

ISSN Print: 2617-4693 ISSN Online: 2617-4707 IJABR 2024; 8(3): 368-372 www.biochemjournal.com Received: 02-12-2023 Accepted: 03-01-2024

Abhimanyu Patel

Guest Teacher, Floriculture and landscaping College of Horticulture and Research Station Kunkuri Jashpur MGUVV Raipur, Chhattisgarh, India

Johnson Lakra

Assistant Professor, Department of Fruit Sciences, MGUVV, Sankra, Patan, Durg, Chhattisgarh, India

Shashi Kant Ekka

Research Scholar, Department of Horticulture, Fruit sciences, SHUATS, Prayagraj, Uttar Pradesh, India

Sunny Sharma

Assistant Professor, School of Agriculture, Lovely Professional University, Phagwara, Punjab, India

Reena Kujur

Research Scholar, Department of Biological Sciences, SHUATS, Prayagraj, Uttar Pradesh, India

Rajiv Kumar Kurrey

Lecturer, Department of Agricultural processing and Food engineering, College of Horticulture and Research Station, MGUVV, Kunkuri, Jashpur, Chhattisgarh, India

Ravi Kumar

Post-Graduate, Department of Horticulture, SHUATS, Prayagraj, Uttar Pradesh, India

Corresponding Author:

Abhimanyu Patel Guest Teacher, Floriculture and landscaping College of Horticulture and Research Station Kunkuri Jashpur MGUVV Raipur, Chhattisgarh, India

Ornamental plant breeding is tools for new generation

Abhimanyu Patel, Johnson Lakra, Shashi Kant Ekka, Sunny Sharma, Reena Kujur, Rajiv Kumar Kurrey and Ravi Kumar

DOI: https://doi.org/10.33545/26174693.2024.v8.i3e.742

Abstract

Plant breeding for crops and ornamentals has grown in importance over the past century. Mendel's theories about the inheritance of characteristics established the groundwork for contemporary genetics. While chromosomal duplication, mutation breeding, and intra- and interspecific cross-breeding remain the mainstays of ornamental plant breeding, plant breeding has advanced dramatically since Mendel's day. Advanced accuracy breeding and selection towards more challenging to measure or quantify characteristics are now possible because to new genomic techniques. The breeding of ornamental plants nowadays is a challenging endeavor with constantly evolving and new obstacles. Collaborations between research and industry will be necessary to apply current technology to small-scale crops.

Keywords: Genomics, ornamental plants, interspecific hybridization, molecular markers

Introduction

It was during the 17th and 18th centuries that plant hunters, botanists or adventurers brought new plants to Europe from Asia and the Americas that many of today's popular ornamental plants were bred and selected. A new era of plant breeding was initiated by Mendel's discovery of how traits are passed from generation to generation. In addition to crossbreeding and selecting seedlings combining the desired characteristics of both parents, ornamental breeding was gradually applied. It became an industrial activity in private companies starting in the mid-1800s, resulting in the wide variety of ornamental species and cultivars Long et al. Approximately 85,000 to 99,000 ornamental plant species exist worldwide, according to (2018) extrapolations. It determines the huge potential of natural differences and germplasm in addition to the requirement to conserve genetic resources of ornamental plants for breeding and future growth. These facts include the wild relations of educated plants. Reasonable benefit-sharing will encourage the development of conservation of ornamental plants and will conserve imperative genetic variation for future demands and challenges. In recent decades legal organizations as The Convention on Biological Diversity (CBD), the Convention on International Trade in Threatened Species of Wild Fauna and Flora (CITES) and the Nagoya Protocol were recognized to govern the conservation and supportable use of plants.

Intra- and interspecific hybridization

The majority of ornamental species have high levels of heterozygosity, which generates enough variation in F1 populations to allow for selection of new valuable cultivars. Selection of novel phenotypes in progenies from controlled intraspecific crosses or even in open pollination seedling inhabitants has been, and still is, a successful method in various ornamental crops. The limited genetic variation in crossing parents makes it problematic to achieve truly advanced breakthroughs. New crossing mixtures between changed species (interspecific hybridization) in ornamental crops is therefore the most suitable tool to increase variation and represents an excellent way to present new stimulating genes into a breeding gene pool (Huylenbroeck *et al.*, 2020) ^[28]. In rose, only around 8 to 15 species contributed to the original germplasm of the modern cultivars (Leus *et al.*, 2018) ^[29]. In many of the most popular ornamental crops, interspecific hybridization forms the substance of the present variety. Chrysanthemum appeared from natural hybridizations between dissimilar wild species, important to a wide-range cultigens complex (Spaargaren and van Geest, 2018) ^[16].

This has led to a significant shift in the produced assortment (Van Tuyl *et al.*, 2018) ^[30]. Asexual propagation kinds it likely to propagate new types arising from interspecific hybridization even if they are sterile. Further examples are described in Marantaceae (Van Huylenbroeck *et al*, 2018) ^[19] *Asclepias* sp. (Lewis *et al.*, 2021) ^[12], *Pavonia* (Yue and Ruter, 2021) ^[25], and various additional crops.

In order for successful interspecific or extensive intergeneric crossing within a specific genus to occur (Eeckhaut *et al.*, 2006) ^[31], a number of hurdles must be overcome. More and more studies are highlighting the importance of these data as an important indicator to predict crossing efficiency in breeding programs as has been shown for example in Geranium (Akbarzadeh *et al.*, 2021) ^[32], Helleborus (Meiners and Winkelmann, 2012) ^[33] and Hydrangea (Granados-Mendoza *et al.*, 2021) ^[34]. After postzygotic fertilization, numerous interspecific crosses exhibit issues such lower growth vigor, embryo abortion, endosperm development defects, or albinisms.

Chromosome doubling

In ornamental breeding, polyploidy, or chromosome doubling, is still significant. Spontaneous chromosomal doubling is often reported in wild populations.

In ornamental breeding, polyploidy, or chromosome doubling, is still significant. Spontaneous chromosomal doubling is often reported in wild populations. The somatic chromosome number of male or female gametes can spontaneously arise and give rise to new polyploids. This natural process is called gametic polyploidization. In certain instances, when flowers are created under temperature stress or after chemical treatment, there is a noticeable increase in production (Eeckhaut *et al.*,2018) ^[5]. Fertility issues can be resolved with unreduced gamete production, particularly following interspecific hybridization. Moreover, when breeding for triploid progenies, this method likewise produces a one-step process.

Somaclonal variation

The main cause of genetic variability is genetic mutations. Unplanned alterations continue to be a significant source of novel varieties, particularly for decorative plants lacking intentional breeding initiatives. Mutations are the source of new introductions in many woody ornamentals (Laere et al., 2018) ^[20], such as variegated leaf forms or dwarf growing cultivars. The primary factor turning a wild species into a cultivated ornamental is mutations in several common genera of greenhouse-grown plants, particularly leaf plants. Certain examples can be observed in genera likewise Aglaonema, Marantha, Monstera, Ficus, Hedera, and many more. Plastid mutations give rise to a unique category of variegations, which includes leaves with white or yellow cell lineages. Extensive research is currently being conducted in several Asian countries, including as Malaysia, Japan, and South Korea, to improve mutation technology for the purpose of developing new types of ornamentals. (Ibrahim et al., 2018)^[8].

In some cases, it is possible to select genotypes resistant to biotic or abiotic stress factors (salinity resistance, low temperature tolerance) by utilizing somaclonal variation through cell cultures. Fungal toxins or filtrates from cultures can be used as selecting agents to achieve selection towards fungal resistance, as seen in carnations and other ornamentals. (Thakur *et al.*, 2002) ^[35]. Aside from

morphological modifications, different amounts of ploidy have also been noted. Chrysanthemum protoplast regenerants exhibit a variety of somaclonal variations, such as variations in blossom quantity and size, a decrease in plant height, a modified blooming induction time, and varied flower kinds and colors. (Eeckhaut *et al*, 2020) ^[6].

Marker assisted breeding and genomics technology

The sequences of DNA known as molecular markers are those that are closely related to and inherited from the genomic area of concern. These markers can be used in breeding to precisely identify the individuals that carry the desired genetic region. Using marker-assisted selection, floral characteristics like double flowers, flower color, and floral longevity have also been chosen. (Smulders et al., 2012). MAS can be beneficial for difficult-to-assess variables and complicated traits like productivity and flowering time that are regulated by several loci or regions. Even with their benefits, molecular markers are primarily utilized in ornamental breeding for cultivar development of economically significant crops including roses, carnations, chrysanthemums, petunias, and lily. (Onozaki et al., 2004; Von Malek et al., 2000; Su et al., 2019; Tychonievich et al., 2011; Van Tuyl et al., 2018) [36, 37, 17, 38, 30].

The availability of genetic and genomic resources determines the use of molecular markers. Big analyses of data and next generation sequencing have made reference genomes, linkage maps, SSRs, and SNPs for non-model crops more accessible and affordable. Numerous ornamental crops, including gerbera, hydrangea, impatiens, caladium, and others, have benefited from the discovery of genes, SNPs, and SSRs thanks to genome reduction techniques like transcriptome sequencing and genotyping by sequencing. (Bhattarai *et al.*, 2020, Wu *et al.*, 2021; Bhattarai *et al.*, 2018; Cao *et al.*, 2017) ^[1, 23, 39, 2].

Agronomic and horticultural crops are using arrays with a few thousand SNPs more frequently due to advancements in genome resolution and marker-trait connection. For roses and chrysanthemums, these arrays have been established by (van Geest *et al.*, 2017; Koning-Boucoiran *et al.*, 2016) ^[18, 10]. These arrays might be utilized for gene or QTL identification, quality checks (keeping plants true to type), safeguarding plant variety, and analyzing the population structure in the germplasm if they were created for other ornamental crops.

CRISPR genome editing technology

CRISPR, or clustered regularly interspaced short palindromic repeats, is one of the gene-editing techniques that has emerged fastest in recent years for crop enhancement. It's an inexpensive, broadly useful, easy-to-use, and very effective method. Single guide RNA (sgRNA) and Cas9 protein combine to form a complex. The complex is directed by sgRNA to a specific target site next to the protospacer- adjacent motif (PAM), and Cas9 protein cleaves the DNA at the targeted location twice (Jinek *et al.*, 2012)^[40]. There are two techniques for repairing the cleaved site(s): homology-directed repair (HDR) and non-homologous end joining (NHEJ) (Symington and Gautier, 2011)^[41].

NHEJ, which facilitates the creation of minor insertions or deletions, may be applied to the insertion of donor sequences, stacks several genes, and can be used to carry out functional study of genes. (Lieber, 2010) ^[42]. By focusing on

two particular genes—the flavanone 3'-hydroxylase (F3H)A and F3HB coding genes—the CRISPR-Cas9 system, which is currently the most widely used CRISPR-Cas system, has been successfully used in ornamental plants to engineer flower color modifications from purple violet to pale purplish pink (Yu *et al.*, 2021) ^[24]. In I. nil, delayed petal senescence has been attained by disruption of the EPHEMERAL1 gene (Shibuya *et al.*, 2018) ^[15]. With CRISPR-Cas9, the gene carotenoid cleavage dioxygenase 4 (CCD4), which prevents the deposition of carotenoids in I. nil petals, was deleted, resulting in light yellow petals in the mutant lines rather than white petals (Watanabe *et al.*, 2018) ^[22]. A male sterile maternal line in rice has been created using CRISPR-Cas9 based gene knockouts in a variety of crops (Zhou *et al.* 2016) ^[27].

Only a small number of decorative crops, including petunias, morning glory, chrysanthemums, and orchids, to mention a few, have successfully undergone genome editing, despite the fact that the list is anticipated to grow quickly. (Zhang *et al.*, 2016; Kishi-Kobashi *et al.*, 2017; Kui *et al.*, 2017; Watanabe *et al.*, 2017) ^[26,9,11,21].

Root inducing technology

It's a useful tool for encouraging dense plant development. It has proven possible to make genetically engineered flowers in crops such as Dianthus, roses, and chrysanthemums. An intriguing substitute transformation approach solely employs Rhizobium rhizogenes wild type strains. In many dicotyledonous plant species, this group of pathogenic bacteria causes the so-called crazy root disease because they carry a root-inducing (Ri) plasmid. Natural transformation occurs when the bacteria and plants are co-cultivated in a lab setting. Since regenerated Ri phenotypic plants are not thought to be genetically modified, there are no legal restrictions on their commercialization. 2020a; Desmet *et al.* 2021.

These Ri phenotypes can exhibit changes in the morphology of the leaves, flowers, blooming period, and roots, in addition to the most intriguing characteristic: growth behavior. Pre-breeding material is provided by Ri technology and used in traditional cross-breeding procedures. Effective transformation and regeneration tissue culture techniques guarantee the production of several Ri lines within a given genus. Among other things, Kalanchoe blossfeldiana has been shown to successfully employ the technology (Christensen *et al.*, 2008) ^[43].

Challenges faced by breeders

Traditionally, the objective of breeding has been to create cultivars with better esthetic qualities, such as improved plant habit, leaf features, or flower properties (color, shape, aroma, and extended vase life). Increasing output is another key objective for cut flowers. Enhanced resistance to pests and diseases as well as greater tolerance to abiotic stressors are among the new breeding objectives. This is a significant task that is anticipated to grow in importance as a breeding objective. The output of ornamental plants may also be impacted by decreased fertilizer application. Although it has historically primarily been a concern for agricultural crops, nutrient utilization efficiency is expected to become a problem for ornamentals as well.

It will be extremely difficult to meet all of these mediumlong term targets without the cooperation of industry and research, as most breeding programs are carried out by small-scale breeding companies that lack the knowledge and financial resources to accomplish these goals. Better drought-resistant varieties or cultivars—that is, plants that require less water input and can withstand more extreme weather conditions—are needed for application in gardens and public green spaces.

Conclusions

Breeding ornamental plants has grown to be a significant industry. Nowadays, breeding ornamental plants is a complex process that calls for far greater flexibility than the medium- to long-term goals of the past. It's not always the greatest idea to use the newest technology and make large expenditures in today's dynamic world, where quick changes in the global environment call for creative and adaptable solutions. Indeed, the most inventive results in minor crops are frequently being produced by ardent "traditional" breeders and even amateur plant enthusiasts. Only through more active coordination across the various industry and research components can this seeming conflict be resolved.

References

- 1. Bhattarai K, Wang W, Cao Z, Deng Z. Comparative analysis of impatiens leaf transcriptomes reveal candidate genes for resistance to downy mildew caused by *Plasmopara obducens*. International Journal of Molecular Sciences. 2018;19(7):2057.
- 2. Cao Z, Deng Z. De novo assembly, annotation, and characterization of root transcriptomes of three caladium cultivars with a focus on necrotrophic pathogen resistance/defense-related genes. International Journal of Molecular Sciences. 2017;18(4):712.
- 3. Deng Z, Bhattarai K. Gerbera in Van Huylenbroeck. Ornamental Crops. In: Handbook of Plant Breeding, vol 11. Cham: Springer; c2018. p. 407-438.
- 4. Desmet S, Dhooghe E, De Keyser E, Quataert P, Eeckhaut T, Van Huylenbroeck J, *et al.* Segregation of rol genes in two generations of *Sinningia speciosa* engineered through wild type *Rhizobium rhizogenes*. Frontiers in Plant Science. 2020;11:859.
- 5. Eeckhaut T, Van der Veken J, Dhooghe E, Leus L, Van Laere K, Van Huylenbroeck J. Ploidy breeding in ornamentals. Ornamental Crops; c2018. p. 145-173.
- Eeckhaut T, Van Houtven W, Bruznican S, Leus L, Van Huylenbroeck J. Somaclonal variation in *Chrysanthemum× morifolium* protoplast regenerants. Frontiers in Plant Science. 2020;11:607171.
- Feng Z, Mao Y, Xu N, Zhang B, Wei P, Yang DL, et al. Multigeneration analysis reveals the inheritance, specificity, and patterns of CRISPR/Cas-induced gene modifications in *Arabidopsis*. Proceedings of the National Academy of Sciences of the United States of America. 2014;111(12):4632-4637.
- Ibrahim R, Ahmad Z, Salleh S, Hassan AA, Ariffin S. Mutation breeding in ornamentals. Ornamental crops; c2018. p. 175-211.
- Kishi-Kaboshi M, Aida R, Sasaki K. Generation of gene-edited *Chrysanthemum morifolium* using multicopy transgenes as targets and markers. Plant and Cell Physiology. 2017;58(2):216-226.
- 10. Koning-Boucoiran CF, Esselink GD, Vukosavljev M, van't Westende WP, Gitonga VW, Krens FA, *et al.* Using RNA-Seq to assemble a rose transcriptome with more than 13,000 full-length expressed genes and to

develop the WagRhSNP 68k Axiom SNP array for rose (*Rosa L.*). Frontiers in Plant Science. 2015;6:249.

- 11. Kui L, Chen H, Zhang W, He S, Xiong Z, Zhang Y, *et al.* Building a genetic manipulation toolbox for orchid biology: identification of constitutive promoters and application of CRISPR/Cas9 in the orchid, Dendrobium officinale. Frontiers in Plant Science. 2017;7:2036.
- Lewis M, Chappell M, Thomas PA, Maynard RC, Greyvenstein O. Development and verification of an interspecific hybridization protocol for *Asclepias*. Horticulture Science. 2021;56(7):831-837.
- 13. Long C, Chen Z, Zhou Y, Long B. The role of biodiversity and plant conservation for ornamental breeding. Ornamental Crops, 2018, 1-12.
- 14. Salsman J, Dellaire G. Precision genome editing in the CRISPR era. Biochemistry and Cell Biology. 2017;95(2):187-201.
- 15. Shibuya K, Watanabe K, Ono M. CRISPR/Cas9mediated mutagenesis of the *Ephemeral1* locus that regulates petal senescence in Japanese morning glory. Plant Physiology and Biochemistry. 2018;131:53-57.
- 16. Spaargaren J, van Geest G. Chrysanthemum. Ornamental Crops. 2018:319-348.
- 17. Su J, Jiang J, Zhang F, Liu Y, Ding L, Chen S, *et al.* Current achievements and future prospects in the genetic breeding of chrysanthemum: A review. Horticulture Research. 2019, 6.
- 18. van Geest G, Bourke PM, Voorrips RE, Marasek-Ciolakowska A, Liao Y, Post A, *et al.* An ultra-dense integrated linkage map for hexaploid chrysanthemum enables multi-allelic QTL analysis. Theoretical and Applied Genetics. 2017;130:2527-2541.
- 19. Van Huylenbroeck J, Calsyn E, Van den Broeck A, Denis R, Dhooghe E. Calathea. In: Ornamental Crops. Cham: Springer International Publishing, 2018, 301-318.
- 20. Van Laere K, Hokanson SC, Contreras R, Van Huylenbroeck J. Woody ornamentals of the temperate zone. Ornamental Crops; c2018. p. 803-887.
- Watanabe K, Kobayashi A, Endo M, Sage-Ono K, Toki S, Ono M. CRISPR/Cas9-mediated mutagenesis of the dihydroflavonol-4-reductase-B (DFR-B) locus in the Japanese morning glory Ipomoea (Pharbitis) nil. Scientific Reports. 2017;7(1):10028.
- 22. Watanabe K, Oda-Yamamizo C, Sage-Ono K, Ohmiya A, Ono M. Alteration of flower colour in *Ipomoea nil* through CRISPR/Cas9-mediated mutagenesis of carotenoid cleavage dioxygenase 4. Transgenic Research. 2018;27:25-38.
- 23. Wu X, Hulse-Kemp AM, Wadl PA, Smith Z, Mockaitis K, Staton ME, *et al.* Genomic resource development for hydrangea (*Hydrangea macrophylla* (Thunb.) Ser.)—A transcriptome assembly and a high-density genetic linkage map. Horticulture. 2021;7(2):25.
- Yu J, Tu L, Subburaj S, Bae S, Lee GJ. Simultaneous targeting of duplicated genes in *Petunia* protoplasts for flower color modification via CRISPR-Cas9 ribonucleoproteins. Plant Cell Reports. 2021;40:1037-1045.
- 25. Yue Y, Ruter JM. *Pavonia*× *rufula* (Malvaceae): An interspecific hybrid between *Pavonia lasiopetala* and *Pavonia missionum. Hort Science*. 2021;56(6):732-735.
- 26. Zhang B, Yang X, Yang C, Li M, Guo Y. Exploiting the CRISPR/Cas9 system for targeted genome

mutagenesis in petunia. Scientific Reports. 2016;6(1):20315.

- 27. Zhou H, He M, Li J, Chen L, Huang Z, Zheng S, Zhuang C. Development of commercial thermosensitive genic male sterile rice accelerates hybrid rice breeding using the CRISPR/Cas9-mediated TMS5 editing system. Scientific Reports. 2016;6(1):37395.
- 28. Huylenbroeck L, Laslier M, Dufour S, Georges B, Lejeune P, Michez A. Using remote sensing to characterize riparian vegetation: A review of available tools and perspectives for managers. Journal of environmental management. 2020 Aug 1;267:110652.
- 29. Leus IV, Weeks JW, Bonifay V, Smith L, Richardson S, Zgurskaya HI. Substrate specificities and efflux efficiencies of RND efflux pumps of Acinetobacter baumannii. Journal of bacteriology. 2018 Jul 1;200(13):10-128.
- Van Tuyl J, Alves TM, Cherns L. Geometric and depositional responses of carbonate build-ups to Miocene sea level and regional tectonics offshore northwest Australia. Marine and Petroleum Geology. 2018 Jun 1;94:144-65.
- 31. Van Den Eeckhaut M, Vanwalleghem T, Poesen J, Govers G, Verstraeten G, Vandekerckhove L. Prediction of landslide susceptibility using rare events logistic regression: A case-study in the Flemish Ardennes (Belgium). Geomorphology. 2006 Jun 30;76(3-4):392-410.
- 32. Akbarzadeh M, Kalogiannis T, Jaguemont J, Jin L, Behi H, Karimi D, *et al.* A comparative study between air cooling and liquid cooling thermal management systems for a high-energy lithium-ion battery module. Applied Thermal Engineering. 2021 Nov 5;198:117503.
- Meiners J, Winkelmann T. Evaluation of reproductive barriers and realisation of interspecific hybridisations depending on genetic distances between species in the genus Helleborus. Plant Biology. 2012 Jul;14(4):576-85.
- 34. Granados-Aguilar X, Granados Mendoza C, Cervantes CR, Montes JR, Arias S. Unraveling reticulate evolution in Opuntia (Cactaceae) from southern Mexico. Frontiers in Plant Science. 2021 Jan 13;11:606809.
- 35. Thakur V, Guptan RC, Kazim SN, Malhotra V, Sarin SK. Profile, spectrum and significance of HBV genotypes in chronic liver disease patients in the Indian subcontinent. Journal of gastroenterology and hepatology. 2002 Feb;17(2):165-70.
- Onozaki T, Ikeda H, Shibata M. Video evaluation of ethylene sensitivity after anthesis in carnation (*Dianthus caryophyllus* L.) flowers. Scientia horticulturae. 2004 Feb 6;99(2):187-97.
- Von Malek B, Weber WE, Debener T. Identification of molecular markers linked to Rdr1, a gene conferring resistance to blackspot in roses. Theoretical and Applied Genetics. 2000 Oct;101:977-83.
- 38. Tychonievich J, Warner RM. Interspecific cross ability of selected Salvia species and potential use for crop improvement. Journal of the American Society for Horticultural Science. 2011 Jan 1;136(1):41-7.
- 39. Bhattarai Y, Williams BB, Battaglioli EJ, Whitaker WR, Till L, Grover M, Linden DR, Akiba Y, Kandimalla KK, Zachos NC, Kaunitz JD. Gut microbiota-produced tryptamine activates an epithelial

G-protein-coupled receptor to increase colonic secretion. Cell host & microbe. 2018 Jun 13;23(6):775-85.

- 40. Jinek M, Chylinski K, Fonfara I, Hauer M, Doudna JA, Charpentier E. A programmable dual-RNA–guided DNA endonuclease in adaptive bacterial immunity. science. 2012 Aug 17;337(6096):816-21.
- 41. Symington LS, Gautier J. Double-strand break end resection and repair pathway choice. Annual review of genetics. 2011 Dec 15;45:247-71.
- 42. Lieber MR. The mechanism of double-strand DNA break repair by the nonhomologous DNA end-joining pathway. Annual review of biochemistry. 2010 Jul 7;79:181-211.
- 43. Christensen JH, Boberg F, Christensen OB, Lucas-Picher P. On the need for bias correction of regional climate change projections of temperature and precipitation. Geophysical research letters. 2008 Oct;35(20).