

Editorial

# Special Issue “Recent Advances in Genomics, Genetic Resources Evaluation and Breeding of Cucurbitaceae Crops”

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Recent progress in plant genomic technologies has amounted to a revolution, making a huge set of molecular tools available for use in plant breeding. The increased availability of genome sequences, molecular marker techniques and genomic technologies for application to horticultural plant species has allowed their utilisation to solve different crop problems, Transforming and complementing traditional methods of plant selection and gene introgression, these techniques represent an incredible toolkit that will enable the best and most efficient use possible of genetic resources in facing the current challenges for agriculture worldwide. Additionally, they will have use in assessing future challenges that affect yield and productivity, such as those of global warming. They allow to open new possibilities in plant breeding for a wide range of biotic and abiotic stresses, as well for quality crop improvement, combining genotyping and phenotyping knowledge and offering new approaches.

The botanical family Cucurbitaceae (cucurbits) includes several economically important and flavourful nutritious crops consumed globally as vegetables, fruits, and seeds, such as melon (*Cucumis melo* L.), cucumber (*Cucumis sativus* L.), watermelon (*Citrullus* spp.), pumpkin, squash and gourds (*Cucurbita* spp., *Lagenaria* spp.) among others (*Momordica* spp., *Luffa* spp.). Also, this plant family, originating from poor countries in many cases, includes species and varieties used for medical and ornamental purposes, some weeds, and some species that can be considered as food for the future, with more possible edible fruits scarcely used so far. The use of these cucurbit crop species has brought great genomic advances, mainly due to their small genome sizes. The assemblies of draft genome sequences and their databases are available for some cucurbit species to explore genetic diversity and functional genetics, facilitating their application in understanding biological mechanisms such as those involved in cucurbit development, the adaptation to their environments, the achievement of sustainable food production, host–microbe interaction, and plant tolerance to biotic and abiotic stresses, among others. In summary, the availability of these recent advances facilitate their application in understanding multiple biological mechanisms and their application in cucurbit breeding and genetic resource management.

This Special Issue compiles 12 research papers, two of them reviews, showing the results of 51 authors. In particular, these submissions cover different aspects of interest on cucurbit breeding, addressing issues of biotic and abiotic stress tolerance and control, as well as fruit quality traits, with the application of genomic tools as well as the monitoring and management of genetic resources for the promotion of a more sustainable agriculture (Figure 1).

Abiotic stresses represent important constraints for agriculture, affecting plant growth and productivity. Among them, salinity in water and soil is a major cause of reduction in crop yields and food production worldwide. So, addressing environmental stress factors, as well as their consequences and the possible measures required to palliate them, is an active research field, especially in a scenario of global warming and environmental pollution. Chen et al. [1] analyse the differential ion toxicity under salinity stress in cucumber as its tissue tolerance to  $\text{Na}^+$  and  $\text{Cl}^-$  is still unclear, and the uptake restriction caused by



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varieties. Regarding powdery mildew, a fungal disease occurring in field and greenhouse conditions worldwide and reducing productivity and quality, Choi et al. [4] reported the development of a codominant PCR-based marker that can be used to develop resistant melon varieties from MR-1 melon resources.

Plant resistance is an effective and sustainable method to control crop diseases. Two reviews herein examine the current knowledge on cucurbit resistance to viruses and to pathogens co-existing in the rhizosphere of crops, as well as some of the mechanisms involved and the traditional and biotechnological tools used for breeding. Martín-Hernández and Picó [5] review the natural resistances available in Cucurbitaceae to viruses such as Potyviruses, Cucumoviruses, Criniviruses, Ipomoviruses, Tobamoviruses, and Begomoviruses. Many of these genetic resources are multi-resistant but, although many genes have been mapped, higher mapping resolutions and functional genomic research are required to identify them and to advance toward a genomic-assisted breeding against viral diseases in cucurbits. Ayala-Doñas et al. [6] review the breeding status of resistance and grafting methods that allow researchers to manage soil-borne fungi and root-knot nematodes in cucurbits. The authors highlight and comment on the importance of achieving an adequate pathogen diagnosis, given the specificity in the response to fungi and nematode, as well as the resistance mechanisms deployed and involving the hardening of cell walls, pathogenesis-related proteins, plant hormones, antimicrobial molecules, and the increased activity of peroxidases and other enzymes.

Several research papers in this Special Issue deal with some very specific agronomic traits related to fruit quality, emphasizing the use of new genetic resources and the role of domestication. Some of these trait characterisations might encourage future efforts to enhance breeding melon quality since there are still many underexploited landraces and wild accessions. Esteras et al. [7] analysed melon core collection for rind volatile compounds since these substances play a key role in determining consumer preferences. So, the authors identified interesting melon accessions with different combinations of aroma profiles for rind and flesh, also observing the potential introgression origins of some of these important volatile compounds. Many of the interesting melon fruit traits, not to mention the increase in fruit flesh, are the major domestication achievements in this species, which originated from wild melons and produces small fruits with non-edible fruit flesh. Regarding this issue, Riahi et al. [8] observed potential evidence of the involvement of QTL epistatic interactions in the increase in melon fruit flesh content occurring during melon domestication.

Besides the agronomic traits already mentioned, two research papers presented data on the seed oil composition of different species of the genus *Cucurbita*. Cucurbit seed oil meets the requirements for functional nutrition, being a material for the food industry and medicines based on natural ingredients. Shelenga et al. [9] examined seed oil biochemical composition of several *Cucurbita* collections from the N.I. Vavilov Institute (VIR) to extract more data that might allow us to identify the accessions with the most economically important indicators for seed oil. Conversely, Tańska et al. [10] examined the seed oil composition of a series of new Styrian pumpkin hybrids in order to assess their composition and variability in comparison to other melons coming from different growing areas.

New breakthrough technologies open new possibilities for advancing crop improvement and trying to overcome the difficulties that may arise. For plant breeding purposes, in situ parthenogenesis via irradiated pollen is the preferred technique to obtain doubled haploids plantlets. However, this technique presents many limiting factors in cucurbits, even in addition to being a very time-consuming and labour-intensive work, sometimes with low efficiency. Hooghvorst and Nogués [11] review and discuss the progress made towards the development of doubled haploids and haploid inducer genotypes using CRISPR/Cas9 technologies, providing insights for the application of haploid inducer-mediated genome-editing systems in cucurbit species.

Recent advances in all these technologies can definitely support the development of more sustainable agriculture, starting from sustainable plant breeding and production. Dhillon et al. [12] present a perspective on the World Vegetable Center (WorldVeg), an

organisation that operates across Asia and Africa, where cucurbit crops make an important contribution to global food and nutrition security and are economically important to small-holder farmers. Concretely, the authors assess the promoted public–private partnership and consortium developed to share and use the new breeding lines derived from local unexploited landraces in order to increase genetic variability into elite cucurbit hybrid cultivars with enhanced yield and resistance to major diseases.

The availability of genome sequences, the continuous development of new molecular and biotechnological techniques, as well as the implementation of high-throughput phenotyping tools and speed breeding techniques, might make it possible and affordable to face the new challenges and promise to play important roles in the future of agriculture. In summary, this Special Issue includes a diverse collection of original research articles, covering a wide range of research interests, with the increasing use of genomic resources and new technologies as powerful tools for genetic studies. These articles provide a substantial knowledge on gene resources related to disease resistance and quality agronomic traits, offering theoretical references for accelerated cucurbit genetic improvement and breeding.

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