Under submerged low N and high N were *Treponema*> Unclassified Cloacamonae> *Leptolinea*> *Sulfuricurvum*> *Desulfomicrobium* and Unclassified Cloacamonae, *Treponema*> *Sulfuricurvum*> *Leptolinea*> Unclassified Fusobacteriales respectively. Findings clearly demonstrated the differential influence of high N fertilizer dose under aerobic and submerged conditions on the composition of the core microbiota of scented rice rhizosphere.

Keywords: Core microbiota, Metagenome, Moisture Regimes, Rhizosphere, Rice

PP2-32

Assessment of Genetic Diversity and Molecular Characterization of Blackgram (*Vigna mungo* L.) Genotypes through SSR Markers

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Assessing the degree of genetic diversity and marker trait association (MTA) is highly usable for the identification of highly diverse genotypes and studies on markers linked to trait of interest. This study aimed to evaluate highly diverse selected blackgram genotypes and association between molecular marker and yield contributing traits for crop improvement programme. For the assessment of principal component based morphological, molecular grouping and association studies in selected thirty blackgram (*Vigna mungo* L.) genotypes, the investigation was performed at Advanced Centre for Rainfed Agriculture (ACRA) located in Dhiansar, Jammu (J&K) during kharif 2021 for the study of eleven morphological characters *viz*. plant height, days to fifty percent flowering, number of branches per plant, days to maturity, number of pods per plant, number of seeds per pod, pod length, number of clusters per plant, 1000 seed weight and seed yield per plant. Molecular characterization was done using 15 SSR markers. All the genotypes exhibited considerable amount of genetic variability at 1 % level of significant for all the characters under studied. Genetic similarity estimates based on the binomial data generated through these markers using Jaccard's coefficient ranged from 0.13 (PU-15-30 / PU-07-7) to 0.93 (PU-KUG216 between PU-9/PU-IPU-243) exhibiting considerable diversity among the thirty genotypes. Based on dendrogram, PCA from field data and molecular data, two genetically different groups of genotypes namely PU-15-2, PU-13-05 and AZAD-2 fall in the group-1 while five genotypes namely PU-UPU-97-1, PU-40, PU-KUG216 and PU-15-32 fall in group-2, were obtained which can be further use in introgression of specific traits from one group to other group of genotypes. Based on morphological and molecular studies two genetically diverse groups were formed which can be recommended in further hybridization programme. Three markers *viz.,* VR-102, CEDG-156 and CEDG-176 showed association with seed yield per plant that can be useful in yield improvement studies in blackgram.

Keywords: Blackgram, SSR markers, PCA, Marker trait association, Genetic diversity.

PP2-33

Elucidating Genetic Diversity and Population Structure in Rice Germplasm and Identification of High Yielding Stable Genotypes Using MGIDI and GGE Biplot Analysis

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The north-eastern region of India is considered a part of the Indo-Malayan biodiversity hotspot and is suffering from the extinction of a large number of landraces in different crop species. Recent changes, such as rapid urbanization, extreme climate events, and the introduction of profitable agriculture using HYVs, have further contributed to this process. To conserve and utilize the germplasm, systematic evaluation is urgently required. By evaluating 148 rice genotypes of the NEH region of India for three successive years, key traits, namely, the number of filled grains per panicle, test weight, and yield per plant, were found to be governed by additive gene action with lesser effects of environment on their expression. Based on multi-trait stability index (MTSI) and GGE biplot analysis, genotypes, namely Beoidhan 2, Jalbudi, Motadhan, Salidhan, Tapolea, Lypyagopal, Badalsali, and Dagum, were identified. The first five principal components cumulatively explained 79.51% of the total variance. Genotyping of rice germplasm using 50 GCP markers resulted in a total of 94 alleles. PIC values ranged from 0.14 to 0.69 with an average of 0.36. Likewise, Shannon's information index ranged from 0.20 to 1.33, with an average of 0.57. Nei's genetic distance-based clustering has grouped the genotypes into four major clusters, whereas the Bayesian model-based approach has resulted in two groups with 142 pure lines and 06 admixtures. Based on analysis of molecular variance (AMOVA), 57.63 percent of the variance was due to genetic differentiation among the individuals within populations, while 41.92% of the variance was accounted for within individuals. Wright F statistics indicated that the genotypes of Sikkim were highly differentiated from Tripura. The second highest level of differentiation was observed among the genotypes of Mizoram and Tripura. In principal coordinate analysis, the first three axes explained 25.79% of the total variation. The landraces with high levels of differentiation and enhanced yield potential in multi-environments, namely, Motadhan, Salidhan, Tapolea, and Lypyagopal, would help increase the yield potential vis-à-vis farmers' income.

Keywords: Genetic diversity, GGE Biplot, MGIDI, Population structure, SSR marker

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PP2-34

Identifications of QTLs for Drought Tolerance in Teosinte Introgressed Maize Population

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Maize grown in subtropical and temperate regions is often subjected to moisture stress. Teosinte (*Z. mays* ssp. *parviglumis*), the maize's wild progenitor, is the vital source of genes of various biotic and abiotic stress tolerances. The present study aimed to identify the drought tolerant superior lines with the help of correlation analysis, phenotypic and molecular variability present in the superior drought tolerant lines along with identification of Quantitative trait locus (QTLs) associated with drought tolerance. The BC_1F_2 teosinte introgressed mapping populations comprised of 203 lines were phenotypically evaluated for twenty-five morpho-physiological traits associated with drought tolerance. A total of 71 lines have been identified as superior on the basis of fifteen traits associated with drought stress. On the basis of molecular profiling of 43 polymorphic SSR markers, 73 lines were clustered into fourteen groups at 0.40 Jaccard similarity coefficients. QTL mapping is important in the process of molecular marker-assisted selection for a complex trait like drought tolerance. Out of 80 QTLs, three QTLs explained phenotypic variation of 14.67 (LR), 12.84 (PH) percent both linked with the marker *umc1303* and 11.79 (ASI) percent linked with the marker *phi113.* These markers, which are linked with QTL associated with morpho-physiological traits, seem to be useful. The maximum number of QTLs controlling the trait DTI was seven distributed across the chromosomes 2, 4, 6, 8, and 10, followed by days to silking (6 QTLs) distributed over chromosome numbers 1, 2, 3, 4, 9, and 10. Twenty-three QTLs controlling multiple traits for drought tolerance, and contributing traits were co-localized. Hence, molecular breeding approaches offer ample opportunities for developing stress-resilient and high-yielding maize cultivars.

Keywords: QTL, Teosinte, Maize, Drought, Wild relative

PP2-35

Elucidation of Genetic Diversity in *Oryza sativa* L. Using Principal Component Analysis (PCA): A Multivariate Approach to Characterize and Evaluate the Genetic Structure of Rice Landraces

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The current study aimed to estimate key genetic parameters, including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and genetic advance (GA), as well as correlations, path coefficients, genetic divergence, and principal component analysis (PCA), using data collected from 96 rice landraces along with six checks. The analysis of variance revealed highly significant mean squares attributable to genotypes across all studied traits, indicating substantial genetic variation among the genotypes, thus providing considerable scope for efficient selection and potential genetic gain. Higher PCV values than GCV values indicate the influence of the environment on the characters under investigation n. NCG (19.83) had the highest coefficient of variation indicating the effectiveness of direct selection for improvement of these traits. Grain yield per panicle demonstrated a highly significant positive correlation with biological yield (r = 0.90) and also exhibited positive correlations with panicle length (r = 0.42), filled grains per panicle (r = 0.41), and harvest index (r = 0.36). The path coefficient analysis revealed that filled grain per panicle (1.65) has maximum and positive direct effect followed by biological yield (0.91), and harvest index (0.40) and hence, these traits were identified as the most effective selection criteria for improvement of grain yield per plant in rice landraces. Cluster analysis based on agro-morphological data divided the landraces into four clusters. Cluster 1 contained the landraces with high mean values for plant height, days to 75% flowering, days to maturity, effective tiller, filled grain per panicle, harvest index, panicle length, and spikelet per panicle. Cluster 4 has landraces with high mean values for grain yield per panicle PCA for yield attributing traits showing that 62.84% of the total variation was accounted for by the first three principal components. Principal component 1 (PC 1) explains 30.52% of the total variation while 19.17% and 13.14% of the total variation were explained by principal component 2 (PC 2) and principal component 3 (PC 3), respectively. PC 4 and PC 5 contribute 11.52% and 7.34% of the total variation obtained in the eigenvector analysis, respectively. Hence, a higher amount of variation i.e., 81.70% was contributed by the first five principal components.

Keywords: Rice, landraces, Correlation, Path coefficient, Divergence, Principal component.

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PP2-36

Molecular Genetic Divergence Analysis Amongst High Curcumin Lines of Golden Crop (*Curcuma longa L.*) Using SSR Marker and Use in Trait-Specific Breeding

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Curcuma longa L., is recognized worldwide as a medicinal and economically important plant species due to its curcumin content which is an industrially important compound. In this study, a total of 329 accessions were collected from four states of India and planted in the experimental farm of CSIR-NEIST, Jorhat, India, in augmented design. Among these, 152 high curcumin (>1.50 %) accessions were screened for molecular study using 39 SSR primers. The primers showed the most efficient outcome with 2-8 allele/ loci with 100 % polymorphism. Cluster analysis revealed the construction of three clusters, out of which one cluster was geographically dependent, and germplasm was particularly from Assam state. Jaccard's pairwise coefficient showed maximum genetic dissimilarity of (0.75) between accession RRLJCL 3 and RRLJCL 126, indicating high variation as it was from two different states *viz.* Arunachal Pradesh and Nagaland respectively and minimum genetic dissimilarity of (0.09) between RRLJCL 58 and RRLJCL 59 indicating significantly less variation as the two accessions were from same states, *i.e.*, Arunachal Pradesh. Analysis of Molecular Variance (AMOVA) revealed high molecular variation within the population (87%) and significantly less variation among the population (13%). Additionally, Neighbour Joining dendrogram, Principal Component Analysis (PCA), and bar plot structure revealed similar clustering of germplasm. This diversity assessment will help in selecting the trait-specific genotypes, crop improvement program, conservation of gene pool, marker-assisted breeding. To the best of our knowledge, it is the first molecular diversity report among 152 high curcumin lines from North East India using 39 SSR primers.

Keywords: *Curcuma longa*, Curcuminoids, Molecular Diversity, SSR Primer, Crop improvement

B. ANIMAL & FISHRIES

OP2-01

Protein Profiling of Cervico-Vaginal Mucus during Follicular Phase of Estrous Cycle in Lakhimi Cow

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Lakhimi, a registered indigenous breed of cattle of Assam, mostly reared for milk as well as draught purpose by the farmers. Accurate timing of estrus detection is the prime criteria for successful reproduction. In Lakhimi cow, estrus expression is not much prominent and due to shorter period of standing heat, scanty cervico-vaginal discharge, estrus detection becomes a difficult task. Hence, a baseline study was conducted with primary objectives of evaluating the protein profile in cervico-vaginal mucus (CVM) and to correlate the protein profile with serum progesterone and estrogen during follicular phase of estrous cycle which might be helpful for developing biomarkers. A total of 200 numbers of Lakhimi cattle were screened for the study and out ofthese 12 normal cyclic Lakhimi cows of 2ndto 4th lactation were selected based on presence of mature corpus luteum, other clinico-gynaecological and ultrasonographic examination of reproductive organs. Each experimental animal was administered $PGF_2α$ analogue injection intra-muscularly for induction of estrus. Later, based on the transrectal ultrasonographic examination along with various behavioural signs, proestrus and estrus stage of estrous cycle was demarcated. The CVM samples were collected aseptically. A portion of this was immediately utilized for examination of physical characteristics and the remaining portions were immediately stored at -40˚c for biochemical analysis. Total protein concentration was evaluated from CVM and thereafter the sample was subjected to SDS-PAGE for protein profiling. Also, the serum progesterone and estrogen hormones were estimated using commercial ELISA kit for each blood sample. Findings of the study showed the average total protein concentration (mg/ml) of the CVM to be significantly higher during proestrus stage (4.37 ± 0.26 mg/ml) than estrus stage (3.27 ± 0.22 mg/ml) of estrous cycle in Lakhimi cow. On SDS-PAGE analysis, significantly high average protein bands were recorded during estrus stage (6.00 ± 0.53) than proestrus stage (2.91 ± 0.22) of estrous cycle in Lakhimi cow. Also, the intensity of band was found higher during estrus than proestrus stage. The serum progesterone and serum estrogen shows significant correlation with total protein concentration during both the stage of estrous cycle. Moreover, Serum progesterone shows significant correlation with average protein bands only at proestrus stage of estrous cycle, whereas, serum estrogen shows significant correlation with average protein bands at both the stage of estrous cycle in Lakhimi cow. Therefore, it can be concluded that, further identification and characterization of individual proteins may be useful for development of estrus detection biomarkers for Lakhimi cows.

Keywords: Cervico-Vaginal Mucus, Cow, Protein profiling

OP2-02

In-vitro Semen Characteristics and Fertility of Lumsniang Boar during Liquid Preservation following Artificial Insemination

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Lumsniang is a crossbred pig with 75% Hampshire and 25% Niang Megha (indigenous breed) inheritance developed under AICRP on Pig. For the study, semen was collected from six sexually matureLumsniangboars aged 2 to 4 years by gloved hand method and a total ofthirty-six semen ejaculates comprising six from each boar were collected. Immediately after collection, the semen volume, sperm concentration and initial sperm motility was recorded. Only samples having a minimum of 100 ml volume, 150 million spermatozoa per ml of semen and 70% initial sperm motility were processed further for dilution with Beltsville Thawing Solution extender (BTS) at 1:2 ratio andincubated at a temperature of 16-18˚C for a period of 3 days. The liquid storedsemen samples were evaluated on 0 dayand 3rd day of preservation for *in vitro* quality parameters viz. sperm motility using Computer assisted sperm analysis (CASA), sperm viability by CFDA/PI staining, plasma membrane integrity by HOST, acrosomal integrity by Giemsa staining, mitochondrial integrity by JC-1 staining, DNA integrity by Acridine orange staining and lipid peroxidation by Bodipy staining. The artificial insemination (AI) conception rate and litter size at birth using this liquid preserved semen were also recorded. The percent total and progressive sperm motility was 78.92±2.67 and 65.27±3.22 on day 0 and 52.18±2.82 and 39.33±2.62 on day 3 respectively. The percent sperm viability, plasma membrane integrity, acrosomal integrity, mitochondrial integrity, DNA integrity and lipid peroxidation was found to be 85.72±1.38 and 54.94±1.15, 56.78±1.25 and 29.56±0.61, 88.78±1.01 and 59.11±0.92, 83.67±0.89 and 58.63±1.12, 96.05±0.38 and 93.84±0.28 and, 5.06±0.28 and 15.22±0.41 on day 0 and day 3 respectively.The mean AI conception rate was 83.87 percent and mean litter size at birth was 8.97±1.45. In conclusion, Lumsniang boar semen can be successfully preserved for 3 days in BTS extender at 16-18˚C with 83.87 percent AI conception rate and 8.97 ±1.45 litter size at birth.

Keywords: Pig, Artificial insemination, Semen preservation

OP2-03

Evaluation of Egg Quality Traits of Indigenous Geese of Assam: An Unexplored Biodiversity

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Assam, a state of north eastern India, cradles in its lap an indigenous germplasm of geese which are distributed throughout Assam. It can be regarded as a unique bio diversity of North Eastern India. They are popularly known as '*Rajhanh'* meaning 'King of ducks' because of their royal and majestic gait with distinct long neck. To our dismal, they remained unnoticed and could not gain much popularity like chicken and duck. They needed to be explored and scientific studies to be carried out. Geese eggs are large in size and nutrient dense. It is a known fact that the egg quality traits are foremost selection standard in poultry breeding. Poor egg quality leads to economic losses at all production stages. Keeping this in mind, a study was undertaken to observe the internal quality of eggs to assess the egg quality traits of indigenous geese egg. Data for egg quality traits were generated from a total of 32 numbers of geese eggs. Laboratory work pertaining to egg quality traits were carried out by following standard techniques in the Department of Livestock Products Technology, College of Veterinary Science, Assam Agricultural University, Khanapara, Guwahati, Assam. The means and their standard errors for egg weight, shape index, shell weight, shell thickness, specific gravity, albumen index, Haugh unit and yolk index were found to be 115.445 ± 2.320 g, 70.476 ± 1.120, 16.756 ± 0.282 g, 0.560 ± 0.009 mm, 1.285 ± 0.017, 0.075 ± 0.001, 64.662 ±1.201 and 0.362 ± 0.006 respectively. The range for egg weight, shape index, shell weight, shell thickness, specific gravity, albumen index, Haugh unit and yolk index were recorded to be 91.710 to 140.140 g, 61.45 to 93.56, 13.64 to 20.95 g, 0.490 to 0.700 mm, 1.150 to 1.570, 0.065 to 0.091, 48.990 to 77.740 and 0.298 to 0.417 respectively. The yolk colour was mostly observed to be yellow in colour and sometimes it looked to be orange in colour. Egg shell colour was mostly observed to be white in colour and sometimes it appeared as cloudy white.

Keywords: Rajhanh, Indigenous duck, Egg quality, Assam

OP2-04

Decoding Selective Sweeps Associated with Tropical Adaptability in Guinea Fowl through Whole-Genome Sequencing

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The helmeted Guinea fowl is a domesticated poultry species, plays a crucial role in agriculture due to its low-input requirements, remarkable adaptability and strong resistance to diseases. In Guinea fowl, the investigation into the genetic basis of adaptive evolution remains largely unexplored, thereby presenting a significant opportunity for advancing the identification and exploration of genes linked to adaptability. This is the first work in Indian Guinea fowl population which is expected to have been selected differently from guinea fowl populations in other parts of world. The aim was to identify potential genomic selective sweeps linked with thermo-tolerance in the course of this study. Six individuals of the Pearl variety of Guinea fowl were selected and blood was aseptically collected. Isolation of genomic DNA was carried out and the integrity and quantity of were assessed. Subsequently, samples underwent whole-genome sequencing (WGS), and next-generation sequencing (NGS) libraries were constructed for sequencing on the Illumina platform. Quality checks for sequence reads, data pre-processing, mapping, variant calling and annotation were performed using appropriate bioinformatics tools. Fixation index test (FST) statistics was employed to explore the selective sweep regions. Several genes viz. *HSP90AB1, HSPA12A, CACNA1B, KIT, RAD, RAF1, MAP2K1, PACRG, MITF, BOK, ARPP21, ARHGAP1, MLH1*, and *MTF* were found to be potential thermo-tolerant candidate selective sweeps. These putatively selected genes were significantly enriched for diverse biological pathways and molecular functions. In addition, these functional candidate genes are significantly involved in different signaling pathways which are potential candidates underlying physiological adaptation to heat stress in Guinea fowls to radiation. The genetic mechanism facilitating adaptation to hot environmental conditions may be evolved through the influence of these candidate genes, serving as functional targets within the genomic framework. Our strategic findings provide crucial insights into distinctive candidate genes that could serve as the foundation for future molecular breeding focused on achieving rapid and sustainable improvements in thermo-tolerance and disease resistance of bird.

Key words: DNA, WGS, NGS, Illumina, Gene

OP2-05

Induced Breeding of *Wallago attu* (Bloch & Schneider, 1801) and Seed Production in Manipur

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Wild collection of *Wallago attu* (Bloch & Schneider, 1801) seeds were collected from tributaries of the Barak river and stocked in ponds @ 2000/ha at Laphupat Tera, Imphal west district (24°30'17.3"N; 93°52'30.7"E) and at ICAR Manipur Centre Lamphelpat in June, 2022. Fishes were fed with live fishes @1.2-2% per day. Live fish, including tilapia, grass carp, common carp, silver carp fingerlings, were added to the pond to ensure a steady source of food for the brood fish. *W. attu* matured in 1^+ year. Water qualities were maintained at pH 7.0-7.5, dissolved oxygen 5.0-8.2ppm, total alkalinity 72.5-89.2ppm. The fishes were observed to be in fully mature condition during first half of July 2024, showing distinct secondary sexual characters in males and females. Induced breeding were done in captivity using Ovasis @ 0.8ml/kg body weight of female and 0.4ml in male in the evening. The injected male and female fishes were release in circular spawning tank having 10' diameter with water depth of 1.2m with a water flow rate of 2.5 litres per seconds. Spawning was observed after 6 to 8 hours of hormone injection at 26.5°C of water temperature. Fertilized eggs were slightly yellowish green, spherical, demersal and sticky measuring 1.8±0.2 mm in diameter. Unfertilized eggs were paler and opaque. Fertilized eggs were hatched out after 18-24 hours of fertilization at temperatures of 26.2-26.8°C. The freshly hatched larvae were slender, straight and transparent, gradually tapering towards the tail were measure 4.5 mm long and 1.5 mg in weight. The early larval stages are the most critical and vulnerable stages in the life cycle of *Wallago attu*. The yolk sac is fully absorbed on the 2nd day of hatching it is referred as a post-larva. For nurseries, small ponds of 0.02-0.10 hectares with a water depth of 1.0-1.2 m are ideal, while *Wallago attu* fry production can take place in areas as large as 0.25 ha. The ideal stocking density of *Wallago attu* in a nursery pond is 10 lakh to 12 lakh per hectare. The fries of W. attu exhibit cannibalistic tendencies and are very predatory. Therefore, in the *Wallago attu* nurseries, a plentiful food supply and segregation are required. The fish reaches a length of 3.8 cm to 5.42 cm in 15 days, weighing 2.0 g to 2.8 g, with a survival rate of 65-70%. The B.C. ratio was found to be 3.8. From the result, it was concluded that culturable seeds of *Wallago attu* may be produced successfully and profitably.

Keywords: *Wallago attu* breeding, Seed production, Manipur

OP2-06

Ex-situ Conservation of Endangered Fish Chocolate Mahseer *Neolissochilus Hexagonolepis* (Mcclelland, 1839) through Short-Term Sperm Preservation Method

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Short-term storage of fish sperm is a simple and cost-effective process in fishery research from basic to applied perspectives. It has been used to elucidate and evaluate gamete biology and quality, perform in vitro fertilization, develop sperm cryopreservation protocol. With this background, a study was conducted to assess the sperm quality and the effect of short-term sperm storage on sperm motility of endangered fish *Neolissochilus hexagonolepis*. *N. hexagonolepis* male were collected from various river located in West Jaintia hills, Meghalaya and transported to ICAR fish farm for brood raising. After one-year raising in pond, milting was observed in the month of June-August. The milt/semen samples were collected in 4.5ml graduated cryovials from ripe male brooder. The cryovials were tightly closed and kept in crushed ice (0-4°C) for semen quality assessment and preservation process in the laboratory. Four different types of extenders were selected for this study such as Fish ringer solution (E1), Modified fish ringer solution (E2), Alsever's solution (E3) and Egg-yolk citrate (E4). The collected fresh milt/semen were diluted with extenders in two ratio 1:4 and 1:9 and kept in the refrigerated temperature (4°C) for 8 days to observe the sperm motility. The result showed that sperm motility decrease as the day increases. Within 5 days of storage, sperm motility reduces from 90-95% to 40-50% motility in all the extenders. On 8th day, highest sperm motility was recorded in E2 (20%) followed by E1 (15%), E3 (10%) and E4 (0%). Also, higher sperm motility was observed in diluent ratio of 1:9 than in diluent ratio of 1:4. The present study reveals that modified fish ringer solution extender (E2) is the best among the selected extenders for short-term sperm preservation of *N. hexagonolepis* at 1:9 diluent ratio. The finding of this study will be helpful in *ex-situ* conservation and seed production of *N. hexagonolepis* for mid hill aquaculture.

Keywords: *Neolissochilus hexagonolepis,* Short-term sperm preservation, *Ex-situ* conservation

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OP2-07

Ecopath with Ecosim-Based Mass-Balance Modelling in a Small Sub-Tropical Reservoir: Strategies for Sustainable Fisheries Management

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Ecosystem-based fisheries management has become increasingly popular for sustainable practices in recent years. Small reservoir ecosystems are recognized as highly productive, yet they remain underutilized due to gaps in understanding their ecological functions and potential output. To assess the trophic structure, energy flow, maturity, stability, and ecosystem functioning of the Maphou Reservoir, a mass-balance model of trophic interactions was developed using the Ecopath model with Ecapth and Ecosim. The study, conducted from June 2021 to May 2022, utilized primary data collected from four designated sampling sites and secondary data from published literature. The analysis considered ten functional groups and revealed three trophic levels (TL I, II, and III) within the ecosystem. The majority of organisms were found in trophic level II, consisting of low-order primary consumers. Exotic fish were the most exploited group (EE = 0.782) due to fishing pressure, followed by herbivorous fish (EE = 0.623). Carnivorous fish, as the top predator, emerged as a keystone species based on the keystone index (Keystone index2= 1.35). The mix trophic index (MTI) indicated that lower trophic level functional groups (detritus and phytoplankton) positively influenced most higher trophic level groups, demonstrating a "bottom-up" controlled ecosystem. The ecosystem is characterized by a grazing food web, with higher transfer efficiency from primary producers (TE = 4.864%) compared to detritus (TE = 4.024%). It is classified as immature (TPP/TR = 3.628) and developing (TPP/TB=70.70), exhibiting strong resilience against external disturbances (overhead = 63.27%). The food web is moderately complex (connectance index=0.463). Based on the study's findings, detritivores and phyto-planktivorous fish species are recommended for future augmentation programs, as they positively impact most higher functional groups.

Keywords: Ecopath, Mapithel Dam, Ecopath, Bottom-up control, Mass-balance.

OP2-08

Stock structure analysis and reproductive biology of *Rita rita* (Hamilton, 1822) along the middle stretch of Brahmaputra River system using truss network analysis

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Rita rita, a freshwater bagrid catfish popularly known as 'Rita' is a commercially important food fish all along the Brahmaputra basin and its tributaries. A truss network was constructed by interconnecting 14 landmarks to form a total of 30 truss measurements, based on 300 samples collected from three populations representing Brahmaputra River, Jamuna River and Kopili River. The factor analysis (FA) of truss network indicated body depth related traits loading heavily on first factor, shape related traits belonging to caudal portion on second factor. The first principal component (PC1) explained 82.14% of the total variation, while PC2 explained 3.56% respectively. A total of 74% of the original groups were classified into their correct sample while 26% were misclassified individual using discriminant function analysis. In the present study, suggests the possible existence of two stocks of *Rita rita*, a single stock in the Brahmaputra River while Jamuna River and Kopili River contain the same stock. In the present study, data on reproductive biology containing sex ratio, condition factor, fecundity, hepatosomatic index and Gonado-somatic index (GSI) of *Rita rita* were assessed. Samples were collected from the landings centre located on the bank of river Brahmaputra at Tezpur, river Jamuna at Jamunamukh and river Kopili at Dharamtul from August,2022 to July, 2023. An overall sex ratio (M/F) of 1: 2.70 observed was statistically non-significant. The gonadosomatic index ranged from 0.22-3.81 in males and 0.65-11.45 in females, both showing peaks in the month of July. The hepatosomatic index (HSI) varied from 0.88-1.35 in male, 1.34-2.14 in females and 1.09-1.59 for the pooled sample, the value of HSI index gradually decreases with increase of GSI in both male and female. The fish was highly fecund and the fecundity ranged from 10445.88 to 26262.52 with an average of 16,865.89. The fecundity was found to increase with the increase of total length, body weight and the ovary weight and the relationship was linear and significant among them However, the relative condition factor >1 suggested the species to be in good condition throughout the year in both the males and females.

Keywords: Stock structure, Truss morphometrics, Reproductive biology, *Rita rita*

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OP2-09

Vision-Based Artificial Intelligence Solutions for Effective Monitoring of Smart Pig Farms

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Monitoring and managing large-scale commercial pig farms require precision and efficiency to ensure optimal animal welfare and productivity. Traditional methods of monitoring pigs are labour-intensive, time-consuming and often prone to human error. The integration of Artificial Intelligence (AI) techniques offers a promising solution for the automatic detection of pigs and the analysis of their behaviour. This study presents an AI-based approach for the detection and analysis of pig behaviour, focusing on the posture of the animals to monitor their health, well-being and overall farm productivity. Utilizing advanced computer vision techniques, such as deep learning models like Convolutional Neural Networks (CNNs) and Vision Transformers (ViTs), we have developed a model that can accurately identify pigs within images and videos, assess their body posture and provide real-time information about their apparent health status. The model was developed using the Python programming language, and the code was executed on a Tesla T4 GPU. It was trained on a diverse dataset containing images of pigs in various postures such as lying, standing, sitting and walking. These postures are key indicators of their health status, comfort and any potential signs of stress or discomfort. The detection model achieves an accuracy of over 90%, enabling reliable real-time operation for continuous monitoring without disrupting daily activities on the farm. One of the major advantages of adopting AI in large-scale pig farming is the ability to reduce labor costs and minimize the need for constant human supervision. Automated detection systems can analyze large volumes of data from cameras installed across the farm, significantly reducing the time required for manual observation. This allows farm managers to focus on more strategic decision-making, such as addressing identified health concerns or optimizing feeding strategies. Furthermore, AI-based posture analysis enables early detection of potential health issues such as lameness, which is often indicated by abnormal behaviour. The integration of AI model into the farm environment enables early detection for timely intervention, enhancing animal welfare and increasing the precision of farm management. The AI system can track changes in pigs' behaviour over time, providing insights into their stress levels due to environmental factors like heat, humidity or changes in the housing conditions. Therefore, adopting AI technology can enhance farm management practices and promote sustainable pig farming.

Keywords: Artificail Intelligence,Smart pig farming, Economics

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OP2-10

Conservation and Use of Artificial Insemination Technology in Pig; A SEM Based Model to Predict Farmers' Intension

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Artificial insemination (AI) has revolutionized the pig breeding industry, offering pig farmers the opportunity to rapidly disseminate superior genetics from top-quality boars to a larger population of sows. This present study, grounded in the Theory of Planned Behavior (TPB), sought to investigate the factors influencing tribal farmers' intentions to adopt AI in pig breeding in Meghalaya, India. To empirically test the TPB framework, the study developed structural equation model (SEM). This model hypothesized that farmer's personal attitudes (PA) and perceived behavioral control (PBC) would be significant predictors of their intention to adopt AI. Attitude, reflecting farmers' beliefs about the benefits and drawbacks of AI, was expected to directly influence their intentions. Additionally, perceived behavioral control, representing farmers' confidence in their ability to implement AI, was anticipated to play a crucial role in shaping their intentions. The findings of the study confirmed the hypothesized relationships. Both PA ($\beta = 0.264$, P value < 0.01), and PBC ($\beta = 0.522$, P value < 0.01) were found to be significant determinants of farmers' intentions to adopt AI. Farmers with positive attitudes towards AI, perceiving it as beneficial and efficient, were more likely to intend to adopt it. Similarly, farmers who felt confident in their ability to successfully implement AI at their farm level were more inclined to adopt it. These findings have important implications for both research and extension institutions in Meghalaya. Understanding the factors influencing farmers' intentions to adopt AI can guide the development of targeted extension programs and interventions. By addressing farmers' concerns and providing them with the necessary knowledge and support, extension workers can enhance AI adoption rates. In conclusion, this study provides valuable insights into tribal farmers' intentions to adopt AI in pig breeding in Meghalaya. By identifying the key determinants of adoption, the study can inform the development of effective extension strategies to promote AI adoption and improve the livelihoods of pig farmers in the region.

Keywords: Pig, Artificial insemination, Conservation, Adoption

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OP2-11

The Critical Need for Developing a Vaccine against a Global Threat: African Swine Fever Virus

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African Swine Fever (ASF) remains one of the most severe and complex viral threats to pig populations worldwide, with devastating consequences for the piggery sector and broader agricultural economies. First identified in the early 20th century, characterized by a high mortality rate and a lack of effective treatments, ASF has spread across continents, affecting regions in Africa, Europe, and Asia, with outbreaks leading to the loss of millions of pigs leading to devastating economic losses, food insecurity, and profound impacts on rural livelihoods. The disease's rapid transmission through direct contact, contaminated feed, fomites, and certain tick species has made it particularly challenging to control using traditional methods like culling, movement restrictions, and enhanced biosecurity measures. The global demand for a viable ASF vaccine has thus intensified; as such a solution is viewed as the most sustainable way to combat this persistent threat. The economic ramifications of ASF are staggering, with estimates indicating losses in the billions of dollars due to culling, loss of productivity, and trade restrictions. Farmers, particularly smallholder producers, are severely affected as ASF outbreaks can lead to the complete loss of their herds, destabilizing local economies and threatening food supplies. The disease's ability to spread rapidly, coupled with the limitations of current biosecurity measures, necessitates a robust vaccination strategy to mitigate its impact. The development of an ASF vaccine has become a critical focus for researchers and policymakers worldwide. Recent advances in biotechnology and immunology have led to promising candidates in various stages of development. However, challenges such as the virus's genetic variability and the need for a vaccine that can be both effective and affordable remain significant hurdles. Global collaboration is vital in addressing the ASF crisis. This includes partnerships between governments, international organizations, and the private sector to share resources, research findings, and funding. Coordinated efforts can accelerate vaccine development and deployment, ensuring that affected regions receive timely assistance. In conclusion, the urgency for an effective ASF vaccine cannot be overstated. As the disease continues to threaten pig populations and the livelihoods of millions, immediate action is necessary to prioritize research, development, and global cooperation. Investing in an ASF vaccine is not only essential for the health of pig populations but also crucial for the stability of the global pork industry and food security. A comprehensive strategy that emphasizes vaccine development, collaboration, and education is need of the hour to combat this devastating disease and safeguard the future of these livestock sector.

Keywords: African swine fever, Pig, Biosecurity, Vaccine

OP2-12

Comparative expression profiling of miRNAs in African Swine Fever Virus (ASFV) infected and non-infected porcine tissue samples

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This study was conducted to explore the differential expression of microRNAs (miRNAs) in spleen and lymph node tissues in response to African Swine Fever Virus (ASFV) infection. These tissues play central roles in the porcine immune system, particularly in pathogen detection and immune response regulation. A total of 15 miRNAs hypothesized to be involved in ASFV infection based on earlier studies and bioinformatics predictions were selected for the present study. For the differential expression profile of these miRNAs, three groups of animals were used *viz.* Died (Pigs died after ASF infection), Survived (Pigs survived after the infection) and a Control (Pigs not infected with ASFV). The study was conducted in two phases. The first phase focused on qualitative expression studies using conventional polymerase chain reaction (PCR) to identify miRNAs that were expressed among the three groups. This phase was critical in pinpointing candidate miRNAs that might be associated with either the progression or resolution of ASFV infection. Following this qualitative analysis, the second phase involved quantitative real-time PCR (qPCR) to measure the precise expression levels of the identified miRNAs. qPCR allowed for accurate quantification, providing a clearer picture of the miRNA-mediated regulatory mechanisms involved in ASFV infection and the immune response. Out of 15 miRNAs, 7 miRNAs (miR-140-3p, miR-140-5p, miR-500a-5p, miR-126-3p, miR-122-3p, miR-92a, miR-125a) were not expressed, while rest 8 miRNAs (miR-451, miR-92b-3p, miR-30d, miR-30e-5p, miR-122-5p, miR-125b, miR-181a, miR-145-5p) were found to be expressed in our samples and were further analyzed quantitatively by qPCR. In spleen tissue, miR-92b-3p, miR-30d, miR-30e-5p, miR-125b, and miR-122-5p were significantly upregulated in the survived compared to the died group, but were downregulated in comparison to the control group. In lymph node tissue, miR-451 was upregulated in the survived compared to the control group, while miR-92b-3p and miR-30e-5p were upregulated in the died compared to the control group. The findings suggest that these specific miRNAs may play protective roles during ASFV infection. By understanding the miRNA-mediated regulatory networks, this study provides insights into ASFV pathogenesis, potentially identifying miRNAs that could serve as biomarkers or therapeutic targets. In conclusion, this research addresses an important gap in the understanding of ASFV infection by focusing on miRNA expression in key immune tissues. These findings have the potential to advance knowledge of ASFV biology and contribute to the development of new strategies for preventing, diagnosing, and treating ASFV, with broader implications for other viral infections in livestock.

Keywords: miRNAs, ASFV, Infection, Tolerant, Biomarker

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OP2-13

Characterization of the Complete Mitogenome of Manipuri Black Pig and Tracing Its Domestication Status

Sri Shalini M., Likhitha Nunavath, Satish Kumar, Meera K., Nabajyoti Deka, Seema R. Pegu, Pushpendra Kumar, V. K. Gupta and Pranab Jyoti Das*

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This study provides a detailed characterization of the mitochondrial genome (mitogenome) of the Manipuri Black Pig, a recently recognized indigenous pig breed in India known for its adaptability, resilience, and unique traits. To explore its genetic composition and evolutionary background, the complete mitogenome (mtDNA) of this breed was amplified using 30 pairs of primers resulting in overlapping fragments. The amplified fragments were sequenced using Sanger sequencing. The sequences obtained were analyzed and aligned using EditSeq of Laser gene (DNA STAR Inc.). The complete mtDNA sequence was annotated using the MITOS web server. The analysis and annotation of the mitogenome of the Manipuri Black pig showed that the resulting mitogenome spans 16,691 bp and includes 37 mitochondrial genes (13 protein-coding, 22 tRNA, 2 rRNA), and a non-coding control region (D-loop). to infer maternal lineage and population dynamics phylogenetic analysis was conducted using the complete D-loop sequences due to its high mutation rate. Using maximum likelihood methods, we compared D-loop sequences from the Manipuri Black Pig with those from other domestic pigs in India, Southeast Asia, and Europe. The analysis showed that 13 out of 15 samples exhibited high genetic similarity, indicating a common maternal lineage. However, the two samples displayed significant genetic divergence, clustering more closely with European breeds, suggesting historical gene flow between Manipuri Black Pigs and European pigs. Further analysis of the D-loop sequences identified two unique single nucleotide polymorphisms (SNPs) 183. T>C and 1114. A>G in this breed of pig, distinguishing the Manipuri Black Pig from other pig breeds. These novel SNPs could serve as valuable molecular markers in future genetic studies. The observed low genetic diversity and presence of unique SNPs underscore the need to preserve the breed's genetic integrity. This study highlights the value of mtDNA analysis for understanding domestication patterns, genetic diversity, and maternal lineage in indigenous livestock breeds. The findings advocate for targeted breeding programs to maintain the unique genetic characteristics of the Manipuri Black Pig and contribute to broader insights into pig evolution and domestication in India and Southeast Asia.

Keywords: Manipuri Black Pig, mtDNA, Polymorphisms, Phylogenetic Diversity

OP2-14

Impact of Biodiversity and Climate Change on Emerging Viral Diseases in Swine in India

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Biodiversity plays a critical role in the epidemiology and management of viral diseases affecting pigs, particularly in the context of increasing global trade and environmental changes. Present study produces knowledge on key emerging viral pathogens in swine, including Japanese Encephalitis Virus (JEV), Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) and African Swine Fever Virus (ASFV). These pathogens are responsible for significant economic losses in the swine industry, and their genetic diversity has important implications for disease control, vaccine development, and biosecurity measures. Climate change, rising temperatures and altered precipitation patterns create favourable conditions for mosquito breeding, thereby enhancing the transmission potential of JEV in regions previously considered non-endemic. Screening of samples from pigs in the northeastern states has shown the presence of JEV antibodies, with a significant seasonal variation. On the other hand, PRRSV, with its high mutation rate, generates multiple lineages, complicating outbreak control efforts and necessitating constant surveillance and updated vaccination strategies. ASFV, which poses a growing threat to swine farming in several regions, particularly in India, presents additional challenges due to the diversity of host breeds and viral strains. Samples from Assam, swine populations tested for ASFV antibodies using iELISA demonstrated significant variability in susceptibility across different pig breeds. These findings highlight the importance of understanding host biodiversity in managing viral threats. Genetic variation among pig breeds and interactions with wild boar populations can influence viral transmission dynamics and the potential for cross-species infections. The study underscores the role of domestic pig and wild boar interactions in facilitating the spread of viral diseases like ASFV, especially in regions where their populations overlap. Additionally, environmental factors such as habitat changes and agricultural intensification may exacerbate the spread of viral pathogens, affecting livestock health and the broader ecosystem. This study emphasizes that enhancing biodiversity, both within viral populations and among host species, may act as a natural buffer against disease emergence and spread. A more diverse host population could slow viral evolution and transmission, potentially reducing the risk of widespread outbreaks.

Keywords: Biodiversity, Epidemiology, Climate change, PRRSV, ASFV, JEV

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Theme-III:

Integrating Biodiversity for Sustainable Farming

(Role of communities, farmers, Krishi Vigyan Kendras, Non-Governmental Organizations, Farmer Producer Organizations)

ORAL PRESENTATION

OP3-01

Community Based Seed Banks: A Strategy for Biodiversity Conservation and Sustainable Agriculture in Rural Villages

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Seed banks serve as vital repositories for preserving the genetic diversity of crops, safeguarding seeds for future use or to enhance agricultural resilience. This initiative focuses on establishing seed banks dedicated to foxtail millet in rural areas. These seed banks are designed to conserve germplasm, ensuring the survival of indigenous seed varieties while promoting sustainable farming practices. By collecting, conserving, and exchanging traditional seed varieties, seed banks contribute to the preservation of biodiversity, which is essential for creating more stable and resilient farming systems. These systems not only support farmers livelihoods by diversifying their produce and increasing income but also improve human nutrition and protect ecosystems. In this project, each farmer in the adopted village will contribute 10 kg of traditional foxtail millet seeds to the community seed bank, which will be managed by a village committee. This committee will oversee the collection, distribution, and maintenance of the seed bank, fostering a sense of ownership and responsibility within the community. Additionally, the seed bank will facilitate the creation of seed exchange networks with government organizations, NGOs, and other community seed banks, starting within the district and eventually expanding across the entire state. This approach ensures seed, food, and nutrition security at the local level, empowering villagers to plan, manage, and oversee all aspects of food production and distribution, ultimately contributing to long-term food security and agricultural sustainability. The Krishi Vigyan Kendra Phek had established two seed banks one at Porba and the other at Zelome village under the financial support of NABARD, Dimapur.

Keyowrds: Community, Seed bank, Genetic resources, Conservation

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OP3-02

In-Situ Conservation of Indigenous Fruits of Bundelkhand Region by Collaborative Efforts of Local Communities, Agricultural Institutes, KVKs, NGOs, FPOs and Farmers

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Bundelkhand, a region that straddles the states of Uttar Pradesh and Madhya Pradesh in India, is known for its unique geographical features and diverse agricultural practices. Despite facing challenges such as drought, extreme temperature, soil salinity, soil degradation, and economic difficulties, Bundelkhand is home to various indigenous fruits like aonla , bael, ber , Jhar ber, kath ber, *jackal* jujube, chironji, mahua, jamun, karonda, wild karaunda, khirni, lasoda or labhera, phalsa, jackfruit, wood apple, anjir, tamarind, gular, tendu, and paniyala etc., with significant nutritional, economic, and ecological value. The sustainable management of indigenous fruits is crucial for food security and biodiversity. Local communities, agricultural institutes, NGOs, FPOs, and farmers play collaborative roles in *in-situ* conservation strategies, protecting and managing indigenous fruit species in their natural habitats. Traditional knowledge of local communities regarding cultivation practices, pest management, and seasonal variations contributes significantly to the conservation efforts. Community-based approaches, such as conventional agroforestry systems and home gardens, will help to perpetuate indigenous fruit varieties. We should promote local festivals and cultural practices that honor these fruits and also contribute to their preservation by maintaining their relevance in the local culture. Agricultural universities and institutes play a crucial role in researching and conserving indigenous fruit species through biodiversity assessment, ecological studies, and genetic research. Krishi Vigyan Kendras play a vital role in linking research with farmers, offering training programs, and farming demonstrations, and fostering community engagement for sharing traditional knowledge. NGOs should support indigenous fruit conservation through community engagement, financial aid, and technical resources. They must raise awareness, implement conservation projects, and collaborate with stakeholders for sustainable practices. NGOs should assist in establishing community seed banks and nurseries to cultivate and distribute indigenous fruit species. FPOs should facilitate collective action in conserving and commercializing indigenous fruits and help improve market access, credit, and technical services for fruit cultivation in this region. Farmers play a crucial role in conserving genetic diversity and adapting cultivation practices to ensure the survival and productivity of indigenous fruits. The conservation of indigenous fruits in the Bundelkhand region requires the active involvement of local communities, agricultural institutes, KVKs, NGOs, FPOs, and farmers. Collaborative efforts are essential for successful conservation. Moreover, financial incentives from Center /State Government / ICAR-NBPGR / Bioversity International may encourage farmers for care and maintenance of local and precious fruit species.

Keywords: *In-situ* conservation, Bundelkhand, Fruit biodiversity

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OP3-03

Varietal Evaluation of Maize and Buckwheat under Organic Management of Maize-Buckwheat Cropping System

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The results of the maize varietal screening evaluation showed that the growth, yield characteristics, and yield of maize cultivars was significantly impacted by organic management conditions. At the point of flowering stage, Seti makkai achieved the tallest plant (306.87 cm), followed by Baiguini makkai (297.87 cm), yet both were far superior over the other cultivars. Rato makkai achieved the highest dry matter accumulation (81.58 g plant^{-1}) during the tasseling stage, followed by Seti Makkai (73.39 g plant^{-1}) among the cultivars. The highest value of LAI (4.40) was noticed under Vivek Sankul-35 followed by Rato makkai (3.95), Baiguini makkai (4.22) as compared to other varieties respectively. Baiguni makkai matured significantly earlier took (110 days) than other cultivars but it remained statistically at par with Rato makkai. The maximum cob length (15.68 cm) was recorded under RCM 1-1 which was significantly at par with Seti makkai (15.08 cm) and Rato makkai (15.28 cm) but significantly higher than other cultivars, respectively. Significantly highest cob girth (14.07 cm) was registered under Vivek sankul-31 compared to other cultivars but it remained statistically at par with Vivek Sankul-37 (13.57 cm) and Vivek Sankul-35 (13.87 cm) respectively. A significantly higher value of grain yield (3.98 t/ha^{-1}) was observed under Vivek Sankul-35 as compared to other cultivars but remained statistically a par with Seti makkai (3.95 t/ha^{-1}) and Vivek Sankul-31 (3.91 t/ha^{-1}). For buckwheat, the cultivar IC 104727 required a minimum (108 days) for maturity followed by local Meethay (110 days) and IC 15393 (110 days) followed by Local Teethay (113 days), SANGLA B-1 (116 days) IC 109729 (117 days) IC 2018742 (119 days) IC 36805 (119 days) IC 109433 (121 days) PRB -1 (121 days) VL- UGAL (124 days) IC 49671 (126 days). Maximum grain yield (2.18 t ha^{-1}) was recorded under IC 109433 which was statistically at par with local Meethay (2.13 t ha^{-1}), IC109729 (1.98 t ha^{-1}), IC49671 (1.97 t ha^{-1}) but significantly higher than remaining cultivars, respectively. The highest value of gross return (127.52 ×10^3 ha^{-1}), return rupee^{-1} invested (2.96), and profitability (173.42 ₹/ha/day) was noticed under IC 109433 which was statistically at par with local Meethay, IC 109729, IC 49671 but significantly superior over all remaining cultivars. Maximum net return (95.43 ₹×10^3 ha^{-1}), was observed under IC 109433 which was statically at par with Local Meethay and IC 109729 and significantly higher than other cultivars, respectively.

Keywords: Buckwheat, Maize, Varietal evaluation, Organic condition, Cropping system

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OP3-04

Farmer Participatory Evaluation for Conservation and Promotion of Comilla Cotton (*Gossypium arboreum* L.) in the Garo Hills of Meghalaya

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The area under diploid cotton in India has drastically reduced to less than 5 % from 97% in 1947 and presently, the area under *Gossypium arboreum L.* cotton is less than 3%. Cotton grown in the Garo hills of Meghalaya belongs to the Indian cotton species *G. arboreum* race *cernuum*, and this cotton is popularly known as Comilla cotton or Assam Comilla due to its marketing in the Comilla district of Bangladesh during the pre-independence period. The Comilla cotton is present in localized pockets across the North Eastern Indian states and evolved with special features due to continuous natural selections, hybridization and selection pressure for specific traits by the native farmers, who are the true custodians of biodiversity. In comparison to the other two races of *G. arboreum*, the race cernuum is bestowed with unique traits like big boll and higher GOT required by the commercial cotton production industries. Comilla cotton is a major cash crop in the Garo hills of Meghalaya under the traditional mixed farming method, however, its production, productivity, and market supply have declined in recent years due to multiple production constraints. In this context, farmer participatory varietal selection (PVS) was carried out to understand the farmer-preferred traits, the extent of variability, the selection of better genotypes and DUS Characterization. From various exploration trips, 371 individual plant selections were made from different cotton growing villages of West, South and South West Garo hills district of Meghalaya during 2022-23 and 371 individual progenies were evaluated in three locations *viz*., Sadolpara, Sansanggre and College of Community Science, CAU(I), Tura Meghalaya during 2023-24. The results of the study revealed that the farmers' preferred traits were big boll types, more number of bolls per plant, ease of harvest, tolerance to pink bollworm and grey mildew disease. Wide variability was observed for important traits like boll weight (6.3-8.9 g), number of bolls per plant (6-27), seed cotton yield per plant (20 -166 g), ginning outturn (47-50%) and number of seeds per boll (47-51 seeds). Fibre quality analysis revealed, short staple fibre (17.2-24.4 mm), bundle strength (18.2-22.4 g/tex), micronaire (6.6 to 8.0 g inch^{-1}), uniformity index (75-82%) and higher absorbency of water. Wide variability was also recorded for the DUS characters like leaf shape, leaf colour, stem colour, hairiness, boll shape and seed fuzz colour. Based on these evaluations, 226 genotypes were selected and advanced to the next generation and used 4 genotypes as parents in the inter-racial hybridization (involving 3 races of *G. arboreum* L) programs for creating variability for important traits. The present study has increased farmers' awareness on selection of better genotypes, selection bolls for sowing, DUS characterization and management of insect pests. The PVS combined with a formal breeding system should be used for further improvement and conservation of comilla cotton cultivation in the Northeastern India, and promoting this cotton as surgical cotton.

Keywords: Comilla cotton, Custodian farmers, Garo hills, Participatory varietal selection, Surgical cotton

OP3-05

Integrated Pest Management in Cotton for Conservation of Natural Enemies

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Cotton is an important cash crop playing a pivotal role in sustaining the economy of India and livelihood of the Indian farming community. Out of 1328 species of insects recorded in cotton, a dozen arthropods causing economic loss to the crop, need attention to attain better yield. Farmers use heavy doses of chemical pesticides to control pest incidence that adversely affect naturally occurring predators and parasitoids in the ecosystem. Over-reliance on chemical pesticides has caused harm due to pesticide residue, resurgence, secondary pest outbreak and development of resistance against these chemical molecules. Some of the pests, *viz*., pink bollworm, mirid bugs, jassids, whitefly etc. never recorded earlier or recorded in traces in Bt cotton have emerged as serious pests whereas the major pests especially American and spotted bollworms have reduced in their incidence and damage. Emerging pest problems posing threat to cotton production are pink bollworm, sucking pests and miscellaneous insect problems. The baseline information indicated that usually 10-20 sprays (average 14) of pesticides in a cotton crop per season are carried out by the farmers with cocktail of pesticides. Keeping in view, field trial on cotton integrated pest management (IPM) with emphasis on pink bollworm (*Pectinophora gossypiella*) was conducted during Kharif 2022 and 2023 at Khandwa, Madhya Pradesh in farmers' participatory mode in 50 acre and 100 acre respectively. For the management of pink bollworm, a novel technology, SPLAT (Specialized Pheromone and Lure Application Technology (Gossyplure 4% RTU) @ 125 g/acre/application) was used. In addition, application of Neem oil (Azadirachtin 1500 ppm), foliar applications of potassium nitrate fertilizer (NPK 13:0:45) @ 2% during flowering to boll formation stage and need based application of safer pesticides were done. Comparison of population per three leaves of sucking pests indicated lowest population of whitefly (adult), jassid and thrips (nymph and adult) in IPM module (3.45, 1.3 and 7.50) as compared to farmers' practice (6.5, 3.5 and 9.2) and untreated control (9.5, 7.4 and 29.7) respectively. IPM recorded the lower boll damage in IPM (4.5%) as compared to FP (24.4%) and untreated control (30.5%). Among beneficial population of spiders, lady bird beetle and green lacewing remained higher in IPM (0.87, 3.74 and 1.59 adults/plant) as compared to farmers' practice (0.34, 1.3 and 0.85 adults/plant) and untreated control (1.68, 4.33 and 1.93), respectively. Seed cotton yield was significantly higher (35.12%) in IPM fields (11.36q/ha) compared to FP (7.37 q/ha) with higher BC ratio in IPM (1.88) as compared to FP (1.21). It was evident that by adopting IPM strategy, pink bollworms in *Bt* cotton can be successfully managed along with the conservation of natural enemies with minimum application of insecticides. The technology will be helpful in increasing the seed cotton yield and improved quality, especially in terms of improving the socio-economic status of cotton growers of the country.

Keywords: *Bt* cotton, Pest management, Sucking pests, Natural enemies

OP3-06

Integrated Farming System for Sustainability and Livelihood Security- A Success Story of Mr. L. Kanlum

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The Integrated Farming System strategy aims to reduce poverty and promote food security, farmer security, sustainability, and farmer security. When it is possible, it entails using the outputs of one enterprise component as inputs for other connected firms. An integrated agricultural system model was constructed in the field of Mr. L. Kanlum, a 62-year-old resident of Lamphoupasna village, from 2021–2022 to 2023–2024, taking into consideration the physical, social, and economic restrictions of the farmer. The model comprises 1.00 ha under the interventions of ICAR-KVK Chandel under Tribal Sub-Plan, technological interventions were made through high yielding variety Maize (HQPM-5), Soybean (DSb-19), Fieldpea (Prakash), Rapeseed-mustard (NRCHB-101), Broad bean (Local) vegetables cabbage (Rareball), fruits (5 tree bean), banana, citrus, piggery, fishery (Jalkund area), and vermicomposting unit for waste recycling. The beneficiary farmer participated in a number of capacity-building programs on the Integrated Farming System that were held in the village and at the KVK office for those in need. In comparison to growing of the local cultivars Mr. L. Kanlum successfully harvested a larger yield of maize var. HQPM-5, which produced 49.60 q/ha, soybean var. DSb-19, which generated 19.20 q/ha. He was able to harvest 9.65 q/ha of Rapeseed-mustard in maize fallow and 12.90 q/ha of Field Pea. Following intervention, the yield of vegetables grew significantly, yielding Rs. 100000/- (one lakh) net returns from broad beans, cabbage and other vegetables. The cross-bred Hampshire pigs did well in piggery farming yielding 10–12 piglets annually. From 1.00 hectares of land with improved and scientific methods, he could earned the total net returns Rs 2, 76426/ [Maize production (0.5 ha) = Rs. 54150, soybean (0.25 ha) = Rs. 19663, production in rabi season from fieldpea (0.25 ha) = Rs.16313, Rapeseed-mustard (0.50 ha) = Rs. 14300 Cabbage and broad bean) =Rs. 100000, Fruit production (from citrus) = 25000, Piggery (from piglets) = Rs. 42000, Fishery = Rs. 5000]. He is now regarded as an example not only in his community but also in the communities that surround it. The usage of limited resources under the delicate hilly ecosystem was positively impacted by these initiatives, which benefited tribal farmers generally. As a result of this success story and with the assistance of ICAR-KVK, Chandel, many of the active farmers have shown a strong interest in improving the work culture for both the farmers in these areas and the farmers in other places.

Keywords: Integrated Farming System, Livelihood security, Sustainability, Success story

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OP3-07

Using Biodiversity to Protect Its Gifts: A Case of *Chak-Hao* and Its Protection from Storage Pests Using Indigenous Plants in Manipur

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Chak-Hao, the aromatic black rice of Manipur, is God's gift to mankind. Also known as Forbidden rice or Emperor rice, it is a superfood with gluten-free and fibre-rich grains loaded with antioxidants from its Nutri-dense anthocyanin content. It is a GI-tagged crop cultivated organically in less than 5000 ha in Manipur, primarily by small-scale farmers in a small portion of their land holdings. However, despite being a hardy landrace that tolerates pests and pathogens in the field, post-harvest storage pests are a major problem after harvesting and dehusking. Compared to regular rice, *Chak-Hao* is far more susceptible to storage pests, drastically reducing its storage life, quality and quantity while significantly impacting its marketability. The entire supply chain of *Chak-hao* is handled at the farmers' level or that of FPOs and NGOs. The organic tag of *Chak-hao* will be compromised if synthetic chemicals are used for pest protection. Manipur, a treasure trove of diverse flora, fauna, and fungi, is blessed with many plant species capable of protecting against insect pests. Our study found that readily available Indigenous plants such as *Zanthoxylum acanthopodium*, *Goniothalamus sesquipedalis,* and *Isodon ternifolius* protect rice weevil, *Sitophlius oryzae*, which is the major storage pest of *Chak-hao* and posing a massive challenge to its long-term storage, especially on dehusked grains. These plants, in combination and individually on treatment on *Chak-hao* grains, can reduce progeny production and insect infestation. This eco-friendly technology provides an economical, socially feasible, sustainable and accessible organic alternative for farmers and their communities. FPOs dealing with *Chak-hao* sales and marketing can easily tackle post-harvest storage pest problems. *Chak-hao* grains may be treated or packed (for marketing) with these plant parts or their powders to prevent and repel storage pests. These plants are edible medicinal plants and cause no health hazards.

Keywords: Chak-hao, Landrace, Rice, Manipur

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OP3-08

Ecological Structure and Functional Dynamics of Homegardens in the Foothills of Nagaland

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This study evaluates the vegetation composition and carbon stock of homegardens, the predominant agroforestry system in the foothills of Nagaland. A total of fifty-four homegardens, distributed across three elevation zones (EZ_1: <250 m amsl; EZ_2: 250-500 m amsl; EZ_3: >500 m amsl), were assessed. The results revealed that homegardens comprised 4-5 vertical strata, with larger homegardens featuring distinct microzones, each occupying a specific area within the garden, such as arecanut + betel vine groves, banana groves, bamboo groves, vegetable gardens, pond areas, and livestock sheds. A total of 130 plant species were recorded, excluding weeds. The diversity analysis of woody and non-woody perennials indicated that the Shannon-Wiener Index did not vary significantly among the different elevation zones. However, species evenness and species richness showed significant variations, with the highest values in EZ_3 and the lowest in EZ_1. The area of the homegardens varied significantly with elevation, with an average size of 291.46 m^2 in EZ_3 compared to 988.17 m^2 in EZ_1. The total biomass carbon ranged from 11.81 MgC/ha to 85.74 MgC/ha, without significant differences among the elevation zones. A total of 162 composite soil samples, were collected from four different depths (0-15 cm, 15-30 cm, 30-45 cm, and 45-60 cm) across the elevation zones, were analyzed to determine the soil organic carbon (SOC) stock. The results showed that SOC stock varied significantly along the elevation gradient, with the highest values at higher elevations and the lowest at lower elevations. Correlation analysis indicated a negative relationship of home garden size with species evenness, species richness, above-ground biomass (AGB), and SOC stock, while all biodiversity indices showed a positive correlation with SOC stock.

Keywords: Biodiversity, Biomass, Carbon stock, Soil, Species Composition

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OP3-09

Unleashing Agricultural Transformation through Rabi Maize Farming in Assam

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Maize as a staple crop crucial to global food security has demonstrated its transformative potential in various regions. Since 2010, systematic techno-policy interventions by ICAR-IIMR have significantly expanded maize cultivation in West Bengal, increasing the area from 0.89 to 3.93 lakh hectares (L ha) and boosting yields from 4.0 to 6.8 tonnes per hectare (t/ha) during 2010-11 to 2023-24. Currently, West Bengal is a key maize-producing state in India with the highest productivity. To replicate this success in the maize-deficit North Eastern Hill (NEH) region, demonstrations during the *rabi* season under the National Food Security Mission in Assam began after 2020, receiving positive responses from farmers. However, the acreage did not pick up until 2022-23. The IIMR, Ludhiana under the Assam Project on Agribusiness and Rural Transformation (APART) a World Bank-financed project initiated training and awareness programs from July 2023 onwards. This included 12 master training programs for trainers across 12 districts of Assam followed by training sessions for 520 progressive farmers and technical trainings for >1500 farmers. These initiatives emphasized linking farmers to markets and existing feed and grain-based distilleries for ethanol production, which proved crucial for large-scale maize adoption in Assam. Involvement from maize input providers (seed, agrochemicals) resulted in their significant presence before the onset of the 2023-24 *rabi* season. Advanced agricultural techniques and high-yielding maize hybrids demonstrated at farmers' fields across 1440 plots yielded between 8.73 and 12.58 t/ha, averaging 10.94 t/ha. Remarkably, the crop was grown with minimal irrigation due to Assam's significant rainfall, which averages >200 rainy days/year. Economically, this initiative greatly benefited farmers, allowing them to earn Rs. 60-65 thousand from a 0.25 hectare plot by selling maize. Additionally, green fodder harvested after cob maturity provided valuable livestock feed, showcasing maize's dual-purpose value. The IIMR-APART initiatives addressed challenges like knowledge gaps, inadequate irrigation, storage, transportation, and pest control by providing essential training and resources. As a result, *rabi* maize cultivation expanded from no recorded data in 2022-23 to 39,000 ha in 2023-24. Assam needs 25 lakh metric tonnes (LMT) of maize for feed and ethanol production and can add 3.0 L ha under maize by utilizing *rabi* fallows and expanding irrigation with productivity target of 6-7 t/ha. This growth will support the piggery, poultry, and livestock industries in the NEH region. The Government of India has approved a 725 kiloliter per day capacity (KLPD) bioethanol plant in Assam, requiring an additional 10 LMT of maize annually by 2025-26. Therefore, the total maize requirement will exceed 25 LMT against a current production of 4 LMT. This highlights that scaling up maize production based on regional conditions and market opportunities can ensure sustainable livelihood security in Assam through an improved maize value chain.

Keywords: Maize Farming, Farmer Empowerment, Biodiversity, Agricultural Transformation, Sustainable Livelihoods, Assam

OP3-10

Effect of Pollen Storage on Kiwifruit (*Actinidia deliciosa)* Quality and Production under Organic Management Systems

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Asynchronisation in kiwifruit male and female flower anthesis is a common phenomenon across the kiwifruit growing areas worldwide. This situation demands efficient short term pollen storage techniques for production of high quality and high yielding kiwifruits through optimum pollination throughout the flowering season. As tested by *in vitro* germination and acetocarmine tests, the analysis of variance clearly showed that storage method, days of storage, and the interaction between storage methods and days of storage had a highly significant effect ($p \leq 0.0001$) on pollen viability. Room temperature storage revealed a sharp decline in pollen viability as accessed by acetocarmine test and *in vitro* germination test and complete viability was lost within 42 days after pollen storage. The rate of decline of pollen viability was in the order of 0°C>-4°C> -10°C >-20°C. Fruit set, fruit maturity, average fruit weight, percent A grade fruits and yield/plant were recorded highest for −20°C stored pollens, while it was lowest in room temperature storage. Fruit quality in terms of TSS, DPPH and ABTS antioxidant assays showed a positive trend (highest in –4°C and –20°C), while, total acidity and ascorbic acid content showed negative trends (lowest in –20°C) for low temperature stored pollen pollinated fruits as compared to fruits in room temperature stored pollen pollinated fruits. Fruit nutrient content also exhibited a positive trend when pollinated with low temperature stored pollens as compared to room temperature stored pollens. Therefore, our findings point to a dependable approach for preserving kiwifruit pollen that farmer may apply to get good quality and high yielding fruits.

Keywords: Pollen storage, Kiwifruit, Pollen, Low Temperature, *Actinidia deliciosa,* Organic

OP3-11

Conserving Fruit Crop Diversity: VNR Research Centre's Efforts in Promoting Use of Genetic Resources

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The VNR Research Centre in Raipur, Chhattisgarh, leads in managing genetic resources for fruit crops, currently overseeing 58 varieties of tropical, subtropical, and low-chill fruit crops, many of which are suitable for the NEH (North Eastern Hill) region. These include 12 major and 46 minor fruit crops, with a total of 564 accessions. These resources encompass varieties released from different ICAR Institutions, KVKs, SAUs, local selections, landraces, exotic germplasm, and hybrids developed by VNR. The genotypes are maintained as field gene banks at three main locations in Chhattisgarh, spread across two agroclimatic zones, two in Raipur and one in Bastar, Jagdalpur. The centre conserves a total of 22,143 plants over more than 46.5 hectares, including mother orchards and field gene banks. Raipur, with its tropical wet and dry climate, has an average yearly temperature of 30.4ºC, receiving about 37.38 mm of precipitation and experiencing 32.19 rainy days annually. Jagdalpur, also with a tropical wet and dry climate, has an average yearly temperature of 27.69ºC, with about 66.67 mm of precipitation and 44.36 rainy days annually. The soil at the Raipur centres is sandy loam, well-drained, and well-aerated, while Bastar has light rocky soil. Major fruit crops at the VNR Research Centre include pomegranate, apple, grapes, guava, citrus fruits (such as oranges, lime, and lemon), litchi, mango, and pineapple. Minor fruit crops include almond, annona, aonla, avocado, bael, ber, lasoda, breadfruit, cashew, cherry, chironji, coconut, curry leaves, cinnamon, date palm, dragon fruit, fig, flying dragon, ganga imli, grapefruit, hog plum, jackfruit, jamun, carambola, karonda, khirni, kumquat, longan, mangosteen, miracle fruit, moringa, mulberry, noni, olive, passion fruit, pear, phalsa, plum, pummelo, rambutan, rose apple, sapota, tamarind, velvet apple, walnut, wax apple, and wood apple. Mango and guava are trained under the espalier system, while other crops follow the open centre system. These genotypes undergo systematic data collection over three years, focusing on growth performance, fruit quality, yield, stress tolerance, and disease resistance. Notably, five guava genotypes, one lemon variety, three lime genotypes, five mango genotypes, three mandarin and sweet orange varieties, and one grape variety performed superiorly at both locations. One pineapple genotype and one pomegranate variety excelled at the Bastar location, while tropical apple showed below-average performance at both sites. Among minor fruit crops, outstanding performers include annona, bael, ber, lasoda, coconut, curry leaves, date palm, dragon fruit, fig, grapefruit, jackfruit, jamun, carambola, karonda, longan, drumstick, mulberry, passion fruit, pummelo, sapota, and wax apple. The VNR Research Centre's dedicated efforts in genetic resource management are paving the way for improved fruit crop productivity and quality.

Keywords: Fruits, Nursery, Genetic resources, Conservation

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POSTER PRESENTATION

PP3-01

Traditional Institutional Structure of Managing and Conserving Forest Resources in Phayeng Village of Manipur

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Manipur has 77% of its geographical area under forest cover, ~82% of it being in the hill areas. Nearly 18% of the forest cover falling in the valley areas of the state are sparsely located and are prone to degradation due to expanding economic development activities and population pressure. The present study focused on the case of forest protection and management efforts by the community of Phayeng village in the Imphal West district with the objectives of understanding the functional system of community forest management in the village and to examine the problems and constraints in forest management. The Phayeng forest, covering an area of 96.98 Ha (as on 2015), has a rich plant biodiversity with a record 95 tree species with medicinal and timber quality and 41 fruit tree species having been reported in the forest. The village was conferred "First carbon positive village" tag in India in 2019 under National Adaptation Fund for Climate Change (NAFCC) Scheme implemented by NABARD. The forest is traditionally managed by a committee called the Phayeng Umang Kanba Lup (Phayeng Forest Protection Committee) constituted by the members from the village. The committee consists of 60 members in total, exclusively male, constituted every two years from among the households of the village. It has both regular and seasonal duties allotted to the members of the committee throughout its tenureship of two years. The regular duty consists of monitoring the forest every day to safeguard the forest from two major activities viz., felling of trees and hunting. The seasonal duties consisted of two main activities viz., Meiram haiba (Fireline creation) and Dried Wood Collection. Lack of government assistance, unresolved dispute over the ownership of the forest land, lack of capital and technical support in forest management were some of the most important limiting factors in the conservation activities of the forest protection committee.

Keywords: Forest resources, Manipur, conservation

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PP3-02

Role of ICAR-KVK Longleng in Biodiversity Conservation

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The term "biodiversity" refers to biological diversity, which includes the variety of all species that are present on Earth. India is one of the world's 17 mega-biodiversity countries and the world's richest source of biodiversity. But overuse, deforestation, improper land use, unsustainable land management, intensive agriculture, high synthetic inputs, pollution, invasive exotic spice invasions, diseases, shifting cultivation, poaching of wild animals, and other human-sponsored ecosystems disrupt our natural ecosystem's pathway by affecting resources and their depletion. Both in-situ and ex-situ methods of conservation can be used to preserve biodiversity. The most significant role being done in biodiversity protection is by Krishi Vigyan Kendras (KVKs). The most suitable approach to biodiversity conservation is known as "in-situ" conservation, which refers to the preservation of species in their native environments. KVKs play a part in raising awareness of the value of biodiversity and the need to conserve it for a secure and healthy future. It is a one-stop shop for agriculture and related sectors. To the advantage of farmers, KVK has pushed the use of several integrated management techniques, including integrated pest management (IPM), integrated crop management (ICM), and integrated disease management (IDM) technologies. KVKs work to increase the use of natural agricultural methods and foster collaborations within the larger food system, agro-ecology.

Different agro ecological systems, such as Integrated Farming System (IFS) Models have been developed and that has produced a symmetric relation with different crops, shrubs, livestock components. Crop rotations often produce the positive effect due to legume cropping. By following and adoption of more biological and mechanical techniques in crop production as well as crop protection has synchronises the harmony between various biological and soil micro-organism activities. KVKs has developed demonstration unit for farmers, to recycle the animal waste along with farm waste. Recycling organic materials and by-products offers great potential for agro-ecological innovations.

Keywords: Biodiversity, KVK*, In-situ*, Conservation, Deforestation

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PP3-03

Enhancing Cropping Diversity and Sustainable Productivity in Longleng, Nagaland: A Decade of Technologies Interventions

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The North East Region of India is known for a rich source of wild relatives of cultivated crop plants. However, conservation of biodiversity is a big threat or problem in coming future. There is many causes of losing biodiversity *viz.*, natural and human impede. In Longleng the shifting or *jhum* cultivation practice contributes to the extinction of wild germplasm due to its cyclic nature which often leads to soil degradation and loss of biodiversity. To overcome this problem, cultivation of diversified crop species and settle farming methods like establishment of orchards is a viable solution to enhance soil health, increase profit and support biodiversity. Over the past decade, the Krishi Vigyan Kendra (KVK) in Longleng has implemented a range of agricultural initiatives designed to boost productivity, livelihoods and biodiversity in a region known for its challenging hilly terrain and soil erosion issues. Tailored to address local conditions, these initiatives have included the diversified crop species and orchards. It has been estimated that due to allocation of different crop species (Rice, Maize, Pulses, Oilseed and Vegetables) the expansion of total area under crops, productivity and cropping intensity is increased substantially. However, in last 10 years, the KVK Longleng, has been significantly enhance farmers ability through technology interventions leading to replacement of the *jhum* farming for more sustainable agriculture practices and preservation of local biodiversity. A decade-long intervention has effectively transformed rural livelihoods by addressing regional challenges and focusing on sustainable practices. Future efforts should continue to build on these successes by integrating community feedback and advancing innovative agricultural technologies to ensure long time sustainability and prosperity.

Key Word: Biodiversity, Crop diversification, Jhum farming, Sustainable and Technology intervention

PP3-04

Status, Changing Landscape and Farmers' Criteria for the Continuity of Paddy (*Oryza sativa*) Landraces in the Upland Ecosystem of Jharkhand, India: A Conservation Perspective

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The present study involved paddy landraces naturalized widely across Jharkhand, India, at an altitude range of 6 (Sahibganj) to 768 (Garhwa) metres above sea level. They naturalized across diverse niche areas, including fat to sloped uplands, lowlands, rivulet edges, pond/dam basins, swampy regions with varying altitudes, and broad edaphic ranges. The high number of paddy landraces collected from the Central and North-Eastern Plateau (CNEP) sub-zone was well supported by the complementarity analysis. Landraces from iron- and aluminium- (West and East Singhbhum) and mica- (Giridih and Koderma) rich regions are a potential source of extraordinary mineral tolerance and bioaccumulation. These ecologically stressful habitats owing to limitations in soil pH, soil texture, and other factors are considered potential sites for the evolution of unique traditional varieties. However, the resource base was critically genetically eroded from 2005 to 2021, particularly in Ranchi, Hazaribagh, Ramgarh, Chatra, Bokaro, Dhanbad, Koderma, Deoghar, and Palamu. The CNEP sub-zone witnessed the most genetic erosion of landraces. At the same time, the continued cultivation of landraces in the steeper landscape of both the Western Plateau and South Eastern Plateau sub-zones underscored their value in risk aversion under challenging environmental conditions. Selection criteria analysis of continued paddy landraces demonstrated farmers' preference for functional traits that influence livelihood security in the local context. These traits are vital for mainstreaming registered landraces into the production chain under changed climatic conditions

Key words: Conservation, DIVA-GIS, Georeferencing, Genetic Erosion, Paddy

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PP3-05

Knowledge Level of Farmers about Climate Resilient Agro-Technologies: NICRA Project

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National Innovations on Climate Resilient Agriculture (NICRA) project run by Krishi Vigyan Kendra, Amreli since 2015. As per the requirement of the project, four modules were adopted and different activities were carried out at Karjala village which was selected for it. To know what farmers got

from the NICRA project an adoption study was carried out. A total of 300 respondents were selected randomly for the study. The study revealed that after NICRA respondents had knowledge of summer ploughing (80 per cent), Soil sample collection and testing (74 per cent) and summer deep ploughing (every 3rd year) (73 per cent) in case of natural resource management. Whereas in crop production interventions respondents have knowledge about sowing of short duration/ late sowing/ drought resistance/ wilt resistance verities (98 per cent),Seed treatment and Integrated pest and disease management in crop (96 per cent). Moreover, mineral mixture (96 per cent); fodder production around the year (91 per cent) and vaccination & de worming (52 per cent) which related to the livestock interventions. Lastly, in Module four institutional interventions after implementation of the NICRA project knowledge of respondents had about custom hiring centre (100 per cent) and agro advisory (36 per cent).

Key words: NICRA, Agro-technology, Knowledge, Climate change

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PP3-06

Crucial Impact of Ca Nutrition on *Cymbidium* 'PCMV' Orchid Yield: Its Vital Role and Dynamic Distribution across Plant Parts

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This study investigated the influence of Ca nutrition on the growth and yield of *Cymbidium* hybrid 'Pine Clash Moon Venus' (PCMV). The orchids were subjected to six Ca treatments, ranging from 0 to 100 mg Ca L^{-1} in fertigation solutions. The results revealed that plants under the Ca_{100} treatment exhibited a markedly higher vegetative yield and produced twice as many flower spikes as those under Ca_0 treatment. Additionally, the flower spikes from the Ca_{100} treatment were approximately 72% longer and bore 72% more florets per spike. The study also demonstrated that Ca application substantially increased Ca concentrations in various plant parts. Interestingly, flowering-induced Ca removal led to a significant decrease in Ca content in the back bulbs, while other plant parts remained relatively unaffected. Partial regression analysis indicated that for every unit of Ca uptake by flowers, there was a corresponding 0.279-unit decrease in Ca content in the back bulbs. These findings highlight the critical role of Ca in enhancing *Cymbidium* yield and provide new insights into Ca dynamics across different plant parts. The study recommends a weekly application of 100 mg L^{-1} Ca for optimizing *Cymbidium* cultivation practices.

Keywords: Orchid, Ca, Growth, Nutrition

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PP3-07

Response of Soybean (*Glycine max* L. Merrill) Varieties towards Zinc Fertilization in Acidic Soils of Nagaland

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The present study entitled "Biofortification of zinc in Soybean (*Glycine max* (L.) Merrill) under foothills of Nagaland" was conducted during 2018 and 2019 at the Research farm, SASRD, Nagaland University, Medziphema. The field experiment was laid out in factorial RBD replicated thrice consisted of three (3) varieties *viz*., JS-335, JS-97-52 and local cultivar with seven (7) zinc treatments *viz*., Z_0 (control), Z_1 (Soil application of Zn @ 5 kg ha^{-1} through $ZnSO_4.7H_2O$), Z_2 (Soil application of Zn @ 5 kg ha^{-1} through ZnO), Z_3 (Soil application of Zn @ 5 kg ha^{-1} through $ZnSO_4.7H_2O$ + Two foliar spray application of $ZnSO_4$ @ 0.25%), Z_4 (Soil application of Zn @ 5 kg ha^{-1} through ZnO + Two foliar spray application ZnO @ 0.25%), Z_5 (Three foliar spray applications of $ZnSO_4.7H_2O$ @ 0.5%) and Z_6 (Three foliar spray applications of ZnO @ 0.5 %). The results of the experiment revealed that varieties differed significantly in some important growth and yield parameters, where JS 97-52 was found superior in almost all aspects. JS 97-52 (1.88, 1.69 t ha^{-1}) recorded significantly higher seed yield than JS-335 (1.49, 1.52 t ha^{-1}) and local cultivar (1.29, 1.24 t ha^{-1}). Seed yield was found to increase by (19.70, 20.88%) from (1.38, 1.32 t ha^{-1}) in control to (1.65, 1.59 t ha^{-1}) in Z_3 treatment which was at par with Z_5 (1.62, 1.55 t ha^{-1}). Zinc fertilization treatments, Z_5 was found most effective and was at par with Z_3 in many parameters in enhancing growth, yield and grain quality of soybean. Highest protein content was observed in Z_5 (39.76, 39.37%) which was statistically at par with Z_3 (39.27, 39.29%) and Z_4 (38.14, 38.44%). The grain zinc density was observed to be slightly higher in JS-335 and local cultivar over JS-97-52 (9% and 8% higher in zinc content). The highest zinc concentration in grain was observed in Z_5 (34.40, 33.25 mg kg^{-1}) was at par with Z_3. It was observed that there was increase in grain zinc content upon zinc fertilization over control (34.40, 26.97%), (26.98, 24.78%), (22.38, 20.45%) and (16.01, 12.80%) in Z_5, Z_3, Z_4 and Z_1 respectively. Antinutritional factor, phytic acid content was recorded highest (713.17, 724.25 mg/100 g) in local cultivar and least in JS-335 (568.77, 585.46 mg/100 g). Similarly, JS-335 recorded the least phytic acid: zinc molar ratio (18.23, 18.97) and highest value in local cultivar (23.56, 23.15). Zinc Crop recovery efficiency (ZnCRE) and Agronomic efficiency (AE) was highest in Z_5.

Keywords: Biofortification, Quality, Soybean, Varieties, Yield, Zinc

PP3-08

Effect of Different Growing Media on Propagation and Morphological Studies of Black Pepper *cv*. Panniyur-1 through Serpentine Layering

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Black pepper (*Piper nigrum* L.) is known as the "King of Spices" and is one of the most economically essential spice crops in the world. An experiment on "Effect of different growing media on propagation and morphological studies of black pepper cv. Panniyur-1 through serpentine layering" was conducted in the Horticulture farm of the School of Agricultural Sciences, Medziphema Campus, Nagaland during 2021-2022. The experiment was conducted in Randomised block design with eight number of treatments viz., T_0 - Soil (control), T_1 - Soil + FYM (1:1), T_2 - Soil + Cocopeat (1:1), T_3 - Soil + Cocopeat + FYM (1:1:1), T_4 - Soil + Vermicompost (1:1), T_5 - Soil + Cocopeat + Vermicompost (1:1:1), T_6 - Sand + Cocopeat + Vermicompost (1:1:1), T_7 - Soil + Sand (1:1), replicated four times. Among the parameters studied, treatment T 5 (Soil+ Cocopeat+ Vermicompost (1:1:1) showed better results for all the characters viz., survival percentage (79.8.%), rooting percentage (90%), length of roots (20.25 cm), root weight (6.14 g for fresh and 2.08 g for dry), length of the shoots (45.17 cm), number of leaves per plant (6.17), number of nodes per vine (7.00) and stem diameter (0.57 cm). The various combinations of growing media significantly improved the vegetative growth of black pepper under the study.

Keywords: Black pepper, Serpentine layering, Growing media

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PP3-09

Evaluating the Impact of Biofertilizers and Natural Farming Practices on Crop Yield and Soil Quality in the Ri-Bhoi District of Meghalaya

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India predominantly relies on agriculture to meet the current demographic disaster owing to its diversified climate and plenty of natural resources. Natural resources must be preserved without being wasted, especially when it comes to agriculture. Agro-ecology, the foundation of natural farming, emphasizes reducing stress on the production system and utilizing environmentally friendly

practices that promote plant and soil health for long-term results without compromising soil quality, biodiversity, or the general quality of the environment. *Beejamrutha* (seed treatment), *Jeevamrutha* and *Acchadana* (mulching) are the main components under natural farming which helps in growing the crop without disturbing the environment. The native biofertilizer named as CAU-Bioenhancer (NPKZn solubilizers) contributes in enhancing the soils microbial biodiversity. A study has been done in COA research farm with four different crops (Buckwheat; Garden pea; Linseed and Potato) along with the combination of natural farming components with bioenhancer. T_1-*Beejamrutha* + *Jeevamrutha* + Biofertilizer; T_2-*Beejamrutha* + *Jeevamrutha* + *Acchadana*; T_3-*Beejamrutha* + *Jeevamrutha* + *Acchadana* + Biofertilizer; T_4- Control are the four different treatment combinations on four different crops. Among the four treatments T_3 has shown significant difference in soil parameters (N, P, K and Zn; 338.5±3.8 kg/ha, 45.1±0.75 kg/ha, 288.7±5.33 kg/ha and 0.45±0.02 ppm) as well as plant parameters (Buckwheat- no. of flowers/plant; no. of grains/flower; Garden pea- no. of pods/plant; no. of grains/pod; Linseed- no. of primary branches; no. of capsules/plant; Potato- no. of tubers/plant) and nutrient uptake. Significant increase in the plant biomass was observed with T_2. But T_3 has recorded the highest yield in all the four crops (Buckwheat-12q/ha; Garden pea-14q/ha; Linseed-11q/ha; potato-225q/ha) compared to the rest of the treatments followed by T_2. Hence the addition of bioenhancer to the natural farming components shows effective result on soil quality and yield of different crops.

Keywords: Natural farming, Biofertilizer, Soil quality and Nutrient uptake.

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PP3-10

Effect of Different Abiotic Stresses on Soil Microbial Resource and Its Performance in Rice Rhizosphere under Diverse Nutrient Management Regimes

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Soil microbial communities significantly influence the health and fertility of soil. Any external stressor, including chemicals, submersion, and drought, will change the chemistry and physics of the soil, which will impact the biology of the soil. The population and general activity of beneficial microorganisms may be negatively impacted by abiotic stress. An experiment was conducted to study the effect of abiotic stress on soil beneficial microbial load and its performance under diverse nutrient management practices. Abiotic stressors *viz*. arsenic toxicity (10 ppm), moisture stress and excessive fertilization (3 times RFD) were imposed to the rice crop grown in the soils of 13 years old INM experiment, consisting of five diverse nutrient management strategies. It was recorded that along the growing period of rice, irrespective of the management options and abiotic stresses, the

preponderance of nitrogen fixing bacteria, phosphate solubilizing bacteria and cellulose degrading bacteria population in rice rhizosphere attained the highest level at flowering stage and then gradually decreased at harvest. However, changes in the physical and chemical properties of soil due to the exertion of abiotic stressors caused shifting in microbial communities and their functions. In all the cases, the soil from conventional farming plot when exposed to the abiotic stressors, failed to maintain significant number of viable count of beneficial microbial count and hamper its capacity to perform soil functions like nitrogen fixation, phosphate solubilization and cellulose degradation in rice rhizosphere as compared to other management options. Soils treated with integrated nutrient management options, ½ N + ½ P + K of STCR based fertilizer in conjunction with 7.5 ton of FYM and biofertiizer @ of 4.0 kg/ha (T_4), harbored significantly the highest level of benificial microbial abundance and maintained its capacity significantly in rice rhizosphere followed by the organic input based farming.

Keywords: Soil microbial resource, Soil functions, Abiotic stressors, Integrated nutrient management (INM).

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PP3-11

Impact of Microbial Bio-Formulation on Soil Health and Crop Production at Umiam, Meghalaya

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The deterioration of soil fertility and decline in indigenous beneficial soil microbial population led to decrease crop production. An alternative and green approach is the need of the hour to maintain soil health and agricultural productivity. Initial and after harvest soil sample was taken to know the impact of natural farming components on soil health and crop yield at CPGS-AS research farm, Umiam. Finger millets, French bean and Rice bean were grown as intercropped following a recommended standard spacing. Soil available nutrients, bio-chemical properties, yield attributes, plant stress parameters and nutrient uptake were analyzed and recorded to assess the performance of *jeevamrutha, beejamrutha* and biofertilizer - CAU bio-enhancer (NPKZn solubilizer). Seed and seedlings treatment was done following recommended practices for *beejamrutha* and CAU bio-enhancer. Post emergence sprays were carried out systematically as per recommended dose and time. T_1 was control, T_2 was treatment with CAU bio-enhancer, T_3 was treatment with natural farming components (*Beejamrutha and jeevamrutha),* and T_4 – a combination of both T_2 & T_3 treatments. Highest yield of finger millets (10.65 q/ha) and rice bean (4 q/ha), was observed in T_4 treatment, however, French bean yield (29.35 q/ha) was highest in T_2 treatment. Soil reaction increases from initial 5.6 to 6.8 after cultivation, which makes nutrients more easily available for plant uptake. Soil available nitrogen, phosphorus and potassium were found to be highest in T_4 treatment plots at 171.83kgha^{-1}, 13.62 kg ha^{-1} and 312.97 kg ha^{-1}, respectively. Microbial biomass carbon, nitrogen and phosphorus were high in T_4 treatment at 292.82μg g^{-1}, 48.24μg g^{-1} and 10.52μg g^{-1}, respectively. T_4 has highest soil enzymes activity for

dehydrogenase (11.64 µg TPFg^{-1}soil hr^{-1}), acid phosphomonoesterase (256.67µg pNPg^{-1}soil h^{-1}) and aryl sulphatase (219 µg pNPg^{-1}soil h^{-1}) but lowest β-glucosidase (547.89 µg pNPg^{-1}soil h^{-1}) activity. The study reveals that treatment with natural farming components and bio-fertilizer has the potential for enhancing soil health and crop yield and its attributes.

Keywords: Natural farming, Soil health, Yield, Bio-fertilizer

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PP3-12

Integrated Pest Management in Agriculture and Its Role in Managing Natural Biodiversity

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Integrated Pest Management (IPM) is a holistic approach to pest control that integrates multiple strategies to minimize environmental impact and support ecosystem health. This explores the role of IPM in managing natural biodiversity, emphasizing its contributions to maintaining ecological balance and enhancing habitat diversity. IPM practices prioritize reduced chemical use, promote biological control through natural predators and parasitoids, and support habitat conservation through diverse plantings and soil management techniques. By minimizing use of harmful pesticides and promoting judicious use of green label pesticides, IPM reduces harm to non-target species and prevents the development of resistance. Additionally, IPM fosters adaptive management through regular monitoring and data-driven adjustments, ensuring that pest control efforts are aligned with conservation goals. The implementation of IPM strategies not only improves pest management efficiency but also strengthens ecosystem resilience, supports soil health, and promotes a diverse array of beneficial organisms. This approach highlights the importance of integrating pest management with biodiversity conservation to achieve sustainable agricultural and environmental outcomes.

Keywords: Pesticides, IPM, Ecosystem, Biodiversity, Biological Control

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PP3-13

Integrated Pest Management in Direct Seeded Rice and Its Role in Managing Natural Biodiversity

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Integrated Pest Management (IPM) in direct-seeded rice (DSR) systems has emerged as a crucial strategy for managing pest populations while preserving natural biodiversity. Unlike traditional transplanting methods, DSR involves sowing seeds directly into the field, which influences pest dynamics and ecosystem interactions. This explores the application of IPM in DSR, focusing on its effectiveness in controlling pests through a combination of biological, cultural, mechanical, and chemical practices. Emphasizing the role of habitat manipulation, natural predators, and reduced chemical use, IPM in DSR not only targets pest suppression but also fosters a balanced ecosystem. The trial included 70 acre as DSR-IPM, 05 acre as DSR-FP and 05 acre as transplanted rice. The major pest was yellow stem borer, leaf folder, weeds and in some pockets incidence of rodents. Yield in DSR-IPM (Basmati rice) 57q/ha, 55q/ha in DSR-FP and 58q/ha in transplanted rice with b:c ratio 5.46 in DSR-IPM, 5.31 in DSR-FP and 3.48 in transplanted rice, respectively, whereas, in (non basmati) rice yield was 73 q/ha in DSR-IPM, 70q/ha in DSR-FP and 73 q/ha in transplanted rice with b:c ratio 3.28 in DSR-IPM, 3.16 in DSR-FP and 1.92 in transplanted rice respectively. Our results indicate that implementing IPM practices significantly reduces pest populations, with a 40% decrease in the incidence of major rice pests, compared to conventional methods. The DSR IPM approach not only enhances pest control efficiency but also contributes to the conservation of beneficial organisms and overall ecosystem health. This highlights the synergy between pest management and biodiversity conservation in DSR systems, underscoring the potential of IPM to achieve sustainable agricultural practices that benefit both productivity and ecological balance.

Keywords: Direct-Seeded Rice, IPM, Ecosystem, Biodiversity, Biological Control

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PP3-14

Integrated Approach for Management of Pulse Beetle (*Callosobruchus sp.*) in Mungbean

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In the present study it was observed that the pulse beetle damage after 9 months storage was above 1.0% i.e. Indian Minimum Seed Certification Standards (IMSCS) in T_6- Pre-harvest spray of emamectin benzoate 5SG, 0.3g/L at 50% maturity and maturity of green gram and seed treatment with diatomaceous earth 5g/ kg seed + desiccant (MgSO4 5g/kg seed) and T_3- Pre-harvest spray of azadirachtin 10000 ppm, 6ml/L at 50% maturity and maturity of green gram and seed treatment with diatomaceous earth 5g/ kg seed + desiccant (MgSO4, 5g/kg seed). Moreover, the germination was above IMSCS 75.00% in both these treatments. While, the pulse beetle damage after 6 months of storage period was below IMSCS 1.0% in T_3 (1.00%) and T_6 (0.75%) and germination was above IMSCS 75.00%. Looking to the importance of pulse beetle damage, 6 months storage under ambient condition after taking necessary spray and seed treatment for green gram storage can be done.

Keywords: Pulse beetle, Integrated approach, Management, Mungbean

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PP3-15

Fruit Bagging in Guava

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Recently, guava fruits are getting good return price because of their high quality. Inferior quality fruits obtained due to climate change such as abnormal rains, sudden fluctuations in the temperature and fog up to a great extent. Fruit bagging is a simple and phytosanitary procedure widely used for improving the visual quality by promoting fruit colouration and also to enhance internal fruit quality. There for an experiment was conducted at Regional Horticultural Research Station, ASPEE College of Horticulture, Navsari Agricultural University, Navsari during 2021-22 to study the effect of bagging on yield and quality of guava fruit variety Lalit. The experiment was laid out in a Completely Randomized Design with factorial concept and repeated thrice with twelve treatment combination. It comprised of two factors consisting stage of bagging (S) *i.e*., marble stage (S1) and egg stage (S2) and type of bagging materials (B) *i.e*., control-no bagging (B1), news paper bag (B2), butter paper bag (B3), non-woven red bag (B4), non-woven green bag (B5) and non-woven white bag (B6). The results showed that fruit weight (134.79g), fruit length (6.07cm), fruit diameter (6.43cm), fruit volume (133.99 ml), fruit retention (96.11%), shelf life (6.73 days), TSS (11.83 °Brix), reducing sugars (6.48 %), total sugars (8.32 %), ascorbic acid (170.66 mg/100 g pulp) and minimum PLW(7.34 %) and titrable acidity (0.55%) were recorded in egg stage of fruit bagging. Among different type of bagging materials, maximum fruit weight (137.13g), fruit length (6.22cm), fruit diameter (6.53cm), fruit volume (138.81ml), fruit retention (97.22%), shelf life (7.00 days), TSS (12.07°Brix), reducing sugars (6.61 %), total sugars (8.56 %), non-reducing sugars (1.95 %), ascorbic acid (173.46 mg/100 pulp) and minimum PLW (7.04 %) were recorded in non-woven red bag. While, the lowest titrable acidity (0.52 %) was found in newspaper bag. Minimum fruit fly infested fruits and maximum marketable fruits were found in non-woven bagged fruits. No significant effect was found for the physical and quality properties of guava fruits between stage and different bagging material.

Keywords: Guava, Fruit fly, Bagging, Quality

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PP3-16

Incorporation of Natural and Organic Farming Plant Protection Products, a Viable Option for Greenhouse Whitefly, *Trialeurodes vaporariorum* (Westwood) Management in Tomato under Protected Environment

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Presently, the whitefly management techniques are based upon the use of chemical pesticides, in parallel resulting in concurrent rise in the proportion of pests, which increases the demand for hazardous chemicals for their management. With increased public awareness for safe food, the current studies that incorporate biorational pesticides for greenhouse whitefly management programme were carried out in naturally ventilated polyhouses at CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur during 2020-21. Biorationals including cow by-product based natural insecticidal products namely, *Darekastra*, fermented butter milk, *Tamarlassi* and vermiwash which were applied as alternate foliar applications at 10 days intervals. Amongst different insecticidal treatments evaluated the treatment comprised alternate foliar application of vermiwash (10%) & *Tamarlassi* (10%) proved most efficacious in reducing greenhouse whitefly population upto 68 to 70% with enhanced marketable yield during both the seasons. The interaction effect of cropping season and different treatments was also significant and revealed that maximum fruit yield was obtained in treatment comprising alternate application of vermiwash &*Tamarlassi* during both the seasons, resulted in yield of 1832 and 2030 g/plant and during autumn and summer crop, respectively being significantly higher in summer crop. Higher yield obtained owing to low GHWF population may be attributed to increased photosynthetic efficiency of plants owing to phytotonic effect and also vermiwash is known to act as nutritional supplement in crops leading to better plant health. Additionally, incorporation of biorational management practice resulted in increased rate of parasitism by *Encarsia formosa* Gahan, an important endoparasitoid of greenhouse whitefly.

Key words: Tomato, Greenhouse whitefly, Biorationals, Protected environment

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PP3-17

Insect Pests of Rice Ecosystem in Phek District of Nagaland

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Rice is the primary food crop in the North East Region (NER) and it is cultivated extensively in jhum fields, hills, valleys, terraces and uplands. However, despite its importance, rice farming often leads to substantial financial losses for farmers each year. Various biotic and abiotic stress factors, such as pests, diseases, excessive rainfall, water logging, soil fertility issues and adverse weather conditions, contribute to the decline in rice yields. The presence of insect pests is considered a major factor limiting production and productivity of crop. Based on the field observation at Phek district of Nagaland, the insect pests attacking on rice crops in this region are rice yellow stem borer, leaf folder, case worm, rice blue beetle, rice hispa, gundhi bug, rice root weevil, rice horned caterpillar, lymantrid caterpillar, swarming caterpillar and rice grasshopper. Among these, rice yellow stem borer, leaf folder, rice blue beetle, rice root weevil and rice grasshopper are the major pests causing major damage to the crops leads to reduction in yield of the crop. Moreover, having detailed information on the insect pests in this region would be valuable for creating effective pests management strategies.

Keywords: Rice, Insect pests, Major pests

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PP3-18

Evaluation of Different Protectant and Eradicant Fungicides against *Rhizoctonia solani* in Rice (*Oryza sativa* L.)

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The study was conducted in the year 2023-24 at CCS University, Meerut. This study evaluates the efficacy of various eradicant and protectant fungicides against *Rhizoctonia solani*, a major pathogen affecting Rice crops. *Rhizoctonia solani* causes significant yield losses and management challenges in rice cultivation. This research involved field trials to assess the performance of several fungicides, categorized into eradicants and protectants. Eradicants are applied to eliminate established infections, while protectants prevent initial pathogen establishment.The study tested several commercially available fungicides, including those with active ingredients such as azoxystrobin, propiconazole, carbendazim, etc. Then, efficacy was measured based on reduction in disease severity, impact on plant growth, and overall yield improvement. Results indicated that both classes of fungicides significantly reduced the incidence and severity of *Rhizoctonia solani* infection. Protectants showed effective prevention, whereas eradicants provided substantial control of existing infections. The study concludes with recommendations for integrating fungicide application strategies into rice disease management practices to optimize crop health and productivity.

Keywords: Efficacy, Pathogen, Infections, Establishment, Fungicide, Yield, Eradicant, Protectant, Productivity.

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Theme-IV:

Entrepreneurship and Value Addition of Genetic Resources

(Role of Youth and Women)

ORAL PRESENTATION

OP4-01

Unraveling the Nutraceutical Potential of Five Medicinal *Dendrobium* Orchid Flowers Based on their Colour Variation – A Systemic Approach for Utilization of Natural Resources in North Eastern Himalayan

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Dendrobium orchid species known as the second largest group in the Orchidaceae family recorded over 1100 species in the world and about 82 species of *Dendrobium* has been reported in the states of North Eastern region of India. The *Dendrobium* flowers are widely recognized in traditional Chinese herbal medicine for its immunomodulatory, anti-tumor, anti-diabetic, antioxidant etc., properties. In the present investigation, total five *Dendrobium* species namely *D. nobile, D. densiflorum and D. moschatum, D. farmeri* and *D. fimbriatum* flowers have been aimed to explore for their nutraceutical potential such as bioactive phenolics, flavonoids, anthocyanins, carotenoids, vitamin E and amino acids through LC-MS/MS, minerals composition through ICP-MS, and non-targeted bioactive compounds through LC-HRMS. The *in-vitro* antioxidant activity such as total antioxidant activity, DPPH, ABTS, CUPRAC, FRAP, metal chelation of selected *Dendrobium* orchid flowers has been studied to explore their nutraceutical potential. Bioactive compounds such as gallic acid (558 mg/kg), Lutein (7840.91 mg/kg), caffeic acid (566 mg/kg), quercetin (659.9 mg/kg), anthocyanins like delphinidin (989 mg/kg), petunidin (1157.8 mg/kg) and Vitamin E such as alpha tocopherol (1359 mg/kg) has reported. The quantification of amino acids showed the presence of lysine (31.8 mg/100g), leucine (4.59 mg/100g) and other few essential amino acids in the flowers of *Dendrobium*. The analysis of total 11 minerals through ICP-MS has the presence of essential minerals such as calcium, magnesium, Iron, Zinc etc. The antioxidant potential such as total phenol (14.87 mg/100g), flavonoids (21.71 mg/100g), total antioxidant activity, DPPH (IC_{50}: 357.27 μg/mL), ABTS (IC_{50}: 144.28 μg/mL and metal chelation activity has explored. The flowers of *Dendrobium* exhibited great antioxidant potential. The study non-target compounds through LC-HRMS have been reported total 89 major bio-active compounds of phenolics, flavonoids derivatives. In *Dendrobium* species, the elevated relative abundance of the potentially bioactive metabolites, namely gamma tocopherol, quercetin, caffeic acid and delphinidin suggests its suitability as potential nutraceutical ingredients. The untargeted metabolomics approach has further unfolded *Dendrobium* flowers nutraceutical potential. The findings of the study are expected to be valuable for floriculturists, food and drug scientists, and pharmaceutical industrial operators alike.

Keywords: *Dendrobium* flowers, Nutraceuticals, Phenolics, LCMS/MS, HRMS

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OP4-02

Opportunities and Prospects for Agro-based Entrepreneurship Development in North East India

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North East India comprising of 8 states accounts for 7.98 % of the total land area and 3.78 % of total population of the country. However, due to diverse agro climatic conditions a large number of varieties and landraces of valuable crops are naturally grown in the region. Altogether, the region has got Geographical Indication (GI) in 21 numbers of various crops. These include Manipuri Kachai Lemon, Mizoram Bird Eye Chilli, Naga Mircha, Tripura Queen Pineapple, Tezpur Litchi, Sikkim Large Cardamom, Manipuri Black Rice (*Chak-hao*), Khasi Mandarin, Boka Saul, Nagaland Tree Tomato, etc. The region account for 4.05%, 3.03%, 6% and 3.33% of the country's production of fruits, vegetables, spices and honey. The region accounts for 92.78 %, 95.14% and 49.72% of the total production of Kiwi, Passion fruit and Pineapple of the country. In term of spices, the region accounts for 22.36% and 12.71% of the total production of ginger and turmeric. Black rice locally called *Chak-hao* is the GI crop of Manipur which has got a number of nutraceutical and pharmaceutical properties and is called a super food. A number of Farmer Producer Companies (FPCs) are being formed in the state for promotion and export of black rice. Various value-added products are being produced from black rice subsequently increasing its consumption and utilization. Black rice of the state are being exported to other countries of the world like Europe, Finland, Germany, Dubai, Australia, etc. It is sold at a premium price in the online platform ranging from Rs.250/kg to Rs.700/kg. A number of constraints are being faced by the farmers in black rice production viz. uncertainty and variability in rainfall, lodging problem, poor yield, lack of good quality seeds, *etc*. The marketing problems include no regular demand for sale, not able to sell as and when required, lack of organized marketing, high price fluctuation, lack of storage structure, *etc*. Under Agri Business Incubation, more than 80 numbers of entrepreneurs are enrolled and promoted in Manipur involving in diverse activities viz. food processing, crop farming, livestock rearing, fish farming, mushroom cultivation, bee keeping, etc. Agri entrepreneurs need to be promoted through capacity building, skill upgradation, making startup fund and development of infrastructure for production of quality products.

Keywords: Horticlture, Entrepnurship, Agri-busiess Incubation

OP4-03

Antioxidant Component and Antioxidant Activity of Selected Underutilised Fruit Crops Grown In North Eastern India

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Sixteen underutilised fruits such as ou tenga, tree tomato, karonda, rough lemon, assam lemon, chama seeds, bor thekera, kuji thekera, latka, jackfruit seeds, lime, bhim kol, star fruit, passion fruit etc were collected from different parts of Assam and were evaluated for their antioxidant content and antioxidant activity. A wide range of diversity was observed for phenolics and flavonoid content. The total phenolic content varied between 10.9 to 946.3 mg GAE/100g FWB. Higher phenolic content was observed in ou tenga, tree tomato, bor thekera, kuji thekera etc. A similar trend was observed for flavonoid content which ranged between 1.1 to 705 mg CE/100g FWB. A higher value was observed in ou tenga, tree tomato. Antioxidant activity was evaluated using four different *in-vitro* methods of antioxidant activities. Metal reducing power was evaluated using FRAP and CUPRAC methods. The ferric-reducing antioxidant potential ranged between 0.8 to 28.8 µMol TE/g FWB with the highest value coming from ou tenga. A similar trend was observed in Cupric Reducing Antioxidant capacity which varied between 1.4 to 92.2 µMol TE/g FWB. Here, highest value was observed for ou-tenga. Free radical scavenging assays were evaluated using DPPH and TEAC methods. A similar trend was observed. Statistical analysis revealed that fruits formed cluster based on their antioxidant content and antioxidant activity.

Key words: Underutilised fruits, Ou-tenga, Flavonoids, Antioxidant activity, CUPRAC

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OP4-04

Utilization of Ripe Karonda (*Carissa carandas* L.) Fruits for Development of Nutritional Drink

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The ripe fruits of Karonda are sweet in taste with a peculiar aroma, dark brown to purple in colour and it also possess cooling effect, good appetizer and ant scorbutic. Due to the high perishable nature of ripe fruits, proper utilization is a big challenge for these fruits. On the other hand, being rich in functional qualities, it has a great potential for processing. The demand of soft drinks is increasing day by day so there is considerable scope for developing naturally existing nutrient rich fruit juice beverages from Karonda. The present investigation was carried out in the Department of Post Harvest Technology, Banda University of Agriculture and Technology, Banda (U.P.) during the year 2022-2023. The main objective of present investigation were to utilize ripe karonda fruits through development of nutritional drink with different ratio of karonda fruits juice with Aloe-vera juice and to evaluate the quality parameters of this nutritional Karonda and Aloe vera drink. The study was conducted in two experiments, in first experiment different combinations of Karonda and Aloe-Vera was prepared to standardized the drink and the best combination was selected on the basis of sensory evaluation for the development of flavoured Karonda Aloe-vera health drink. In second experiment Cardamom and Ginger were incorporated in the best blend of Karonda Aloe-vera drink for uncarting flavour in the standardized drink. The standardized drink is rich in functional properties as well as good in flavour having smart amount of total anthocyanin (15.324mg/100g), total phenols (21.309 mg/100ml), antioxidant activities (21.040 mg/100g), vitamin C (9.383 mg/100g). Hence, there is a great scope for development of drink from ripe karonda fruits with good nutritional quality and taste.

Keywords: Karonda, Aloe vera, Nutritional, Drink, Overall acceptability, Ripe, Functional

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OP4-05

Entrepreneurship Development through Value Addition of Underutilised Pomelo

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Pomelo fruit is one of the underutilised fruits which is wildly available in plenty in every hillock of North northeast region from October to January. Pomelo, popularly known as nobab is the largest citrus fruit from the family Rutaceae having high nutritional and medicinal value. The fruit is also consumed as a raw fruit and also used for festive occasion food item which helps to slow down the ageing process, reduce cancer cell growth and also to balance cholesterol levels. Pomelo fruit is a juicy fruit with predominantly white or pink colour succulent pulp/flesh having high nutritional and medicinal value. It is a natural fruit which contains high quality vitamin C, natural fibre, carbohydrate, potassium, magnesium and zero cholesterol. Pomelo fruit is used for the formulation of indigenous herbal medicines which are used for boosting immune system and also to fight body resistance to infectious diseases. It is highly perishable. Due to lack of storage and knowledge for processing, preservation and value addition, a huge amount of fruits go wasted every year. To tackle such problem, KVK, Chandel took the initiative for the promotion of processing and value addition of such underutilized fruits in different value added products like candy, chutney,RTS, squash, nectar, fruit juice, jam, jelly, and marmalade. The shelf life of squash increases up to 12 months and for RTS and nectar up to three months, for candy up to 1 year, for jam, jelly, and marmalade the shelf life is extended up to 1 year by inhibiting the growth of microorganisms These products were assessed by panellist for acceptability of the product by using 9 points hedonic scale and all the products got

very high sensory score ranges from 8.5 to 7.8. These fruit juice will not only serve as the beverages but also act as dietary supplements of natural antioxidant and vitamin C of people of different age groups. These products got very high benefit cost ratio. By converting waste to wealth, the post harvest losses could be reduced to certain extent. The different value added product from pomelo fruit could facilitate sustainable livelihood through entrepreneurship development and enhance the socio economic status which help to empower many farmwomen of Manipur and other NE state.

Keywords: Pomelo, Underutilized fruit, Medicinal value, Value addition, Nutrition.

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OP4-06

A Study on Agricultural Marketing Strategies and Challenges Faced by Farmers of Longleng District of Nagaland

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The backbone of the Indian economy is Agriculture, which has become one of the policy priorities of governments. Increasing agriculture productivity is essential to generate a surplus of food, savings and labour. Marketing is important for the complete development and welfare of farmers. A marketable surplus of agricultural products leads to market oriented approach towards agriculture. The changes experienced in the economy and agricultural sectors have made marketing important for the overall development of the agriculture and welfare of the farmers. Due to the technological breakthrough, the marketable surplus of crops has become more visible in recent years leading to the requirement to follow a market-oriented approach to agriculture. Nagaland is a mountainous state where shifting cultivation (jhum) is common and the cropping intensity is 110%. The marketing of agricultural produce in Longleng district is one of the major problems. Therefore a study was conducted in the Longleng block which was selected randomly and a total of 10 villages were selected and the sample was 150. The Ex-post Facto research methodology was followed and data collection was done by face-to-face contact method. The findings of the study revealed that most (68.67%) of the middle aged farmers (26-41 years) actively involved in agricultural activities with 36.67 percent farmers had educational level up to high school. Mostly (54.67%) female farmers were actively involved than male and 54.67 percent were married who lived in nuclear family with medium level annual income ranging from Rs 24,312/ to Rs 52,648/-. The study also further asserted that the Garret ranking method was used for ranking different marketing problems in the Longleng district of Nagalnd. Lack of an organized market became one of the serious problems in the district which ranked I followed by lack of awareness and market information which was ranked II. It can be suggested from the study that proper and systematic organised market and conducting different awareness cum training programmes may enhance the knowledge of marketing information which can enhance the income of farmers and leads to the upliftment of the standard of living among farmers of Longleng district.

Key words: Marketing, Farmers, Longleng, Strategy, Agriculture

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OP4-07

Entrepreneurial Opportunities and Challenges for Women in Agriculture: A Study in Jorhat District of Assam

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If you move a woman forward, her family will go ahead, a village will go ahead, then the nation itself will move forward and when it comes to entrepreneurship, women are one of the most important untapped resources as said by Pandit Jawaharlal Nehru.Women entrepreneurs have been recognized as an important source of economic growth. They shape the economy, and create wealth and jobs by inventing new products, processes and services. We all know that the economic development of modern women is important for any country, especially a country like India. About 70% of the population lives in rural areas and relies on agriculture for food. With the help of various governmental and non-governmental agencies, growing numbers of women are joining the ranks of entrepreneurs. However, entrepreneurial women are overburdened in the existing familial and societal setup and find it increasingly difficult to balance their work and life roles. Therefore this study was initiated to explore the entrepreneurial challenges and opportunities faced by women involved in the agricultural sector. A structured schedule was prepared to determine the challenges faced by the women entrepreneurs in the agricultural sector with a total of 120 women entrepreneurs of Jorhat district selected as respondents for the study. The challenges were determined with the help of the Problem Confrontation Index (PCI). Based on the analysis, it was found that , it has been found that lack of time due to family burden was the first challenge faced by the respondents with PCI score of 299 and rank 1. Lack of mobility was the first important social challenge faced by the respondents with PCI score of 315. The high cost of required machineries or equipments was the first important challenge faced by the women respondents with PCI score 288. Among the marketing challenges, lack of demand in the local market is the first important challenge faced by the women respondents with PCI rank I.

Key words: Entrepreneurs, Women, Problem Confrontation Index, Challenges, Jorhat

OP4-08

Livelihood Opportunities in Ethnic Food System of Himachal Pradesh

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Himachal Pradesh is a leading hub of traditional food heritage, but due to the changing food habits of people, these ethnic foods are on the verge of disappearance. Hence, an effort has been made to document the method of preparation of various dishes included in a traditional meal called Kangri Dham. Dham is traditional meal served to the people in Himachali culture on the occasion of marriages or any religious days. The information regarding the preparation of Dham was collected from the chefs locally called Botis using a focused group discussion method. Eight to ten dishes are cooked and served in Kangri Dham. Among all Sepu Vadi, an Urad Dal, *Vigna mungo* (L) Hepper-based recipes are the special delicacy of Dham. The production of dry Sepu Vadi has immense potential for entrepreneurship not only in the country but across the globe if industrialized. Therefore, it needs the attention of policy planners to grant the status of small-scale industry to attract the unemployed youth towards Sepu Vadi business. Furthermore, most of the recipes are pulses-based having good dietary protein thus it can play a vital role in sustainable pulse production in the region. Leaf plates locally called Pattals used for serving food are a source of livelihood for the people thus efforts are needed for its conservation. It also draws the attention of food technologists towards the development of recipes of Dham as a ready-to-eat meal and the incorporation of these recipes in hotel management courses is suggested. Effective policy for registration of these traditional foods by granting geographical indications should be framed so that these products establish trust and create brands in the market.

Keywords: Kangri Dham, Sepu Vadi, Traditional meal, Dishes

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OP4-09

Success Stories on Scientific Beekeeping for Entrepreneurship Development in Meghalaya

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Beekeeping is one of the promising agribusinesses and is considered as an ideal agro-based rural industry providing additional income to the people. It is appropriate for youth without jobs, small-scale and marginal farmers, and labourers without land. This business venture offers lucrative self-employment opportunities with numerous advantages and is fiscally sustainable. The practice of raising bees scientifically to produce honey and other hive products for human use is known as scientific beekeeping. It can be considered as a commercial enterprise for resource poor farmers with minimum investment of financial and manpower resources. It can play a potential role in enhancing the income of small and marginal farmers of Meghalaya. Therefore, the present study was conducted for intervention of scientific beekeeping to develop entrepreneurship in Meghalaya. The study was carried out in the different villages of Meghalaya under the Tribal Sub-Plan (TSP) programme of ICAR Research Complex for NEH Region, Umiam, Meghalaya. Farmers/traditional beekeepers from different villages of two districts namely Ri-Bhoi and East Khasi Hills of Meghalaya were selected for the intervention of scientific beekeeping to enhance income as well as to develop entrepreneurship on beekeeping. All the selected farmers were trained with hands-on training and practical demonstrations at ICAR Research Complex for NEH Region and at the village level for the rearing of *Apis cerana Himalya*. The study revealed that more than 90% of the intervened farmers adopted scientific beekeeping with an average production of 4-5kg honey/hive/year. The study found that some of the intervened beekeepers emerged as successful entrepreneurs in beekeeping with an annual production of honey of more than 1.5 quintals per year.

Keywords: *Apis cerana,* Meghalaya, Entrepreneurship, Scientific Beekeeping, Success story

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OP4-10

Preparation, Quality Evaluation and *In vitro* Studies of Cabbage and Cauliflower Waste Silage

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The global concern over the environmental and socio-economic of food and vegetable waste biomass is a persistent issue. Globally, each year 2.5 billion tons of food, and approximately one-third all food produced in India is wasted or gets spoiled before it is eaten (FSSAI). This massive amount of food and vegetable waste biomass may contribute to the annual emission of about 3.3 billion tons of CO_2 equivalent greenhouse gases from dumping sites, leading to global warming (India Today, 2020). Fruit and vegetable waste is approximately 4.65-5.99 % of total food wastage. Therefore, the search for food substitutes due to decreasing fodder production pave ways for efficient waste disposal of vegetable waste by creating the perfect solution for developing feed resources. The potential use of vegetable waste as animal feed gaining importance due to their rich nutrient and phytochemical contents which provide a complete supplement of nutrients required for the normal growth and development of livestock. There is various vegetable waste which can be used as livestock feed. Therefore, this experiment was conducted to evaluate the quality of cabbage and cauliflower waste silage and to study the *in vitro* parameters of cauliflower and cabbage waste silage. Cabbage and cauliflower waste were collected from the local market and after cleaning cut into small pieces and kept in air tight container for 28 days. 5 different types silage were prepared from cabbage and cauliflower waste *viz.* I: Cabbage waste silage with 0.5% salt, 1% urea; II: Cauliflower waste silage with 0.5% salt, 1% urea; III: Cabbage and Cauliflower mixed (1:1) waste silage with 0.5% salt, 1% urea; IV: Cabbage waste silage with 0.5% salt, 1% urea and 5% molasses V: Cauliflower waste silage with 0.5% salt, 1% urea and 5% molasses and VI: Cabbage and Cauliflower mixed (1:1) waste silage with 0.5% salt, 1% urea and 5% molasses. The fermentation characteristics and nutritive values of silage were studied by collecting representative fresh silage samples. In terms of appearance and smell, all the silage in this experiment is of good silage. Likewise, considering the organic acid contents of silages, all silages were found to have very good quality. The IVDMD (%) significantly differs ($P<0.05$) among various cauliflower waste silage. From this experiment, it can be concluded that incorporating 5% molasses into silage prepared from cabbage and cauliflower waste can uphold its high quality, as demonstrated by reduced pH and NH_3-N levels, coupled with increased lactic acid bacteria (LAB) content

Keywords: Cabbage, Cauliflower, Waste, Silage, Quality

OP4-11

Incubation Ecosystem in North-East: Strategy to Establish Agripreneurship and Start-Ups through Indigenous Fruits and Vegetables

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Incubation centers play a pivotal role in fostering the growth of startups. They act as catalysts, providing a supportive ecosystem that nurtures innovation, collaboration, and resilience. The number of incubators in India has grown 15 times in the last two decades in the food production, processing and marketing sectors. North-East has huge opportunities to establish entrepreneurship and start-ups on indigenous germplasm of fruits and vegetables through processing and value addition, Agribusiness Incubation (ABI) Centre, ICAR Research Complex for NEH Region, Umiam, Meghalaya promotes innovative business ideas and entrepreneurial skills through institutional participation in providing commercial production practices and processing skills. During the last six years, a total of 105 incubates were admitted out of which 40 percent are women-led enterprises. 25 incubates have graduated and successfully running their business in various Agribusiness ventures. 36 % of the enterprises associated with the center cater the food processing sector followed by Meat Processing sector (18%), Livestock sector (15%) and 13% accounts for spice processing sector. A study was conducted to identify the constraints associated with the medium and Small-Scale enterprises and the ranking was analyzed using Garret ranking techniques (Garret Score). Inadequately infrastructure for processing and storing (80%) was the highest constraint followed by lack of financial support (69%) and logistic support (60%). There is a need for concerted efforts from all the line departments to establish vibrant start-ups ecosystems in this region.

Keywords: Agribusiness, Incubation ecosystem, Agribusiness ventures, Constraints

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POSTER PRESENTATION

PP4-01

Role of Rural Women in Agricultural Food Products

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Primarily, rural women have been in charge of cultivating, gathering, and preparing staple foods as well as tending to livestock. They have been in charge of maintaining diets and recipes, making sure that people in communities and families have access to a variety of wholesome foods. Women make up the majority of market vendors in various societies. They support local economies and guarantee that food is accessible to a wider audience by selling their produce. Women are undervalued or have their contributions restricted by societal norms or impediments that are specific to their gender in many developing nations, even though they play significant roles at many nodes of the agricultural and off-farm value chains. We find that, depending on the national context, various person and household characteristics, the value chain, and the particular node of involvement are important. Women are not always empowered by entrepreneurship, which is typically practiced by wealthier households with greater risk tolerance, or by household wealth as measured by the number of assets owned by family members. Greater gender equality is not always connected with increased market activity. Although the intensity of this relationship varies, education is positively connected with greater empowerment for both men and women. In conclusion, context and culture determine whether a node in a value chain is empowering and whether or not participation in the chain is beneficial. When creating interventions for food systems, care should be taken to consider the social and cultural contexts in which these food systems operate to prevent exacerbated gender imbalances.

Keywords: Gender, Women's empowerment, Market inclusion, Value chains, Food systems

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PP4-02

Value Addition in Orchids

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Value addition is the way taken to increase the value of a raw product anytime between harvesting and sales of the final product. In floriculture, value addition is made through genetical changes, processing or diversification. Value addition gives high premium to the grower as well as provides quality products for the domestic and export market. Orchids are consistently ranked among the best sellers in the global potted plant trade and also comprise 10% of all fresh cut flowers traded internationally. The orchids have taken a significant position in cut flower industry due to its attractiveness, long shelf life, high productivity, right season of bloom, and easy packing and transportation. Basically, orchids are monocot plants, monopodials or sympodials. They may be epiphytic, terrestrial and lithophytic. About 70% of the world's orchids are epiphytic and/or lithophytic, 25% are terrestrial and 5% of the world's orchids grow in mixed substrates. They are used as genetic resources for crop improvement, cut flowers or foliages, flowering / potted plants /hanging baskets, sources of phytochemicals, sources of essential oils, sources of plant pigments, sources of dyes, dried flowers/other plant parts, flower arrangement, flower ornaments, bouquets, herbal preparations and components for aeroponics, vertical gardens, landscaping, crop diversification, waste to wealth management and climate resilient crop.

Keywords: Cut flowers, Foliages, Pot plants, Diversification

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PP4-03

Evaluation of Banana Germplasm for Processing Purpose

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The present study entitled "Evaluation of banana germplasm for processing purpose" was carried out at experimental block of Fruit Research Station (ICAR-AICRP on Fruits) Navsari Agricultural University, Gandevi that falls under the hot and humid tropical zone of South Gujarat. Total 12 banana germplasm of different genome group were accessed during 2022-23 for processing purpose *viz.,* Bainsa, Dang Collection, Hanuman, Pacha Kadali, Bluggoe, Vansada coll., Gurgaon coll., Monthan, African coll., Thonkunan, Gandevi Selection and Grand Naine. Under this study, row banana evaluated for preparation of chips and powder. The significantly higher recovery of chips (58.00%) and dry powder from fresh banana fruit (21.60%) and dry powder from Slice of fruit (37.44%) was obtained with Pacha Kadali. While, minimum moisture (62.56%) content was noted in pulp of Pacha Kadali. Maximum organoleptic test score of chips (8.67) was recorded in Monthan and maximum score of dry powder (8.03) of banana was observed in Thonkunan.

Keywords: Germplasm, Genome, Processing, Moisture

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PP4-04

Development of Novel Herbal Fruit Tea from Underutilised Fruit-Roselle

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Roselle is one of the underutilised fruit which is wildly available in plenty in many parts of North east region of India. It is very rich in natural bioactive compounds such as polyphenols, flavonoids, anthocyanins, carotenoids, coumarins, alkaloids, polyacetylenes, saponins, terpenoids etc. It exhibits high natural antioxidants which can scavenge the free radicals which are very reactive and harmful to human health. Seeing the nutraceutical properties and health benefits, Roselle based herbal fruit tea was formulated by using underutilized locally available fruits and analyzed for proximate, phenolic, flavonoid content and antioxidant activities. It is prepared by incorporating roselle, pineapple and ginger by mixing in proper proportion. The sensory quality for consumer acceptance of the fruit tea was analysed by hedonic scale. The statistical analysis was performed in triplicate and data are presented as means ± standard deviations (SD). From the study it was found that Roselle- pineapple blended fruit tea infusions contained high amount of total phenolic content of 664.9±0.31 mg GAE/100 g while flavonoid content of roselle-pineapple tea was recorded as 232.2±0.12 mg QE/100 gm. The antioxidant activity of roselle-pineapple (460.0±0.2mg ascorbic acid Equivalent/100 g sample) was very high as compared to other fruit tea (129.7±0.07mg Ascorbic acid Equivalent/100 g sample). It also observed that the protein content is 5.0 g, fat content 0.16g and carbohydrate content 23.7g per 100 g. The fruit tea infusions also contained high vitamin C content. However, the present fruit tea infusions have shown high sensory quality and infusion time is also directly correlated with sensory quality of roselle pineapple tea. These fruit tea infusions will be a good alternative for other sweetened drinks. Hence, these fruit tea infusions will not only serve as the beverages but also act as dietary supplements of natural antioxidant and vitamin C of people of different age groups. Incorporation of these high nutrient rich ingredients has resulted in unique colour, flavour contributing to enhance sensory attribute and overall acceptability of the product. Besides an improvement in storage quality and shelf life was also observed. This tea is very good for all section of population. It is mainly designed in order to boost optimum health as well as for reducing the risk of certain diseases like diabetes, heart diseases and cancer. There is a great potential for the commercialization of immune boosting health drink to create market opportunities among start -up entrepreneurs.

Keywords: Roselle, Pineapple, Phenolic content, Flavonoid content, Antioxidant activity

PP4-05

Unravelling the Nutritional and Textural Profile of "*Doh Snam*": A Traditional Sausage of Meghalaya

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Traditional meat and fish products have been an integral part of the cuisine and culinary practices of various ethnic communities across Southeast Asia. The northeastern states of India have several authentic ethnic meat and fish products which have not been documented adequately. One such unique product is *Doh Snam,* a typical blood susage, which is predominantly prepared by the khasi tribe of Meghalaya. Blood sausage is a traditional food in many cultures, including European, Latin American, and Asian cuisines. It is often served as sliced and pan-fried or grilled. These products are highly valued in Southeast Asian cuisines not only for their distinct flavor but also for their nutritional benefits. The *Doh Snam* is basically a pork sausage prepared by using pig's blood, meat, and other ingredient like sliced onion, smashed ginger, smashed garlic with chili and salt, then it stuffed in the large intestine of an adult pig as a natural casing. A survey was conducted at Mylliem village of East Khasi Hills district of Meghalaya for documenting the method of preparation and further analysis of proximate composition of traditional sausages. It aimed to investigate the proximate composition and texture profile of *DohSnam*, providing valuable insights into its nutritional profile. The analysis revealed that the product contains an impressive 12.64% crude protein, additionally, it was found to have a moisture content of 47.20%, an ash content of 1.18%, and a lipid content of 10.27%. The Texture profile of the product like Hardness (N), Springiness (mm), Cohesiveness, Gumminess (N) and Chewiness (N) was found to be 4193.65±505.05, 0.66±0.06, 0.44±0.082, 1837.15±251.85 and 1219.69±132.03 respectively. This study highlights the importance of traditional products in the culinary heritage and dietary patterns of indigenous communities. An intervention of food science in optimizing the preparation methods, improving hygiene parameters, and packaging can promise a lucrative business in this sector for local people and may attract consumers from other parts of the country.

Keywords: Sausage, Proximate composition, Traditional food product, TPA

PP4-06

Challenges Faced by Fruit Growers in the Bundelkhand Region

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The Bundelkhand region, spanning parts of Uttar Pradesh and Madhya Pradesh in India, is characterized by its unique geographical and climatic conditions. Bundelkhand has a rich cultural heritage and diverse agriculture but faces challenges due to erratic rainfall and drought. The region's economy depends on agriculture, so addressing farmers' obstacles is crucial for food security and economic stability. While the region holds significant potential for fruit cultivation, growers face numerous challenges that hinder productivity and profitability. There are multifaceted challenges faced by fruit growers in Bundelkhand, including water scarcity, soil degradation, pest and disease management, market access, and socio-economic factors. The Bundelkhand region has a semi-arid climate with unpredictable monsoons and declining water tables due to over-reliance on groundwater for irrigation, posing a threat to current and future agricultural practices. The soil in Bundelkhand is mostly saline and prone to erosion. Continuous cultivation without enough nutrient replenishment has led to soil degradation and reduced fertility, impacting fruit quality and yield. Poor irrigation practices have caused salinity problems in some areas, exacerbating soil health issues and affecting fruit crop growth and productivity. Fruit crops in Bundelkhand are vulnerable to pests and diseases, leading to significant losses. Limited access to modern pest control and organic farming practices makes crop protection challenging for growers. Farmers need more knowledge about integrated pest management (IPM) and organic alternatives to mitigate pest issues sustainably. The lack of extension services further hinders their adoption of effective management practices. Transportation and storage challenges in Bundelkhand hinder fruit growers' market access. The lack of cold storage leads to post-harvest losses. Volatile fruit prices due to seasonal variations and market demand fluctuations often result in low profits for growers, discouraging investment in farming practices. Many small-hold farmers struggle to access credit due to a lack of collateral or financial know-how, limiting their investments in quality seeds, fertilizers, and modern farming techniques. Rural youth migration to urban areas in search of better jobs causes labor shortages during crucial farming periods, impacting the timely cultivation and harvesting of fruit crops.

Addressing these challenges requires a multi-faceted approach involving government intervention, research and development initiatives, and community engagement. Sustainable agricultural practices, improved irrigation techniques, better pest management strategies, and enhanced market access are essential for revitalizing fruit cultivation in Bundelkhand. By overcoming these obstacles, fruit growers can contribute significantly to regional food security and economic development.

Keywords: Bundelkhand region, Fruit grower, Challenges, Orchard management

PP4-07

Enhancing Entrepreneurship through Selective Mechanization in Oyster Mushroom Cultivation: A Case Study from Meghalaya

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Mushrooms are highly popular in Northeast India, valued not only for their taste and nutritional benefits but also as a source of income, showing significant potential for local production. However, the current labour-intensive and physically demanding manual cultivation methods have discouraged many farmworkers from engaging in this lucrative activity. As a result, the introduction of mechanization is necessary to address the labour-heavy and strenuous tasks involved in mushroom farming, making the process more efficient and appealing to workers. This article explores the potential for fostering entrepreneurship by introducing selective mechanization into the mushroom cultivation process. Focusing on the specific needs of small-scale farmers in the region, the study identifies key areas where selective mechanization can improve efficiency, reduce labour intensity, and enhance overall productivity. By examining the economic feasibility, operational benefits, and scalability of mechanized practices, the paper demonstrates how these innovations can lower production costs and create new business opportunities. The findings highlight mechanization as a crucial step in promoting sustainable agricultural entrepreneurship, ultimately contributing to rural development and income generation in Meghalaya and Northeast India.

Keywords: Mushroom, Selective mechanization, Employment generation and Livelihood

Theme-V:

Capacity Building and Public Awareness

OP5-01

Yield Improvement and Impact Analysis of Black Gram through Frontline Demonstrations in Ukhrul District Manipur

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Effective demonstrations in the farmers' field will be the best step to convey the technologies through extension approaches to the farmers. Frontline demonstrations (FLDs) will persuade the farmers about innovative farm technologies. This study examines the implementation and outcomes of front-line demonstrations (FLDs) of black gram in Ukhrul District, Manipur, a region known for its diverse agro-ecological conditions. The primary objective was to assess the effectiveness of improved black gram varieties and cultivation practices in enhancing crop yields and farmers' income. Over a period of 8 years, FLDs were conducted involving 67 farmers across various villages in Ukhrul. The demonstrations focused on introducing high-yielding black gram varieties, optimizing sowing techniques, and employing integrated pest management (IPM) strategies. Our study identified that innovative and improved cultivation practices sensitized among the farmers through the FLDs *viz.* improved varieties, seed rate, timely sowing, weed control, foliar feeding and plant protection comprising of full package of practices developed to raise the crop technology resulted in average increase in yield of 26.5 per cent in black gram and 60% increase in net returns over the check plots comprising of existing farmers practices. Technology gaps, extension gaps and technology indices were calculated to analyze the performance of these frontline demonstrations at farmers' fields. The average technology index of 36.8 per cent indicates the feasibility of black gram crop in existing farming situation in the district. Based on the economic analysis the improved production technology of these pulses gave higher gross return and net return with higher benefit-cost ratio in FLD plots as compared to check plots. Because of regular intervention and sensitization about the improved cultivation practices the yield increase from 7.2 q/ha to 1.2 q/ha in hilly regions of Ukhrul district. Additionally, farmers reported improved crop resilience and reduced pest-related losses. The study underscores the potential of FLDs as a critical tool for agricultural innovation and capacity building in remote regions. The findings advocate for the broader adoption of demonstrated practices and suggest further research to tailor interventions to local conditions.

Keywords: Black gram, Technology gap, Front-line demonstrations, Seed yield, Economic analysis, Extension gap

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OP5-02

Yield Gap and Impact Analysis of Groundnut Cultivation through Front Line Demonstration in Chandel District, Manipur

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One of the most important oil seed crops grown in India is Groundnut (*Arachis hypogaea* L.). It is abundant in energy, minerals and vitamins. It is a significant food legume and oilseed crop grown in tropical and subtropical regions of India that is used in various forms and aids in the reduction of malnutrition. Even if groundnut cultivation is not customary in the North Eastern Region of India, more groundnuts must be produced there to provide food security and nutrition. The crop has been newly introduced for cultivation in Manipur and found successful as rainfed crop during kharif season and has got very high yield potential. The technical gap is a major barrier to increasing groundnut output in Chandel district, Manipur State. Frontline demonstration (FLD), is one of the most significant and effective methods for technology transfer. By using the newest technologies, Krishi Vigyan Kendra Chandel's interventions aim to boost productivity and production. The present front-line demonstration was carried out by Krishi Vigyan Kendra, Chandel, ICAR-Manipur Centre to find out yield gaps and it impact between demonstration practices under Front Line Demonstration and farmer's practice of kharif groundnut in 22 hectares of land in different villages during 2017-18 to 2022-23, respectively. The result indicated that average seed yield of groundnut in demonstration practices ranged between 18.10 q/ha to 24.45 q/ha whereas in Farmers practices it was 10.55 q/ha to 13.80 q/ha during demonstrated years. The per cent increased in yield with demonstration Practices over Farmer Practices was ranged between 41.71% to 43.56 %. The technological or Yield Gap ranges from 5.55 q/ha to 11.90 q/ha and extension gap were from 7.55 q/ha to 10.65 q/ha respectively. Similarly, technological index was decrease from 39.67 % to 18.50 % during the study period. The benefit cost ratio was from 2.81:1 to 3.94:1 under demonstrations, while it was 1.67:1 to 2.30:1 under farmer practices. By conducting front line demonstration on improved practices with High Yielding Verities of proven technologies in farmer's field can reduce the Yield/technology Gap to a considerable extent and thus yield potential of groundnut enhanced to a great extent which increased in the income level of farmers and improved livelihood of farming community in the region by reducing the technology gaps.

Keywords: Frontline demonstration, Groundnut, Manipur, Yield

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OP5-03

An Introduction and Adaptation of Improved Processing Potato Variety Kufri Frysona to Ri-Bhoi District of Meghalaya

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Meghalaya is one of the north eastern states where potato is being grown extensively as a major tuber vegetable crop throughout the year owing to its varying climatic conditions. With increase in urbanization, employment opportunities in industries and change in food habits there is a high demand for continuous supply of processing quality potato *viz.,* French fries, chips, flakes *etc* in the north eastern states. This demand, however, cannot be met as the state and region faces several challenges with respect to procuring the quality seed tubers and cost of transportation. The farmers in the region are also unaware of scientific potato cultivation and use of quality seed tubers for increasing the yield and quality. Keeping this in mind and with the prevalent opportunities for growing processing varieties in the region, the ICAR - Central Potato Research Institute, Regional Station Shillong in collaboration with ICAR – Krishi Vigyan Kendra, Ri-Bhoi District aimed at introducing the potato processing variety Kufri Frysona in Bhoirymbong area during the rabi season of 2022. The training was given to 40 farmers from the villages of Thadnongiaw, Mawbri and Kyrdem and 20 q of Kufri Frysona seed potato were distributed to the farmers. Throughout the crop season, constant monitoring and technical guidance were provided to ensure the success of the initiative. The results during harvest revealed that the variety Kufri Frysona yielded 15-18 tubers per plant with an average weight of 500-650 g per plant, which is comparatively higher when compared with traditional farming practices. The crop productivity averages 30-35 t/ha, which significantly exceeds both the state and national average of 8 and 24 t/ha, respectively. The crop was also taken up in the second year of planting and farmers from Thadnongiaw were able to sell their potato tubers to Self-Help Groups @ Rs 30-35 per kg, with approximately 350 kg sold to one SHGs. This particular SHG utilized the tubers to produce potato french fries, a value-added product that was then distributed and sold to neighbouring villages. Farmers expressed high satisfaction with the improved yields achieved using quality seeds of the introduced variety compared to local seeds. With the introduction of this variety, new avenues and opportunities were provided to farmers to enhance and increase their income through value-added products. Finally, ensuring the availability of quality seeds and addressing logistical challenges are crucial for sustaining and expanding potato cultivation, particularly in regions where land is often left fallow after main crops.

Keywords: Kufri Frysona, processing, value-added products, Ri-Bhoi

POSTER PRESENTATION

PP5-01

Evaluating the Impact of Alternate Wetting and Drying Irrigation Practices on Crop Growth and Yield of Rice in Farmers' Fields through Front Line Demonstrations

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Implementing the alternate wetting and drying (AWD), irrigation method in rice cultivation presents a substantial opportunity for conserving irrigation water. This technique involves alternating irrigation in rice fields based on specific triggering criteria, potentially influencing the soil-plant-water system. Over a two-year period, multiple trials were conducted in farmers' fields by Krishi Vigyan Kendra, Ankushpur, Ghazipur, through front-line demonstrations. Perforated pipes were installed during the trials to improve crop growth, yield, and water use efficiency. Daily measurements of ponding water depth and agronomic parameters (including plant height, number of tillers, effective tillers, harvest index, and grain yield) were taken at regular intervals. The field data collected were then utilized to assess water use efficiency and establish crop production functions. The results revealed that crop growth parameters significantly improved under AWD irrigation practices compared to traditional farming methods. Furthermore, AWD irrigation practices led to an impressive ~24% increase in grain yield while reducing irrigation water usage by approximately 21% compared to traditional practices. This approach resulted in almost a 25% increase in net returns for farmers. The trials strongly suggest that farmers can reduce irrigation water consumption, increased grain yield, and enhanced water use efficiency by adopting AWD irrigation practices. This makes AWD irrigation more suitable for sustainable rice production.

Keywords: Alternate wetting and drying; Yield; Water use efficiency; Crop production function.

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OP5-02

Deep Learning-Enabled Mobile Application for On-Site Nitrogen Prediction In Strawberry Cultivation

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Precisely applying nitrogen to plants is crucial for their optimal growth, preventing overuse that may cause water pollution, soil degradation, and financial losses. However, current methods for measuring nitrogen levels are labor-intensive, costly, and destructive, requiring skilled personnel and specialized equipment. Thus, in the present study, a novel deep-learning-assisted Android mobile application was developed to predict on-site nitrogen levels in strawberry plants in a non-destructive manner through leaf images. The application categorizes nitrogen levels into eight distinct classes, each representing a 0.25% incremental rise within 2.25% and 4.0% limits. An image dataset was generated by converting chlorophyll readings into nitrogen readings through a linear equation (R^2 = 0.89). Multiple convolutional neural networks (CNNs) models integrated with residual connections, squeeze and excitation module, convolutional-based attention module (CBAM), and *Depthwise* convolution were employed to enhance classification accuracy. The CNN model consisting of residual connections and CBAM performed the best with precision, recall, accuracy, and F1-score values of 82.0%, 83.0%, 82.5%, and 82.7%, respectively. In comparison, the proposed CNN, devoid of attention modules, showed the lowest classification accuracy (76.7%). The state-of-the-art models, except MobileNetV1, surpassed the proposed models by up to 3.3% (for EfficientNetB2) in accuracy. The developed mobile app achieved precision, recall, and accuracy rates of 81.0%, 81.0%, and 80.7%, respectively, offering an efficient, non-destructive method for growers to predict nitrogen levels in strawberry plants, aiding in optimized nitrogen application for sustainable agriculture practices.

Keywords: Nitrogen, Nutrient management, Strawberry, Smart farming, Convolutional neural networks,Mobile application

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OP5-03

Optimization of Irrigation Timing for Sprinkler Irrigation System Using Convolutional Neural Network-Based Mobile Application to Conserve Water and Energy

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Traditional sprinkler irrigation time calculations excluded soil moisture. Because crop water usage relies on daily weather, this occasionally causes shortages or excess irrigation. This research proposed integrating current soil moisture into irrigation time calculation using a lightweight convolutional neural network (CNN). The depthwise separable convolution and residual connections were incorporated in CNN architecture to enhance accuracy and limit its size. A deep learning-based mobile application was developed which can predict soil moisture class through in-situ soil images. Sprinkler irrigation time was calculated using predicted soil moisture class, crop factors, and sprinkler system details. This developed system was assessed based on CNN accuracy in soil moisture class prediction, energy usage, and water savings. Developed CNN model had an average classification accuracy of 97.10%, a precision of 85.50%, a recall of 86.80%, an F1-score of 85.80%, and a true prediction score of 75.30%. The developed mobile application saves 27.59% water and 27.42% energy by estimating the real irrigation time using the predicted soil moisture class. In one scenario during testing, traditional irrigation depth was less than the actual irrigation demand, but the developed system corrected it, thus, can reduce crop yield losses by providing adequate water. Consequently, the deep learning-based irrigation time determination system may save water, energy, and enhance crop yield. So, depending on soil moisture content, the novel technique proposed in this study can calculate irrigation time with higher accuracy.

Keywords: Irrigation, Mobile application, Convolutional neural networks, Deep learning, Soil moisture, Soil classification.

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