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Recent Advances in Breeding of Mango *(Mangifera indica)*: A Review

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Authors' contributions

This work was carried out in collaboration among all authors. Author SB designed the study, performed the statistical analysis, wrote the protocol, and wrote the first draft of the manuscript. Author AJ and Author SS managed the analyses of the study. Author SS managed the literature searches. All authors read and approved the final manuscript.

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Review Article

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ABSTRACT

Mango stands as a significant fruit crop with global importance, thriving primarily in tropical and subtropical regions across the world. (*Mangifera indica* L.) belongs to the Anacardiaceae family. This evergreen, sizable tree bears a beloved tropical fruit that enjoys local consumption and international trade. The choice of preferred mango varieties varies from one country to another. Generally, mango types from subcontinental Asian regions are monoembryonic, while those from South East Asian regions tend to be polyembryonic. Despite *Mangifera indica*'s prevalence within the Mangifera genus, several other species within this genus share grafting and pollination compatibility with M. indica. These species can serve as valuable rootstocks or sources of novel genetic traits for breeders. Growing mango presents challenges due to the rapid decline in seed viability shortly after fruit maturity, typically within weeks. While a diverse array of mango varieties is available, inherent limitations exist, including extended juvenility, high clonal heterozygosity, the

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presence of only one seed per fruit, resilient seeds, polyembryony, early post-zygotic auto-incompatibility, and a substantial land requirement for hybrid evaluation. Breeders, however, benefit from the extensive variation and the ease of vegetative hybrid production. A successful mango cultivar must exhibit traits such as dwarfness, precocity, regular and prolific fruit bearing, appealing fruit of good size and quality, resistance to physiological issues, diseases, and insects, and an extended shelf life. A comprehensive understanding of mango phenology, inheritance patterns, and advanced techniques for hybridization has proven invaluable in addressing challenges like irregular fruit bearing, susceptibility to disorders and pests, and issues with taste and quality. The development of genetic markers has further reduced uncertainties in mango breeding and improved the management of hybrid populations.

Keywords: Breeding; mango; physiological problems; disease and insect resistance.

1. INTRODUCTION

Mango (*Mangifera indica* L.) is a member of the Anacardiaceae family, which includes a range of dicotyledonous trees and shrubs. These mango trees are characterized by their evergreen nature and possess branched canopies that can either grow upright or spread widely, reaching impressive heights of up to 30 meters. The tree is well-supported by one or several deep taproots and numerous surface feeder roots. Mango trees are known for their longevity, often living for more than a century. The canopy of the mango tree is adorned with dark green leaves that are simple, alternate in arrangement, and generally have an oval-lanceolate to roundish-oblong shape. The emergence of new leaves occurs periodically, and the color of expanding leaves varies from tan to red. The tree produces numerous flowers, which include hermaphrodite and male blooms. These flowers are borne on branched conical panicles that sprout from the tips of branches [1]. The mango fruit itself is a fleshy drupe, displaying variations in size, shape, and color. The most appealing and edible part of the fruit is the fleshy mesocarp. Within each mango fruit lies a single seed enclosed within a stony endocarp [2].

Breeding programs for mango have faced significant challenges due to certain inherent characteristics of the plant species, which include:

(i) An extended juvenile phase.
(ii) High levels of heterozygosity, leading to unpredictable results in hybridization.
(iii) The presence of only one seed per fruit.
(iv) A high rate of fruit drop, resulting in a low retention of cross-pollinated fruits.
(v) Polyembryony observed in many cultivars.
(vi) The substantial land area needed for a meaningful evaluation of hybrid offspring.

Mangoes are believed to have originated in the South East Asian or Indo-Myanmar region, where they grew as forest trees bearing fibrous and resinous fruits. Estimates regarding the number of Mangifera species vary widely. In northeastern India, one can find wild *Mangifera indica*. From a botanical standpoint, it shares connections with other species such as M. sylvatica, M. caloneura, M. zeylanica, and M. petandra. Some sources have documented as many as 69 distinct species within the Mangifera genus [3]. Among these 69 species, at least 12 fall into the category of species incertae sedis, meaning they cannot be definitively categorized due to insufficient confirming evidence. In the majority of Mangifera species and cultivars examined thus far, the chromosomal count is 2n= 2x= 40.

In a study conducted by Plooy et al. [4], the cytological nature of lenticel discoloration in mango fruit was investigated as part of a broader examination of affected mango fruits. Lenticels, which are small openings in the fruit's skin, were dissected from physiologically mature fruit categorized into different groups based on the extent of discoloration. Through the use of transmission electron microscopy and light microscopy, the researchers examined the mesophyll cells in the affected tissue. The findings revealed that cellular structures and endomembranes remained intact in all cases of discoloration, indicating that the accumulation of phenolic compounds in the cell wall did not result from structural damage such as vacuolar collapse or membrane disintegration. Instead, the results suggested that a signal for the deposition of phenolics occurs via apoplastic transport. This accumulation of phenolic compounds in a specific region of the affected tissue surrounding the lenticel serves as a barrier between the external atmosphere and the rest of the mesophyll [5,6]. It's important to note that

while lenticel discoloration represents an inherent self-defense mechanism supported by ongoing metabolic activity, it remains a superficial cosmetic defect in mango fruit.

In the context of chromosome numbers in Mangifera species, it's worth noting that *Mangifera indica* L., M. sylvatica Roxb., M. caloneura Kurz, M. zeylanica Hooker, and M. odorata Ariff are typically reported as diploid (2x) species, each having a chromosome number of 2n=40. However, an interesting observation was made regarding the Vellai Kolumban variety, which is known for its polyembryonic trait. In an earlier study, it was reported that one plant of the polyembryonic Vellai Kolumban variety exhibited tetraploidy, with a chromosome count of 2n=80. This finding led to some confusion because Manjumbder and Sharma [7] had previously reported that the Vellai Kolumban variety was diploid, with 2n=40 chromosomes. The discrepancy between these two reports seems to arise from the fact that the earlier report was based on one specific plant of the Vellai Kolumban variety, which may have naturally undergone tetraploidy. This particular tree might not have been available for subsequent studies. As a result, the later study has been given more weight, and Vellai Kolumban is generally considered a diploid variety [8].

2. GENETICS OF IMPORTANT TRAITS AND THEIR INHERITANCE PATTERN

Mango breeding has encountered several challenges over the years, primarily stemming from limited knowledge regarding the inheritance of specific traits, the presence of high levels of heterozygosity in the cultivars, and a relatively low number of successful hybrid progenies resulting from crossbreeding efforts. In terms of tree growth habit, the dominant trait is the upright growth habit, which tends to prevail over the spreading growth habit. Conversely, dwarfness, regularity in fruit-bearing, precocity, and resistance to malformation are controlled by recessive genes. There appears to be a correlation between regularity in fruit-bearing and precocity. The color of the fruit pulp is influenced by additive genes, indicating that multiple genes contribute to determining pulp color. Additionally, the biennial bearing habit, where a tree produces a significant crop every other year, is a dominant trait compared to regular, consistent fruit-bearing. These genetic insights provide valuable information for mango breeders seeking to develop cultivars with desirable characteristics [9].

2.1 Incompatibility

The phenomenon of self-incompatibility in mango was not well-understood until Singh et al. [10] reported it in the North Indian mango cultivar 'Dushehari.' This discovery led to the development of the caging technique for pollination in mango, as described by Sharma and Singh [11]. Subsequent embryological studies have revealed that in mango, pollen tubes grow down the style and achieve fertilization, but the development of the zygote is blocked, resulting in a sporophytic type of self-incompatibility [12]. The effects of self-pollination and open-pollination on various aspects of mango fruit development were investigated in four different mango cultivars: 'Amrapali,' 'Mallika,' 'Pusa Arunima,' and 'Pusa Surya' [13]. The results showed that self-pollination led to a rapid decline in fruit setting compared to open-pollination, especially in 'Amrapali' and 'Mallika' in contrast to 'Pusa Arunima' and 'Pusa Surya' [14]. Within 48 hours after self-pollination, the growth of pollen tubes in the stylar region of 'Amrapali' and 'Mallika' was notably slower compared to 'Pusa Arunima' and 'Pusa Surya.' In the former two cultivars, pollen tubes reached up to two-thirds of the stylar region, while in the latter two, they extended up to the micropylar end [15]. Furthermore, self-pollination resulted in a significant percentage (75%) of degenerated ovules in 'Amrapali' and 'Mallika,' which dropped within 21 days after pollination (DAP). In contrast, open pollination led to only 20% of ovule degeneration in these mango cultivars. The growth of fruitlets and ovules obtained from self-pollination versus open-pollination indicated that fruitlet weight, dimensions, and ovule characteristics were significantly inferior in self-pollinated 'Amrapali,' 'Mallika,' and 'Pusa Arunima' compared to their open-pollinated counterparts. However, no significant differences were observed in fruitlet weight and dimensions or ovule characteristics between self-pollination and open-pollination in 'Pusa Surya.' In summary, these findings clearly establish that 'Mallika' and 'Amrapali' are self-incompatible mango cultivars, while 'Pusa Arunima' and 'Pusa Surya' are self-compatible [16].

Maklad [17] research findings highlight the significance of self and cross incompatibility as a critical factor affecting fruit set in various mango cultivars. Mango (*Mangifera indica* L.) holds the distinction of being one of the oldest cultivated trees globally. Some mango cultivars exhibit low productivity due to challenges related to low fruit

setting and/or the premature dropping of immature fruits. In the study, five mango cultivars, namely Alphonse, Ewais, Hindi khassa, Keitt, and Zebda, were employed as potential pollinators for the Langra cultivar, which served as the female parent. The aim was to assess the degree of cross compatibility or incompatibility among these cultivars and to examine the effects of self-pollination. The results of this investigation revealed that Langra cultivar exhibited signs of incompatibility after self-pollination, with microscopic examination showing the presence of numerous callus plugs along the pollen tubes. Among the different combinations, Keitt and Zebda cultivars exhibited a higher number of pollen tubes in Langra styles, reaching the base of the style within four days after pollination. This suggests a high level of cross-compatibility between these two cultivars and Langra. In contrast, Alphonse, Ewais, and Hindi khassa took longer to reach the base of the style, yielding the lowest percentage of pistils with pollen tubes reaching the base seven days after cross-pollination with Langra styles. Furthermore, when Zebda pollens were used for cross-pollination, it resulted in a higher initial number of fruits per panicle (55.93 and 73.25) compared to the other cultivars. However, fruit drop percentages dramatically increased and reached their peak 45 days after self-pollination, particularly when crossed with Alphonse pollens. These findings shed light on the complexities of mango pollination and fruit set, emphasizing the importance of considering cross-compatibility when selecting pollinators for mango cultivars.

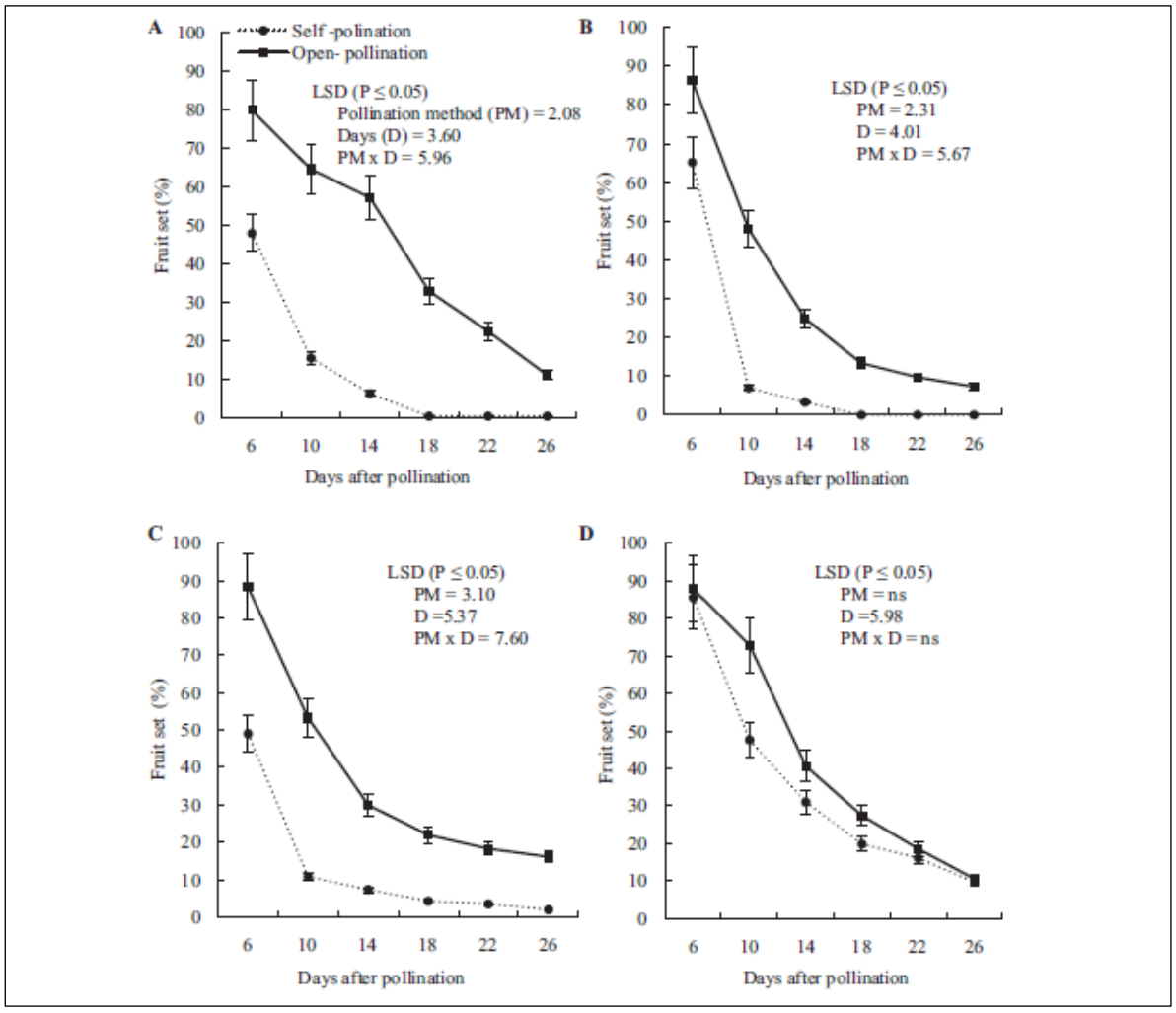

Fig. 1. Fruit set under self- and open-pollination in 'Amrapali' (A), 'Mallika' (B), 'Pusa Arunima' (C) and 'Pusa Surya' (D)

2.2 Plant Genetic Resources

India stands as the world's most diverse center for mango germplasm, boasting over a thousand vegetatively propagated varieties or clones. These mango varieties exhibit a wide range of characteristics, including variations in fruit shape, size, skin color, maturity period, seed size, pulp quality, yield, and fruit-bearing consistency. Singh et al. [10] reported that in the Punjab province of India, the area dedicated to mango (*Mangifera indica* L.) fruit cultivation has significantly declined over time. This decline can be attributed to factors such as deforestation, population pressure, the shift to more financially rewarding crop systems, recurrent cold spells, infrastructure development, increased incidence of pests and diseases, and more. Consequently, a survey was conducted to document the extent of diversity present in the native mango landraces and strains. The study involved the evaluation of twenty-eight elite mango strains that were favored locally for various purposes, including table consumption, sucking, and the preparation of pickles, canning, beverages, and amb leather. This evaluation was based on both physical appearance and chemical attributes. The physico-chemical analysis of fruit samples unveiled a significant level of variability within the indigenous mango population, encompassing various qualitative and quantitative attributes. This diversity not only contributes to biological diversity but also plays a crucial role in ensuring nutritional security and livelihoods. Additionally, it offers valuable resources for future crop improvement efforts [18]. In light of these findings, the study emphasizes the importance of conserving and protecting such biologically rich areas in Punjab, India, to benefit future generations, in alignment with the cultural and environmental values cherished by the Punjabi folklore.

The region has revealed some fascinating mango strains with distinctive characteristics. These strains have acquired local names that reflect their unique features. For instance:

1. **Anda Dusehree:** This mango strain exhibits a flavor and taste reminiscent of the popular Indian table-purpose mango variety 'Dashehari,' but its fruit shape resembles an egg.
2. **Laddu Amb:** This mango strain is known for its distinctive fruit shape.
3. **Gola Ghassipur:** Another mango strain with a unique fruit shape.
4. **Ber Amb:** This strain stands out due to its fruit shape as well.

In Punjabi folklore, these native mango strains are collectively referred to as 'Chhalli' due to their oblong shape and relatively large fruit size, which resembles a small-sized corn cob. Additionally, several of these mango strains display attractive characteristics such as a bright yellow fruit color with a red blush on the shoulders. These strains include Anami Chhalli, Choe Sindhuri, Ghassipur di Chhalli, Laddu Amb, Mahantan di Laltain, and Sindhuri Chusa [19].

The mango strains in the area exhibit a diverse range of fruit colors, spanning from yellowish to light yellow, deep chrome, greenish, spinach green, and dark green. Among these strains, fully colored fruits are locally preferred and referred to as "Arru Amb" and "Pencil Amb." These mangoes are particularly favored for their suitability for consumption by sucking due to their thin and abundant juice content, soft flesh, and fewer coarse fibers. Consequently, these mango varieties command higher prices in the local market. In terms of fruit characteristics, one strain, in particular, stands out. Strain "Jogiya Chhalli," collected from the Government Orchard in Bhunga, boasts the maximum fruit weight at 380.4 grams and the longest fruit length at 12.52 centimeters. Additionally, this strain exhibits a notable percentage distribution of pulp, peel, and stone within the fruit, with pulp accounting for 70.3%, peel for 16.0%, and the stone for 13.7%. In fact, "Jogiya Chhalli" also records the highest fruit pulp weight at 267.5 grams [20].

Several mango strains, including Charan Achari, Gola Desi, and Banta strains No.1, 2, and 3, exhibit characteristics that make them ideal candidates for preservation and utilization in pickle-type mango preparations. These strains possess attributes such as higher juice acidity, a favorable pulp-to-stone ratio, a sour-sweet taste profile, an almost roundish fruit shape, and a medium to abundant fiber content. These qualities make them well-suited for the production of pickled mango products. In a study conducted by Kaur et al. [21], various mango germplasm was evaluated, revealing interesting findings:

1. **Kala Gola** exhibited the maximum tree height.
2. **Chausa** had the widest tree spread.
3. **Chausa** also had the highest fruit weight and pulp-to-stone ratio among the evaluated germplasm.

4. **Dashehari** yielded the highest fruit production, with a remarkable 148.90 kilograms per tree.
5. **Local selection-1** stood out as an early maturing variety with consistent fruit-bearing habits.
6. **Rattaul** was noted for its excellent flavor.

These insights provide valuable information for selecting and utilizing mango varieties for specific purposes, whether it be for pickling, fresh consumption, or other uses.

Table 1. Pulp percentage, pulp stone ratio, TSS, acidity and yield of different genetic resources of mango

S/N	Genetic resources	PP %	P/S ratio	TSS (°brix)	Acidity (%)	TSS/Acid ratio	Yield (kg)
T1	'local Selection-I'	54.16	1.80	13 25	1.33	9.96	112.70
T2	Dashehari	78.56	3.36	17.40	0.30	58.00	148.90
T3	Gob	62.36	3.03	16.85	4.81	3.50	107.84
T4	Langra Banarasi	87.74	7.29	19.95	0.34	58.67	97.30
T5	Langra	79.23	4.54	21.68	1.57	13.81	104.56
T6	Kala Gob	73.66	2.52	16.95	7.86	2.16	97.35
T7	Dharbhanga	73.16	4.56	12.06	0.22	54.82	93.71
T8	Alphonso	72.1	3.11	26.84	0.33	81.33	93.33
T9	Hundel	41.73	2.98	15.88	0.20	79.42	113.31
T10	Malda	65.8	4.03	28.95	0.56	51.70	108.74
T11	Amarpali	63.59	5.82	23 25	0.40	58.12	44.03
T12	Rattaul	64.53	4.58	24.34	0.95	25.62	126.73
T13	Chausa	89.78	8.80	27.08	0.34	79.64	114.00
T14	'Local Selection-II'	84.34	5.43	11.35	0.34	33.82	93.60
	Mean	64.09	4.81	19.70	1.15	46.36	107.46
	C.D	**2.87**	**.93**	**.94**	**0.77**	**0.59**	**2.64**
	Range	41.7-89.78	1.80-8.80	11.35-28.95	0.20-7.86	2.16-81.33	44.03-148.90

PP- Pulp Percentage. P/S- Pulp Stone Ratio. TSS- Total Soluble Solids. RS- Reducing Sugar. TS- Total Sugar.

Table 2. Time of maturity and organolaptic ratio of different genetic recourse of mango

S/N	Genetic resources	Colour of fruit	OR	TM
T1	'local Selection-I'	Yellowish Green 151^{A}	3.0	Ist week of July
T2	Dashehari	Yellowish Green 144 ^{A}	6.6	IInd week of July
T3	Gob	Yellowish Green 152 ^{B}	0.2	IVth week of July
T4	Langra Banarasi	Yellowish Green 144 ^{A}	7.5	IInd week of July
T5	Langra	Yellowish Green 144 ^{B}	6.8	IInd week of July
T6	Kala Gob	Yellowish Green 144^{C}	1.5	IVth week of July
T7	Dharbhanga	Yellowish Green 144^{B}	0.5	IInd week of July
T8	Alphonso	Yellowish Green 153^{B}	8.0	IInd week of July
T9	Hundel	Yellowish Green 151^{A}	7.0	IInd week of July
T10	Malda	Yellowish Green 152^{A}	8.0	IIIrd week of July
T11	Amarpali	Yellowish Green 153^{D}	7.6	IVth week of July
T12	Rattaul	Greenish Yellowish 163^{C}	6.8	IVth week of July
T13	Chausa	Yellowish Green 151^{A}	8.8	IVth week of July
T14	'Local Selection-II'	Yellowish Green 153^{A}	6.0	IIIrd week of July

OR- Organoleptic Rating at 10 Point Scale. TM- Time of Maturity

Dinesh et al. [22] conducted a comprehensive evaluation of seedling diversity, focusing on morphological traits in the Chittoor region of Andhra Pradesh, India. Their study involved both morphological and molecular characterizations of various mango varieties. When analyzing the fruit characteristics, the researchers found significant differences among the varieties concerning various fruit traits. To gain deeper insights into the genetic diversity, molecular characterization was carried out using microsatellite markers. Interestingly, most of the indigenous mango varieties from the Kalepalli region were grouped together in the same cluster. This alignment between morphological and molecular characterizations suggests that the genetic makeup plays a significant role in determining these fruit characteristics. The study's findings underscore the notion that the observed diversity within a particular geographic region can be attributed to the varieties cultivated in that area. Identifying promising seedling varieties with desirable traits not only benefits farmers but also supports the concept of benefit sharing when these varieties are registered. Moreover, it aids in the conservation efforts, known as "on-farm conservation," and can contribute to the improvement of mango crops through breeding and improvement programs. This holistic approach enhances the sustainability and utilization of local mango genetic resources.

Mangoes can be broadly categorized into two main types:

1. **Indian Types:** These mangoes typically have monoembryonic seeds, and they are susceptible to anthracnose, a fungal disease.
2. **Indo-Chinese Types:** These mangoes are characterized by polyembryonic seeds, and they display tolerance to anthracnose.

Breeding methods for mango improvement involve several techniques and strategies, including:

1. **Selection from Open-Pollinated Seedlings:** Natural open pollination results in seedlings with diverse characteristics. Selecting superior individuals from these seedlings is one way to identify desirable traits.
2. **Controlled Pollinations:** This method involves hand pollinating specific flowers on a large number of panicles, ensuring that specific parent plants are involved in the crossbreeding process.
3. **Enclosing Self-Incompatible Parents:** To achieve controlled cross-pollination, self-incompatible male and female parent plants can be enclosed to prevent unwanted pollination, ensuring that the desired genetic material is transferred.
4. **Cross Pollination with Houseflies:** Houseflies can be used as pollinators to facilitate controlled crossbreeding.
5. **Maintaining Hybrid Populations:** Grafting scions (cuttings) from hybrid plants onto established rootstock plants allows for the maintenance of hybrid populations with desirable traits.
6. **Pre-selection of Mango Hybrids:** Before committing to further breeding efforts, pre-selection can be employed to identify and discard undesired material, streamlining the breeding process [23,24].

These breeding methods are crucial for developing new mango cultivars with improved characteristics, including taste, disease resistance, and fruit quality, to meet the diverse needs of consumers and growers.

2.3 Methods of improvement

The techniques employed for the enhancement of mango crops encompass various approaches such as introduction, selection, hybridization, and mutation. A notable instance is the introduction of the Exotic cultivar known as Eldon, which exhibited impressive performance in India. This variety has been officially released for commercial cultivation under the name Pusa Surya by the Indian Agricultural Research Institute, New Delhi, through the Delhi State Seed Sub-Committee. The characteristics of this cultivar include a medium-sized tree canopy, consistent fruit bearing, medium-sized fruit (approximately 240 grams) with a thick red peel on the sun-exposed surface, firm and fiberless pulp, a sweet taste profile (with 18.6% Total Soluble Solids and 0.22% acidity), and suitability for long-distance transportation. Extensive testing is currently underway to evaluate its performance on a national scale. Additionally, various other introduced cultivars have been assessed in India, including Ametista, Carabao, Edward, Extrema, Florigon, Haden, Irwin, Keitt, Kensington, Kent, Sensation, Simmonds X, Tommy Atkins, and more [25].

Table 3. Characteristics of the 8 microsatellite markers with repeat motif, number of alleles, observed Heterozygosity (HO), expected heterozygosity (HE) and polymorphic breeding methods

Loans	Primer (5'-3)	Repeat motif	No. of alleles	Allele size range (bp)	He	Ho	PIC
MilIHR17	F: GCITGCTTCCAACTGAGACC R: GCAAAATGCICGGAGAAGC	$(GT)_{16}GAGT(GA)_{10}$	10	230-269	0.867	0.477	0.841
MilIHR18	F: TCTGACGTCACCICCTITCA R ATACTCGTGCCTCGTCCTGT	$(GT)_{12}$	11	148-193	0.724	0.023	0.693
MilIHR23	F: TCTGACCCAACAAAGAACCA R: TCCTCCTCGTCCTCATCATC	$(GA)_{17}GG(GA)_{6}$	13	117-156	0.693	0.409	0.667
MilIHR26	F: GCGAAAGAGGAGAGTGCAAG R: TCTATAAGTGCCCCCPCACG	$(GA)_{14}GGA(GAA)_{2}$	19	127-171	0.889	0.523	0.869
MilIHR30	F: AGCFAICGCCACAGCAAATC R: GTOWTTCTGGCTGCCAAC	$(CT)_{13}$	11	190-213	0.857	0.674	0.831
MilIHR31	F: TTCTGITAGTGGCGGTGITG R: CACCTCCTCCTCCTCCTCTT	$(GAC)_{6}$	10	207-260	0.752	0.523	0.718
MilIHR34	F: CTGAGITTGGCAAGGGAGAG R: TTGATCCITCACCACCATA	$(GGT)_{9}$ $(GAT)_{5}$	09	203-245	0.771	0.364	0.734
MilIHR36	F: TCTATAAGTGCCCCCFCACG R: ACTGCCACCGTGGAAAGTAG	$(TC)_{17}$	14	210-250	0.834	0.545	0.805

2.4 Hybridization

Hybridization of mango in India was first initiated in 1911 with the objectives of breeding varieties having regular bearing habit, good fruit quality, high yield and resistance to insect pests and diseases.

2.5 Intervarietal Hybridization

Pinto and colleagues [26] engaged in the intervarietal hybridization of mangoes, where they observed that among 2088 mango seedlings initially established in the field, 209 seedlings were singled out for further consideration during the first year of evaluation. From this group of 209 seedlings, 42 were identified as having significant promise, ultimately leading to the release of four of them as distinct mango cultivars:

1. **Alfa** - Hybrid cultivar from the cross 'Mallika' x 'Van Dyke', semi-dwarf and high yielding, regular bearing, fruit 435 g, pink/red peel, firm and medium fiber pulp with good quality (Brix 16%, acidity 0,23%, Brix/Acidity ratio 70), resistant to oidium and moderately resistance to anthracnose, without malformation or pulp soft-nose.
2. **Beta** - A hybrid cultivar known as Selection CPAC 98/86, resulting from the cross between 'Amrapali' and 'Winter', exhibits moderate vigor and high yield potential. While its bearing pattern can be irregular, the fruits it produces weigh approximately 310 grams each. These fruits feature a yellow peel and contain a firm, low-fiber pulp of outstanding quality, suitable for both fresh consumption and processing. The pulp boasts remarkable attributes with a Brix content of 24.8% and acidity at 0.16%. The Brix/acidity ratio falls within the range of 155, indicating a superb balance of sweetness and acidity. Furthermore, this cultivar demonstrates moderate resistance to anthracnose and oidium, making it a suitable choice for cultivation. Importantly, it does not exhibit malformation issues.
3. **Roxa** - A hybrid cultivar resulting from the cross between 'Amrapali' and 'Tommy Atkins' is characterized by moderate vigor and medium yield. It exhibits consistent fruit production with an average fruit weight of 287 grams. The fruits are distinguished by their purple-reddish coloration and possess a very firm and fiberless pulp of exceptional quality, boasting a Brix content of 19-21% and low acidity at 0.12%. The Brix/acidity ratio falls within the range of 158-175, signifying an excellent balance of sweetness and acidity. However, it's worth noting that this cultivar is susceptible to cochineals and displays moderate to low resistance against anthracnose, oidium, and malformation.
4. **Lita** - A hybrid cultivar known as Selection CPAC 136/86, resulting from the cross between 'Amrapali' and 'Tommy Atkins', exhibits robust growth and high yield. It consistently produces fruits weighing 414 grams, characterized by their remarkable firmness and minimal pulp fiber content, offering excellent quality with a Brix content of 18-20% and acidity at 0.20%. The Brix/acidity ratio falls within the range of 90-100, highlighting its exceptional taste balance. Additionally, this cultivar displays moderate resistance to anthracnose, oidium, and malformation.

Among the outstanding hybrid seedling selections, CPAC 165/93 and CPAC 256/94 stand out, both featuring a red-yellowish peel, firm texture, and a remarkably sweet pulp. Notably, the hybrid progeny CPAC 256/94 boasts a high pulp yield ranging from 82-85%, primarily attributed to its thin seed content.

Rajwana and their team [27] successfully created a hybrid mango variety called 'Faiz Kareem' by crossbreeding two commercially established mango cultivars, namely Anwar Ratole and Chaunsa. These investigations aimed to assess and compare the ripening characteristics and overall fruit quality of the newly developed 'Faiz Kareem' hybrid with its parent cultivars under standard ambient conditions (at approximately 28±2°C with a relative humidity of 65-70%). Throughout the ripening process, various physico-chemical attributes were meticulously recorded on a daily basis for up to seven days. These attributes included the percentage of physiological fruit weight loss, fruit softness, visual peel color, titratable acidity, total soluble solids, sugar content, vitamin C concentration, and total carotenoid levels. Interestingly, all three cultivars exhibited a seven-day ripening period under the ambient conditions. However, 'Faiz Kareem' demonstrated superior firmness, suggesting its potential for an extended shelf life. While the highest levels of total sugars (25.88%), total soluble solids (26.75°Brix), and total carotenoids (69.99µg g-1) were found in Chaunsa, 'Faiz Kareem' exhibited lower values

Table 4. Physical characteristics of F1 population of mango

Cross combinations	Tree type	Inflorescence	Bearing Habit	Hermaphodite flower %
Langra x Vanraj [Hybrid-1]	Medium erect	Pink coloured	Regular	45.24
Langra x Vanraj [Off Type-1]	Medium erect	Yellow	Alternate	25.62
Langra x Kesar [Off Type-2]	Medium erect	Yellow	Alternate	23.89
Langra x Kesar [Hybrid-2]	Medium spreading	Golden Yellow	Alternate	54.65
Langra x Swarnarekha [Off Type-3]	Wild type	Yellow	Alternate	24.96
Langra x Swarnarekha [Off type-4]	Wild type	Yellow	Alternate	18.75
Chausa x Vanraj [Hybrid-3]	Medium spreading	Yellow	Alternate	19.67
Chausa x Swarnarekha [Off type-5]	Dwarf	Redish yellow	Alternate	22.82
Chausa x Swarnarekha [Off type-6]	Medium Spreading	Yellow	Alternate	16.25
Dashehari x Kesar [Off type-7]	Dwarf	Deep Yellow	Alternate	19.64
Dashehari x Swarnarekha [Hybrid -4]	Dwarf	Greenish Yellow	Alternate	35.32
[CRD] CD at 5%	--	---	----	5.86

Table 5. Fruit characteristics

Cross combinations	Fruit weight (g)	TSS (°B)	Total Sugar (%)	Plant yield (Kg/plant)
Langra x Vanraj [Hybrid-1]	230.56	19.5	11.42	10.07
Langra x Vanraj [Off Type-1]	200.45	16.3	9.87	4.25
Langra x Kesar [Off Type-2]	212.85	15.7	8.88	5.63
Langra x Kesar [Hybrid-2]	250.12	20.5	1237	12.50
Langra x Swarnarekha [Off Type-3]	152.00	14.8	8.24	5.97
Langra x Swarnarekha [Off type-4]	174.64	12.8	7.99	3.89
Chausa x Vanraj [Hybrid-3]	140.67	11.5	8.88	4.05
Chausa x Swarnarekha [Off type-5]	262.75	11.5	7.45	8.72
Chausa x Swarnarekha [Off type-6]	128.45	11.5	7.41	8.42
Dashehari x Kesar [Off type -7]	205.86	10.31	6.65	7.69
Dashehari x Swarnarekha [Hybrid -4]	188.52	12.25	7.58	6.83
[CRD] CD at 5%	34.08	2.49	1.82	2.61

(23.71%, 25.54°Brix, and 24.60 µg g-1, respectively), which could be advantageous for prolonged storage and appeal to health-conscious consumers.

Additionally, sensory evaluations conducted by a taste panel clearly indicated a strong preference for the hybrid cultivar 'Faiz Kareem,' with Chaunsa and Anwar Ratole following in rank. These findings offer valuable insights into the potential market appeal of 'Faiz Kareem,' both domestically and for export purposes. In a separate study by Jana [28], a varietal improvement program was carried out at ICAR-RCER, Research Centre, Ranchi, India. During this program, three mango cultivars, namely Langra, Dashehai, and Chausa, served as the female plants, while the pollen grains from Swarnarekhan, Kesar, and Vanraj were used as the male parents in diallel crosses. The study's results unveiled that hybrids resulting from the cross between Langra and Vanraj (referred to as Hybrid 1) and Langra and Kesar (referred to as Hybrid 2) exhibited superior characteristics in terms of tree growth, bearing habits, and fruit quality. Among the various hybrids obtained, Hybrid 2 (Langra x Kesar) displayed the highest Total Soluble Solids (TSS) content at 20.50°B and the highest total sugar content at 12.37%, featuring a yellow coloration. It was followed by Hybrid 1 with a TSS of 19.50°B and Hybrid 3 with 11.50°B. Regarding regular fruit bearing, Hybrid 1 exhibited the most promising traits, closely followed by Hybrid 3 (Chausa x Vanraj). Furthermore, in terms of yield potential, Hybrid 2 outperformed the other two hybrids, with 7-year-old plants yielding 12.5 kg of fruit per year.

3. INTERSPECIFIC HYBRIDIZATION

3.1 Resistance Breeding

Numerous diseases have a substantial economic impact on mango production and distribution, with anthracnose, primarily caused by Colletotrichum gloeosporioides Penz, being the most significant. This disease manifests in various forms: as leaf blight on mango flushes and leaves, blossom blight on flower panicles, tree dieback on mature trees, and postharvest rots on ripened fruits. The presence of postharvest anthracnose on fruits leads to notable losses in fruit quality during storage and transportation [29]. At present, the management of this disease relies on a combination of cultural and chemical practices, both in the field and during postharvest handling. However, these control measures do not offer complete efficacy, resulting in substantial reductions in fruit quality and shelf life. While some commercial mango cultivars do display varying degrees of resistance to anthracnose, this resistance is generally weak and can falter under specific environmental, storage, and transportation conditions. The establishment of robust, genetics-based resistance to anthracnose in mangoes would have a profound impact. It would significantly reduce current production costs by diminishing the need for extensive chemical and cultural management practices. Additionally, it would greatly enhance postharvest shelf life and the overall fruit quality that consumers receive.

Bally and colleagues conducted an experiment aimed at screening and breeding for genetic resistance to anthracnose in mango, as documented in their study [30]. The germplasm that underwent screening displayed a broad spectrum of reactions to C. gloeosporioides in both natural and artificially induced assessments. An accession of M. laurina known as 'Lomboc' exhibited promising resistance to artificial inoculation across three seasons when exposed to two virulent isolates of C. gloeosporioides. 'Lomboc' was also utilized as a male parent in hybridization experiments with M. indica.

In a separate study by Ebrahim and colleagues [31], resistance gene analogues (RGAs) in mango against mango malformation were reported. Mango malformation is a significant disease that limits mango cultivation. While some mango cultivars exhibit disease resistance, it is a desirable trait that can be harnessed to develop mango varieties resistant to malformation. RGAs cloned from various plant species have displayed similarities in DNA sequences and structural motifs. This similarity allows for the potential isolation of resistance genes using polymerase chain reaction (PCR) with degenerate oligonucleotide primers designed from highly conserved regions of the nucleotide binding site (NBS). In their study, eight combinations of oligonucleotide primers were employed, designed based on the P-loop and hydrophobic domains of conserved NBS-leucine rich repeat (LRR) protein sequences. These primers were used to amplify resistance gene analogues (RGAs) in eight mango cultivars and hybrids that

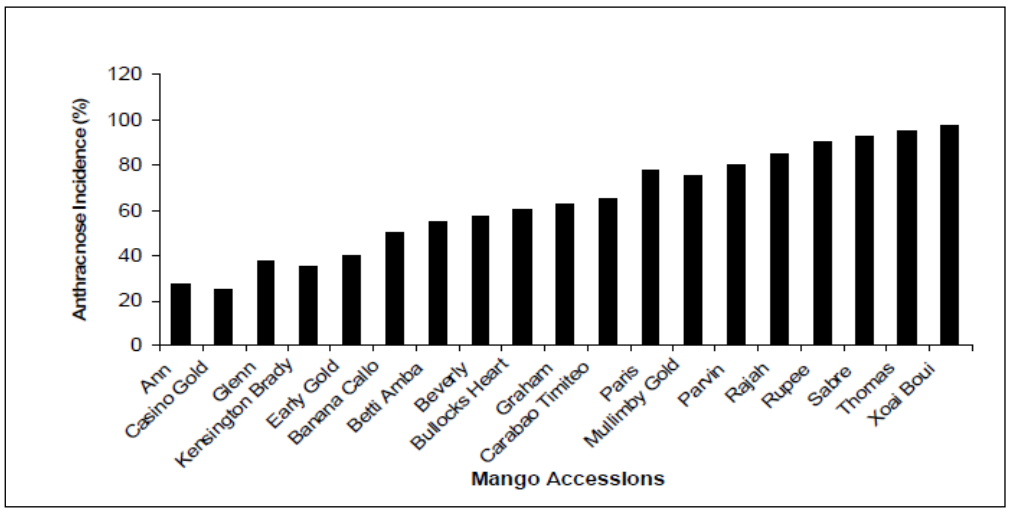

Fig. 2. Disease incidence of anthracnose from natural fruit infections on mango accessions screened during 2008

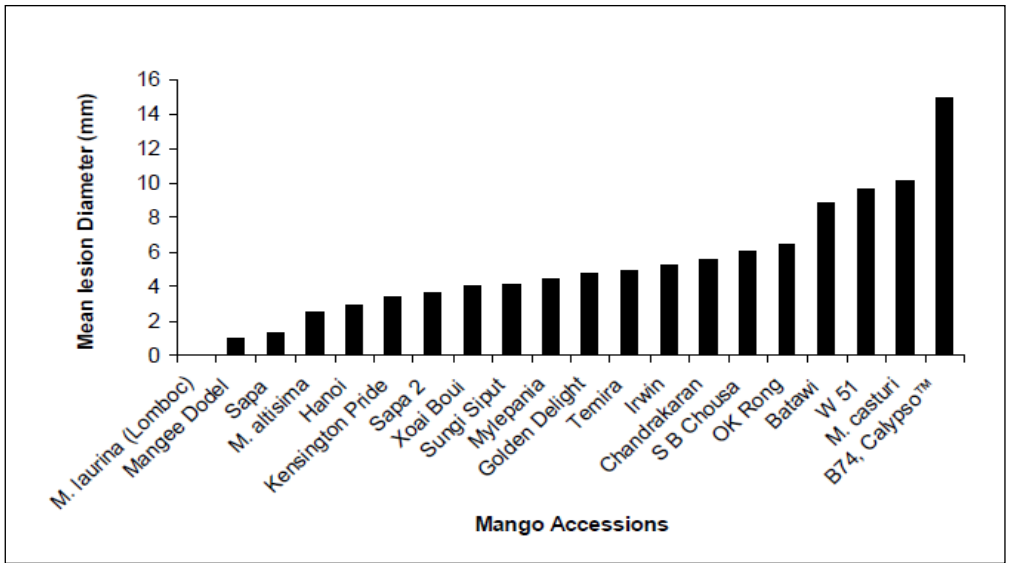

Fig. 3. Disease severity of anthracnose on fruit artificially inoculated with *Colletotrichum gloeosporioides during 2007/2008*

demonstrated varying degrees of resistance to mango malformation disease. A single band of approximately 500 bp was consistently obtained from all mango cultivars using the s2+as2 primer combination. The RGAs isolated from mango exhibited a 73% similarity with RGAs found in existing databases, confirming their isolation from mango. This obtained sequence can serve as a basis for isolating full-length R-genes. In conclusion, PCR amplification of resistance gene analogues based on degenerate primer combinations from conserved motifs of NBS-LRR resistance genes holds promise for identifying and isolating resistance genes in mango against mango malformation and other diseases. Further research is necessary to fully isolate these resistance genes from mango cultivars resistant to malformation.

4. BIOTECHNOLOGY AND MANGO IMPROVEMENT

Over the last twenty years, there has been a scarcity of newly developed mango cultivars through traditional breeding methods. The substantial requirements for a successful breeding program, such as substantial investments in land, time, genetic resources, and more, have constrained the scope, accomplishments, and the quantity of mango

breeding initiatives [32,33]. However, genetic engineering, which emerged as an alternative approach for enhancing mango production just a little over a decade ago, provides a sustainable avenue for addressing specific essential breeding objectives.

4.1 The Fundamental Elements of Mango Genetic Engineering Encompass

1. The development of efficient somatic embryogenesis and successful plant regeneration from elite, typically nucellar, material.
2. The induction of random mutations within embryogenic cultures and the selection for resistance to a specific selective agent.
3. The process of transforming mango plants with a gene responsible for a desired horticultural trait.

4.2 The Key Components of Mango Genetic Engineering Comprise

1. Establishing efficient somatic embryogenesis and successful plant regeneration from elite material, often nucellar in origin.
2. Inducing random mutations within embryogenic cultures and subjecting them to selection for resistance to a specific selective agent.
3. Transforming mango plants by introducing a gene that controls a desirable horticultural trait.

Based on both past and ongoing research, it is likely that specific breeding priorities can be effectively addressed using different techniques:

1. Mutation breeding can be employed to address priorities such as enhancing resistance to abiotic soil stress (e.g., drought, salinity) and providing resistance to certain diseases. This approach leverages induced mutations to create genetic variation and select for desired traits.
2. Genetic transformation techniques offer the potential to address breeding priorities related to the control of fruit ripening, achieving seedlessness, and conferring resistance to specific diseases. Genetic transformation involves the introduction of specific genes that govern these traits, enabling precise control over the desired characteristics in mango plants.

Studies across various research centers worldwide are actively engaged in a range of biotechnological approaches to advance mango cultivation and address several challenges [34]. These approaches include in vitro culture and selection, micropropagation, embryo rescue, genetic transformation, marker-assisted characterization, and DNA fingerprinting, among others. In the realm of in vitro culture, researchers have successfully achieved somatic embryogenesis for various mango genotypes. The nucellus, excised from immature fruit, has proven to be a suitable explant for initiating embryogenic cultures. While high-frequency somatic embryogenesis has been achieved in some genotypes, certain abnormalities can arise during somatic embryo germination. Embryo rescue from young and dropped fruit can enhance hybridization success, particularly in situations with a limited flowering season. Additionally, protocols for protoplast culture and regeneration have been developed. However, micropropagation of mango has not attained the same commercial success as in other fruit crops like pineapple, banana, and strawberry. This is due to challenges such as latent microbial infections, excessive polyphenol exudation, and early explant necrosis, among others. Biotechnological methods hold promise for addressing these issues and improving mango production.

Molecular methods are also playing a crucial role in characterizing mango cultivars, understanding the regulation and expression of important traits, and more. The primary challenge facing mango production is the scarcity of superior cultivars. This is attributed to the complexities of conventional mango breeding, including factors such as limited seed production, intricate flower structures, excessive fruit drop, lengthy juvenility, high heterozygosity, and polyembryony in some cultivars. Most existing mango cultivars have been selected from open-pollinated seedling populations. Protoplast fusion and somatic hybridization techniques offer a means to overcome conventional breeding barriers by directly transferring cytoplasmic and nuclear genomes into plant cells [35]. Somatic hybridization, in particular, holds the potential to introduce desirable traits, such as tolerance to biotic and abiotic stresses, from mango cultivars and wild species into mango rootstocks, thereby enhancing mango cultivation.

In-Vitro **Culture:** In vitro selection techniques hold significant promise for identifying mango

varieties that exhibit favorable mutations or variations resulting from somaclonal variation. Researchers have developed a range of regeneration protocols, including callus induction, somatic embryogenesis, and organogenesis. These protocols involve various explants such as cotyledons, nucellus tissues, leaf disks, and shoot tips of mango plants. Notably, somatic embryos have been successfully generated from nucellus tissues of young mango fruits. However, the critical step lies in the standardization of culture media for the maturation and subsequent germination of these somatic embryos, a process that requires substantial attention and refinement [36].

Somatic Embryogenesis: In a study conducted by Tomar and colleagues [37], twenty mango cultivars (*Mangifera indica* Linn) obtained from the Gir region of Saurashtra were examined using ISSR markers. Out of the 50 primers initially screened, 21 primers were selected due to their ability to produce consistent and polymorphic DNA amplification patterns. These 21 selected primers were then utilized to create a DNA fingerprinting map for distinguishing between mango genotypes. The banding patterns generated by these 21 selected primers allowed for the differentiation of all the tested mango cultivars in the study, except for Jamadar and Kesar. This finding indicated that ISSR-PCR proved to be an effective method for identifying and distinguishing mango cultivars based on their genetic profiles. Using the data obtained from 125 selected bands, the Gir mango landraces were categorized into three major groups through UPGMA (Unweighted Pair Group Method with Arithmetic Mean) analysis. The first group included 'Kaju' and 'Khodi,' the second group consisted of 'Dudh Pendo,' 'Sopari,' 'Jamadar,' 'Kesar,' and 'Ashadhiya,' while the third cluster was composed of 'Agargato,' 'Amir Pasand,' 'Pethal,' 'Gajariyo,' 'Chhappaniyo,' 'Alphanso,' 'Neelum,' 'Jamrukhiyo,' 'Kavasji Patel,' 'Giriraj,' 'Amrutiyo,' 'Dasheri,' and 'Deshi.' This clustering revealed that certain Gir mango landraces shared a close genetic relationship with each other, while others were notably distinct from the rest of the landraces.

In a study conducted by Shukla et al. [38], research focused on nucellar embryogenesis and plantlet regeneration in both monoembryonic and polyembryonic mango (*Mangifera indica* L.) cultivars. Nucellar tissues from immature mango fruits of monoembryonic cultivars, namely Alphonso, Amrapali, Dashehari, and Zafran, as well as polyembryonic cultivars Carabao and Turpentine, were utilized as explants to initiate somatic embryogenesis for plantlet production. For the culture media, a standard basal medium consisting of Gamborg's B5 macronutrients, Murashige and Skoog micronutrients, an iron source, vitamins, and organics was employed at various stages of somatic embryo development and regeneration. The results revealed that different induction media led to the highest percentages of primary somatic embryos for specific cultivars. For instance, induction medium 2, containing 2 mg/l 2,4-Dichlorophenoxyacetic acid and 0.5 mg/l 6-Benzylaminopurine, induced the highest percentage of primary somatic embryos for Alphonso (22.08%). In contrast, induction medium 3, with 1 mg/l 2,4-Dichlorophenoxyacetic acid and 60 gm/l sucrose, and induction medium 1, containing 1 mg/l 2,4-Dichlorophenoxyacetic acid and 0.25 mg/l 6-Benzylaminopurine, induced the highest percentages of primary somatic embryos in Carabao (29.17%) and Turpentine (42.71%), respectively.

Subsequently, the maximum somatic embryo germination rates were achieved under different germination media conditions. For Alphonso (7.34%) and Turpentine (3.34%), germination medium 2 containing 0.1 mg/l Indole-3-acetic acid and 0.5 mg/l Gibberellic acid proved effective. In contrast, for Carabao (18.59%), germination medium 1, which did not contain any plant growth regulators, yielded the best results. Furthermore, the germinated plantlets exhibited robust survival rates in ex-vitro conditions after four months of transfer to a greenhouse. The survival rate reached 66.66% for Alphonso, 26.68% for Carabao, and 49.16% for Turpentine, indicating the successful regeneration of mango plantlets through somatic embryogenesis.

Genetic Mapping: In a study conducted by Surapaneni et al. [39], a genetic analysis was performed on 90 mango genotypes, which included various types such as juicy, table, dual-purpose, and pickle mangoes, originating from different regions of Andhra Pradesh, India. The analysis utilized 143 mango-specific microsatellite markers, including 34 new mango-specific microsatellite loci that were isolated during the study by constructing a genomic library enriched for (CA)n and (TG)n repeats. Characterizing the 90 mango genotypes revealed the presence of 301 alleles from 106 polymorphic loci, with an average of 2.87 alleles per locus and a polymorphism information content (PIC) of

Table 6. Hardening and ex-vitro survival of tissue culture raised mango plants

Cultivars	Batch No.	No. of plants transferred to green house for hardening	No. of plants survived after 1 month of transfer	No. of plants survived after 3 months of transfer	% plants survived after 3 months of transfer	Mean % survival after 3 months of transfer
Alphonso	Batch 1	12	7	7	58.33	
	Batch 2	8	5	4	88.68	88.68
	Batch 3	8	8	8	75.00	
Carabao	Batch 1	28	2	2	7.14	
	Batch 2	18	7	5	31.25	28.88
	Batch 3	12	8	5	41.68	
Turpentine	Batch 1	8	5	3	37.50	
	Batch 2	8	5	3	50.00	49.18
	Batch 3	5	4	3	80.00	

0.67. The UPGMA (Unweighted Pair Group Method with Arithmetic Mean) cluster analysis organized all the genotypes into two primary groups, exhibiting a genetic similarity range spanning from 47% to 88%. Interestingly, when grouping the genotypes based on their utility types (juicy, table, dual-purpose, pickle), such categorization was observed only at the sub-cluster level. A study of population structure, conducted using model-based STRUCTURE analysis, revealed the presence of four gene pools within the germplasm. The overall Fst value of 0.11 suggested that genetic differentiation between the populations was relatively low. An analysis of molecular variance indicated that the majority of the genetic variation was within individual genotypes (62.25%). This molecular marker-based assessment of genetic diversity highlights that the studied germplasm, encompassing diverse varieties of mangoes, represents a valuable genetic resource. It holds significant potential for future breeding programs and association mapping efforts aimed at identifying new and novel alleles that can contribute to mango improvement and breeding efforts.

Bajpai et al. [40] studied the molecular and morphological diversity of locally grown non-commercial (heirloom) mango varieties in North India was examined. The study included a total of 37 mango types, consisting of 27 heirloom varieties from the Malihabad region and 10 commercial varieties cultivated in North and Eastern India. To assess diversity, the researchers used SSR (Simple Sequence Repeat) markers, which individually amplified 2-13 alleles, resulting in a cumulative amplification of 124 alleles. These alleles were then analyzed for allelic diversity, and the genetic dissimilarity among the varieties ranged from 0.035 to 0.892. Based on this genetic dissimilarity, the varieties were grouped into three major clusters.vThe results of this study highlighted that the majority of unique heirloom mangoes from the Malihabad region were distinct from those found in the eastern part of the country. Notably, Dashehari, a commercial variety from Malihabad, did not cluster with the heirloom varieties, indicating its genetic uniqueness or distinctiveness from these heirloom mangoes.

In a study conducted by Ravishankar et al. [41], the focus was on the development and characterization of microsatellite loci (SSR markers) from mango. They characterized twenty sequence-tagged microsatellite site loci using the M13-tailed PCR technique. All twenty microsatellite loci were found to be efficient in discriminating and identifying the 20 diverse mango cultivars utilized in the study. The genetic analysis of these loci revealed several important parameters:

1. Expected heterozygosity values ranged from 0.350 to 0.850, with a mean of 0.505. This indicates the degree of genetic diversity within the studied cultivars.
2. Polymorphic information content (PIC) values varied from 0.624 to 0.938, with a mean PIC of 0.860. PIC is a measure of the informativeness of a genetic marker, reflecting its ability to distinguish between different alleles.
3. The probability of identity (PI) values ranged from 0.012 to 0.182, with a mean PI of 0.050. PI measures the likelihood of two individuals having the same genetic profile based on the marker.

Notably, the total PI value was extremely low at 1.06 x 10^-28, indicating a very low probability of two individuals having identical genetic profiles based on these microsatellite markers. These novel SSR markers have significant potential for various applications in genetic studies, including cultivar identification, linkage map development, association studies, and assessments of genetic diversity and relatedness in mango cultivars.

5. CONCLUSION

Mango breeding is thoroughly covered in the current review. Mango breeding has faced several challenges over the years, primarily stemming from limited knowledge regarding the inheritance of specific traits, the presence of high levels of heterozygosity in the cultivars, and a relatively low number of successful hybrid progenies resulting from crossbreeding efforts. The development of genetic markers has significantly decreased uncertainties in mango breeding and enhanced hybrid population management.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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