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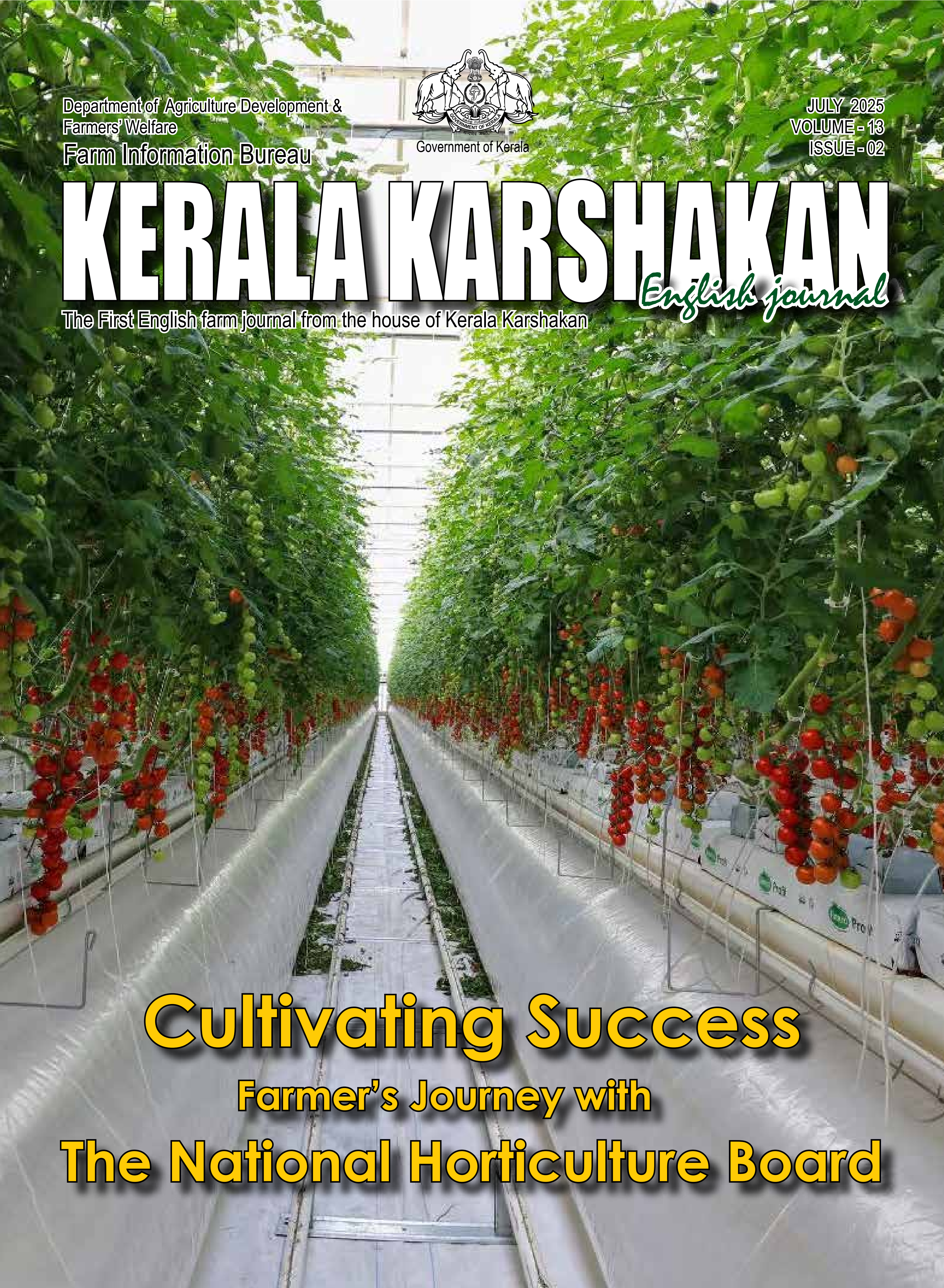
KERALA KARSHAKAN

English journal

The First English farm journal from the house of Kerala Karshakan



Cultivating Success

Farmer's Journey with The National Horticulture Board

INSIDE

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Mail: editorejournalkkfib@gmail.com Log on to http://www.fibkerala.gov.in
Phone: 0471-2314358

The First English farm journal from the house of Kerala Karshakan

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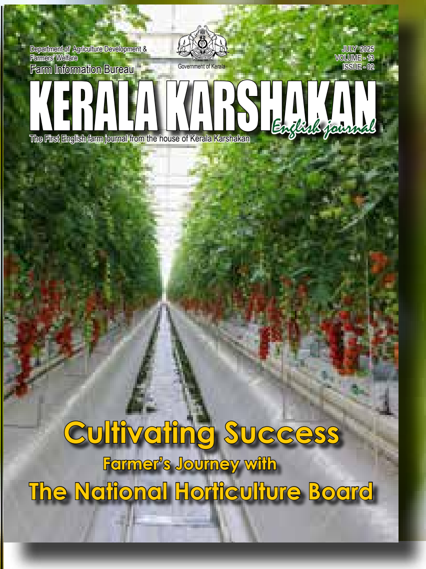

Articles/ Features appearing in this e-journal are either commissioned or assigned neverthless, other articles of farm relevance are also welcome. A maximum of 750 wordage is appreciated. Such items should be addressed to The Editor, Kerala Karshakan e-journal, Farm Information Bureau, Kowdiar PO, Thiruvananthapuram, Pin: 695003
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Editorial

In the evolving journey of Kerala's agriculture, every new challenge brings with it a call for innovation, and every success story lights the path forward for others to follow. This edition of Kerala Karshakan celebrates one such inspiring story as its cover feature: a farmer's successful venture into Gerbera cultivation, made possible through the support of the National Horticulture Board. This isn't just a tale of individual triumph, this story is a blueprint that is detailing the practical steps of project proposal, navigating government schemes, and effectively using subsidies. It is a testament to what becomes possible when farmer ambition meets institutional backing.

Our pages are rich with insights, starting with the articles that deepen our understanding of both promise and peril in agriculture today. Whether it is the potential of the tree tomato, or the revival of Kerala's naturally organic Kaipad rice through some sustainable models, each piece brings scholarly insight into real world applicability. Alongside innovation, we also confront the biological challenges threatening productivity of mixed viral infections in cassava, the need of conservation of a critically endangered native slipper orchid of India, and the technological hurdles in cashew cultivation and so on. These topics may appear scientific at first glance, but at their core, they are about safeguarding livelihoods and ensuring that our crops thrive under mounting pressure.

As editors, we believe that meaningful agricultural progress happens when researchers, farmers, and policymakers engage in dialogue. This issue aims to bridge knowledge gaps, not just in rice genomes or plant virology but in how we share and act on that knowledge. We hope that whether you are a scholar who decodes genes or a farmer nurturing fields, you will find something in these pages that speaks to your experience, encourages curiosity, and inspires action. After all, the future of farming lies in both science, soil and in the hands of those who believe in both.

In the bustling landscape of Bangalore Urban District, Karnataka, lies a beacon of modern agricultural success: Somashekara Reddy's polyhouse project. At 70 years young, Mr. Reddy embodies the spirit of a true agricultural innovator, proving that age is just a number when it comes to embracing new techniques and achieving remarkable profitability.

His story, featured in **"TAMIZHAGA VIVASAYI ULAGAM,"** is a testament to the power of vision, hard work, and the crucial support provided by the National Horticulture Board (NHB).

The Visionary Project: Mr. Somashekara Reddy embarked on a hi-tech Gerbera cultivation project under a polyhouse cover, spanning 5828

Cultivating Success

Farmer's Journey with the National Horticulture Board

Deputy Director
National Horticulture Board
Ministry of Agriculture & Farmer's Welfare, Govt. of India
Uppalam Road, Statue, Thiruvanathapuram, Kerala-695 001
Phone: 0471-2740505, 2470506, 9880273019
E-mail : kerala.nhb@gov.innhbtvm@gmail.com

square meters (1.46 acres) at Sarjapura Village. With a remarkable 50,000 Gerbera plants thriving in disease-free conditions, his polyhouse is a hub of vibrant blooms.

Key Infrastructure & Financial Support: The project was meticulously designed and executed with modern infrastructure:

- A state-of-the-art polyhouse built to NHB specifications.
- An efficient drip irrigation and fertigation system.
- A bore well (850 feet deep with a 15 HP motor) and a large substantial water harvesting tank (19.50m x 14m x 5m, with 500 micron plastic polyfilm sheet) to ensure consistent water supply.
- A 120-meter 4-inch PVC pipeline for efficient water distribution.
- A functional labor room for the convenience of farm workers.
- Essential horticulture equipment, including a power sprayer and five other farm tools.

The total project cost was Rs 88.70 lakh, with a bank loan of Rs 64.00 lakh. Mr. Reddy's commitment was evident in his promoter margin of Rs 24.70 lakh. What truly made this venture accessible and highly profitable was the significant NHB subsidy of Rs 40.88 lakh, received promptly.

Impressive Returns: The results speak for themselves. Mr. Reddy's polyhouse yields an astounding 145,700 Gerbera bunches per year, translating to a net profit of Rs 31 lakh annually

from just 1.46 acres! His marketing strategy involves both local agencies and direct sales in Bangalore, ensuring his beautiful flowers reach a wide market.

A Message of Motivation: "The good profit and the timely subsidy from the National Horticulture Board have been instrumental," shares a grateful Somashekara Reddy. His success story is a powerful encouragement for aspiring farmers and entrepreneurs.

National Horticulture Board (NHB) Schemes: Empowering Farmers for Profitable Horticulture

The National Horticulture Board (NHB) offers comprehensive financial and technical support to boost commercial Horticulture across India. Below is a concise overview of key schemes and benefits available to farmers, entrepreneurs, and allied stakeholders.

1. Protected Cultivation (Greenhouse/ Polyhouse, Shade Net House)

Eligible Crops: High-value vegetables (Tomato, Cucumber, Capsicum) and flowers (Gerbera, Orchids, Anthurium, Rose, Carnation, Lilium, Chrysanthemum).

Area: Above 2,500 sq. m.

- **Project Cost:** Up to ₹200 lakh per project.
- **Subsidy:** 50% of project cost, maximum ₹100 lakh per applicant.
- **Supported Components:** Land development (up to 15% of project cost), construction of Polyhouse/Shadenet, planting material,

Sl No	Crop	Maximum Project	Subsidy for 5 cost (Lakh/5 Acre)	Subsidy for 1 Acre* Acre (Lakh)*
1	Banana (Sucker)	6.25	2.5	50,000
2	Banana (Tissue culture)	8.75	3.5	70,000
3	Pineapple (Sucker)	10	4	80,000
4	Pineapple (Tissue culture)	11.25	4.5	90,000
5	Cardamom	11.5	4.6	92,000
6	Black pepper	7.5	3	60,000
7	Cashew	10	4	80,000
8	Coconut	7.5	3	60,000
9	Jack fruit	6.25	2.5	50,000
10	Avocado, Rambutan, Mangosteen	6.25	2.5	50,000
11	Passion fruit (With support system)	12.5	5	1,00,000
12	Mango: Regular spacing	7.5	3	60,000
13	Mango: HDP	8.75	3.5	70,000
14	Date palm (Tissue culture)	7.5	3	60,000
15	Papaya	7.5	3	60,000

* Approximate estimation

4. Construction/Expansion/Modernization of Cold Storage for Horticulture Produce

Capacity of cold storage	Maximum Project Cost	Maximum subsidy
6000 MT (Cold storage type-1)	547 lakh (9120/MT)	191 lakh
10000 MT (Cold storage type-1)	816 lakh (8160/MT)	285 lakh
6000 MT (Cold storage type-2)	684 lakh (11400/MT)	239 lakh
10000 MT (Cold storage type-2)	1020 lakh (10200/MT)	357 lakh

cultivation expenses, Inputs (manures, fertilizers and pesticides), drip irrigation with fertigation, irrigation infrastructure (Bore well/ open well, pipeline, water harvesting structure, water tank), mechanization, pack house/on-farm collection unit, vermicomposting, plastic mulching, GAP certification, and more.

2. Open Field Cultivation

- **Eligible Crops:** Mango, Banana, Pineapple, Papaya, Jackfruit, Mangosteen, Rambutan Coconut, Passion Fruit, Cashew nut, Black pepper, Cardamom, Guava, Pomegranate, Citrus fruits, Strawberry, Date palm, Blueberry, Blue berry, Citronella, Stevia, Geranium, Palmarosa, Mint, Celery etc
- **Minimum Area:** More than 2 hectares (5 acres). Leased land (minimum lease: 10 years).
- **Project Cost:** Up to ₹100 lakh (Cashew nut/
- **Date palm:** up to ₹200 lakh for >20 ha).
- **Subsidy:** 40% of project cost, up to ₹40 lakh (Cashew nut/Date palm: up to ₹80 lakh).
- **Supported Components:** Land development, cultivation expenses (Planting material, labour, fertilizer and manures, pesticides etc), drip irrigation with fertigation unit, irrigation infrastructure (Bore well/ open well, pipeline, water harvesting structure, water tank etc), mechanization, precision farming, GAP certification, storage,

Sl No	Component	Project Cost (Approx.)	Subsidy (Approx.)
1	Farmgate Pack House (9m x 6m)	25 lakh/unit	12.5 lakh/unit (50%)
2	Integrated Pack House (9m x 18m)	160 lakh	56 lakh
3	Collection Aggregation Centre (22m x 26m)	320 lakh	112 lakh
4	Non-Pressurized Ripening Chamber	1 lakh/MT	35,000/MT
5	Pressurized Ripening Chamber	1.2 lakh/MT	42,000/MT
6	Refrigerated Transport (Refer van >15 MT)	80 lakh	28 lakh
7	Retail Outlets	20 lakh/unit	7.0 lakh /unit
8	Mobile Pre-cooling Unit	30 lakh	10.5 lakh
9	Cold Room	52 lakh	18.20 lakh
10	Primary Processing Unit	35 lakh/unit	12.25 lakh/unit
11	Secondary Processing Unit	100 lakh	35 lakh
12	Integrated Post-Harvest Management	145 lakh	50.75 lakh

vermicompost unit, plastic mulching, and more.

3. Post-Harvest Management

- **Subsidy:** Up to 35% of total project cost (credit-linked back-ended subsidy).

5. Tissue Culture and Mushroom Production Units

- **Tissue Culture:** Project cost up to ₹250 lakh (For production capacity of 25 lakh plant/year and minimum 10 lakh plants/year); subsidy up to ₹90 lakh (40% of project cost)
- **Button Mushroom:** Project cost up to ₹30 lakh (for production capacity of 300 MT/year with minimum capacity to produce 50 MT annually); subsidy up to ₹12 lakh (40% of project cost).

Eligibility for NHB Schemes:

Individuals, groups of farmers, FPOs, SHGs, NGOs, companies, cooperatives, marketing federations, municipal corporations, agro-industries, SAUs,

Steps in Project Proposal and Subsidy Claim

1. Preparation of DPR (By Applicant)
2. Submission of DPR & relevant documents to lending bank (By Applicant)
3. Sanction of term loan (By Lending Bank):
4. Application for GoC (By Applicant):Apply online through the NHB website.
5. Issue of GoC (By NHB):
6. Disbursement of term loan (By Lending Bank):
7. Implementation of project (By Applicant):
8. Submission of Project Completion Report to NHB (By Applicant):
9. Joint inspection of the project site and Release of subsidy (By NHB):

Two Viruse, One Plant

The Rise of Mixed Cassava Mosaic Infections in Kerala

B. Lohitha [1,2,] **T. Makeshkumar**[1],
K. Krishnaveni [1,2,] **S. Divya**[1,3,] **V. Pravi**[1]
[1]ICAR- Central Tuber Crops Research Institute, Thiruvananthapuram, Kerala
[2]ICAR-IARI-Indian Institute of Horticultural Research, Bengaluru, Karnataka
[3]ICAR-Indian Agricultural Research Institute, New Delhi, Delhi

Abstract

Cassava *(Manihot esculenta)*, a staple crop deeply rooted in Kerala's agriculture and cuisine, is now facing a serious threat from mixed infections of cassava mosaic viruses. Caused by Indian cassava mosaic virus (ICMV) and Sri Lankan cassava mosaic virus (SLCMV), these begomoviruses significantly reduce cassava yields—up to 30% losses annually—impacting smallholder farmers' livelihoods. Both viruses have bipartite genomes and are spread by the whitefly vector. Recent studies in Kerala reveal that co-infection by ICMV and SLCMV is becoming common, leading to more severe disease symptoms and challenging existing management practices. This mixed infection accelerates viral recombination and compromises the plant's resistance, making control efforts more difficult. To safeguard cassava production and ensure regional food security, integrated strategies are urgently needed. These include the use of clean planting materials, improved diagnostics, vector management, and breeding of resistant varieties. Continued research combined with farmer-focused approaches will be key to combating this evolving threat and sustaining cassava cultivation in Kerala.

Single infection

Introduction

In the sun-drenched fields of Kerala, Cassava (Manihot esculenta Crantz), locally known as kappa or maracheenihas long been a vital crop, interwoven with the culinary traditions and livelihoods of millions. Introduced to the region centuries ago, this hardy tuber has earned its place as a staple food and an economic lifeline, especially for smallholder farmers across the state. But today, this once-reliable crop faces a growing and complex biological threat that is redefining plant pathology in the region: the rise of mixed cassava mosaic infections.

Cassava mosaic disease (CMD), caused by cassava mosaic geminiviruses (CMGs), is a major constraint to cassava cultivation, resulting in 30% of yield losses annually (Jose et al., 2011). These viruses belong to the family Geminiviridae and the genus Begomovirus, transmitted by vector whitefly (Bemesiatabaci). In India, two viruses are primarily associated with CMD, viz., Indian cassava mosaic virus (ICMV) and Sri Lankan cassava mosaic virus (SLCMV) (Hong et al., 1993; Saunders et al., 2002).

CMGs have circular single-stranded DNA genomesencapsidated in twinned icosahedral particles. They exhibit two types of genome organizations, Bipartite genome: Consists of two components, DNA-A and DNA-B. Monopartite genome: contains only a DNA-A–like component. ICMV is bipartite, with both DNA-A and DNA-B components. SLCMV was initially thought to be monopartite based on its DNA-A, but later studies confirmed it as bipartite, capable of trans-replicating a DNA-B component similar to ICMV DNA-B.Each genomic component contains distinct genes.DNA-A encodes replication-associated protein (Rep), coat protein (CP), transcriptional activator protein (TrAP), replication enhancer (REn), and AC4.DNA-B encodes movement proteins, including the nuclear shuttle protein (NSP) and movement protein (MP), essential for virus movement within the plant(Hanley-Bowdoin et al., 2013).

Mixed infection

These viruses have caused significant damage to cassava crops in various parts of Kerala and Tamil Nadu. Together, however, their impact is becoming alarmingly synergistic. Recent field observations and genetic studies in Kerala have confirmed a disturbing trend,plants are increasingly being co-infected by both viruses, resulting in "mixed infections".

Rise of mixed infections

The progression from single infections to mixed infections of cassava mosaic virusesspecifically Indian cassava mosaic virus (ICMV) and Sri Lankan cassava mosaic virus (SLCMV)is a complex process shaped by ecological interactions, molecular compatibility, and human agricultural practices. Initially, ICMV was the predominant virus in India, particularly in cassava-growing regions like Kerala and Tamil Nadu, where it was first identified in 1956 and later confirmed and sequenced in the 1990s. SLCMV, on the other hand, was initially identified in Sri Lanka in 2002 and was introduced into India by 2005, most likely through the unregulated movement of infected cassava stem cuttings, a common propagation method for the crop. Once SLCMV entered regions already endemic to ICMV, both viruses began to co-exist in the same agroecological zones, creating the opportunity for co-infection in cassava plants.

The situation was exacerbated by the presence of insect vector, the whitefly (Bemisiatabaci), which can acquire both viruses from co-infected plants and transmit them to healthy plants during feeding. This vector-mediated transmission significantly facilitated the spread of mixed infections across fields. Moreover, SLCMV DNA-A has been found capable of replicating ICMV DNA-B through a process known as pseudo recombination, where the genomic components of different viruses functionally interact without nucleotide-level recombination. This compatibility enhances the infectivity and stability of the viral complex, contributing to more severe disease symptoms and broader systemic infection (Kushawahaet al., 2018; Hareesh et al., 2023).

Over time, molecular recombination between the two viruses has also been documented, giving rise to genetically novel recombinant forms with potentially increased virulence and a broader host range. These recombinants may also have an enhanced ability to overcome cassava's natural or bred resistance mechanisms, thereby complicating control strategies. Furthermore, the lack of virus-indexed planting material, poor monitoring, and the widespread use of asymptomatic but infected cuttings by farmers have led to the widespread establishment of mixed infections. Monoculture practices may further intensify the issue, providing ideal conditions for the viruses and their vectors to thrive.

Why it is concerning

Mixed infections are a significant concern due to their far-reaching implications on crop health, yield, and food security. Unlike single infections, mixed infections often result in synergistic interactions between viruses (Fig 1,2) leading to enhanced symptom severity such as severe leaf distortion, chlorosis, stunting, and drastic reductions in tuber yield and quality. These intensified symptoms not only reduce the yield of the crop but also threaten the livelihoods of farmers dependent on cassava cultivation.

One of the primary dangers of mixed infections lies in their ability to facilitate the evolution of more virulent viral strains. When two or more viruses co-infect a host plant, they create an environment conducive to genetic recombination and pseudorecombination, processes through which segments of DNA from different viruses can combine or functionally interact(Crespo-Bellidoet al., 2021). Such interactions can result in increased viral fitness, broader host range, enhanced pathogenicity, and the potential to overcome resistance mechanisms in cassava varieties. These newly evolved strains often escape detection using conventional diagnostic tools and can evade the resistance traits bred into cassava cultivars, making them more challenging to control.

Furthermore, mixed infections complicate field-level disease diagnosis and management. Symptoms may be atypical or masked, making visual identification unreliable. Laboratory detection becomes more demanding, requiring advanced molecular tools like multiplex PCR or next-generation sequencing to accurately identify and distinguish co-infecting viruses. This diagnostic complexity delays timely interventions, allowing the viruses to spread unchecked.

In regions like Kerala, where cassava mosaic disease (CMD) was originally observed, mixed infections have now become increasingly common and are associated with higher crop losses and more severe symptom expression compared to single-virus infections. The transition from single to mixed infections reflects a broader pattern of viral evolution and disease emergence, underscoring the urgent need for improved diagnostic tools, certified virus-free planting materials, and integrated disease management practices to mitigate the ongoing threat of CMD in India and beyond.

The Way Forward for Control

1. Use of Virus-Free Planting Material

The most effective control measure is the use of certified virus-free cassava stem cuttings. Establishing decentralized, community-level tissue culture labs or screen houses for producing clean planting materials can help prevent the introduction of viruses at the beginning of the cropping cycle.

2. Surveillance and Mapping: Ongoing disease surveys in Kerala should be expanded with GPS-based mapping and molecular diagnostics to track the spatial distribution of mixed infections.

3. Regular Field Monitoring and Early Diagnosis

Farmers should be trained to recognize early symptoms and report unusual disease patterns. The adoption of field-based rapid diagnostic kits, point of care devices like LFD (Lateral flow device) or mobile PCR-based units can enable early detection of mixed infections before they spread.

4. Integrated Pest Management (IPM)

Controlling the whitefly vector (Bemisiatabaci) is crucial. IPM strategies should include: Biological control agents (e.g., parasitoids), Botanical insecticides or insecticide rotation to delay resistance, Reflective mulches or trap crops to reduce vector landings, cultural practices like removing infected plants, plant spacing, and intercropping.

5. Breeding for Broad-Spectrum and Durable Resistance

Breeding programs must focus on developing cassava varieties with resistance to both ICMV and SLCMV, including their recombinants and Molecular tools such as marker-assisted selection and gene editing (e.g., CRISPR) can accelerate this process.Currently four cassava varieties released from ICAR-CTCRI viz., Sree Reksha, Sree Kaveri, Sree Sakthi, Sree Suvarna are resistant to both virueses

6. Farmer Awareness and Capacity Building

Empowering farmers through awareness campaigns, training, and access to diagnostic and extension services is vital. Farmer field schools and participatory approaches can help in community-wide adoption of best practices.

7. Strict Phytosanitary Regulations

Movement of planting material across districts and states should be regulated. Government and research institutions should enforce quarantine and certification systems to prevent the spread of infected material.

8. Research and Surveillance

Continuous monitoring of viral diversity and evolution using genomic tools is essential for forecasting outbreaks and updating control strategies. Collaborative networks for data sharing among research institutions, extension agencies, and policymakers can strengthen regional preparedness.

Conclusion

The emergence of mixed infections involving ICMV and SLCMV in Kerala represents a significant shift in cassava mosaic disease epidemiology, driven by viral recombination, vector dynamics, and the widespread use of infected planting materials. These synergistic interactions exacerbate symptom severity, compromise resistance, and hinder effective management. Addressing this complex threat requires integrated strategies focused on clean planting materials, advanced diagnostics, vector control, and resilient cultivar development. Sustained research and farmer-centric interventions are essential to mitigate the evolving impact on cassava productivity and regional food security.

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Paphiopedilum druryi The Endangered Slipper Orchid of the Western Ghats

Sabu V. U.
Eunoia Orchids Garden Native Orchid
Conservationist, Ambalavayal, Wayanad.

Introduction

Among the many botanical treasures of the Western Ghats, Paphiopedilum druryi—India's only native species of the world-renowned "Slipper Orchids"—holds a place of rare ecological and horticultural significance. Endemic to the southern stretches of the Western Ghats, particularly the Agasthyamalai hills of Kerala and Tamil Nadu, this orchid is a striking emblem of both biodiversity and fragility.

Named in honor of Colonel Heber Drury, a 19th-century British botanist, P. druryi is instantly recognizable by its exotic slipper-shaped pouch or labellum, designed to trap and guide insect pollinators. This unique floral adaptation not only adds to its visual charm but plays a crucial role in its reproductive biology. Flowering typically occurs from June to August, with each plant bearing a solitary, long-lasting bloom.

Thriving in shaded, moist, high-elevation evergreen forests, Paphiopedilum druryi is extremely sensitive to habitat disturbance. Deforestation, illegal collection for the horticultural trade, and climate change have pushed this species into the critically endangered category. As an indicator species, its presence often reflects the health and integrity of the surrounding forest ecosystem.

Conservation efforts now focus on both in-situ protection within designated sanctuaries and ex-situ propagation using seed banking and tissue culture. Native orchid conservationists in Kerala have taken commendable steps to study and reintroduce this orchid back into protected zones.

Raising awareness among local communities and enforcing strict wildlife protection laws are crucial for ensuring that Paphiopedilum druryi, a floral gem of the Western Ghats, continues to thrive for generations to come.

Taxonomy and Identification

Scientific Name: Paphiopedilum druryi (Bedd.) Stein

Family: Orchidaceae

Common Name: Drury's Paphiopedilum or Indian Slipper Orchid

Conservation Status: Critically Endangered (IUCN Red List); Listed in CITES Appendix IThis orchid can be recognized by its strap-like leaves and solitary, striking greenish-yellow flower with dark spots and a slipper-shaped labellum. It blooms typically from June to August, with each plant producing a single flower per season.

Paphiopedilum druryi: A Jewel of the Western Ghats

The Western Ghats of India, a UNESCO World Heritage Site and biodiversity hotspot, is home to an extraordinary variety of flora, including a wide array of native and endemic orchids. Among these is the rare and elegant Paphiopedilum druryi, commonly referred to as Drury's Slipper Orchid. This species is of exceptional interest not only due to its aesthetic beauty but also because of its limited geographic range and ecological significance.

Habitat and Distribution

Paphiopedilum druryi is endemic to the

Agasthyamalai Hills in the southern Western Ghats, straddling the Kerala–Tamil Nadu border. It is predominantly found at elevations between 800 and 1200 meters above sea level, favoring moist, shaded rocky outcrops in evergreen and semi-evergreen forests. This orchid is epilithic in nature, meaning it typically grows on rocks, especially in crevices that collect moisture and organic debris. The species thrives in cool temperatures, high humidity, and diffused light—a delicate combination that makes its survival heavily reliant on undisturbed microhabitat conditions.

Its highly localized distribution and specific habitat requirements make P. druryi particularly vulnerable to habitat degradation, illegal collection, and climate-induced changes. The species is now extremely rare in the wild and is listed under CITES Appendix I, highlighting its critical conservation status.

Ecological Importance

Beyond its rarity, Paphiopedilum druryi holds considerable ecological value. As a rock-dwelling orchid, it plays a role in stabilizing micro-ecosystems within rocky forest zones. Its flowering cycle supports specialized pollinators, such as small bees and flies, that have co-evolved with this unique orchid. The presence of this orchid often signifies pristine forest conditions, making it an important bioindicator of ecological health. Furthermore, the species contributes to the genetic and botanical uniqueness of the Western Ghats. Its conservation is not merely about preserving a single orchid species but about maintaining the integrity of a fragile and richly interdependent ecosystem.

The urgent need to conserve P. druryi calls for an integrated strategy involving habitat protection, regulated ex-situ cultivation, and local community awareness. Initiatives such as in-situ habitat monitoring and cultivation protocols could play a key role in ensuring the survival of this irreplaceable jewel of the Western Ghats.

Conservation Initiatives

Fortunately, growing awareness and conservation efforts are underway to protect and restore this botanical treasure.

1. In-situ Conservation

Several protected forest areas in Kerala—particularly within the Agasthyamalai Biosphere Reserve—now serve as potential safe zones for remnant P. druryi populations. Forest officials, local ecologists, and tribal watchers are working together to monitor these habitats and prevent further extraction.

2. Ex-situ Conservation and Propagation

The Jawaharlal Nehru Tropical Botanic Garden and Research Institute (JNTBGRI)have established dedicated orchid houses for the propagation and study of rare orchids, including P. druryi. Advanced tissue culture techniques and seed propagation protocols are being developed to strengthen the species' ex-situ population.

Recently, collaborative Memoranda of Understanding (MoUs) have been signed with the ICAR–National Research Centre for Orchids (NRCO) in Sikkim to share expertise and promote long-term germplasm conservation. These partnerships are critical for building a coordinated conservation strategy across states and ecosystems.

3. Community-Based Conservation

One of the most promising developments in the conservation of P. druryi is the involvement of local communities. In districts like Wayanad and Idukki, native orchid collectors, tribal farmers, and conservation educators are taking the lead in awareness-building. Private orchid gardens, school-based biodiversity clubs, and eco-tourism guides are helping demystify orchids and reduce destructive curiosity.

Orchid conservation gardens run by individuals and NGOs have begun showcasing P. druryi under controlled conditions, providing both educational and scientific value. Outreach programs engage schoolchildren, local elected bodies, and forest-dependent communities in the shared responsibility of orchid preservation.

Looking Ahead

While Paphiopedilum druryi remains one of the most endangered orchids in India, it also represents a powerful symbol of hope for conservation in the Western Ghats. Its story is not just one of rarity and beauty, but also of resilience and recovery—when supported by science, policy, and community partnership.

For this effort to succeed, sustained action is necessary: stricter enforcement against poaching, habitat restoration, enhanced scientific research, and continued public engagement. Only through a coordinated approach can we ensure that this irreplaceable species survives for future generations to admire—not just in collections, but in the wild forests where it truly belongs.

The Way Forward: A Conservation Roadmap for Paphiopedilum druryi

The conservation of Paphiopedilum druryi—India's only known species of slipper orchid—is a botanical priority that demands immediate and sustained attention. Endemic to the southern Western Ghats, particularly the Agasthyamalai Hills of Kerala and Tamil Nadu, this critically endangered orchid is emblematic of the unique and fragile flora of the region. Once widespread, its population has sharply declined due to habitat destruction, over-collection, and the effects of climate change.

Moving forward, a successful conservation strategy for P. druryi must adopt a multi-pronged approach grounded in science, community participation, policy enforcement, and public awareness.

Firstly, scientific propagation is crucial. Ex-situ conservation through seed germination, tissue culture, and symbiotic mycorrhizal techniques must be scaled up in botanical gardens and orchid conservation centers. Organizations such as the Jawaharlal Nehru Tropical Botanic Garden and Research Institute (JNTBGRI) and the Kerala Forest Research Institute (KFRI) could play key roles in conserving genetic stock and supporting reintroduction programs.

Secondly, habitat protection is non-negotiable. Paphiopedilum druryi prefers shaded, moist, evergreen forest environments along rocky slopes. These microhabitats, often unprotected, must be identified, demarcated, and conserved through legal measures. Forest departments should collaborate with local communities to prevent illegal orchid harvesting and monitor sensitive areas using technology such as GIS mapping and drone-based surveys.

Thirdly, the role of local communities and indigenous knowledge systems must be recognized and empowered. Tribal and forest-dwelling communities often possess keen ecological knowledge regarding orchid blooming patterns, habitat cues, and sustainable harvesting practices. Incentivizing their involvement as community-based conservation stewards or eco-guides not only supports livelihoods but also ensures on-ground protection.

Further, policy-level support is critical. Strict enforcement of international regulations under CITES (Convention on International Trade in Endangered Species) must be prioritized, especially given the global demand for Paphiopedilums in the horticulture trade. While P. druryi is listed in Appendix I of CITES, indicating the highest level of protection, enforcement gaps remain. Training customs officials and forest guards, along with public awareness campaigns, can curb illegal trade.

Additionally, integrating native orchid conservation into eco-tourism and environmental education programs can yield dual benefits. Interpretive trails in biodiversity parks, orchid-themed learning modules in schools, and orchid festivals in collaboration with tourism boards can help generate public interest, while subtly communicating the conservation message.

Collaboration with international orchid conservation bodies—such as the Orchid Conservation Alliance and the Royal Botanic Gardens, Kew—can enhance access to resources, research tools, and conservation networks.

Conclusion: Protecting a Living Jewel

Paphiopedilum druryi is not just an orchid; it is a symbol of the rich biodiversity, ecological sensitivity, and botanical uniqueness of the Western Ghats. Its slipper-shaped bloom, once abundant on the shaded slopes of Agasthyamalai, now hangs in the balance—its survival intimately tied to our conservation choices.

Orchids like P. druryi are bioindicators—species whose presence, absence, or abundance reflects the health of ecosystems. When we protect this orchid, we are not merely saving a plant; we are preserving an entire micro-ecosystem of mosses, insects, pollinators, and soil fungi that coexist with it.

In a time of global biodiversity loss and climate crisis, Paphiopedilum druryi reminds us of the urgency of local conservation with global implications. From scientists and forest managers to schoolchildren and policymakers, the responsibility to protect this orchid is a collective one.

As Kerala advances in environmental planning, integrating P. druryi conservation into broader ecological policies will serve as a model for orchid conservation not just in India, but across tropical biodiversity hotspots. It is our duty to ensure that future generations inherit not just stories, but living examples of the region's botanical heritage.

Preserving Paphiopedilum druryi is more than an act of conservation—it is an affirmation of our commitment to Kerala's natural legacy, one orchid at a time.

Unlocking the Hidden Potential of the Tree Tomato

(*Solanum betaceum*)

Kalieswari K[1], Selvakumar R[2], Thendral U S[3]
Division of Fruits and Horticultural Technology, ICAR-IARI, New Delhi-110012,
Centre for Protected Cultivation Technology, ICAR-IARI, New Delhi-110012
Division of Plant Genetic Resources, NBPGR, New Delhi-110012

The tree tomato, scientifically known as *Solanum betaceum*, is a captivating fruit-bearing crop from the Solanaceae (nightshade) family. Historically, it was classified under the *Cyphomandra genus* before being reassigned to the genus *Solanum*, subgenus

Bassovia, based on detailed morphological and genetic studies. Commonly referred to as "Tamarillo," it is celebrated for its vibrant, elongated fruits that resemble large eggs or plums. Its unique flavor, which combines the tanginess of kiwi with the richness of passion fruit, makes it a versatile ingredient that can be used as both a fruit and a vegetable.

Origin and History

The tree tomato is believed to have originated in South America, particularly in the Peruvian Andes. It is speculated that the Incas incorporated tree tomatoes into their diet alongside staples like potatoes and maize. By the late 1800s, tree tomato seeds were introduced to India, where they adapted well to hilly terrains. Around 1890, missionaries from India carried tamarillo seeds to New Zealand. Subsequently, these plants were introduced to Sri Lanka and Nepal. During the 1930s, the crop entered commercial production in New Zealand, gaining popularity during World War II when imports of fruits like bananas and oranges were restricted. In 1967, the crop's commercial name was officially changed to "tamarillo" to distinguish it from traditional tomatoes. Today, tamarillo cultivation is concentrated in countries such as Colombia, Ecuador, Australia, and specific regions in the United States, including California.

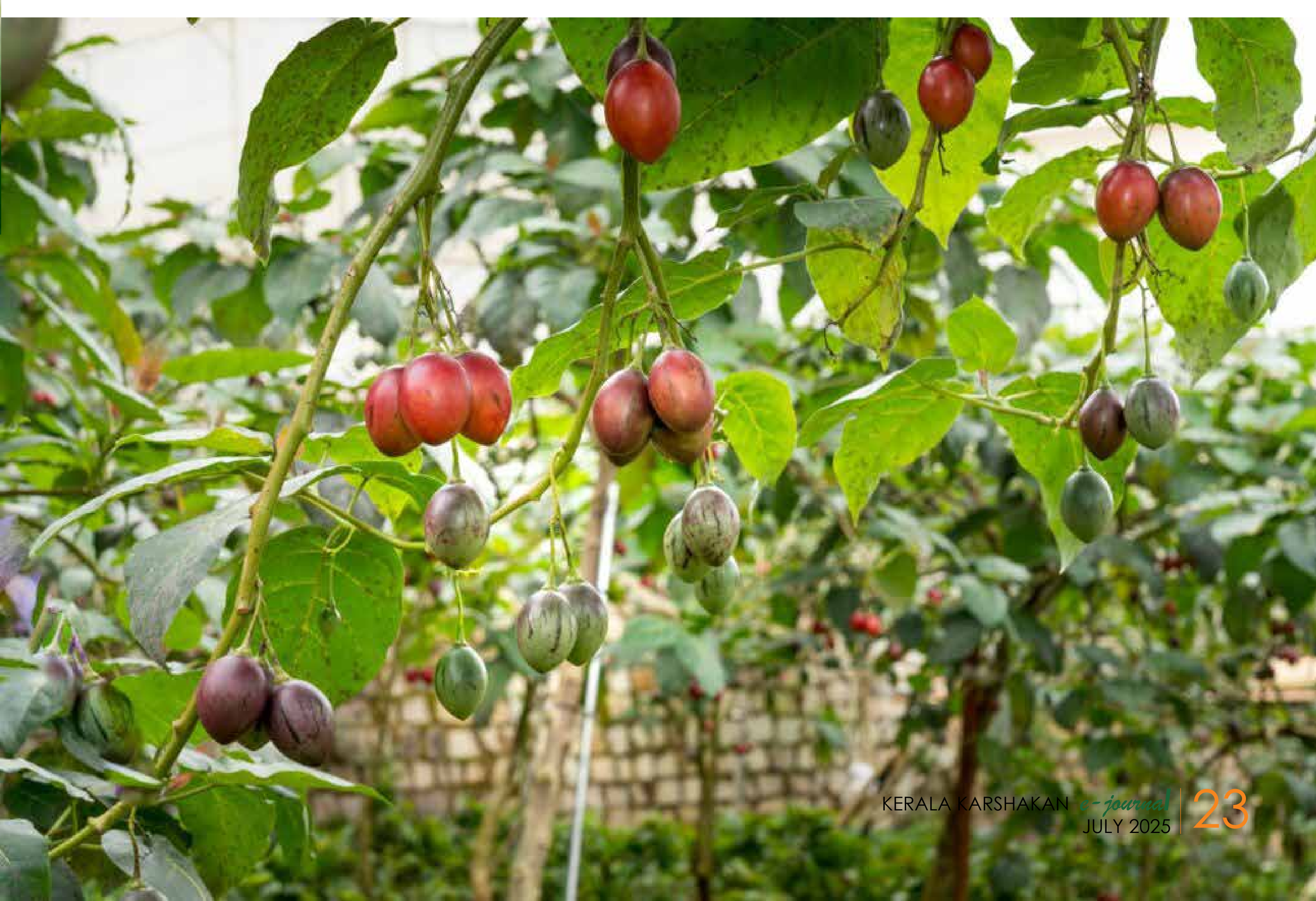
From Peru to Nagaland

In India, tree tomatoes are cultivated in the hilly regions of West Bengal, Maharashtra, Assam, Uttarakhand, Nagaland, and Himachal Pradesh. In South India, they thrive in the Nilgiris and Kodaikanal hills of Tamil Nadu, as well as select high-altitude areas in Kerala and Karnataka. These regions provide the cool climates essential for successful cultivation.

Nagaland was awarded a Geographical Indication (GI) tag for its tree tomato, locally known as "Naga Tree Tomato" or sei bangenuo in the local dialect. The North Eastern Regional Agricultural Marketing Corporation (NERAMAC) has actively promoted its cultivation, with the fruit being a common feature in kitchen gardens across Kohima and other districts of the Naga hills.

Botany

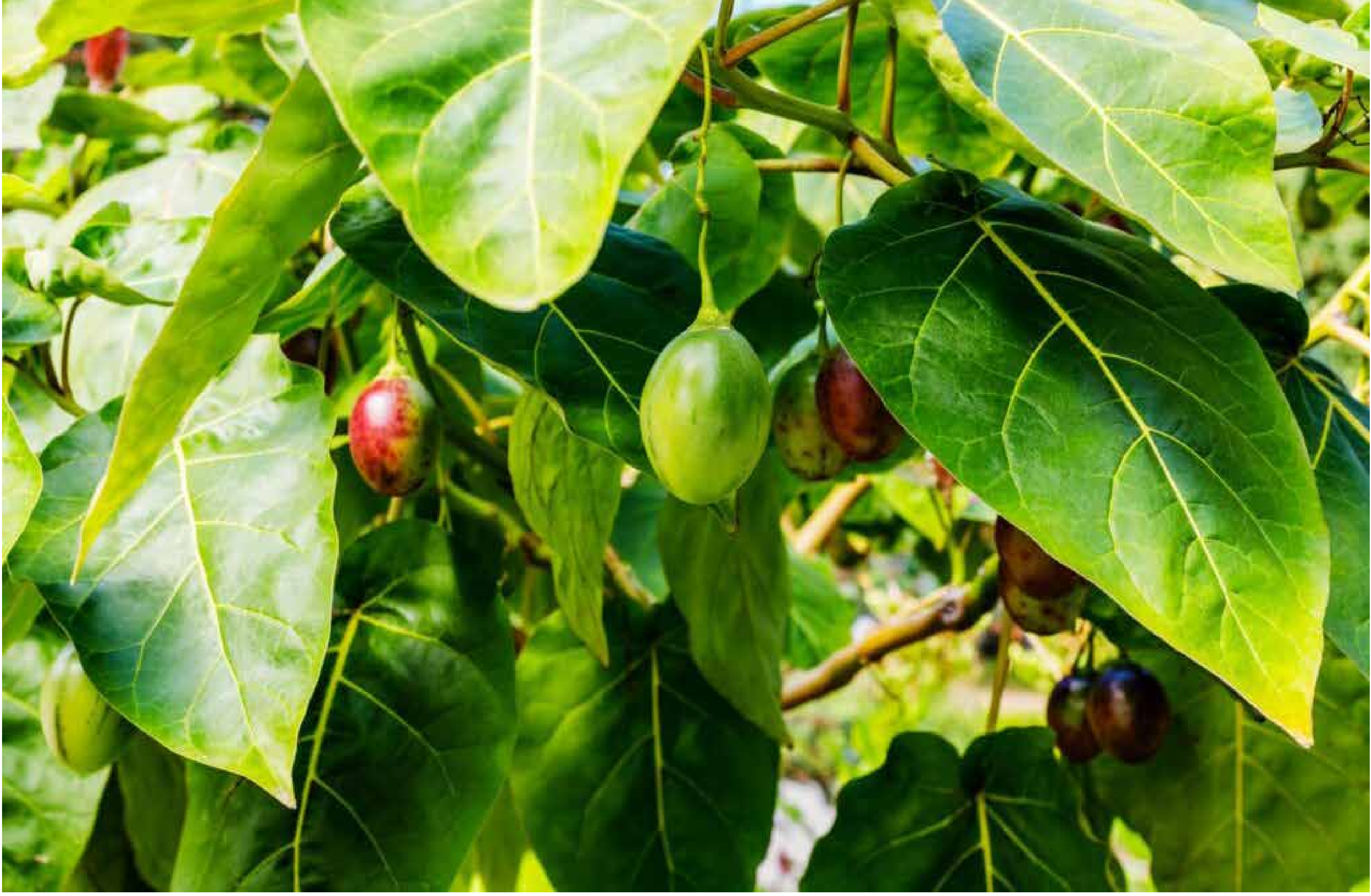
The tree tomato is a small, fast-growing shrub that typically reaches heights of 3 to 5.5 meters but can grow as tall as 7.5 meters under optimal conditions. It is evergreen to semi-deciduous, with characteristic dichasial branching that contributes to its shrubby form.



Seed-grown plants experience a prolonged juvenile phase, with initial branching occurring after approximately 30 nodes of growth. Due to its shallow root system, the plant is sensitive to drought stress and strong winds.

The plant bears simple, heart-shaped leaves that are ovate and pointed at the apex, emitting a musky aroma when young. Its fragrant flowers are borne in small clusters near the branch tips, featuring pale pink or lavender petals, prominent yellow stamens, and a greenish-purple calyx. Tree tomatoes are self-pollinated, with flowers capable of producing fruits without the need for cross-pollination.

The egg-shaped fruits vary in color, including red, orange, yellow, and red-and-yellow combinations, with flesh colors ranging from orange-red to cream-yellow. The fruit is soft and juicy, with tough, bitter seeds. Tree tomatoes typically begin bearing fruit within the first or second year of planting, achieving peak production by the fourth year. They have



a relatively short lifespan of 5 to 12 years and form a wide, spreading crown supported by a single upright woody trunk.

Favorable Conditions

Tamarillos thrive in subtropical climates, particularly at altitudes ranging from 1,000 to 7,500 feet above mean sea level. They prefer frost-free, temperate climates with temperatures between 12°C and 24°C. The plant is sensitive to strong winds and requires sheltered growing areas or windbreaks. Propagation is carried out through seeds or cuttings, and annual pruning of fruit-bearing branches promotes new growth and productivity. Tamarillo plants are self-pollinating and produce abundant clusters of flowers and fruits. Remarkably, full fruiting occurs within 18

Nutritional Value per 100g of Fruit

Nutrient	Amount
Protein	1.5 g
Fat	0.2 g
Crude Fiber	4.2 g
Carbohydrates	6.7 g
Energy	35 kcal
Calcium	12 mg
Phosphorus	46 mg
Carotene	324 µg
Magnesium	34 mg
Potassium	539 mg
Beta-Carotene (Vit A)	4.80 mg/100 g DW
Ascorbic Acid (Vit C)	55.90 mg/100 g DW

months of planting.

Varieties

Tamarillos are available in two primary types:

- Purplish-Red: More acidic, with reddish-golden flesh.
- Golden-Yellow: Sweeter, with golden flesh.

Culinary Applications

Tamarillos are highly versatile in the kitchen:

- Green or unripe fruits are used in curries.
- Ripe fruits can be consumed raw or cooked in sauces, jams, chutneys, sambars, and desserts.
- Tamarillo chutney, prepared by peeling the fruit and mixing it with onions, offers flavors similar to tomato chutney.
- The high pectin content makes it ideal for jams, jellies, and preserves.

Health Benefits

- Rich in Vitamin A: Supports vision health, maintains skin integrity, and aids in sustaining optimal red blood cell levels.

Traditional Remedies:

- In Ecuador, warmed leaves are wrapped around the neck to alleviate sore throats.
- In Colombia, a poultice is prepared by cooking the fruit pulp in embers to soothe inflamed tonsils.

Cultural Beliefs: Jamaicans refer to tree tomatoes as "vegetable mercury," attributing liver-healing properties to the fruit.

Antimutagenic Properties: Proteins in tree tomatoes exhibit antimutagenic effects, reducing oxidative damage and inhibiting uric acid formation.

Anaemia Treatment: The fruit is traditionally used to combat anaemia.

High in Anthocyanins: Offers protection against diabetes, ageing, certain cancers, and neurological disorders.

Contains Lycopene: A powerful compound that helps prevent degenerative diseases, supports heart health, and enhances skin resilience against UV radiation.

Conclusion

Tamarillo, an underutilized crop, holds immense potential for cultivation and marketing. Its dual role as a fruit and vegetable offers farmers and entrepreneurs opportunities for diversification in subtropical regions. With its distinctive flavor, rich nutritional profile, and versatility as a tomato substitute, tamarillo cultivation not only enhances agricultural diversity but also opens new economic avenues.

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Reviving Tradition

The Success Of Rejuvenating Kerala's Naturally Organic Kaipad Rice Tracts Through A Holistic 4C Approach – Conservation, Cultivation, Consumption, And Commerce

Vanaja T[1], Atheena U P[2]
[1]Professor& Associate Director of Research (North Zone),
[2]Assistant Professor (Contract),
Regional Agricultural Research Station,
Pilicode, Kasargod,
Kerala- 671310

Introduction

Kaipad is an exceptional naturally organic coastal wetland rice cultivation tract in North Kerala, which is prone to salinity, spanning 4100 hectares in the districts of Kozhikode, Kannur, and Kasaragod. It is an integrated organic farming technique that uses coastal brackish water marshes rich in organic matter for both rice and aquaculture. The land becomes salinized due to the network of estuaries and backwaters acting as an inlet of sea water.Kaipad tracts are characterised by mangroves, which are found on the fringes of estuaries and backwaters.

Kaipad rice cultivation

Rice cultivation in the Kaipad paddy tracts is unique due to frequent sea water flooding. Small farmers grow a single crop during the low to medium saline phase of the monsoon. Mounds are prepared in March and April, and sprouted seeds are sown on raked mound tops in June. Once the

Kaipad paddy field

seedlings grow to an age of 30-35 days, they are spread across the field mounds during the southwest monsoon. No further cultural practices or chemical inputs are needed until harvest, which occurs by the end of October. The harvested rice is transported by yachts, and traditional fishing and shrimp cultivation begin in November, lasting until April.

The traditional land races of'Kuthiru' and 'Orkayama' are abundantly farmed in in the past along with other landraces, in limited area including'Kandorkutty', 'Orpandy', 'Odiyan', 'Orissa', 'Punchakayama', 'Mundon'and 'Kuttadan'. These yield on average between 1.0 and 1.5 tonnesper hectare, makescultivation unprofitable, and are susceptible to lodging. Their Poor grain qualities like awn on grains, long bold, and heavy shattering of grainsmakesthe harvest time consuming and laborious. In response, Kerala Agricultural University developedhigh-yielding, saline-tolerant rice varieties- 'Ezhome-1', 'Ezhome-2', 'Ezhome-3', 'Ezhome-4', and 'Mithila', through a 20-year breeding programusing native land races in hybridization programme, conducting all trials including filial generations in farmers' field.

All five varieties are saline tolerant and having good cooking qualities and tolerant to lodging. 'Ezhome-1' and 'Ezhome-4' are long duration varieties with 130-135 days duration. 'Ezhome-2', 'Ezhome-3' and 'Mithila" are medium duration varieties with 120-125 days. Development and commercialisation of these high-yielding rice varieties facilitated the conversion of large, naturally organic, saline-prone, and less productive tracts of Kaipad into an arable, highly productive farming land (60-70%).

Malabar Kaipad Farmers' Society (MKFS)

The lack of stake holder society for this speciality zone of North Kerala had an impact

Farmer participatory plant breeding researchat Kaipad

Various value-added products from Kaipad rice

on the farmers of Kaipad tract as they needed more organised support and representation. This led to the establishment of Malabar Kaipad Farmers' Society (MKFS) in 2010,as part of the Rashtriya Krishi Vikas Yojana (RKVY) Paddy mission project of Kerala Agricultural University. The society aims to support Kaipad rice cultivation and address obstacles these farmers encounter. Itimproves the welfare of the Kaipad farmers and artisans in Kannur, Kozhikode and Kasaragod districtsincluding rejuvenated Kattampally Kaipad of Kannur district.MKFS has four regional societies and 58 local-level Kaipad samities across these districts.

In 2010, MKFS launched the Food Security Army (FSA) to boost rice production with support from the RKVY-Paddy Mission project. Twenty-member FSA units were formed in the panchayats of Ezhome, Pattuvam, Kannapuram, and Cherukunnu, and trained through a network development activity. In November 2018, Kaipad Area Development Society (KADS) was established as the apex body of MKFS, chaired by the agriculture minister. This strengthened the society's network, with 58 panchayath-level samithies and four regional societies, and helped address the area's mechanization challenges.

Geographical Indication Tag

In 2014, this distinct, nutrient-dense Kaipad rice secured Geographical Indication Tag. Obtaining the GI tag gave small and marginal farmers of Kaipad tract anexcellent opportunity to increase their livelihood security by selling their produce for a premium price.

Plant genome saviour community award

In 2021-22, the Malabar Kaipad Farmers' Society received the 'Plant Genome Saviour Community Award' from the Protection of Plant Varieties and Farmers' Rights Authority (PPVFRA) for its efforts in conserving genetic resources of land races, wild relatives of economic plants, and improving them through selection and preservation.

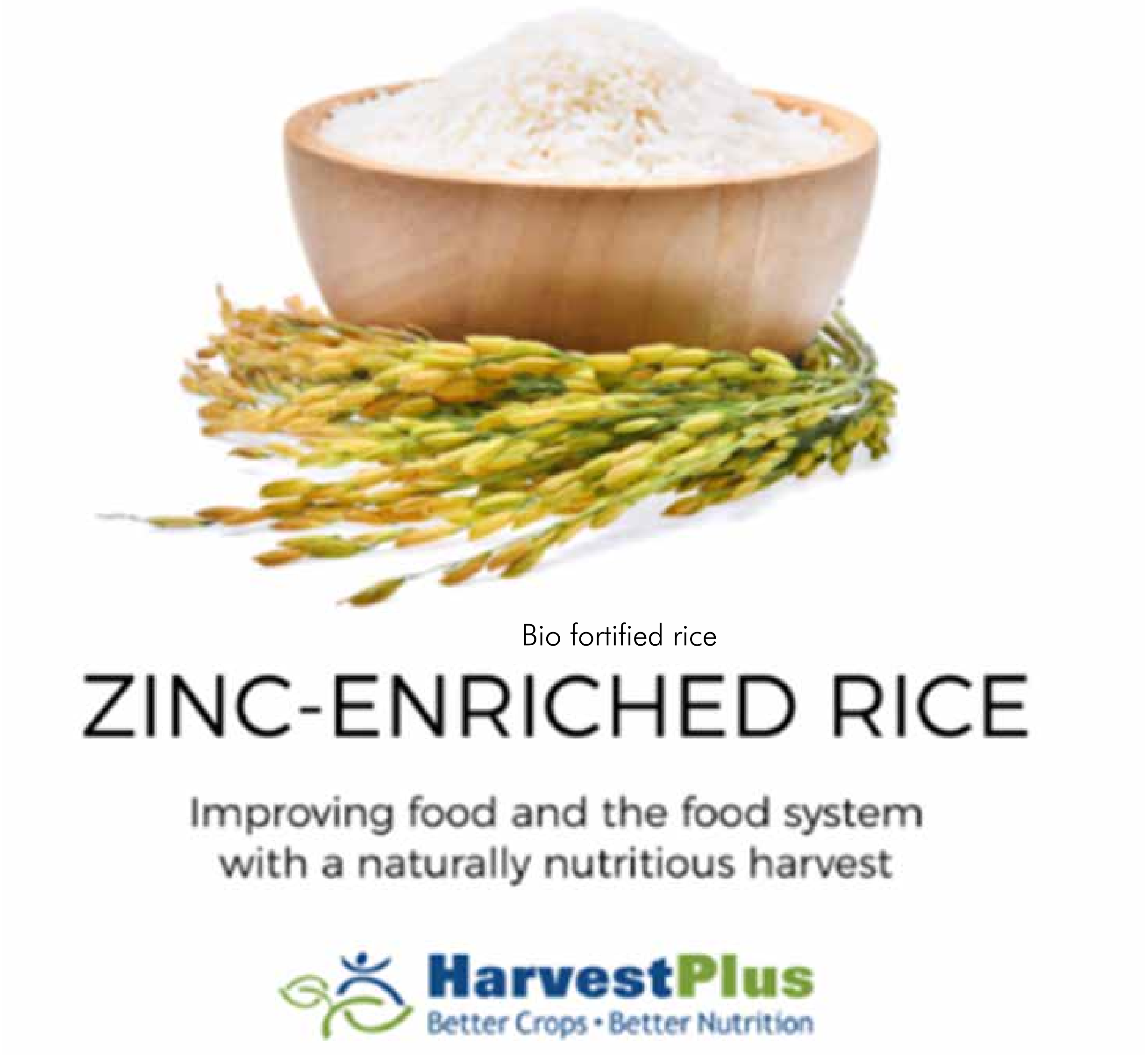
Malabar Kaipad farmer producer company (MKFPO)

In 2021, a farmer producer company was formed with Kaipad farmers being shareholders. It markets Kaipad rice and various value-added products from Kaipad rice namely, rice flakes, puttupodi, pathiripodi, payasamada, Poshananutrimix, health mix, ariyunda and sweet gruel, both domestically and for export. MKFPOalso operates a food park promoting healthy and nutritious food and runs an agro service centre.

Kaipad Farm Tourism

A farm tourism mission was launched in the Kaipad tract, to create awareness on farming culture and significance of preservation of nature. This project, the first of its kind in Kannur district, promotes organic agriculture and aquaculture in the Kaipad area.Visitors can explore paddy fields, enjoy boat rides, and taste traditional cuisine. The initiative also focuses on preserving rice germplasm and mangroves.

The Regional Agricultural Research Station, Pilicode, is currently establishing a R&D centre for organic agriculture, with processing and marketing facilities. Since 2000, Kerala Agricultural University's efforts have improved food, nutritional, water, and livelihood security for small farmers, using the 4C approach—Conservation, Cultivation, Consumption, and Commerce. This revitalization has significantly boosted community development, enhancing economic, social, cultural, and environmental well-being.



Bio fortified rice

Bridging Genomic Gaps Omics and Bioinformatics for nutri-dense rice

Abstract

Amid global challenges such as the post-COVID socio-economic downturn, climate change, and geopolitical instability, nutritional insecurity has become more pressing than ever—particularly in rice-dependent regions across the Pacific-Asian belt. Biofortification breeding emerges as a strategic approach to address hidden hunger and promote global nutritional security. India, especially Kerala, is home to a rich diversity of Traditional Rice Varieties (TRVs) with promising nutritional potential. The integration of advanced genomic tools, bioinformatics, and multi-omics approaches has revolutionized the identification and incorporation of beneficial traits into breeding pipelines. These technologies enable deeper insights into the genetic architecture of nutrient traits, facilitating

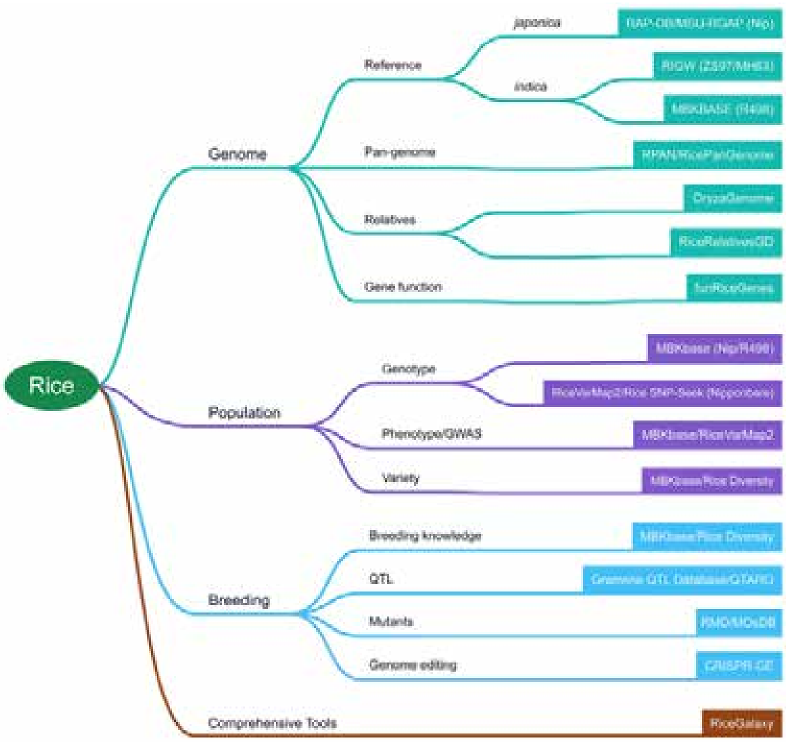


Figure 2. Tree of genomic data base and bioinformatic tools for rice

the development of nutrient-dense and resilient rice varieties. Bioinformatics plays a central role in this transformation—supporting gene discovery, trait mapping, and optimized breeding strategies. The synergy between omics sciences and computational biology not only accelerates the creation of biofortified and potentially genetically modified rice but also represents a vital step toward overcoming global nutritional challenges and securing food systems for the future.

Introduction

Nutritional quality enhancement through biofortification breeding is the key to beat hidden hunger and to ensure global nutritional security. The current scenario of post covid socio-economic depression, international wars and extreme climatic changes exacerbates nutritional insecurity on a global scale. Many developing and underdeveloped countries in the Pacific-Asiatic belt rely on rice as their staple food. Thus, biofortification programmes of rice will be an efficient strategy to address food and nutritional security.

India harbours a rich diversity of rice germplasm and several Traditional Rice Varieties (TRVs) from Kerala have been found to possess promising nutritional and beneficial qualities. The need of precise characterisation of this rich genetic repository is at alarming stage. In the genomic era, several sophisticated techniques are in shelf to pick out beneficial biofortification traits followed by strategic integration into the breeding pipeline. The observable trait is cumulative output of its genetic value, environment and interaction effects.Thus, an uphold in genotypic value of any trait will yield better phenotype in desired direction. The powerful bioinformatics tools and multi-omics approaches open the door to decipher deeper genomic insights and thus paving the way to design future nutrient-dense rice varieties.

The knowledge and skill on bioinformatic tools and computational algorithms will assist breeders to scale up breeding goals. Bioinformatics plays a pivotal role in agriculture by leveraging computational tools and data analysis to enhance crop yield, quality and resilience.In agriculture, bioinformatics plays a vital role as it is employed for tasks such as deciphering plant genomes, identifying beneficial traits, optimizing breeding programs and understanding the molecular mechanisms behind crop responses to environmental factors. This synergy between biology and informatics fosters development of future bio-fortified varieties.

Role of bioinformatics tools in bio-fortification research

The large quantum of biological data produced from various experiment demanded the birth of a new branch in science in order to deal with data storage, analysis, integration and interpretation, known as "Bioinformatics". The secrets of nature are encoded in the genetic material (DNA/RNA) using simple genetic code comprising of four nucleotides (A, T, G, C). Hence the genomic sequence information yielded from various sequencing platforms will be long stretches of codons and only bioinformatics tools can extract meaningful insights from the same. The sequence-level variations composed of copy number variations (CNVs), presence-absence variations (PAVs), InDels, or simple point mutations (SNPs), are fundamental under players of phenotypic variation.Scientists working on biofortification aspect of rice genotypes are certainly interested in the sequence level variation underpinning nutrient remobilization, metal homeostasis (Eg: Zn, Fe), acquisition, utilization etc. Certain TRVs (Traditional rice varieties) have evolved innate mechanism for essential metal homeostasis viz.,specific metal transport channels, metal uptake, accumulation, utilization etc. bioinformatics and multi-omics studies help to highlight genomic region, molecular mechanism and cellular interacting partners which govern promising biofortification traits.

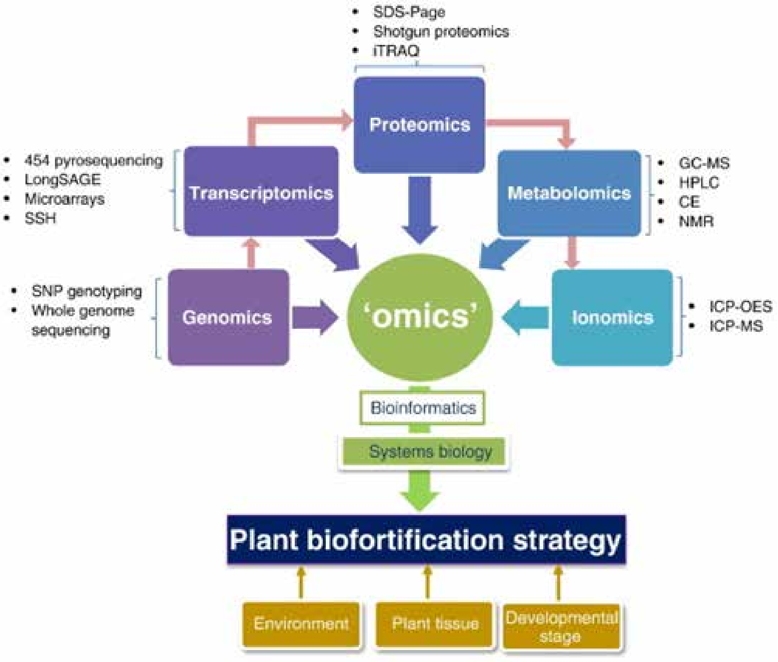
The genomic insight on sequence level variation, candidate genes and specific biochemical pathways associated with biofortification pipeline need to be explored. For instance,the sequence variation associated with high Fe and Zn levels in particular rice germplasm could be mined out using transcriptome sequencing and computational analysis. The genome wide association study or QTL mapping establishes functional relationship between trait of interest and genomic regions. This information is further amenable to integrate with breeding programme for nutrient-dense rice varieties.

Thus, a thorough understanding on type of our data and strategic choice on correct bioinformatic tools is inevitable to produce significant end results. The bulk and detailed multi-omic data regarding nutritional traits in rice along with sophisticated bioinformatic tools assist deep exploration into trait of interest to boost genetic gain in the desired direction.

Role of bioinformatics in integrating Omics data

The data reduction, simplifications followed by focus on key genes, transcripts, metabolites and pathways underpinning nutrient metabolism and accumulation is necessary to

Figure 3. An Outline of Multi-Omics Approach for Biofortification



establish significant association by reducing false positive and negative results.

Genome-Wide Association Studies (GWAS) helps scientists to make significant strides in improving the nutritional value of rice through biofortification. It utilizes genetic variations across a population to identify genes linked to specific traits, including nutrient content. In a study by (Descalsota et al., 2018), 144 different rice varieties were examined to pinpoint specific genetic markers (QTLs and SNPs) related to biofortification. They discovered key regulators, like OsMTP6 and others that play a crucial role in balancing iron and zinc levels. By identifying rice varieties with a combination of these key markers, which show both high zinc content and good yields, GWAS is proving to be instrumental in customizing rice varieties for better nutrition. Another study by (Liu et al., 2021)expanded on this approach, using 212 different rice populations. They identified specific genetic markers associated with zinc content in different parts of the rice plant, providing valuable information for targeted efforts in improving rice nutrition through breeding programs. These studies collectively highlight how GWAS is helping uncover the genetic basis of nutritional traits in rice, paving the way for the development of rice varieties with enhanced nutritional value.

1.2 Rice genome databases

The advances in NGS and the birth of third-generation sequencing platforms, including ONT (Oxford Nanopore Sequencing) and SMRT (Single Molecule Real-Time Sequencing), have improved read length while reducing sequencing time within a reasonable budget. This has necessitated a shift from whole-genome information of model organisms to several non-model organisms. Moreover, the availability of more efficient unique genes involved in nutrient accumulation, while expression profiling identifies those actively engaged in nutrient metabolism. Metabolic pathway analysis uncovers genes contributing to nutrient content and databases like the Rice Genome Annotation Project (RGAP) provide genomic information. Machine learning predicts nutrient-related genes and functional genomics tools like CRISPR/Cas9 validate their roles. This integrated approach advances our understanding of rice genetics, aiding in the development of biofortified varieties.Some key tools, databases and approaches are detailed below:

1.1 Genome-Wide Association Studies (GWAS)

Association mapping accounts ancestral recombination events occurred in the natural population by working on the principle of linkage disequilibrium to uncover trait associated genomic region with precision. Moreover, this approach does not demand time required for construction of a mapping population. Thus, it opens door for immediate scanning and evaluation of our rich genetic resource to uncover key genes governing biofortification (Eg: Zn/ Fe homeostasis) and to incorporate those into breeding pipeline for accelerated genetic gain. A high throughput phenotyping platform offering multi-environment/ multi-season trait phenotypic data coupled with the genome wide marker data (Whole genome scan) is utmost important associate functional variants (allels/SNP) to phenotype with precision. Apart from this, the knowledge on mating system of crop, familiar relatedness (Kinship/K matrix), Population structure (Q matrix) etc are pre-requisite for choice of number of markers and to

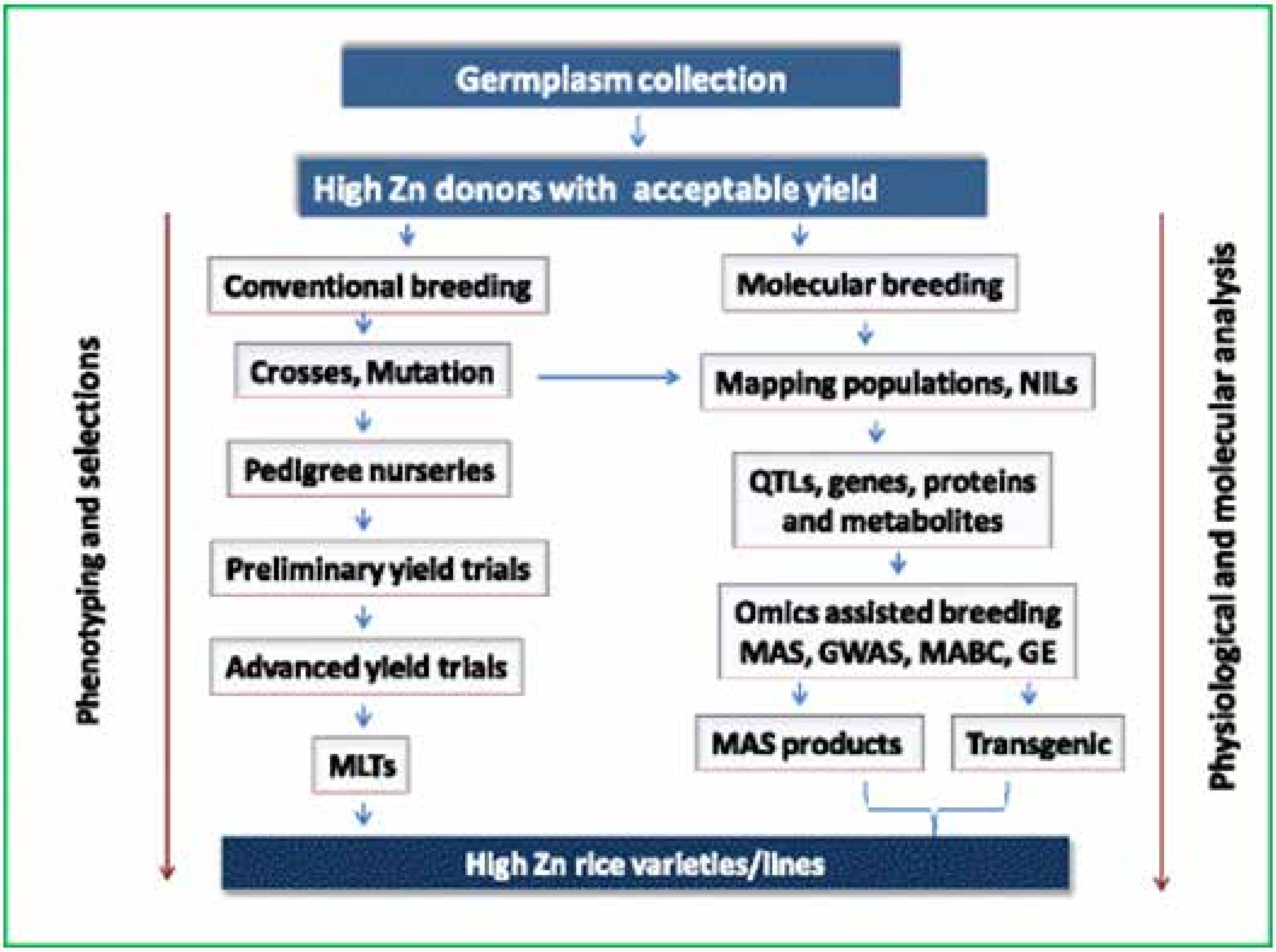


Figure 4: Approach to produce high Zn rice

synthesise future bio-fortified rice varieties.The significance of bioinformatics and computer based approaches in various aspects of development of biofortified varieties are detailed below.

1. Genomics Approaches

Genomic data analysis is crucial for rice biofortification, a process aimed at enhancing the nutritional content of rice varieties. Bioinformatics tools enable researchers to sift through vast genomic datasets, identifying genes related to essential nutrients such as vitamins and minerals. By pinpointing these genes, scientists can strategically modify or breed rice varieties with heightened nutritional profiles. It not only accelerates the identification of key genes but also aids in understanding the complex interactions within the genome that influence nutrient content. This computationally aided targeted approach, holds promise for addressing nutritional deficiencies and improving the health impact of rice consumption globally.

Bioinformatics provides an array of tools to identify genes associated with nutrient content in crops like rice. Through tools like Genome-Wide Association Studies (GWAS) and Quantitative Trait Loci (QTL) analysis, genes linked to specific traits and genomic regions associated with nutrient levels may be identified. Comparative genomics reveals sequence assembly platforms and multi-omic data from various branches such as transcriptomics, proteomics, ionomics and metabolomics, generated across different species and functional tiers, demands specific specialized databases for easy and organized data storage, analysis and retrieval. International Rice Genome Sequencing Project (IRGSP) sequenced whole genome of rice; Oryza sativa ssp. japonica cv. Nipponbare and at present 430Mb of genome size is estimated and resequencing are progressing. The chromosome wise sequence information's are made available in public domain. The Rice SNP-seek database is online repository for rice re-sequencing data harbours extensive source of genetic variation data for 'The 3000 Rice Genomes Project' and having data regarding about 20 million rice SNPs and InDels. Some notable specialized genomic databases of rice are presented in a flowchart in Figure2.

Figure 2. Tree of genomic data base and bioinformatic tools for rice

2.Transcriptomics Approach

Scientists have used various methods like studying specific tissues, examining gene activity and looking at metabolic processes to find key genes responsible for maintaining the balance of essential metals like iron and zinc in rice. Certain gene families, such as RT/IRT (ZIP), HMA, YSL and NRAMP are crucial for metal homeostasis. Transcription factors like OsNAC, OsIDEF andOsIRO also play important roles in boosting the activity of genes related to metal balance. Some traditional rice varieties naturally have high levels of essential metals due to their built-in mechanisms and specific transporter genes. Identifying and studying these important transporter genes, along with transcription factors and metabolic pathways, is essential for developing rice varieties rich in nutrients. Once these key genes are identified, the goal is to transfer them into high-yielding commercial rice varieties. Comparing gene activity during grain filling in regular and zinc-enriched rice varieties, using comparative RNA-seq analysis, helps identify specific genes involved in zinc balance (Figure 2). The genes that are overexpressed or underexpressed, especially in high zinc types, can be pinpointed using Differential Gene Expression analysis (DGE). By employing genomics-assisted breeding with accurate and consistent quantitative trait loci (QTLs), genes and haplotypes, scientists can swiftly create rice varieties fortified with zinc and iron.

The transcriptomic data (eg: microarray data) and proteomic data (eg: GCMS) regarding Zn and Fe homeostasis generated from various omics platforms gives an extensive list of co-expressed transcripts. The next crucial step is the correct interpretation of the huge data to mine out the underlying biological significance. A spectrum of bioinformatics tools and associated computer algorithms assist to interpret data. The clustering computer algorithm is such a tool to organise, visualise patterns in large expression datasets and to group transcripts for mineral homeostasis based on co-expression. Thus, it is possible to derive a functional relationship by integrating multi omics data. Apart from this, the high-throughput expression data from tiers helps to group transcripts based on their predicted or known functions. The GO ontology (http://www.geneontology.org) resource can be used for this purpose to pool omics data to gain insight on biological functions. Expasy, aSwiss bioinformatics resource portal, harbours various tools for genomic, transcriptomic, proteomic, metabolic data analysis and for interaction study and associated visualization tools.

3.Proteomics Approach

For a comprehensive understanding of cellular biology, transcriptomics and genomictechniques may be combined with modern techniques such as tandem-MS and LC-MS/MS to generate proteomics data. Mass spectrometers combined with gas chromatographs are widely used to profile volatile and metabolite compositions in homogenized rice flour. Bioinformatics plays a crucial role in analyzing and interpreting proteomic data for rice biofortification. Proteomic data analysis involves acquiring, pre-processing, identifying and quantifying proteins, as well as annotating their functions. The steps include data acquisition using mass spectrometry, data pre-processing to clean and standardize the data, protein identification by comparing experimental spectra and quantitative analysis to measure protein quantities. Functional annotation involves categorizing proteins based on their biological roles, such as Gene Ontology (GO) annotation, Cluster of Orthologous Groups (COG) analysis and metabolic pathway annotation using databases like KEGG.

Pathway analysis tools, including KEGG, DAVID, Reactome and others, help identify enriched pathways and biological processes related to differentially expressed proteins. These tools offer insights into the underlying biological mechanisms, contributing to a better understanding of rice biofortification.In a comparative proteomic study by(Sarkar et al., 2015), they analysed two rice lines, finding higher levels of phenolic compounds, anthocyanins and antioxidants in red rice (Mali Daeng) compared to white rice (KDML105). This suggests a nutritional advantage in the red rice variety. Proteomics methods also help understand gene expression changes in transgenic rice, affecting translation activity and food quality. (Ramli & Md. Zin, 2015)in 2015 studied seed storage proteins in rice varieties, associating them with nutritional quality. Additionally, proteomic analysis of chalky rice grains under high-temperature stress revealed insights into starch degradation's role in chalkiness (Kaneko et al., 2016). By combining proteome analysis with crop genetics, researchers gain valuable information about protein content and related genes in different plant parts under varying conditions.

4. Metabolomics Approach

Metabolomics is the study of small molecules in a biological system, providing insights into the qualitative and quantitative differences in bioactive compounds among various rice varieties. For instance, a study identified over 3,000 compounds and genetic variations related to nutritional pathways in rice. This research explored how genetic variations affect nutritional compounds like vitamin E and phenolics, along with changes in the cooked rice metabolome. Another study comparing normal and giant embryo rice found that the latter has higher quality attributed to increased bioactive compounds. However, the major challenge in metabolomicslies in extracting and interpreting large amounts of data within a biological context.

In studying the metabolomics of rice, tools like MetaboAnalyst process metabolite data, conduct statistical analysis and explore pathways by normalizing data and visualizing metabolomic patterns. XCMS Online pre-processes and analyzes liquid chromatography-mass spectrometry (LC-MS) data, detecting peaks and aligning profiles for statistical analysis. MZmine processes mass spectrometry data, detecting peaks and quantifying metabolites. Metabolite Set Enrichment Analysis (MSEA) identifies pathways based on metabolite sets, aiding in pattern recognition. MetaboLights serves as a repository for sharing metabolomics data and provides analysis tools. ChemSpider is a database for chemical compounds, facilitating metabolite identification. KEGG and HMDB map and analyze metabolic pathways, aiding in metabolite mapping. Cytoscape visualizes network data, helping researchers understand metabolite interactions. MassBank is a mass spectral database enabling metabolite identification. These tools collectively contribute to processing, analyzing and interpreting metabolomic data, enhancing our comprehension of rice's metabolic processes.

5. Ionomics Approach

Ionomics focuses on studying the mineral nutrients and trace elements in plants across different growth stages and environments. It's an effective method that uses techniques like X-ray crystallography and mass spectrometry to identify genes and gene networks regulating the ionome. For example, a genome-wide association study (GWAS) on 17 mineral elements in rice grains from 529 accessions provided insights into variations in mineral compositions among different rice types(Yang et al., 2018). Another study analyzed trace elements in 1,763 rice accessions to identify germplasm with increased mineral content and better nutritional quality(Pinson et al., 2015). These efforts are crucial for exploring genetic resources and understanding how mineral levels change in rice tissue.

Designing Genetically Modified Rice for Enhanced Nutrition

Bioinformatics plays a pivotal role in designing genetically modified (GM) rice with enhanced nutrition by providing valuable insights and tools throughout the development process. In this process, it first identifies target genes through approaches like Genome-Wide Association Studies (GWAS), analyzing genomic data to unveil genetic variations linked to desirable nutritional traits. Subsequently, CRISPR Design Tools(e.g., CRISPRdirect, Benchling) aid in the precise selection of gene targets for CRISPR/Cas9 editing, ensuring the focused enhancement of specific nutrient-related genes. Additionally, tools for promoter and regulatory element analysis(PlantPAN 3.0, PLACE) contribute to optimizing gene expression by scrutinizing promoter regions and regulatory elements.

Comparative genomics tools(Ensembl, Phytozome) facilitate the selection of genes from species with naturally elevated nutrient levels. The understanding of genetic networks is enhanced through network analysis tools(Cytoscape and STRING), enabling the selection of multiple targets for a comprehensive nutrient boost. Tools predicting off-target effects(CRISPOR, CCTop), coupled with expression profiling through RNA-Seq analysis(DESeq2, edgeR), ensure the safety and precision of GM rice modifications. Data integration platforms like Galaxy and Bioconductor offer a holistic view of genetic and molecular changes induced by modifications. Finally, risk assessment tools such as AllergenOnline and PROVEAN analyze the modified genome and its protein products, ensuring a meticulous evaluation of potential unintended consequences or allergenicity. By leveraging these bioinformatics tools, researchers adeptly navigate each stage, guaranteeing precision and safety in the design of genetically modified rice for enhanced nutrition. All these steps are summarised in Figure 3.

Trait mapping and marker-assisted selection (MAS) in rice breeding benefit significantly from the application of bioinformatics tools. During trait mapping, QTL (Quantitative Trait Loci) mapping tools such as QGene and MapQTL are employed to analyze genetic markers across populations, identifying specific genomic regions associated with traits like yield, disease resistance, or nutritional content. Concurrently, genetic marker identification utilizes Single Nucleotide Polymorphism (SNP) discovery tools like TASSEL and GATK to pinpoint SNPs and other markers within the rice genome, crucial for correlating variations with desired traits. Genome browsers like GBrowse and UCSC Genome Browser aid in visualizing and analyzing genomic data, facilitating the interpretation of marker locations within the rice genome. Marker-trait association analysis is conducted using tools like PLINK and TASSEL, which assesses correlations between genetic markers and target traits, identifying markers significantly associated with the trait of interest.

In the subsequent phase of MAS, decision support tools like Flapjack and Breeding View assist breeders in selecting plants based on favourable markers, streamlining the breeding process through informed and efficient plant selection. Integration with breeding databases, such as Crop Breeding Database and Breedbase, ensures the storage, management and analysis of extensive genetic and phenotypic data, fostering collaboration and providing a comprehensive resource for ongoing breeding programs. Finally, data visualization tools like R and ggplot2 facilitate the creation of clear and interpretable plots and graphs for presenting trait mapping and MAS results. Through the systematic application of bioinformatics tools at each stage, rice breeders can accelerate the identification of desirable traits, enhance the efficiency of marker-assisted selection and contribute significantly to the development of improved rice varieties. The breeding approach for high Zn rice varieties are given in Figure 4.

Bioinformatics to unwind interactions for mineral homeostasis at molecular levels

The protein-protein interaction and the knowledge on interacting partners of a candidate gene is necessary to predict the functional consequence of over expression, knock-down and knock-out at the biological/phenotypic scale. The Fe/Zn accumulation and distribution in rice grains involves various tiers of interacting partners and co-regulation. Phosphorus in rice seeds is converted into inositol hexaphosphate (InsP6), which mainly accumulates in the aleurone layer. Phytic acid (InsP6) serves as a storage compound for phosphorus and forms salts with metal cations such as calcium, potassium and iron, with zinc being loosely bound. Iron, primarily bound to phytic acid, is regulated by the iron-chelate transporter OsYSL9. Zinc initially accumulates around the aleurone layer during seed development and then moves to other parts. Through transgenic approaches, the co-expression of genes like OsNAS1 and HvNAATb can enhance the levels of iron and zinc in rice grains, thereby improving their nutritional value.The putative interacting partners can be estimated in silico using various interaction database/tools like STRING (Search Tool for the Retrieval of Interacting Genes/Proteins), BioGRID(Biological General Repository for Interaction Datasets), STITCH (Search Tool for Interactions of Chemicals), Interologous Interaction Database (I2D) etc. Cytoscape facilitates the merging of interaction data with various biological data types to enable comprehensive analysis. A practical scenario on use of these tools is described by Kandwal and co-workers in 2022. They identified a nonsense OsVIT2 Mutant in rice showing increased grain Fe and Zn level without reduction in yield. We can easily figure out the interacting partner genes using STRING platform and visualize using Cytoscape tool. It generates idea on interacting genes which we can subject to study further for its expressions in mutant (OsVIT2). These extension in studies establishes functional relationship among genes and help to estimate functional scale changes imparted upon manipulation in single gene or transcript.

Nowadays, rice research is increasingly relying on the applications of machine learning algorithms, showcasing their efficacy in tasks such as predicting DNA N6-adenine methylation sites and ranking causal genes associated with quantitative trait loci (QTL). Machine learning applications extend to predicting grain quality parameters and help to choose appropriate donors from the vast germplasm resources cost effectively.

Conclusion

In essence, the collaboration between omics sciences and bioinformatics holds immense promise for enhancing the nutritional quality of rice. By leveraging advanced tools and methods, scientists can uncover the genetic secrets that contribute to nutrient levels in rice varieties. This knowledge not only aids in the development of nutrient-rich rice but also guides the creation of genetically modified varieties. Bioinformatics tools play a crucial role in every step, from identifying key genes to designing genetically modified rice. Moreover, they assist in the efficient breeding of rice varieties with desirable traits. As we embrace these technological advancements, the journey towards healthier and more nutritious rice varieties becomes an encouraging step in combating global nutritional challenges.

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Momordica cymbalaria Phoenix of Vegetable

Raman Selvakumar

ICAR-Indian Agricultural Research Institute,
Pusa Campus, New Delhi, India

Momordica cymbalaria is a Momordica genus of *Cucurbitaceae* species. *Momordica tuberosa Roxb.* and Luffa tuberosa Roxb. are synonyms. It is commonly known as Athalakkai (Tamil), Karchikai (Kannada) or Kasarakayee (Andhra Pradesh). The plant is a perennial climber found in the South Indian states of Andhra Pradesh, Karnataka, Madhya Pradesh, Maharastra, and Tamil Nadu, and is only available during the monsoon season as a weed. Plant can withstand extreme drought and waterlogged condition without effect of its growth due to the reason it is known as 'Phoenix of Vegetable'. Even though it produces well during the Kharif and Rabi seasons, this crop is not cultivated by farmers as a normal crop. It was once thought

Femiale Flower

Male Flower

Perannial herbaceous vine

to be a weed, although the tubers were used in ancient times for medical purposes. The edible parts of this species are the fruits, which are rich in nutritional value. It is utilised as a vegetable in Tamil Nadu particularly Tuticorin, Virudunagar, Sivaganga Districts. It is classified as a medicinal plant in India, and different parts of the plant can be used to cure a variety of illnesses. As a leafy vegetable, not only the fruits but also the leaves can be used. In traditional medicine, the fruits of M. *cymbalaria* have been used as tonic, stomachic, stimulant, laxative, and diuretic. Most commonly, M. *cymbalaria* fruit juice and leaf tea are used to treat diabetes, malaria and colic, as well as to treat infections, worms, and parasites, measles, hepatitis, and fever. As an astringent, abortifacient, and aphrodisiac, the root can help with constipation, indigestion, diabetes and diarrhoea, as well as a number of other ailments. Citric acid, malic acid, and vitamin C have all been found in fruits. Palmitic acid, oleic acid, stearic acid, α-Eleostearic acid, and γ-Linolenic acid are all reported to be present in the fixed oil of Momordica cymbalaria fruits.


Tubers

Botanical description

M. *cymbalaria* is a tropical species native to India and Southeast Asia. The species natural habitat is unknown, however it is believed to be in the tropics. The plant is a thin, scandent, branching, and striate annual or perennial herbaceous herb with a slender, scandent, branched, and striate stem. The leaves have an orbicular-reniform shape to them, are deeply cordate at the base, and are obtusely lobed with five to seven lobes. The fruits are 20-25 mm long, pyriform with 8 sharp ridges, 24 mm × 15 mm attenuated at the apex, and constricted at the base into the

Athalakkai

Rapid Fruit

fleshy, dark green, and ribbed peduncle. The seeds are 4.6 mm in length, are oval in shape, and are smooth and lustrous. Flowers have only one sex. The male flower peduncle is filiform, puberulous, and ebracteate, with 2-5 flowers in racemes, each with a pale yellow corolla and two stamens. On a 28 mm long peduncle, the female bloom is solitary. Fruits are collected from November to January after flowering in October. Each plant produces 1.25 to 1.5 kilogramme of fruit. The tender fruits resemble those of a small bitter gourd species. The roots are perennial, woody, tuberous, and woody. For the sake of fruits, the plant is allowed to grow along bunds (field boundaries), fences, and even in the fields. However, there is no regular cultivation. Only a small percentage of perennial tubers survive in the soil and produce a single plant the following season.

Nutritional composition

Athalakkai has three times the calcium amount of bitter gourd. Calcium is necessary for bone and tooth growth, as well as regular heart rhythm, blood coagulation, muscular contraction, and nerve responses. This nutrient's higher concentration in athalakkai can be harnessed and employed. The iron content of both vegetables is nearly same. The concentration of ascorbic acid (Vitamin C) in athalakkai is two times that of bitter gourd. This is significant in areas where vitamin C consumption is low. The potassium level of athalakkai is also two times that of bitter gourd. The amount of β-carotene in athalakkai is extremely low. Citric acid, malic acid, and vitamin C are all said to be present in fruits.

Therapeutic uses

The fruits of *M. cymbalaria* were used as a tonic, stomachic, stimulant, laxative, and alterative.

Gout, rheumatism, and subacute spleen and liver illnesses can all be treated with this fruit. It has also been proven in animal and human tests to have hypoglycaemic effects. M. *cymbalaria's* fruit juice and leaf tea are used to treat diabetes, malaria, colic, sores and wounds, infections, worms and parasites, as well as measles, hepatitis, and fevers. Antihelimintic action can be found in fruit pulp, leaf juice, and seeds. Root is used to cure constipation, indigestion, diabetes, diarrhoea, and rheumatism and is astringent, abortifacient, and aphrodisiac. The medicinal usefulness of plants has been recognised for several decades. Many plant extracts include a varied array of secondary metabolites, most of which have antioxidant effects, in addition to minerals and primary metabolites. Momordica species plants have been employed as medicinal agents in the treatment of diabetes mellitus. Momordica charantia and Momordica foetida, two other species in this genus, have been shown to have hypoglycemic properties.

Anti cancer activity

When compared to normal cyclophosphamide, a methanol extract of aerial portions of M. cymbalaria (200 mg/kg of body weight) showed substantial anticancer efficacy in mice with ascites carcinoma.

Nephroprotective activity

Momordica cymbalaria tuberosa tubers exhibit strong nephroprotective properties and could be useful in the treatment of acute renal injury caused by nephrotoxins. Its antioxidant properties may be responsible for this activity.

Anti microbial activity

When compared to typical antibiotics, M. cymbalaria extracts (Petroleum ether, chloroform, ethanol, and aqueous) have a very good inhibitory activity against Staphylococcus aureus, Klebsiella pneumonia, Escherichia coli, Pseudomonas aeruginosa, and Aspergillus niger. The zone of inhibition of typical antibiotics was lower than that of M. cymbalaria extracts, indicating that this plant is effective against these species.

Anti ulcer activity

Momordica tuberosa aqueous extract has been shown to have anti-ulcer properties. The presence of polyphenolic contents may be responsible for the anti ulcer action of the aqueous extract of Momordica tuberosa, as evidenced by the reduction in nonprotein sulfhydryls concentration, stomach content, haemorrhage, and ulceration in ulcer caused Wistar rats.

Anti diarrhoeal activity

In rats, a methanol extract of Momordica cymabalaria fruit showed considerable anti-diarrheal action when used to treat castor oil-induced diarrhoea. When evaluated at 200, 400, and 600 mg/kg, the extract demonstrated similar effectiveness to the anti-diarrhoeal medicine diphenoxylate, with a statistically significant

- **Treatment for diabetes, ulcer rhematism**
- **Absorb iron and alleviate anemia**

- **Prevents cancer**
- **Boost immune system of the body**

- **Reduce the high blood pressure**
- **Reduce the and maintain normal cholesterol**

- **Protect Kidney**
- **Give strength to bones and teeth**

reduction in the frequency of defecation and the wetness of faecal droppings when compared to untreated control rats.

Momordica cymbalaria role in current therapy

Oral antidiabetic drugs and insulin administration are currently used to treat diabetes; however, these approaches do not mimic the way insulin is secreted by native islets for glucose regulation in real time, nor do they provide tight blood glucose control to prevent late complications of the disease. Isolated islet cells from a donor pancreas have been proven to successfully manage glucose levels after transplantation. It is a better alternative to pancreas transplantation because it is less invasive, but the benefits of islet transplantation are not universally accepted due to a lack of donors, the maintenance of islet functions such as cell growth and survival in vitro, and concerns about the side effects of the lifelong immunosuppressant used to prevent graft rejection. M. cymbalaria not only has antihyperglycemic properties, but it also has anti-diabetic properties, possibly due to its role in cell regeneration and insulin production.

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Challenges in enhancing Cashew Crop Production and Modern technological solutions to address the challenges

Introduction

Cashew is an important plantation tree crop of India and several other developing countries. Cashew cultivation has been contributing significantly towards improving the socio-economic status of farmers and rural people in India. Currently cashew nut ranks second in

Siddanna Savadi
Manju Manuel
Manjunatha K.
Muralidharaz B.M.
ICAR- Directorate of Cashew Research (DCR), Puttur- 574 202, D.K., Karnataka, India
ICAR-Indian Institute of Horticultural Research (IIHR), CHES, Chettalli, Kodagu, Karnataka, India

edible nut trades and is worth $ 9 billion. Cashew is considered as the low volume and high value crop and it earnssubstantial foreign exchange. The demand for cashewnuts is increasing annually in both domestic and international markets due to increasing demand for cashew kernels as snacks and other valuable byproducts such as CNSL and cashew apple-based products as raw materials in industries. India was the pioneering country in cashew industry and dominated the global cashew production and trade for long. The global raw cashew nuts production is about 3.7 million tons (FAOSTAT 2021) and India is the second major cashew producing country after CÃ´te d'Ivoire. In the area, India stands second with 1.06 m ha (18% of total) and produces about 7.5lakh tonnes of RCNs (FAOSTAT 2021). In India, cashew is grown in 17 states andnearly 95% of the RCNs production is from the seven states viz. Maharashtra, Andhra Pradesh, Odisha, Karnataka, Kerala, Tamil Nadu, and Goa (DCCD 2019). National productivity of cashew is about 750 kgs per hectare. However, India imports about 7-8 lakh tonnes of RCNs every year mainly from African countries to meet its total processing capacity of about 16.50 lakh MT per year. The RCNs import costs India about Rs. 9000 crores.

Low cashew nut yieldsand in recent times, the increasing domestic consumption have resulted in increased imports while reducing the exports. Hence, a lot of foreign exchange is spent on importing RCNswhichwarrants enhancingthe domestic production and productivity of cashew. However, there are several challenges such as old orchards with low yielding andsenile trees, lack of scientific management of the crop, pest and disease infestations, abiotic stresses such as drought and high temperatures, poor pollination and fruit set, labourshortage and lack of mechanization, high production costs, and limited market access and price fluctuations, which are hinderingthe cashew crop productivity, quality, and profitability. These challenges are further aggravated the changes in the climate change, reduced land and water and the need for reduced use of chemical

inputs. With growing demand for cashew nuts in the domestic and international markets, it is crucial to address these challenges to ensure sustainable and efficient farming practices.This could be achieved by integration of modern agricultural practices and technologies which focus on efficiency, sustainability, and precisionwith cashew production technologies.

Challenges in cashew production and Modern technological solutions

1. Old orchards with low yielding and senile trees

Before 1980's, most of cashew planting materials used in the traditional cashew growing areas were of seedling origin (Kumar et al. 2012) and are currentlyaged and often infested by pests giving very low yields. Besides, in the beginning, cashew was promoted as waste utilization tree and grown on mainly on waste lands with poor soil fertility and inadequate nutrient management. Thus, the cashew productions from these old orchards and waste lands are suboptimal. Further, other crop management practices such as pruning and poor canopy management are not practised which also contribute to limiting thepotential yields. The technological solutionsto this problem are replacing or rejuvenating the old trees with superior high yielding and grafted varieties fo renhancing nut production. Besides there is need for adopting precision nutrient management based on soil testing to provide right nutrients at the right time and adopting standardised pruning practices with efficient tree pruners to maintain optimal canopy structuresthatallow better sunlight penetration and airflow for improved flowering and nut set.

2. Yield losses due to Pests and Diseases

Cashew trees are infested by several pests, and major two pests are the tea mosquito bug (TMB) and root and stem borers (CSRB) (Vidya et al. 2011). TMB is a sucking pest which can cause severe damage to the new flushes, flower panicles and fruits resulting huge yield losses. CSRB is borer insect that feeds on the phloem tissue and infested trees would yellow and die within few months few months. Cashew is also affected by diseases such as powdery mildew, anthracnose, and root rot which significantly affect tree growth and nut production and quality. Further, in the view of sustainable and ecofriendly agricultural practices the use of chemical inputs (such as pesticides) needs reduction, which makes pest management even more challenging. Modern agricultural technological solution to managing the insect pests and diseases efficiently is to deploy UAVs to regularly monitor for pests population and diseases symptoms to take preventive measures before pests population or disease spread increases to avoid significant yield losses. Besides, UAVs could be used to apply pesticides efficiently andin targeted arears of infestations with precision to effectively control pests and diseases while minimizing pesticide use. Further, developing and promoting disease-resistant cashew varieties cultivation is the most effective and sustainable means managing diseases affecting cashew nut production.

3. Yield losses due to Abiotic stresses and Climatic Changes

Generally, cashew tree is considered hardy and can sustain heat and moisture stress to a certain extent. However, sever conditions of drought especially during flowering and fruiting will impact the yield to great extent. Cashew is mainly cultivated in rainfed conditions and often faces drought stress, and high temperatures especially in tropical and subtropical climates where flowering coincides with moisture and heat stress, which negatively affect flowering, fruiting, and overall yield (Rupa et al. 2013). To overcome these losses due to abiotic stresses adoption of smart irrigation technologies such as drip irrigation with soil moisture sensors can help toenhance the water use efficiency as well as enhance the nut yields undertropical and subtropical climates. Besides, deployment of drought-resistant cashew varieties can help to cultivate cashew under water stress conditions with lesser yield penalty

4. Yield losses due to Poor Pollination & Fruit Set

Cashew is cross pollinated crop and pollination is mainly mediated by insects like bees and ants. Among the bees, wild type bees are the major pollinators. The reduction in the pollinator's population due to over use of pesticide or abiotic stresses will impact the nut setting and production. The solutions to this problem are conserving natural pollinators and promoting apiculture can help improve pollination rates. Further, for conserving the wild bees flowering plants should be planted at the borders of the orchards.

5. Labour shortage and lack of mechanization

Most of the operations in cashew from weeding to the harvesting and processing are labour-intensive tasks. However, there is drastic reduction in the labour forces involved in agricultural activities including cashew cultivation due to migration of rural population to urban areas. Labour shortage results in untimely or no proper cultural operations causing huge yield and quality losses in crop cultivation. These issues can be addressed by mechanization of most of the operations which can help in taking up timely farm operations, reduce drudgery and cost of labour. Further, lack of mechanization for operationsspecific to cashew such collection and fruit and nut separation, which are tedious andlabour intensive adds to cost of cashew cultivation. Recently, machines have been developed for these specific operations which could be utilized efficiently to reduce the drudgery and the cost of cultivation.

6. High Production Costs

Rising labour costs and the input costs (fertilizers, pesticides) have resulted in increase in overall production costs, making cashew farming less profitable for smallholder farmers. The costs of cashew nut production can be reduced by adoption of Precision Farming technologies involving use of drones, sensors, and aerial imagery can help farmers optimize use of inputs (like water, fertilizers, and pesticides), reducing waste and costs. Besides it helps in reducing non target effects and environmental pollution concerns. The precision farming technologies facility needs to be created at community or block level may be created and on custom hiring basis it can be used by the farmers.

7. Price Fluctuations and Limited Market Access

Cashew farmers of North eastern (NE) India and nontraditional cashew growing areas often struggle to get access to bigger markets and often face challenges like lower prices for their produce. Besides, sale of produce through middlemen reduces the profit margins. The issues related to market access and price could be addressed by leveraging digital marketing and e-commerce platforms to access consumers or processing industries directly and get better profit margins. In the traditional cashew growing areas i.e., coastal areas, lesser prices and price fluctuations compared other remunerative crops like areca is an major issue. To overcome these market related issues forming farmer producer organizations (FPOs) wherein farmers can collectively negotiate better prices and get access markets more effectively and also share resources created for preliminary processing.

Conclusion

Cashew farming faces severalchallenges, but modern solutions ranging from precision farming and mechanization to digital market access and climate-smart strategies can empower farmers to overcome these challenges in enhancingcashew productivity and production and ensure sustainability, and profitability.

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