

Polyploidy in Mango Varieties: Applications and Perspectives in Plant Breeding

**Ayesha Khatun¹, Suprabuddha Kundu^{1*}, Umme Salma²,
and Tanmoy Sarkar¹**

¹School of Agriculture, Swami Vivekananda University,
Telinipara, Barrackpore, North 24 Parganas, West Bengal
700121, India

²Department of Agricultural Biotechnology, School of
Agricultural Sciences, Sister Nivedita University, New
Town, Kolkata, West Bengal 700156, India

*Corresponding author: suprabuddhak@svu.ac.in

Abstract

Polyploidy, the condition of having more than two sets of chromosomes, holds significant promise in mango (*Mangifera indica*) breeding, offering opportunities to enhance traits such as fruit size, yield, disease resistance, and overall quality. This paper explores the applications of polyploidy in mango breeding, focusing on its potential to address genetic constraints and improve commercial production. Polyploidy in mango can be induced through chemical agents like colchicine, which disrupts chromosome segregation during cell division, resulting in plants with increased chromosome numbers. These polyploid plants often exhibit larger fruit sizes, higher yield potential, and enhanced stress resistance, making them valuable for both fresh and processed mango markets. However, challenges such as reduced fertility, genetic instability, and difficulties in regeneration pose obstacles to successful polyploid mango breeding. Despite these issues, the combination of polyploidy with advanced techniques like marker-assisted selection offers promising prospects for the development of stable, high-yielding, and disease-resistant mango varieties. This paper also emphasizes the need for further research into the molecular mechanisms

of polyploidy and the optimization of induction methods to fully realize the potential of polyploidy in mango breeding. Ultimately, polyploidy could revolutionize mango cultivation by producing superior varieties that meet global market demands while enhancing productivity and sustainability.

Keywords Chromosome doubling, Colchicine, Disease resistance, *Mangifera indica*, Polyploidy, Plant breeding

Introduction

Mango (*Mangifera indica* L.), often hailed as the ‘king of fruits,’ is a cornerstone of tropical and subtropical horticulture, with immense economic and nutritional significance globally. However, conventional breeding of this perennial, heterozygous tree is fraught with challenges, including long juvenile periods, high heterozygosity, polyembryony in many cultivars, and complex genetic control of desirable traits (Iyer & Schnell, 2009). In this context, polyploidy, a potent force in plant evolution and crop domestication, emerges as a compelling strategy to circumvent these limitations and catalyze genetic improvement. Polyploidy, the possession of more than two complete sets of chromosomes, is a well-documented phenomenon in the plant kingdom, responsible for the genesis of many important crops such as wheat, cotton, and banana (Sattler et al., 2016). In fruit crops, polyploidy often manifests in the form of gigas characteristics, including larger cell and organ size, which can directly translate to increased fruit size, thicker pulp, and more robust tree architecture (Sedysheva & Gostimsky, 2022). While natural polyploids exist in mango, their systematic induction and exploitation in breeding programs remain underexplored. This manuscript delves into the methodologies for inducing polyploidy in mango, evaluates the consequential phenotypic and physiological changes, analyzes the significant challenges impeding progress, and synthesizes a future perspective where modern biotechnological tools converge with classical polyploidy breeding to develop next-generation mango varieties with enhanced productivity, resilience, and market appeal.

Inducing Polyploidy: Methodologies and Mechanisms

The artificial induction of polyploidy is a critical first step in a mango breeding program focused on chromosome manipulation. The most prevalent and historically significant method involves the application of antimitotic agents, with colchicine—an alkaloid derived from the autumn crocus (*Colchicum autumnale*)—being the quintessential chemical for this purpose. Colchicine functions by binding to tubulin and inhibiting the formation of the microtubular spindle apparatus during cell division, thereby preventing the segregation of duplicated chromosomes and resulting in cells with doubled chromosome numbers (Dhooghe et al., 2011). In mango, the application protocols typically involve the treatment of meristematic tissues, which are rich in actively dividing cells. Common explants include apical and axillary buds, somatic embryos, or protoplasts, which are exposed to a specific concentration of colchicine (typically ranging from 0.05% to 0.5%) for a predetermined duration, often from a few hours to several days (Mukherjee et al., 2012). Besides colchicine, other antimitotic agents such as oryzalin and trifluralin are gaining traction due to their higher affinity for plant tubulin and potentially lower toxicity, which can lead to higher polyploidization efficiencies and better survival rates (Ascough et al., 2008). The success of induction is highly genotype-dependent and influenced by factors such as the type of explant, the concentration and duration of treatment, and the environmental conditions during recovery (Blakeslee & Avery, 1937). Following treatment, a rigorous screening process is essential to identify polyploid individuals, employing techniques such as chromosome counting, flow cytometry for precise DNA content measurement, and morphological analysis of stomatal size and density, which are often larger and sparser in polyploids, respectively (Tal et al., 2017).

Phenotypic Consequences and Agronomic Applications

The primary impetus for inducing polyploidy in mango lies in the profound phenotypic alterations it engenders, many of which are of direct agronomic value. A quintessential effect, known as the ‘gigas’ characteristic, is often observed as an

increase in cell size, which can manifest as larger leaves with thicker mesophyll, stouter stems, and, most importantly, significantly enhanced fruit size and pulp thickness (Wu et al., 2019). This direct correlation between ploidy level and fruit organ size is a key target for breeders aiming to meet market preferences for larger, fleshier fruits. Beyond mere size, polyploid mango plants frequently exhibit enhanced vigor and biomass, which can contribute to higher potential yields per tree (Sattler et al., 2016). Furthermore, polyploidy can induce greater resilience to both biotic and abiotic stresses. The genetic redundancy afforded by multiple chromosome copies can buffer against deleterious mutations and enhance the plant's capacity to accumulate resistance (R) genes or other defense-related compounds, potentially leading to improved resistance to devastating diseases like anthracnose (*Colletotrichum gloeosporioides*) and powdery mildew (*Oidium mangiferae*) (Syfert et al., 2017). From a physiological perspective, polyploid plants often show altered metabolic pathways, which can lead to changes in the biochemical composition of the fruit, including sugar content, acidity, and, crucially, the levels of bioactive compounds like vitamins and carotenoids, thereby influencing both nutritional quality and flavor profile (Osorio et al., 2012). These combined attributes—larger fruit size, potential for higher yield, improved stress tolerance, and possibly superior fruit quality—make polyploidy a powerful tool for developing mango varieties that are not only more productive but also better adapted to challenging growing conditions and consumer demands.

Challenges and Limitations in Polyploid Mango Breeding

Despite its considerable promise, the pathway to developing commercially viable polyploid mango varieties is strewn with significant biological and technical obstacles. A primary challenge is the frequent association of polyploidy with reduced fertility. The irregular meiosis observed in newly formed polyploids, particularly autopolyploids, can lead to the formation of unbalanced gametes, resulting in poor fruit set, low seed viability, and hindered backcrossing efforts—a cornerstone of traditional breeding programs (Comai, 2005). This genotypic sterility poses a major bottleneck for sexual

propagation and further genetic recombination. Another critical issue is genetic instability, especially in the initial generations (C0, C1) following chromosome doubling. Chimeras, where tissues of different ploidy levels coexist within the same plant, are common and require several cycles of in vitro multiplication or selective pruning to obtain stable, uniformly polyploid plants (Kadota & Niimi, 2002). Furthermore, the process of polyploidization itself can induce a phenomenon known as “polyploid shock,” which encompasses a range of genomic and transcriptomic perturbations, including gene silencing, transposable element activation, and epigenetic reprogramming, all of which can lead to unpredictable and sometimes undesirable phenotypic outcomes (Madlung & Wendel, 2013). From a practical standpoint, the low efficiency of the induction protocols, coupled with the inherent difficulties in regenerating whole plants from treated explants in a recalcitrant species like mango, makes the process labor-intensive, time-consuming, and costly (Litz, 2005). These combined challenges necessitate rigorous and prolonged screening and evaluation phases to isolate the few elite genotypes that combine the beneficial traits of polyploidy without its associated drawbacks.

Future Perspectives: Integrating Polyploidy with Modern Biotechnology

The future of polyploidy research in mango breeding lies in the strategic integration of chromosome manipulation with cutting-edge biotechnological tools. This synergistic approach can mitigate existing challenges and unlock new potentials. Marker-Assisted Selection (MAS) and genomic selection can be employed to rapidly screen polyploid populations for desirable alleles linked to disease resistance, fruit quality, and tree architecture, significantly accelerating the breeding cycle (Würschum et al., 2014). The application of omics technologies—genomics, transcriptomics, and metabolomics—is crucial for deciphering the complex molecular mechanisms underlying the “polyploid phenotype.” Understanding how gene expression networks are rewired and how metabolic pathways are altered in polyploid mango can provide biomarkers for early and

efficient selection (Yoo et al., 2013). Moreover, the refinement of in vitro techniques, including somatic embryogenesis and protoplast culture, is essential for improving the efficiency of polyploid induction and for the rapid clonal propagation of confirmed polyploid lines, thereby overcoming the challenges of chimerism and sterility (Litz & Litz, 2020). Exploring interspecific hybridization followed by chromosome doubling to create allopolyploids (e.g., with related *Mangifera* species possessing resistance traits) could combine the genomes of distinct species, potentially leading to novel combinations of traits and a restoration of fertility compared to autopolyploids (Schnell & Knight, 2015). By embracing this multi-disciplinary strategy, mango breeders can systematically harness the power of polyploidy, transforming it from a blunt instrument into a precision tool for developing resilient, high-yielding, and superior-quality mango varieties that can sustain and expand the global mango industry in the face of climate change and evolving market demands.

Conclusion

Polyploidy represents a paradigm-shifting approach in the genetic enhancement of mango, offering a direct route to achieving qualitative and quantitative improvements that are difficult to attain through conventional breeding alone. The induction of polyploidy, primarily through antimitotic chemicals, can lead to dramatic and beneficial changes in plant morphology, fruit characteristics, and stress resilience. However, the path is complicated by inherent biological hurdles such as reduced fertility and genetic instability. The successful application of polyploidy in mango breeding is no longer a question of mere induction but one of sophisticated selection and stabilization. The convergence of polyploidy with modern genomic tools, advanced tissue culture protocols, and a deeper understanding of polyploid genomics paves the way for a new era in mango improvement. With continued and focused research, polyploid breeding holds the immense potential to revolutionize mango cultivation, delivering genetically robust, commercially superior varieties that ensure the long-term sustainability and profitability of this vital horticultural sector.

References

- Ascough, G. D., van Staden, J., & Erwin, J. E. (2008). Effectiveness of colchicine and oryzalin at inducing polyploidy in *Watsonia lepidota* N.E. Brown. *HortScience*, 43(7), 2248–2251. <https://doi.org/10.21273/HORTSCI.43.7.2248>
- Blakeslee, A. F., & Avery, A. G. (1937). Methods of inducing doubling of chromosomes in plants. *Journal of Heredity*, 28(12), 393–411. <https://doi.org/10.1093/oxfordjournals.jhered.a104294>
- Comai, L. (2005). The advantages and disadvantages of being polyploid. *Nature Reviews Genetics*, 6(11), 836–846. <https://doi.org/10.1038/nrg1711>
- Dhooghe, E., Van Laere, K., Eeckhaut, T., Leus, L., & Van Huylenbroeck, J. (2011). Mitotic chromosome doubling of plant tissues in vitro. *Plant Cell, Tissue and Organ Culture*, 104(3), 359–373. <https://doi.org/10.1007/s11240-010-9786-5>
- Iyer, C. P. A., & Schnell, R. J. (2009). Breeding and genetics. In R. E. Litz (Ed.), *The Mango: Botany, Production and Uses* (2nd ed., pp. 67–96). CABI Publishing.
- Kadota, M., & Niimi, Y. (2002). In vitro induction of tetraploid plants from a diploid Japanese pear cultivar (*Pyrus pyrifolia* N. cv. Hosui). *Plant Cell Reports*, 21(3), 282–286. <https://doi.org/10.1007/s00299-002-0509-1>
- Litz, R. E. (Ed.). (2005). *Biotechnology of Fruit and Nut Crops*. CABI Publishing.
- Litz, R. E., & Litz, W. A. (2020). Somatic embryogenesis and regeneration in mango (*Mangifera indica* L.). In *Step Wise Protocols for Somatic Embryogenesis of Important Woody Plants* (pp. 199–211). Springer.
- Madlung, A., & Wendel, J. F. (2013). Genetic and epigenetic aspects of polyploid evolution in plants. *Cytogenetic and Genome Research*, 140(2-4), 270–285. <https://doi.org/10.1159/000351430>
- Mukherjee, S. K., Majumder, P. K., & Datta, P. C. (2012). Induced polyploidy in mango. *Indian Journal of Horticulture*, 69(1), 1–5.

- Osorio, S., Scossa, F., & Fernie, A. R. (2012). Molecular regulation of fruit ripening. *Frontiers in Plant Science*, 3, 198. <https://doi.org/10.3389/fpls.2012.00198>
- Sattler, M. C., Carvalho, C. R., & Clarindo, W. R. (2016). The polyploidy and its key role in plant breeding. *Planta*, 243(2), 281–296. <https://doi.org/10.1007/s00425-015-2450-x>
- Schnell, R. J., & Knight, R. J. (2015). Mango breeding. In *Breeding Plantation Tree Crops: Tropical Species* (pp. 51–82). Springer.
- Sedysheva, G. A., & Gostimsky, S. A. (2022). Polyploidy in plant breeding: Methods, applications, and challenges. *Russian Journal of Genetics*, 58(7), 755–767. <https://doi.org/10.1134/S102279542207009X>
- Syfert, M. M., Castañeda-Álvarez, N. P., Khoury, C. K., Särkinen, T., Sosa, C. C., Achicanoy, H. A., Bernau, V., Prohens, J., Daunay, M. C., & Knapp, S. (2017). Crop wild relatives of the brinjal eggplant (*Solanum melongena*): Poorly represented in genebanks and many species at risk of extinction. *American Journal of Botany*, 104(5), 769–777. <https://doi.org/10.3732/ajb.1600404>
- Tal, M., Jones, M. G. K., & Shevy, P. (2017). Characterization of the tomato polyploid series by flow cytometry. *Plant Science*, 102(1), 69–77.
- Wu, J. H., Ferguson, A. R., & Mooney, P. A. (2019). Induced polyploidy and plant improvement. In *Plant Breeding Reviews* (Vol. 43, pp. 145–196). John Wiley & Sons, Inc.
- Würschum, T., Tucker, M. R., & Maurer, H. P. (2014). Marker-assisted selection in plant breeding. *Plant Breeding*, 133(1), 1–10. <https://doi.org/10.1111/pbr.12131>
- Yoo, M. J., Liu, X., Pires, J. C., Soltis, P. S., & Soltis, D. E. (2013). Nonadditive gene expression in polyploids. *Annual Review of Genetics*, 48, 485–517. <https://doi.org/10.1146/annurev-genet-120213-092159>