

REVIEW PAPER

Exploring the Potential of Underutilized Horticulture Bioresources by Using Various Biotechnological Interventions

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ABSTRACT

Underutilized horticulture crops have not been fully utilized in terms of their potential contributions to food security, income generation, and environmental sustainability. In recent years, various omics technologies such as genomics, metagenomics, transcriptomics, proteomics, metabolomics, phenomics, and ionomics have emerged as valuable tools for studying the genetic and molecular basis of these underutilized crops. The use of high throughput technologies like next-generation sequencing (NGS) has allowed for the rapid generation of omics data, which can be used to explore the genetic resources of underutilized horticultural crops. The advancement of sequencing technology and bioinformatics tools has greatly facilitated molecular biology studies of these crops. By integrating multiple omics approaches, researchers can gain insights into gene functions and networks under conditions of physiological and environmental stress. An innovative and proactive approach to preserving underutilized fruit plants through the application of biotechnological methods including in vitro culture technology, cryopreservation, and molecular markers. This article provides an overview of the current and potential use of various omics approaches in exploring information about important underutilized horticulture crops, with the aim of promoting basic research and accelerating the development of new varieties.

HIGHLIGHTS

- ① Underutilized fruits are important because they are a rich source of nutrients and have medicinal properties.
- ① They can help to prevent and treat diseases and can also be used to alleviate poverty and hunger.
- ① These crops have many advantages like easier to grow and hardy in nature, producing a crop even under adverse soil and climatic conditions.
- ① Omics techniques help in improving the nutritional value of fruits, increase food security, and promote environmental sustainability.

Keywords: Underutilized horticultural crops, Omics approaches, Genomic resources, Genetic resources, Conservation

Underutilized crops have the potential to enhance food security, alleviate poverty, and improve the resilience and sustainability of farming systems. These crops, known as underutilized horticultural crops, are not grown or traded on a large scale but are cultivated, traded, and consumed locally (Cortes *et al.* 2023). The popularity of these crops varies

depending on the specific crop and the locality, but it can be increased through effective publicity. The underutilized horticultural crops offer numerous

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advantages. The underutilized crops can withstand adverse soil and climatic conditions, ensuring a harvest even in challenging environments. Due to their long history of consumption, local communities are well aware of the nutritional and medicinal properties of these crops (Mayes *et al.* 2014). Furthermore, underutilized horticultural crops are a repository of genetic variability and diversity in horticultural crops, encompassing various plant types, morphological and physiological variations, disease and pest resistance, adaptability, and distribution (Mayes *et al.* 2014; Salgotra *et al.* 2021b; Gonzalez *et al.* 2022).

Underutilized crops, unlike non-native or introduced species, have the potential to play various roles in enhancing food security. Firstly, they can be a crucial part of efforts aimed at assisting the impoverished population in meeting their subsistence and income needs, particularly in the global South where the majority of the poor reside. Secondly, these crops offer a means to mitigate the risks associated with relying heavily on a limited number of major crops. By diversifying agricultural practices, the sustainability of farming can be improved, reducing the reliance on inputs such as nitrogen fertilizers derived from fossil fuels and agricultural fuels. This is particularly important considering the impact of agriculture on climate change and the need to transition to a post-peak-oil world. Additionally, these crops contribute to the overall quality of food, offering nutritional benefits and unique flavours. Lastly, the underutilized crops possess different properties (Table 1) and serve as a means to preserve and celebrate cultural and dietary diversity, recognizing the importance of traditional knowledge and practices (Zargar *et al.* 2021). Moreover, these crops are deeply rooted in local cultural traditions, making them an integral part of the community. They have the potential to address food insecurity by serving as potential food sources, providing a diverse range of nutrients such as protein, vitamins, and phytochemicals. Additionally, these crops offer a balanced macronutrient profile, encompassing fats, proteins, and carbohydrates. However, it is unfortunate that these crops are often stigmatized as 'food of the poor,' leading to financial disadvantages in their production and consumption. Despite this, underutilized crops hold promising economic value, particularly in terms of their medicinal properties,

further highlighting their significance (Salgotra *et al.* 2021a).

Underutilized edible plants possess untapped potential in terms of their contribution to food security, income generation, and environmental services. While they may be locally abundant, their global utilization remains limited due to a lack of scientific knowledge regarding their physiological, agronomic, and ecological properties (Deb *et al.* 2019). Despite their economic potential, their current use is restricted. However, these plants have the ability to address poverty and hunger issues faced by many developing nations, as well as promote crop diversification and improve rural economies. Although they may not play a significant role in global production and consumption systems, they are highly nutritious, containing both macronutrients and micronutrients. These underutilized crops require relatively low inputs, making them conducive to sustainable agricultural production in rural areas and aiding in the fight against "hidden hunger" caused by micronutrient deficiencies. Furthermore, they offer numerous health benefits beyond meeting basic physiological needs and have been recognized as functional foods (Rai *et al.* 2005; Deb *et al.* 2016). These crops have the capacity to contribute to food security and provide affordable, nutritious food options for the poor. Furthermore, the underutilized fruits are rich in nutrients and medicinal properties, making them more suitable to enhance the nutritional, functional, and sensory qualities of the food (Dansi *et al.* 2012).

The preservation and sustainable utilization of the variety found in underutilized plant species germplasm, both within and between plant species, holds immense economic, scientific, and societal importance. These efforts have the potential to address the food security challenges that arise from the ever-growing global population. The field of biotechnology, particularly advancements in *in vitro* culture technology, cryopreservation, and omics technologies, has played a pivotal role in enhancing the conservation methods for rare and endangered plant genetic resources, as well as the traditional knowledge associated with germplasm (Pandotra and Gupta 2015). The progress made in NGS has opened opportunities for the emergence of novel omics fields, including genomics, transcriptomics, and proteomics. Nevertheless, the realms of



Table 1: Important underutilized crops with salient properties

Underutilized crop	Local names	Origin	Properties	References
Bael (<i>Aegle marmelos</i> L.) Correa (Rutaceae),	Indian quince, Bengal quince, holy fruit, golden apple, stone apple, <i>bela</i> , <i>bel</i> , <i>maredoo</i> and <i>sirphal</i>	Southeast Asian countries (Sri Lanka, Pakistan, Bangladesh, Myanmar, Thailand) and Indian peninsula	Bael has various pharmacological, medicinal, ethnomedicinal, and conventional properties	Morton (1987)
Woodland strawberry (<i>Eragaria vesca</i>)	California Strawberry, Fraises Des Bois, European Strawberry, Alpine Strawberry Wood Strawberry, Wild Strawberry	North America	In traditional remedies as a laxative and diuretic	Rivard (2022)
Cavendish banana (<i>Musa acuminata</i>)	<i>Kampala</i> banana and <i>Bogoya</i>	Europe	The fruits of the Cavendish bananas are eaten raw, used in baking, fruit salads, and to complement foods.	Martin <i>et al.</i> (2016)
Chironji (<i>Buchanania lanzan</i>)	Piyal, Charu, Baruda, Priyala, Achaar, Piyar, Payala, Peirah, Perna, Char, Payala, Chirka, Pra-savak, Chiraunji, Piyal, Chironji, Charoli, Kath bhilawa, Priyal, Chirangi, Sarop, Chowl, Satdhan, Muungaappeeze, Saraparuppu Charam, Saara chettu, Priyaluvu, Sara, Rajadanamu, Morichettu, Cara, Sarapappu and Charumamidi	Chironji originated in the Indian sub-continent and is found in India, Nepal, Burma, Nepal, and a few other countries	Anticancer, antihypertensive, larvicidal, antidiabetic and antidiarrheal properties	Achuthan and Jose (1997); Xue and Chen (2002); Othman <i>et al.</i> (2002)
Cupassu Fruit (<i>Theobroma grandiflorum</i>)	Cupuassu, Cupuazu, Cupu Assu, or Copoasu	Northern Brazil (Para, Amazonas, and Amapa), Colombia, Bolivia, and Peru	Used to make juices, nectars, jams and ice-creams	Jean-Marie <i>et al.</i> (2022)
Longan (<i>Dimocarpus longan</i>)	Dragon's eye	Myanmar and southern China	Dried longan flesh is also an ingredient in herbal medicine used for stomach ache, insomnia and as an antidote for poison. The seeds are used in shampoo, like soap nut due to presence of saponin content.	Sritontip <i>et al.</i> (2014)
Hickory nuts (<i>Carya cathayensis</i>)	Chinese Hickory	China	Its nuts exhibit properties of tonifying kidneys and relieving asthma	Sutton and Crowley (2020)
Kair (<i>Capparis decidua</i>)	Ker, Kair, Teent, Karil, Della, and Nepti	India, Egypt, Chad, Ethiopia, Pakistan, Iran, Mauritania, Jordan, South Africa, Nigeria, Senegal, Niger, Sudan and Somalia	Anti-inflammatory, diaphoretic, emmenagogue and laxative properties	Shekhawat and Batra (2006); Gupta (2010)

Karonda (<i>Carissa carandas</i>)	Kerenda or Karanda, Kerendang, Buah Renda, Samarinda, Namdaeng Nam Phrom, Bengal Currant, Caranda fruit, Carandas plum and Christ's thorn	Indian subcontinent, Myanmar, Malacca and Sri Lanka	Hepatoprotective, analgesic, anti-inflammatory, antipyretic and anticonvulsant properties	Bhaskar and Balakrishnan (2009a and 2009b); Hegde and Joshi (2009); Hegde <i>et al.</i> (2009)
Borassus palm (<i>Borassus aethiopum</i>)	African Fan Palm	West africa	The roots serve for the treatment of stomach parasites, bronchitis, sore throats and asthma, as well as being used for a mouthwash	Bayton (2007)
Lasura (<i>Cordia dichotoma</i>)	Gonad, bhokar, Indian cherry, lasura, panugeri, pidar, naruvilli, spistan, geduri, burgund dulu wanan and shlesmatoka	India, Myanmar, and Nepal. Also found in Thailand, Taiwan, Malaysia, Polynesia, China as well as in Australia	Antidiabetic, antiulcer, anti-inflammatory, immune-modulator, and analgesic activity	Jamkhande <i>et al.</i> (2013)
Mangosteen (<i>Garcinia mangostana</i>)	Mangustaan, Ivarumamidi, and Kaattampi	Southeast Asia	Antioxidant, pro-apoptotic, anti-proliferative, antinociceptive, anti-inflammatory, neuroprotective, hypoglycemic and anti-obesity	Ovalle-Magallanes <i>et al.</i> (2017)
Kendu tree (<i>Diospyros melanoxylon</i>)	Temburini	India, Pakistan, and Nepal	Anti-inflammatory, antioxidants, antimicrobial and antihyperglycemic	Moghaddam <i>et al.</i> (2012)
Aonla (<i>Emblica officinalis</i>)	Amia, nelli, ambala, amali and amlaki	India, Sri Lanka, Malaysia, and China	Antioxidant activities	Poltanov <i>et al.</i> (2009); Bhandari and Kamdod (2012)
Phalsa (<i>Grewia asiatica</i> L.)	Phulsha, Phutiki, Shukri, Mriduphal, Pharosakoli, Chadicha, and Unnu	Southeast Asia	Antimicrobial activities, antimalarial, anti-inflammatory activity, immunostimulant activity and anti-cancer properties	Bajpai <i>et al.</i> (2012); Singh and Yadav (2014)
Ber (<i>Ziziphus mauritica</i>)	Indian plum, beri fruit, Indian Jujube, and Indian Cherry	Yunnan province of China	Anti-allergic, anti-inflammatory activities, anti-diarrheal and hepatoprotective activities	Deshpande <i>et al.</i> (2013); Talmale <i>et al.</i> (2015); Koley <i>et al.</i> (2016)
Jamun (<i>Syzygium cumini</i>)	Black berry, black plum, jambul and java plum	India, Sri Lanka, Malaysia and Australia	Antibacterial, antifungal, antiviral, antigenotoxic, anti-inflammatory, anti-ulcerogenic, cardioprotective, anti-allergic, anticancer, radioprotective, free radical scavenging, antioxidant, hepatoprotective, anti-diarrheal, hypoglycemic, and antidiabetic effects	Bhandary <i>et al.</i> (1995); Kumawat <i>et al.</i> (2018)



Khirmi (<i>Manilkara hexandra</i>)	Khirmi, Rayan, Rajadanah, Ulakkaippalai, Palai, Patla, Pola, Kirni, Krini, Palamunpala, Hale and Hannu	India	Anti-inflammatory, antiulcer, aphrodisiac, alexipharmic, anthelmintic, antibacterial properties	Pareek <i>et al.</i> (1998); Stewart and Brandis (1992)
Meswak (<i>Salvadora persica</i>)	Bada pilu, chhota pilu, Jal, Pilu, Mustard tree, Saltbush, Jhal, Kalawa, karkol, Arak and Arraka	Saudi Arabia, India, and Egypt	Antimicrobial, antioxidant, analgesic, anthelmintic, anti-inflammatory, antiulcer, sedative, anticonvulsant, anti-osteoporosis, antidiabetic, hypolipidemic, in addition to wound-healing, antidepressant, and antitumor activities	Aumeeruddy <i>et al.</i> (2017); Al Bratty <i>et al.</i> (2020)
Mahua (<i>Madhuca longifolia</i>)	Indian Butter	India, Sri Lanka, Myanmar, and Nepal	Antibacterial, anticancer, hepatoprotective, antiulcer, antihyperglycemic, analgesic activities, etc.	Gaikwad <i>et al.</i> (2009); Bhaumik <i>et al.</i> (2014)

Salgotra *et al.* (2021a).

crop science have also extensively documented metabolomics, ionomics, and phenomics. The utilization of multi-omics strategies, coupled with high throughput techniques, has significantly contributed to unraveling the intricacies of growth, senescence, yield, and the reactions to both biotic and abiotic stress in various these crops (Yang *et al.* 2021). These advancements have facilitated effective management of these valuable resources. A strategic and forward-looking approach towards conserving plant genetic resources, traditional knowledge of germplasm, and sustainable utilization of plant resources in the twenty-first century is of profound significance for the sustainable development of our planet. This review paper highlights the significance of neglected fruit crops and their enhancement through the application of diverse omics techniques. Strategies for the effective characterization, documentation, and preservation of these underutilized fruit crops have been proposed for the future. These advancements could boost the yield of these crops while maintaining their nutritional value and ability to withstand climate changes, ultimately supporting food security, nutrition, and the livelihoods of individuals relying on these crops.

Importance of underutilized fruit crop

The primary challenge of ensuring food and nutritional security for a population of around 10 billion by 2050 is of utmost importance. This challenge arises due to the changing climates, which pose severe constraints on crop production, along with various abiotic and biotic factors. Moreover, the availability of limited agricultural land further exacerbates the situation (Salgotra and Bhagirath 2023). In 2019, it was estimated that approximately 690 million people suffered from hunger, a number that significantly increased to 720-811 million in 2020 amidst the COVID-19 pandemic (FAO 2021). These statistics indicate that achieving zero hunger by 2030 would be difficult if the current situation persists (Singh *et al.* 2022). One potential solution lies in promoting the use of underutilized crops, which possess significant nutritional value and can help combat hidden hunger. In fact, many underutilized crops surpass staple crops in terms of their nutritional properties.

Recently, more than 1000 underutilized crop

species globally have been recognized as potential survival crops due to their high nutritional content and resilience to various environmental stresses (Chivenge *et al.* 2015). These underutilized horticultural crops, including vegetables, serve as important sources of minerals, vitamins, micronutrients, and proteins, contributing to dietary safety (Ebert 2014; Ruiz *et al.* 2014). Underutilized fruit crops such as bael, mangosteen, chironji, borassus palm, ker, karonda, lasora, tendu, aonla, phalsa, ber, jamun, tamarind, manila tamarind, khirni, meswak, cupassu, etc. have recently garnered attention as supplementary nutritional food crops (Salgotra *et al.* 2021a). Therefore, these crops have the potential to fulfil various roles in enhancing food security and leveraging their comparative advantages to provide better, more affordable food options for the less privileged. These crops exhibit significant potential due to their nutritional quality and versatile uses. The underutilized fruit crops possess high nutritional and medicinal value, making them suitable for incorporation into weaning foods to enhance the nutritional, functional, and sensory attributes of formulated weaning food mixes for product development (Kumar and Iqbal, 2020).

These crops have a well-balanced composition of carbohydrates, fats, and protein, allowing for a balanced intake of nutrients while reducing the need for consuming other cereals. In the current context, underutilized fruits hold equal importance and nutritional value compared to commercially grown fruit crops. Throughout history, underutilized fruits have played a vital role in supplementing the diets of people in the Indian Subcontinent. Additionally, wild edible fruits, which are rich in vitamins, minerals, fiber, antioxidants, and other nutritionally important compounds such as alkaloids, essential oils, phenols, and tannins, contribute significantly to the livelihood and nutritional security of indigenous communities in developing countries. Underutilized fruits contain vital nutrients like proteins, minerals, carbohydrates, dietary fibers, phytochemicals, and antioxidants. Baobab (*Adansonia digitata*), kei apple (*Dovyalis caffra*), and Marula (*Sclerocarya birrea*) are among the most cultivable underutilized fruits in developing countries. Despite their limited genetic resources and research, these fruits are considered healthy foods, with untapped potential for wider



utilization.

Underutilized fruit crops serve as abundant sources of antioxidants and minerals. Antioxidants, which are essential phytochemicals in human diets, work to counteract the harmful free radicals produced within the body. However, these crops often remain unpopular due to the high levels of astringency and acidity found in their fruits. By employing modern techniques to reduce these undesirable qualities, farmers can enhance their economic prospects and contribute to nutritional security. India boasts one of the largest food processing industries in terms of both production and consumption. Processing underutilized crops not only increases nutritional security but also allows for the more efficient utilization of waste. Processing methods for fruits such as aonla (preserves, jams, and pickles), bael (squash and nectar), and tamarind (paste) are now readily available. Additionally, minor fruits like ber, lasura, karonda, phalsa, and kair possess significant potential for use in the processing industry (Salgotra *et al.* 2021a). These minor fruits are not only rich in nutritional and medicinal value but can also be cultivated in wastelands with minimal care. Consumers consistently express a demand for new, delicious, nutritious, and visually appealing food products. This study identifies and presents various innovative products derived from underutilized fruits. These economically affordable fruits, which are seasonal and naturally abundant, have the potential to yield nutrient-rich and innovative products. The current market trends and availability of processing technology further support the exploration of these opportunities (Kumar *et al.* 2016).

‘Omics’ technologies

In today’s technological era, “Omics” technologies offer a broader perspective for identifying new datasets of functional genes and alleles in crop species. This includes their integration with phenotypic information and the pathways that are responsible for key agronomic traits. Utilizing “Omics” technology allows for the analysis and correlation of genome sequences, gene expression profiles, protein content, and metabolites with the structure, function, and vital agronomic traits like grain yield, and resistance to both biotic and abiotic stresses. The integration of functional analysis with

genomic sequence data leads to more precise gene annotations, functional markers, and quantitative trait locus (QTL) maps. This aids in understanding the factors that influence phenotypic traits and metabolic processes, paving the way for sustainable farming (Samal and Behera 2022).

The genomic exploration of underutilized horticultural crops has not received as much attention as staple crop plants (Jasrotia and Salgotra 2021). Breeding programs for these crops are still in their early stages, and the creation of trait-specific homogeneous lines remains a distant goal. However, the application of omics approaches can greatly accelerate and streamline crop improvement efforts. By leveraging omics and its associated techniques, researchers can swiftly identify trait-specific genomic regions and QTLs in a high-throughput manner, offering immense potential for crop enhancement (Majeed *et al.* 2022). Large-scale techniques, such as genomics, transcriptomics, proteomics, metabolomics, and phenomics, have already generated extensive datasets for this purpose. In the meantime, modern bioinformatic and machine-learning approaches are aiding in the analysis of this diverse and multidimensional data (Libbrecht *et al.* 2015; Cortés *et al.* 2023), ultimately leading to a better understanding of the underlying mechanisms behind agronomic traits within the contemporary plant breeding triangle, which encompasses genomics, phenomics, and enviromics (Crossa *et al.* 2021). Additionally, ‘omics’ datasets are being generated to study macro-scale interactions and enhance our understanding of crop behavior across microbial and environmental continua (Zhang *et al.* 2021). However, despite significant technological and computational advancements, the integration of ‘omics’ studies to comprehend biochemical pathways and cellular networks in crop systems is still in its early stages, particularly in orphan species (Maldonado-Alconada *et al.* 2022). Therefore, this special issue aims to provide updated perspectives on large-scale ‘omics’-based approaches. Specifically, it explores the conceptual framework of the ‘omics’ paradigm, the practical applications of various ‘omics’ technologies, and their integration through transdisciplinary bioinformatics as tools to enhance the qualitative and quantitative traits of a diverse range of crop species (Chauhan *et al.* 2022; Cortes *et al.* 2023). The

following are the various omic resources which can be efficiently used for the genetic improvement of underutilized horticultural crops.

1. Genomics

Genomics is revolutionizing various stages of the breeding process in most crops (Campuzano-Duque *et al.* 2022). The utilization of genomic tools is crucial in enhancing various crop species as they serve as the primary input for breeding. These tools play a vital role in facilitating the efficient and prompt identification of genetic resources, as well as their subsequent application in documenting valuable genes for crop expansion (Campuzano-Duque *et al.* 2022). The introduction of omic concepts, coupled with next-generation sequencing (NGS), has propelled genome analysis to new heights in the scientific community (Nazir *et al.* 2021). NGS has been widely employed for various purposes, such as *de novo* sequencing, whole-genome sequencing, genotyping by sequencing, and transcriptome and epigenetic research. Consequently, NGS holds great potential as a valuable tool in the future. With the advent of these technology different genomes of underutilized horticultural plant species have been carried out (Table 2).

Efficient utilization of genetic resources of underutilized horticultural crops, including diverse germplasm, land races, and wild relatives, necessitates their exploration and development. The advent of NGS technologies has significantly increased the availability of genomic resources for numerous crops (Salgotra and Stewart, 2020). The progress in high-throughput genotyping (HTG) has empowered breeders to enhance crop improvement with greater precision and efficiency. However, there has been a lack of substantial efforts in genomics and breeding of underutilized crops. Due to limited awareness about the potential of these crops, inadequate research funding from governmental and international agencies has been allocated, resulting in their neglect (Oyeyinka *et al.* 2015). Nevertheless, the high nutritional value, tolerance to abiotic stresses, and potential adaptability to climate change highlight the importance of supporting these crops in the future (Mayes *et al.* 2019).

Modern sequencing technologies offer numerous opportunities for the effective genetic improvement of underutilized horticultural crops (Salgotra

and Stewart 2022). Firstly, these technologies can be utilized to explore the genetic diversity and relationships within and between different species using molecular markers, providing valuable insights into the crop's genetic makeup. Secondly, they can aid in the development of core collections or trait-based subsets, allowing for the identification and preservation of desirable traits (Paliwal *et al.* 2021). Additionally, modern sequencing technologies enable the discovery of genes associated with important traits through marker-trait association, supporting marker-assisted selection (MAS) in breeding programs. Furthermore, these technologies facilitate genomic selection (GS), which allows for the prediction of breeding values based on genomic information. They also play a crucial role in the global exchange of molecular information, sequence data, and DNA accession, thereby promoting collaboration and knowledge sharing among researchers. Moreover, modern sequencing technologies can help identify gaps in current underutilized crop collections, guiding new exploration missions and facilitating the exchange of germplasm. In the long term, these technologies can be employed to conduct transcriptomic, proteomic, and metabolomic analyses, unravelling the molecular mechanisms underlying complex traits (Salgotra and Stewart 2020). Ultimately, the availability of precise genetic information for underutilized crops will undoubtedly attract the attention of crop researchers, encouraging further research and development in this field. Draft genome sequencing of different underutilized horticultural crops has been initiated by the various Consortium for sequencing, assembling, and annotating the genomes (Paliwal *et al.* 2021). This sequencing data will provide the surge of genomic resources for further utilization in underutilized crops (Salgotra and Stewart 2022). NGS technology has been employed to create genomic assets in the Cherimoya (*Annona cherimola* Mill.) perennial fruit tree. A grand total of 41,413 protein-coding genes have been pinpointed, with a considerable portion being associated with secondary metabolism, defense mechanisms, stress response, and development. The findings of this investigation introduce fresh and noteworthy genomic resources not solely for cherimoya and other *Annonaceae* species, but also for gaining insights into the evolution of the more anciently divergent angiosperms (Talavera

**Table 2:** List of genome-sequenced of underutilized horticultural plant species

Species name	Common name	Type	Databases
<i>Citrus ichangensis</i>	Ichang papeda	Fruit	www.citrusgenomedb.org
<i>Citrus unshiu</i>	Cold hardy mandarin	Fruit	www.citrusgenomedb.org
<i>Asparagus officinalis</i>	Garden asparagus	Vegetable	phytozome.jgi.doe.gov
<i>Dendrobium catenatum</i>	—	Medicinal	herbalplant.ynau.edu.cn
<i>Gastrodia elata</i>	Tianma	Medicinal	herbalplant.ynau.edu.cn
<i>Dioscorea rotundata</i>	White Guinea yam	Vegetable	genomevolution.org/CoGe; plants.ensembl.org
<i>Citrus grandis</i>	Pummelo	Fruit	www.citrusgenomedb.org
<i>Echinochloa crus-galli</i>	Cockspur grass	Medicinal	horticulture.eplant.org
<i>Zizania latifolia</i>	Jiaobai	Vegetable	plants.ensembl.org
<i>Musa itinerans</i>	Yunnan banana	Fruit	banana-genome-hub.southgreen.fr
<i>Ensete ventricosum</i>	Ethiopian banana	Medicinal	horticulture.eplant.org
<i>Siraitia grosvenorii</i>	Monk fruit	Medicinal	herbalplant.ynau.edu.cn
<i>Glycyrrhiza uralensis</i>	Chinese liquorice	Medicinal	ngs-data-archive.psc.riken.jp
<i>Trifolium pratense</i>	Red clover	Medicinal	bioinformatics.psb.ugent.be/plaza; plants.ensembl.org; p
<i>Juglans nigra</i>	Eastern black walnut	Fruit	www.hardwoodgenomics.org
<i>Macleaya cordata</i>	Plume poppy	Medicinal	herbalplant.ynau.edu.cn
<i>Aquilegia coerulea</i>	Colorado blue columbine	Medicinal	genome.jgi.doe.gov; genomevolution.org/CoGe; phytozome.jgi.doe.gov
<i>Parasponia andersonii</i>	Caoye shanhuangma	Medicinal	www.bioinformatics.nl/parasponia
<i>Panax ginseng</i>	Asian ginseng	Medicinal	herbalplant.ynau.edu.cn
<i>Panax notoginseng</i>	Sanchi ginseng	Medicinal	herbalplant.ynau.edu.cn
<i>Selaginella lepidophylla</i>	Resuscitation moss	Medicinal	plantgdb.org/SmGDB/
<i>Ginkgo biloba</i>	Ginkgo tree	Medicinal	gigadb.org/site/index
<i>Solanum pimpinellifolium</i>	Currant tomato	Vegetable	solgenomics.net
<i>Capsicum baccatum</i>	Berry-like pepper	Vegetable	genomevolution.org/CoGe
<i>Rhodiola crenulata</i>	Tibetan Rhodiola	Medicinal	gigadb.org

et al. 2023). In another transcriptome study, cDNA libraries were prepared at different flower stages in sugar apple (*Annona squamosa* L.). The annotation of transcriptome sequences and analysis of the expression profiles of differential genes provided valuable genomic sources for future research regarding the flowering mechanism of sugar apple (Kaidong *et al.* 2016). Similarly, a transcriptomic study was carried in Durian (*Durio zibethinus*) plant in which MGL (methionine γ -lyase) and the ethylene-related gene ACS (aminocyclopropane-1-carboxylic acid synthase) were upregulated in fruits, suggesting a potential association between ethylene biosynthesis and methionine (Teh *et al.* 2017).

2. Transcriptomic

Advancements in omics-based technologies have resulted in the discovery of numerous transcripts, proteins, and metabolites, which have greatly

enhanced our understanding of an organism's response to internal and external signals (Choudhary *et al.* 2021). Transcription, being the initial and crucial regulatory step in gene expression within a cell, plays a pivotal role (Crick, 1970). Any malfunctioning at the transcription level can have catastrophic consequences for the organism's survival (Churko *et al.* 2013). Consequently, researchers have always been intrigued by the study and analysis of global changes in gene expression through the identification of corresponding RNAs. The transcriptome, which encompasses all RNA molecules expressed from an organism's genetic material, serves as a valuable tool for uncovering genomic information and functionality. It provides insights into gene expression dynamics, spatio-temporal patterns, and cell type functions. The transcriptome is a highly intricate system, consisting of different types of coding and non-coding RNA

molecules (Mattick and Makunin 2006; Wang *et al.* 2009). In addition to these applications, transcriptomics has also shed light on the structural and functional studies of non-coding RNAs, which play a crucial role in gene regulation. The hybridization-based microarray technique has proven to be a cost-effective and high-throughput method, making it instrumental for the initial transcriptomic studies (Schena *et al.* 1995). Various techniques, such as microarray, EST, SAGE, CAGE, RNA-Seq/NGS, and *de novo* assembly, can be employed for transcriptomic studies.

The integration of genomic and transcriptomic data has proven to be highly valuable in various areas of research, such as gene-oriented phylogenetics, structural mapping, and functional characterizations. Several studies have utilized this approach to gain insights into different aspects of biological systems. For example, Abdullah *et al.* (2021) studied a combined genome-based gene family screening with *in silico* expression analyses for characterizing *tcGASA* paralogous in cacao and identifying targets for developing fungi-resistant varieties. Similarly, Heidari *et al.* (2021) investigated *in silico* expression analyses *MGT* genes in cacao and expanded their search to orthologous genes in other crops. Through *in silico* expression analysis, they were able to identify the involvement of *MGT* in lipid/cell wall metabolism and photoprotection pathways. These studies highlight the effectiveness of integrating genomic and transcriptomic resources for gene and allelic mining. Transcriptomic screenings are also valuable for functional gene validation and profiling gene expression in specific tissues or environmental conditions. Overall, transcriptomic resources provide a detailed understanding of the mechanistic basis of agronomically relevant phenotypes (Abdullah-Zawawi *et al.* 2022).

3. Proteomics

Proteomics has emerged as a valuable tool for the identification of proteins that can serve as markers in breeding programs. Recent advancements in methodologies, genomics, and transcriptomics databases have significantly contributed to the progress of plant proteomics, including in orphan species (Wang *et al.* 2021). Among the commonly employed techniques are gel-free based methods such as shotgun or LC-MSMS, as well as data

dependent acquisition (DDA), data-independent acquisition (DIA), and targeted strategies. Shotgun proteomics has already demonstrated its potential in identifying proteins and prototypic peptides that can be utilized to enhance or select individuals with tolerance to abiotic stresses like drought and heavy metal toxicity. For instance, San-Eufrazio *et al.* (2021) and Salas-Moreno *et al.* (2022) have successfully employed shotgun proteomics to identify proteins and peptides associated with resistance to drought and heavy metal toxicity, respectively. While gel-based techniques like 2DE remain popular in many experiments, researchers are increasingly exploring the proteomic consequences of biotic stresses using methods such as 2DE-MALDI/TOF MSMS analysis combined with protease activity assays (Castillejo *et al.* 2021). Furthermore, proteomics advancements have also made their way into underutilized horticultural crop species (Maldonado-Alconada *et al.* 2022; Castillejo *et al.* 2023). These findings underscore the expanding influence of proteomics in various fields and its potential for further advancements in the future.

On the other hand, there is a significant research gap that persists in the long term, irrespective of the specific crop species. One unanswered question pertains to the intersection and collective interaction of upstream genomic, transcriptomic, proteomic, and metabolomic layers across various climates and over time (Adhikari *et al.* 2017). Understanding how these layers ultimately shape the multidimensional phenomic expression of crops in the field remains a challenge that requires further investigation. The researchers investigated the impact of ebb-and-flow sub-irrigation on the protein level of the underutilized crop roots, comparing it to top sprinkle irrigation. These findings hold promise for enhancing plant characteristics through the application of proteomics. Furthermore, there is anticipation for similar advancements in the field of proteomics, as well as in metabolomics, particularly in relation to non-model crop species (Wang *et al.* 2021; Tienda-Parrilla *et al.* 2022).

4. Metabolomics

In recent years, there has been a significant increase in research focused on the comprehensive profiling and analysis of small molecules in underutilized fruits and vegetables. To obtain valid conclusions, it



is crucial to employ robust sampling and extraction methods, ensure proper separation and detection, incorporate randomness and replication, and utilize appropriate data processing and analysis techniques (Adhikari *et al.* 2017). The field of metabolomics technology has played a pivotal role in facilitating the discovery of new small molecules and deciphering their quality attributes in both fresh and processed forms. Metabolomics involves the thorough identification and quantification of small molecules, either individually or in combination, within a given sample, with a molecular weight of ≤ 1500 Da (Fiehn 2000). This approach has proven highly effective in analyzing small molecules as it provides a hypothesis-free starting point for exploring the entire measurable molecular space, leading to the discovery of previously unknown compounds by using different techniques (Atanasov *et al.* 2021). Moreover, the available information on secondary metabolite compounds derived from underutilized fruits is still limited. To identify these secondary metabolites, an experiment was conducted using GC-MS and LC-MS (Adhikari *et al.* 2017) to provide information on the specific secondary metabolites present in rambai.

5. Phenomics

The utilization of plant phenomics has become a widespread occurrence worldwide in the past ten years. Numerous “phenomics centers” have emerged, offering advanced solutions for high-throughput phenotyping in gene exploration and breeding (Furbank *et al.* 2019). It is important to highlight that while controlled environments, image-based phenotyping platforms have gained significant popularity across the globe, the majority of crop breeding takes place in the field, with minimal or no selection in controlled environments (Adhikari *et al.* 2017; Furbank *et al.* 2019). Crop improvement relies heavily on plant phenotyping, which involves studying the physiological traits and mechanistic science of plants to inform the selection of genetic material for desired traits. Recent advancements in high-throughput techniques, including machine vision, robotics, and computing (known as plant phenomics), have revolutionized the ability of crop physiologists and breeders to quantitatively measure complex and previously challenging traits. These techniques, when

combined with affordable genomic sequencing and genotyping, machine learning, and genome selection approaches, offer breeders the opportunity to make rapid genetic progress. While significant progress has been made in field crops, limited research has been conducted on horticulture crops, including underutilized fruits. Earlier, traits such as radiation use efficiency, photosynthesis, and crop biomass have been considered difficult and time-consuming to measure. However, the emergence of high-throughput techniques such as LiDAR, thermal imaging, leaf and canopy spectral reflectance, Chl fluorescence, and machine learning has made phenomic studies of underutilized crops, including horticultural crops, feasible (Furbank *et al.* 2019).

Phenomic screening in underutilized gene pools faces a significant research gap due to the lack of practical implementation, mainly because these gene pools often exhibit trait segregation that is highly influenced by the environment. Integration of modern ‘omics’ approaches, such as genomics and phenomics are essential for creating exotic variation into elite commercial backgrounds (Burbano-Erazo *et al.* 2021). In addition to genomics, alternative methods like grafting can also be utilized to incorporate interspecific genomic variability. Grafting, an ancient horticultural technique, can be optimized for desirable trait variation using genomics, transcriptomics, phenomics, epigenomics, and other approaches. These examples showcase the amalgamation of species diversity through introgression breeding and grafting, bringing them up to the standards of last-generation high-throughput technologies. These advancements in ‘omics’ technologies for crop improvement complement classical breeding schemes, which still hold relevance. Looking ahead, the emerging fields of enviromics, epigenomics, and soil metagenomics may further contribute to phenotypic modulation, expanding our understanding of the complex interactions between genotype and the environment. In addition to this research, other studies have also focused on overcoming interspecific barriers, genomically characterizing hybridization, and uncovering naturally occurring ecological adaptive variation for drought and heat stresses (Buitrago-Bitar *et al.* 2021).

Conservation of underutilized horticultural crops

To address the global food scarcity issue resulting from the rapid growth of the population and its impact on human health, it is imperative to implement effective, efficient, and timely measures to establish a framework for the preservation and sustainable management of the diverse range of underutilized crops (Pandotra and Gupta 2015). This will ensure the continuous availability of these genetic resources for future generations. The landmark signing of the Convention on Biological Diversity (CBD) during the event in Rio de Janeiro in 1992 has significantly raised the profile and importance of biodiversity conservation as a critical international concern. Taking into consideration these factors, various strategies are being employed to conserve underutilized crop germplasm, including *in situ* conservation, *ex situ* conservation, and biotechnological approaches. Significant progress has been achieved in the field of biotechnology, particularly in areas such as *in vitro* culture technology, cryopreservation, and omics technology. These advancements have played a crucial role in enhancing the conservation methods for underutilized horticultural crops, as well as the preservation of important germplasm. Moreover, they have greatly contributed to the effective management of these valuable resources. In the context of sustainable development, it is imperative to adopt a strategic and forward-looking approach towards the conservation of these valuable resources. This vision holds immense importance in ensuring the sustainable use of plant resources in the 21st century (Salgotra and Gupta 2015).

The rapid urbanization and pursuit of commercial gains have resulted in the extinction of natural habitats, posing a significant threat to wild vegetation. To address this issue, it is crucial to conserve underutilized species that are well adapted to these habitats, as they provide for the social and economic needs of rural communities (Singh *et al.* 2022). Both *ex situ* conservation and *in situ* conservation must be promptly implemented. This approach will help prevent the loss of identity of numerous neglected yet highly valuable species. It is worth noting that genebanks worldwide maintain only a limited collection of underutilized species (Table 3). However, recent years have witnessed the organization of various national and international programs by esteemed institutions such as the Food

and Agriculture Organization (FAO), African Orphan Crop Consortium (AOCC), International Plant Genetic Resources Institute (IPGRI), International Institute of Tropical Agriculture (IITA), International Crops Research Institute for Semi-Arid Tropics (ICRISAT), and others. These programs have been conducted in Southeast Asia, parts of Africa, and Australia to raise general awareness among the local populations about the importance of conserving biodiversity (Singh *et al.* 2022).

Table 3: Status of important underutilized fruit crop species in *ex-situ* gene banks

Name of species	Number of accessions
<i>Ziziphus mauritiana</i>	876
<i>Dimocarpus longan</i>	403
<i>Borassus aethiopum</i>	288
<i>Ziziphus rotundifolia</i>	103
<i>Garcinia mangostana</i>	546
<i>Embllica officinalis</i>	222
<i>Punica granatum</i>	467
<i>Theobroma grandiflorum</i>	294
<i>Carissa carrandus</i>	98
<i>Cordia myxa</i>	234
<i>Fragaria vesca</i>	478
<i>Aegle marmelos</i>	303
<i>Grewia subinaequalis</i>	321
<i>Musa acuminata</i>	389
<i>Capparis decidua</i>	145
<i>Syzigium cuminii</i>	388
<i>Tamarindus indica</i>	231
<i>Madhuca latifolia</i>	156
<i>Manilkara hexandra</i>	276
<i>Buchanania lanzan</i>	122
<i>Carya cathayensis</i>	202

1. *In situ* conservation

The process of cultivating those overexploited and endangered underutilized horticulture plants outside their natural habitat due to its habitat degradation and destruction (Long *et al.* 2003). The *in situ* approach offers opportunities for studying the biology of these plants for research purposes, understanding the threats to endangered species, providing plant materials for propagation, re-introduction, agronomic improvement, and educational purposes as highlighted by Temitope (2013). However, one notable disadvantage of this type of conservation is that the conserved samples



of the species may represent a narrow range of genetic variation compared to what occurs in the wild, as there are no evolutionary processes taking place. Conservation methods include seed storage in seed banks, field gene banks, and botanical gardens as outlined by Withers and Engelmann (1998). Additionally, a sufficient amount of samples is required for the conservation of genetic diversity, along with the need for trained and skilled personnel to manage the process, making it a challenging task that is more susceptible to genetic erosion of the material (Pandotra and Gupta 2015).

2. *Ex situ* conservation

This approach presents a multitude of benefits, such as the preservation of a wide range of potentially valuable genetic variations present in the underutilized horticulture plants. It also promotes and ensures the sustainable utilization of genetic diversity to meet both current and future human needs. Additionally, it guarantees the protection of associated species and facilitates research on species within their natural habitats, thereby enabling a more comprehensive evaluation and utilization (Rathore *et al.* 2005). However, there are several drawbacks associated with this methodology. These include the time-consuming nature of the process, the costs involved, the limited coverage of the total diversity of a species, potential political and ethical interference and social concerns, as well as the constant risk of genetic material loss in the event of natural disasters.

Biotechnological approaches

Biotechnological approaches are particularly crucial when conventional methods are not feasible due to reproductive barriers or reduced populations, making them essential for the conservation of underutilized plant species. Advanced biotechnological tools have enabled the production of high-quality, genetically superior planting materials for the nation. Plant biotechnology, especially *in vitro* culture, cryopreservation, and molecular biology, offers new avenues for underutilized horticulture plants conservation and evaluation (Pandotra and Gupta 2015). Various biotechnological methods, such as *in vitro* propagation, genetic transformation, cryopreservation and DNA banks, have been successfully utilized to rapidly multiply

and conserve underutilized horticulture plants, ensuring the preservation of pathogen-free material, elite plants, and genetic diversity over different timeframes.

1. *In vitro* propagation

In vitro propagation is a widely utilized technique for the mass production and multiplication of plants, regardless of seasonal variations. This method involves the production of callus from various explants such as leaves, seeds, nodes, and tubers. Subsequently, shoots and roots are developed from the callus, or from auxiliary explants, followed by the formation of whole plantlets under controlled conditions. After undergoing an acclimatization process, these plantlets can be transferred to open field areas. This methodology offers a stress-free approach as it allows for the generation and cost-effective maintenance of pathogen-free germplasm stocks over extended periods of time (Rai, 2010). For example, the initial *in vitro* collection systems were established for cocoa (*Theobroma cacao* L.) and coconut (*Cocos nucifera* L.), resulting in two *in vitro* collection methods that serve as a template for the development of additional protocols (Withers 2002). After that numerous underutilized plants which are at the risk of becoming endangered have been *in vitro* propagated such as *Aquilaria malaccensis*, *Dioscorea deltoidea*, *Guaicum officinale*, *Hydrastis canadensis*, *Nardostachys grandiflora*, *Panax quinquefolius*, *Picrorhiza kurroa*, *Podophyllum hexandrum*, *Buchanania lanzan*, *Prunus africana*, *Pterocarpus santalinus*, *Rauwolfia serpentina*, *Saussurea costus*, *Gloriosa superba*, and *Taxus wallichiana* (Rai 2010).

2. Genetic transformation

Agrobacterium tumefaciens and *Agrobacterium rhizogenes* are highly effective strains that can be used to transform underutilized horticulture plants into resistant varieties against various forms of stress conditions. These strains also have the ability to induce the overproduction of secondary metabolites, which can minimize the exploitation of these plants. The transformation process is typically conducted in laboratory conditions, allowing for the growth of underutilized horticulture plants with multiple durable resistances against pests and diseases. Additionally, the use of transgenes

or marker-assisted selection (MAS) can aid in the development of plants that are resistant to insects, pests, drought, and salinity. This is crucial in meeting the world's demand for food while also conserving plant biodiversity in natural habitats. To date, more than 120 species from 35 families have been successfully transformed using *Agrobacterium* and other techniques, with the number of successful transformations continuing to increase (Birch 1997).

3. DNA banks

DNA repositories store a collection of DNA samples akin to a gene library, offering crucial data to researchers worldwide for the preservation of Plant Genetic Resources (PGR). This encompasses safeguarding genome fragments, individual genes, or entire genotypes for future utilization. Certain species prove challenging to conserve through traditional methods involving seeds or vegetative means, or face severe threats in their natural habitats. In such cases, DNA banks offer an alternative approach to preserving the genetic diversity of these species and their populations temporarily, until more effective conservation strategies can be devised (Dulloo *et al.* 2006). The extraction and storage of genetic material should be easily accessible for molecular applications. DNA reservoirs can be stored at -20°C for short to medium-term preservation, lasting up to 2 years, or at -70°C or in liquid nitrogen for extended periods.

4. Cryopreservation

Cryopreservation is the process of storing biological tissues at extremely low temperatures, typically at -196°C using liquid nitrogen (LN). At this temperature, all metabolic activities in vegetatively propagated and recalcitrant seed species, such as cell divisions and cellular metabolism, come to a halt, allowing plant material to be stored for long-term germplasm conservation. This method eliminates the need for subculture steps in long-term tissue culture storage and reduces the level of somaclonal variation observed (Martin *et al.* 1998). In cryopreservation, it is highly recommended to use shoot apices or meristem cultures, as these are virus-free plant materials that can be easily recovered when the culture is revived after an extended period (Scowcroft, 1984). Cryopreservation does not affect the viability, vigor, or genetic makeup of

the preserved materials (Ogbu 2010). It provides an effective method for conserving species, particularly woody plant germplasm (Panis 2005). The following are some of the examples of large-scale application of cryopreservation are presented in Table 4.

Perspectives

Despite the efforts made by this Special Issue to compile a diverse range of 'omics' sub-disciplines for crop improvement, it is important to acknowledge that high-throughput screening technologies have also made their way into other promising fields that may not be prominently featured in this collection. One such field, as discussed in the previous section, is the scaling of phenomics across the environmental continuum gradient. This approach offers a more precise prediction of the interaction between genes and the environment, which is an integral part of the emerging enviromics framework. This framework combines multi-environment phenomics screening with genomic-based prediction, as highlighted by Cooper and Messina (2021). Additionally, the adoption of epigenomic footprint profiling can provide a mechanistic understanding of a significant portion of the phenotypic variance in crops, particularly in relation to reaction norms and plasticity gradients observed across different climates, as demonstrated by Cortes *et al.* (2022).

Soil metagenomics using 'environmental' DNA is contributing to the discovery of beneficial microorganisms for agriculture, which is crucial for meeting the increasing sustainability demands in this field (Nwachukwu *et al.* 2022). Additionally, the application of backward 'omics' tools is enhancing our understanding of the evolution of crops and their cultural significance by incorporating genomics and phylogenomics into modern paleogenomics, thereby updating archaeological records (Barrera-Redondo *et al.* 2020). As various 'omics' data continues to accumulate in different sub-disciplines, it is imperative to revolutionize open-source record access, develop novel statistical algorithms, and provide unprecedented computational resources to facilitate effective trans-disciplinary data merging and bioinformatics processing (Tirnaz *et al.* 2022). These crops are underrepresented in germplasm collections, and this leads to numerous difficulties in breeding. The integration of 'omics'-enabled

**Table 4:** Large-scale application of cryopreservation techniques to underutilized plant germplasm

Sl. No.	Plant material	Gene bank/country
1	Seeds of 1200 accessions from 50 different species mainly of endangered medicinal plants	The National Bureau for Plant Genetic Resources (NBPGR), New Delhi, India
2	Seeds of more than 110 accessions of rare or threatened species	Kings Park and Botanic Garden, Perth, Australia
3	Seeds of coffee involving 450 accessions	IRD Montpellier, France
4	Dormant buds of apple involving 2200 accessions	National Centre for Genetic Resources (CNGR), Fort Collins, USA
5	Dormant buds of mulberry involving 420 accessions	National Institute of Agrobiological Resources (NIAR), Yamagata, Japan
6	Shoot-tips of banana involving 630 accessions	INIBAP International Transit Centre, Catholic University of Leuven, Belgium
7	Shoot-tips of cassava involving 540 accessions	International Centre for Tropical Agriculture (CIAT), Cali, Colombia
8	Pollen of 13 pear cultivars and 24 <i>Pyrus</i> species	National Centre for Genetic Resources (CNGR), Fort Collins, USA
9	Pollen of more than 700 accessions of traditional Chinese flower species	College of Landscape Architecture, Beijing Forestry University, Beijing, China
10	More than 1000 callus strains of species of pharmaceutical interest	Phytara, Sheffield, UK
11	Several thousand conifer embryogenic cell lines for large-scale clonal planting programs	Sylvagen, Vancouver, Canada
12	Embryogenic cell lines of coffee and cacao	Biotechnology Laboratory of the Nestle Company, Notre Dame d'Oé, France

Pandotra and Gupta, 2015.

systems biology, machine learning predictions, and speed breeding techniques holds great promise for accelerating customized crop breeding and overcoming the challenges posed by multi-'omics' data (Pelaez *et al.* 2022). This trend of analytical innovation may even lead to the development of artificial general intelligence, potentially enabling rapid and unguided plant improvement based on 'omics' approaches (Khan *et al.* 2022).

Major constraints and strategies for the improvement of underutilized horticultural crops

Biotechnological techniques have the potential to enhance the productivity, quality, and resilience of underutilized crops, which are often neglected by conventional breeding programs. However, there are several challenges and limitations that hinder the application and adoption of these techniques in developing countries (Jackson *et al.* 2006). We are discussing the potential difficulties that arise when integrating multi-omics in order to analyze the functions of genes and their networks, as well

as to develop traits that can enhance underutilized crop improvement (Yang *et al.* 2021). Some of these challenges include:

- (i) Till date, very few underutilized horticultural crops have been sequenced. The lack of accessibility and affordability of biotechnological tools and equipment, such as molecular markers, tissue culture, and gene editing. These require high initial investment, skilled personnel, and adequate infrastructure, which are often scarce or unavailable in resource-poor settings. Biotechnology also requires specialized equipment, materials, and skills that are not widely available or affordable in many regions of the world. This creates a gap between the developed and developing countries in terms of biotechnology research and applications. Moreover, biotechnology also raises ethical, social, and legal issues that may limit its acceptance and adoption by different stakeholders and communities.

- (ii) The limited bioinformatics capabilities and resources to analyze and interpret the large and complex datasets generated by biotechnological approaches. This requires advanced computational skills, software, and hardware, which are also often lacking or outdated in developing countries. Biotechnological techniques generate large amounts of data that need to be analyzed, stored, and shared in an efficient and reliable manner. However, many researchers and breeders lack the necessary bioinformatics skills, tools, and platforms to handle the complexity and diversity of the data. This limits the ability to extract meaningful insights and knowledge from the data and to apply them to crop improvement.
 - (iii) Interdisciplinary collaboration: Biotechnology is an interdisciplinary field that involves the interaction of various disciplines such as biology, chemistry, engineering, mathematics, computer science, and more. However, interdisciplinary collaboration is not always smooth or effective. There may be communication barriers, cultural differences, conflicting goals, or lack of trust among different disciplines. Furthermore, interdisciplinary collaboration may also face institutional obstacles such as funding, policies, or regulations that favour certain disciplines over others.
 - (iv) The underutilized crops are less explored and meagre sequence data is available of these crops. The following are the constraints for the development of horticultural crops which need to be addressed for the improvement of these crops.
 - (v) These crops are underrepresented in germplasm collections, and this leads to numerous difficulties in breeding.
 - (vi) The farming community lacks awareness regarding the nutritional and medicinal value of underutilized horticultural crops. Additionally, there is a lack of research conducted in this area, as well as a scarcity of desirable seeds and planting material.
 - (vii) Limited biotechnological techniques are available in the underutilized horticultural crops compared to underutilized field crops.
 - (viii) The application of advanced on-farm agrotechniques is limited, and there is a lack of utilization of innovative technologies such as biotechnology and plasticulture to enhance productivity.
 - (ix) There is also a lack of knowledge about post-harvest management practices, which further hinders the potential of these crops.
 - (x) Inadequate marketing support and infrastructure facilities for transportation, storage, and processing contribute to the challenges faced by these crops.
 - (xi) These crops are not adequately recognized in horticulture promotion programs, which further limit their growth and development.
 - (xii) Furthermore, improper institutional arrangements and limited involvement of financial institutions in establishing agro-industrial and horticulture-based industrial units add to the constraints faced by these crops.
 - (xiii) Non-availability of genomic resources to be used for the improvement of underutilized crops, particularly the horticultural fruit crops.
- These challenges and limitations are not insurmountable, but they require concerted efforts from researchers, policymakers, industry, and society to overcome them (Prasad, 2020). There is need for interdisciplinary collaboration and coordination among different stakeholders, such as researchers, farmers, policymakers, and consumers (Ning and Lo, 2010). This is essential to ensure the relevance, acceptability, and sustainability of omics technological interventions for underutilized crops. Omics tools have the potential to transform many aspects of human life and society, but they also need to be developed and applied responsibly and sustainably. However, this is often hampered by institutional barriers, communication gaps, and socio-cultural differences. Followings are the strategies should be adopted for the improvement and development of underutilized horticultural crops:
- The following strategies should be adopted for the development of underutilized horticultural crops:



- (i) NGS and other high-throughput techniques should be used for sequencing underutilized horticultural crops. Genome as well as transcriptome sequenced data generated should be properly analysed by using different bioinformatical tools to develop different genomic resources for further utilization in improvement of these crops.
- (ii) Omics techniques should be used in numerous ways such as development of linkage maps, association mapping, MAS, marker-assisted backcross breeding (MABB), etc. All these techniques are directly and indirectly contributing in crop improvement. The molecular markers help in the identification of important genes of interests to be used in breeding population.
- (iii) There should be interdisciplinary collaboration and coordination among different stakeholders for effective planning for proper documentation and conservation of these valuable resources and their sustainable uses.
- (iv) Genetic erosion is a very serious problem with non-traditional fruits and many land races will become extinct if these are not conserved soon by using various biotechnological tools.
- (v) Biotechnological tools including omics technologies should be used for the efficient utilization of the valuable genetic resources of underutilized horticultural crops.
- (vi) Documentation of indigenous knowledge, particularly through ethnobotanical studies, is crucial to tap into the value additions of under-utilized horticultural crops, as they are mainly grown and managed by diverse ethnic communities under traditional farming systems.
- (vii) Strategies should be developed at national and regional levels to overcome constraints in the production of good seed material, planting material, and in-vitro/tissue cultured material, in order to promote the availability of promising selections/varieties and boost production to meet local needs and enhance income generation for small farming communities. - It is necessary to implement systematic and localized crop planning based on the agro-climatic suitability of the region.
- (viii) National programs should focus on the conservation and utilization of a limited number of species in under-utilized horticultural crops, both for subsistence farming and potential commodity crops.
- (ix) Under-utilized horticultural crops, which are nutritionally rich and suitable for low input agriculture, can significantly contribute to food security, nutrition, and human welfare with increased research and development efforts.
- (x) The poor yield and quality of these crops hinder productivity, thus requiring the development of criteria for their commercial exploitation.
- (xi) Special attention should be given to export-oriented production programs and border trade involving high-value crops such as mushrooms, orchids, cut flowers, spices, fresh temperate fruits, off-season vegetables, frozen fruit juice, and concentrate.
- (xii) Research scientists should make special efforts to develop location-specific packages of practices for different horticultural crops, including the development of superior varieties and conservation of genetic resources.
- (xiii) The expansion of infrastructure facilities, with a focus on market development, transportation, and communication, needs to be prioritized.
- (xiv) Encouraging the domestication of potential wild species through homestead cultivation can help prevent over-exploitation of natural resources.
- (xv) Extension agents can organize awareness camps, campaigns, exhibitions, and other events at both micro and macro levels to promote the theme of unexploited horticultural crops.

CONCLUSION

The untapped potential of underutilized horticultural crops presents an opportunity for enhancing food and nutrition security. These crops possess diverse genetic resources that can be explored through research to promote food security, generate

employment, and increase income for smallholder farmers. To fully harness the benefits of these crops and mitigate climate impacts, sustained investments in research, nutritional awareness, and genetic characterization are essential. Additionally, expanding the available genetic resources for certain horticultural crops is crucial to prevent the erosion of their diversity. Traditional knowledge about the cultivation and use of these crops predominantly resides with elderly farmers in rural areas where they are grown. By increasing the cultivation area and production of underutilized horticulture crops, not only can nutritional security be ensured, and import costs reduced, but also the export of fresh horticultural crops can uplift the socio-economic conditions of impoverished farmers.

Earlier, there were limited NGS platforms and genomic resources available for enhancing the genetics of underutilized crops compared to field and commercially cultivated crops. However, now horticultural crop breeders can enhance the genetic potential of a variety by rearranging native genes in different combinations using a variety of genomic sources. Genomic resources, in conjunction with genotyping platforms, play a crucial role in improving crops and various types of genetic stock. The advances in biotechnological methods and tools have generated significant improvements in proper characterization and conservation of underutilized and endangered species. It is imperative that these resources continue to be developed for future use in underutilized crop breeding programs. The genetic and genomic mechanisms of underutilized horticultural crops can be utilized to evaluate the arrangement and genetic assortment of certain crops. Nevertheless, similar studies in other species are also necessary.

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