

Editorial

Molecular Genetics, Genomics and Biotechnology in Crop Plant Breeding, Series II

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This second volume of this series of Special Issues provides research papers and reviews on the use of molecular marker technologies, genomics selection, site-directed mutagenesis, gene-discovery by genome-wide association studies and biotechnology in important grain crops, tubers, fruit bearing shrub and small fruit crops. Breeding crop plants for end-product use such as quality traits are greatly facilitated by the use of DNA molecular markers. Cost-efficient sequence technologies are available that allow markers to be developed even for orphan crops. Marker-assisted selection also facilitates the introgressive hybridisation of a new site-directed mutation developed in a pre-breeding line into elite cultivars. Other applications of molecular markers make it possible to monitor F1 hybrid seed production and the authenticity of plant-based products. The Nobel Prize in Chemistry 2020 was awarded to Emmanuelle Charpentier and Jennifer Doudna for the discovery of CRISPR-Cas9 scissors that facilitate site directed mutagenesis in all living organisms including the plant kingdom. In this Special Issue, the first paper presents the principles of this new mutation method [1] with instructive illustrations of the mechanism its uses in plants and the review presents recent developments of the methodology. The versatility of site-directed mutagenesis is shown by a survey of a diverse set of 11 crop plants and a wide range of quality traits, yield and disease targets demonstrate its versatility. There is a need for adaptation in soybean (*Glycine max* (L.) Merr.) for Sub-Sahara Africa to overcome yield-drag compared to the global average production and by using single nucleotide polymorphism (SNP) in a Tropical *Glycine max* germplasm interesting genetic material could be identified for future soybean breeding [2]. To support marker-assisted selection and cultivar identification in a germplasm of gooseberry (*Ribes uva-crispa*) with varying berry colours (green, yellow, red and black) the nucleotide sequence of eight genes involved in flavonoid biosynthesis were used to design simple sequence repeat (SSR) markers [3]. The colour of the edible part is also an important trait to breed for in cabbage (*B. oleracea* var. *capitata* f. *alba*) [4] and to support this trait, specific SNPs that are closely associated with anthocyanin accumulation at low temperature were identified. Resistance and susceptibility to pathogens is an important breeding target in red and black raspberry (*Rubus* L.) canes [5], where a waxy locus is controlling the epicuticular wax; SSR markers could be developed and used for breeding. A limitation of the use of SSR markers is that they were found to be difficult to transfer between the two subgenera raspberries. Saline soils cause problems in pomegranate (*Punica granatum* L.) production, where Na/H antiporter genes have an important function in mitigating salt stress. SNP markers were designed by genome-wide analysis to discriminate between members of the gene family in pomegranate and their response to salinity [6]. The grain legume grasspea (*Lathyrus sativus* L.) would require a significant breeding effort in order to be revived as a protein legume for Italian husbandry and this study develops SSR markers that show their feasibility to support selection in a breeding nursery [7]. Marker trait associations (MTAs) for freezing tolerance in canola (*Brassica napus* L.) was carried out on a large and wide germplasm of winter-type canola [8]. Many MTAs were located in genes previously identified to be good candidate genes for freeze tolerance in plants. Molecular markers



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were used for sex determination in Beninese yam (*Dioscorea rotundata* Poir) [9]. The crop plant is grown for its tubers, which are an important staple food in Benin; however, very little breeding is going on in yam. In a study of maize (*Zea mays* L.) hybrids, SSR markers were found to be very useful in breeding due to their codominant nature, high number of alleles, easiness of automation and the ability to differentiate inbred lines, and three markers were identified to be particularly informative in relation to quantitative trait loci (QTL) [10]. A bibliographic survey for publications using modern molecular plant breeding methods such as QTL mapping, GWAS and genomic selection for the following key traits in crop improvement: abiotic stresses and nutrient limitations for the three most important grain crops, rice, wheat and maize, based on global production [11]. The review gives a comprehensive historic overview, such as which year these methods (QTL mapping, GWAS and genomic selection) were first published, and it includes 265 primary references. The current Special Issue II starts out with a review on site-directed mutagenesis in plant breeding and closes with a survey of the plant molecular biology used in the most important cereal crops worldwide. The CRISPR-Cas9 is dependent on the availability of nucleotide sequence and the functional analysis of the candidate gene. Furthermore, the use of the technology is not exempt from the genetic modification regulation in the European Union in the same way that induced mutagenesis is, but, fortunately, it can be used in research. Taken together, the two review papers that embrace this collection of original research will give students and breeders key references on the most recent and strongest method in molecular plant breeding, together with the use of molecular methods in the three main crops that feed the world.

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