



Breeding, Genetics, and Genomics of Ornamental Plants

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Ornamental crops include a broad range of plants, including herbaceous seasonal flowers to woody perennial trees. Due to their wide diversity, different breeding methods have been utilized in ornamental crops to develop new cultivars. Cultivar development in ornamental crops is currently performed by making intraspecific and interspecific crosses, ploidy manipulation, mutation breeding, and molecular breeding. Except for a few floral species, limited genetic, genomic, and breeding information is publicly available, owing to the fact that the majority of breeding work is performed by the private sector. Compared to agricultural or vegetable crops, ornamental crops are diverse, which means that each individual species has a relatively low economic turnover, and subsequent lower budgets are attributed to research and developmental activities. However, public research programs are participating in ornamental cultivar development and genetic studies. This has contributed to the identification of important genes, genetic architecture, and the genomic information of some economically important ornamental crops. To date, limited genome-informed breeding strategies have been applied in ornamental crops. However, with the decreasing sequencing costs and availability of reference genomes of flowers, it is likely that genomics-assisted breeding will be applied in cultivar development as observed in other row, vegetable, and fruit crops.

This Special Issue (SI) was developed to present the advancements made in the field of ornamental crops, with a focus on understanding the genetics, genomics, and breeding frontiers leading to cultivar development. More specifically, the objectives of this SI were to report novel genes; their functionality and cross talks with other genes; breeding activities, including the development and characterization of new cultivars; and the development of genomic resources, including high-density linkage map and transcriptome, and their applications in breeding. This SI gathered six research papers [1–6] based on a wide array of herbaceous and perennial ornamental crops in the fields of gene identification and interactions, ploidy manipulation, and genomics research.

Ploidy manipulation has been commonly used in ornamental crops for cultivar development. In many species, it has led to the creation of new cultivars with altered morphology and increased stress resistance. In addition to obtaining valuable morphological or physiological variations, one of the driving factors for using ploidy manipulation is to develop reproductive sterility in plants to check the invasiveness of the species and the extent to which it is endangering native plants in the environment. Currently, three maple species have been listed as noxious weeds in Connecticut and Massachusetts due to their ability to produce an undesirable number of seedlings, posing an extreme threat to encroaching natural vegetation. Although measures to check the spread of these species are implemented in only two states, the naturalization of these species has already occurred in large areas in different regions of the United States [1]. The development of maple plants that do not produce viable seeds can help in controlling the spread of maple in the wild. Using ploidy manipulation, triploid plants can be developed, which are found to be sterile and do not produce viable seeds. Contreras and Hoskins developed triploid maple by ploidy manipulation and backcrossing methods [1]. Oryzalin treatment of seedling meristem is



Citation: Bhattarai, K.; Van Huylbroeck, J. Breeding, Genetics, and Genomics of Ornamental Plants. *Horticulturae* **2022**, *8*, 148. <https://doi.org/10.3390/horticulturae8020148>

Received: 2 February 2022

Accepted: 6 February 2022

Published: 9 February 2022

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used to develop tetraploid maple, which is then crossed with diploid maple and results in triploid maple [1]. Several years of screening of triploid maple plants have shown that the triploid maple does not produce flowers, or if the flowers are produced, they are sterile [1]. This triploid maple showed the potential to be released as new cultivars for nursery growers and land managers [1].

Polyploids show enhanced desirable traits, such as larger flowers, as compared to their diploid counterparts, which make them more appealing to consumers. Increased organ enlargement due to polyploidy is attributed to the chromosomal doubling and gene dosage effects. Polyploidy has been used in ornamental plants showing narrow genetic diversity and compatibility issues in search of novel or improved traits and make interspecific and intergeneric crosses. *Limonium sinuatum* flowers are desired for their wide range of colors and longer vase life [4]. However, developing new cultivars with novel attractive traits is not easy due to their narrow genetic diversity and the difficulty of crossbreeding with related species, with few exceptions. The development of polyploid plants can potentially result in larger flowers and increased vigor in *L. sinuatum*, making it more desirable for consumers. The in vivo treatment of seedling meristem with oryzalin successfully developed polyploid individuals, including tetraploids and mixoploids [4]. Tetraploid plants showed increased leaf width, stomatal size, and flower length; however, a significant improvement in ornamental value was not obtained [4]. Further study is needed to cross tetraploid and diploid *L. sinuatum* individuals to develop triploid plants and assess them for potential cultivar development with enhanced traits [4]. While traits such as larger flower size are highly desirable to the ornamental industry, not all morphological changes caused by polyploidy positively impact the consumer. Tetraploid *L. sinuatum* exhibited thickened stem wings and inflorescence clogging, which are not desirable ornamental traits [4]. These traits can potentially be improved or eliminated with the use of breeding strategies while retaining the desirable novel traits obtained by ploidy manipulation.

Despite high demand and global production, ornamental crops fall behind in the public availability of genomic resources owing to their high level of heterozygosity, varying ploidy level within the same species and wide range of complex genome sizes. Recently, efforts are being made to develop genomic resources in some widely cultivated and economically important ornamental crops, such as hydrangea (*Hydrangea macrophylla*) [2]. Hydrangea, being a woody ornamental, requires a longer conventional breeding time. The development and incorporation of molecular markers can reduce generation interval times and expedite breeding using marker-assisted selection. Wu et al. used genome reduction techniques, such as genotyping by sequencing (GBS) and transcriptome sequencing, to identify simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) markers and construct a linkage map in hydrangea [2]. Genome reduction techniques, such as GBS and transcriptome sequencing, can be used to identify SNPs and develop molecular markers to facilitate marker-assisted selection in ornamental crops with highly heterozygous, complex, and relatively large genome sizes. When reference genomes or physical maps are not available, linkage maps are used in identifying genomic regions conferring phenotypic traits of interest and developing molecular markers. Wu et al. constructed a linkage map consisting of 18 linkage groups incorporating 1621 SNPs and 146 SSRs [2]. These efforts help in realizing the application of marker-assisted and genome-informed selections in ornamental crops in addition to facilitating QTL mapping, association mapping, gene identification and gene cloning. With the decreasing sequencing cost, the availability of genomic resources for more ornamental crops are expected to be available in future.

The identification of gene functions has led to a better understanding of flower development and physiology. Jones et al. cloned *Petunia hybrida* Endonuclease 1 (*PhENDO1*) gene using two-dimensional gel electrophoresis based on endonuclease enzyme (PhNUC1) activity encoded by the gene [3]. The downregulation of *PhENDO1* using virus-induced gene silencing revealed the role of *PhENDO1* in decreased nucleic acid content in the corolla; however, it did not independently play any role in delaying flower senescence [3]. Similarly, gene expression studies have led to a greater understanding of plant acclimatization to

abiotic stresses. During cold acclimation, the higher expression of dehydrins and increased sugar accumulation played an important role in roses [5]. This was verified by the increased transcript levels of *Rosa hybrida* sucrose-phosphate synthase (*RhSPS*) and *Rosa hybrida* invertase 2 (*RhINV*) genes in “Yesterday” and *R. wichurana*, respectively, while *R. hybrida* sucrose synthase (*RhSUS*) expression was downregulated in both cultivars during the cold months [5]. Meanwhile, the expression of *RhSPS* and *RhINV2* was found to be decreased during the warmer months of April, which signifies the involvement of oligosaccharides in cold acclimation [5].

The pursuit of novel traits in ornamental crops has led to the adoption of distant crosses. Crosses between plants with high genetic distance provide the opportunity to inherit a high amount of variation in the offspring. Interspecific and intergeneric crosses are made in ornamental crops in efforts to develop cultivars with new and improved ornamental traits. However, not all distant crosses are successful due to pre- or post-fertilization barriers. In an intertribal cross between *Anemone coronaria* and *Ranunculus asiaticus*, pre-fertilization barriers were observed due to the interstylar growth of pollen tubes, whereas minimal stigmatic incongruity was observed between the two species [6]. This barrier was minimized by increasing the ratio of pollen tube length to the total style length using 2,4-D treatment [6]. A full seed set without the necessity of pollination indicated apomictic seed generation [6]. Overcoming the pre- and post-fertilization barrier due to artificial treatment can assist in distant crosses and viable seed production and harness the wide genetic variation inherited from distant crosses and use in ornamental breeding.

This SI provides an insight into the application of breeding, genetics, and genomic tools to understand the biology of the ornamental plants and develop new cultivars for ornamental nurseries. In the era where sequencing-based tools are being increasingly applied in ornamental crops, it is expected that future research will incorporate these techniques to develop cultivars and discover or understand biological phenomena in ornamental crops. In the future, once the genetic bases of (complex) traits are resolved, the breeding of ornamental plants will become more efficient.

Author Contributions: Writing, review and editing, K.B. and J.V.H. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: Not applicable.

Conflicts of Interest: The authors declare no conflict of interest.

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