



Molecular Breeding for Introgression of Drought Tolerance Traits in Major Crops

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INTRODUCTION

Drought is the multidimensional and metrological events affects crop production in tropical and subtropical region across the world. Limited rainfall and water deficit condition are the major cause of drought. Drought affects all stages of the crops including seed germination, vegetative growth, flowering and maturity stage (Sallam, et al., 2019). Acute drought due to long-term water deficit condition influenced crop production are decreases economic yield (Ahmad, et al., 2019). Due to lack of drought tolerant crop cultivars, crop production in water deficit condition are under trouble. Crop production in the water deficit condition becomes a challenging issue due to lack of the availability of crop cultivars gives better performance (Gosal and Wani, 2018). Therefore, development of drought tolerant crop cultivars is the challenging issue in the era of global warming and climate change. Drought is the complex phenomenon, difficult to manage through conventional breeding approaches.

Recent trends of marker-assisted breeding have resulted in the identification of mechanism underlying drought stress tolerance in cereals. There are various strategies of molecular breeding like marker-assisted selection, marker-assisted introgression, marker-assisted backcross breeding, Marker-assisted recurrent selection, genome-wide selection and genomic-selection acting as robust platform for introgression of traits from one to other cultivars to achieve durable resistance for the particular traits (Chen, et al., 2016). Therefore, advancement in the genomic tools has resulted in targeted and précised identification of mechanism under laying drought stress tolerance in the major cereal crops. In context to identification of genes and QTLs, association mapping studies gives platform in the detection of desirable quantitative trait loci and several major and minor genes governing drought tolerance mechanism (Wani, et al., 2018).

In this article, recent advances for achieving drought tolerance in major cereal crops through genomic-assisted breeding have been discussed.

2. High throughput genotyping for identification of desirable traits

Identification and introgression of drought tolerance responsive traits into major cereal crops based on the availability of the tightly linked molecular markers frequently distributed throughout the genome. The responsible genes and QTLs available on the various chromosomal location of the genome needed to be tagged with tightly linked molecular markers using high-throughput technology (Wani, et al., 2019). High-throughput technology provide the wide range of molecular markers like RFLP, RAPD, AFLP, CAPs, SCARs, SSR, ISSR, TRAP, DRAT, DArT, SNP etc. (Moose and Mumm, 2008). However, availability of molecular markers are an alternative approach to the molecular breeders to significantly improve the crop cultivars for the abiotic threats like drought, heat, salinity, and submergence (Rana, et al., 2019). Drought is the complex trait and can be governed by many genes. Physiological parameters associated with growth and development of the plants determines the level of drought in the case of plant species. Particularly in the case of cereal crops, the level of drought varies in major cereal crops at various crop stages of the growth and development (Hussain, et al. 2009). Large number of quantitative traits loci (QTLs) and genes are involved in the development of drought tolerance and some of them are then governed by additive and non-additive gene action (Iqbal, et al., 2007).

3. Mapping of genomic region of the major cereal crops for drought stress tolerance

Rice, wheat and maize are the major cereal crops frequently grown for the food grain production across the world. These cereal crops are influenced by the water deficit condition at various crop stages. Survey of genomic region of these crops for the

identification of traits expressed under water deficit condition for the development of drought tolerance is one of the primitive practices for searching particular region of the various chromosomal location of the genome.

In case of rice, large number of QTLs and genes have been identified on the various chromosomal location and conferring resistance under water deficit condition. Three QTLs namely RM8085, I12S and RM6836 mapped on the rice chromosomal region for physiological and yield attributing traits using IR 20 x Nootripathu RIL population by Price, et al., (2015) conferring resistance under water deficit condition. These three QTLs are exploited for introgression into elite rice cultivars for targeting drought prone region. Similarly, more than 14 QTLs have been identified from Nagina-22 derived RILs population for the various roots and shoots responsive traits governing drought tolerance. In several studies, it has been found that the maximum numbers of QTLs governing drought tolerance mechanism were identified on the rice chromosome 1 (Bhattarai, et al., 2018). Genome-wide association studies carried out by Hoang, et al. (2019), using more than 180 rice landraces using more than 20,000 SNPs markers and identified more than 17 drought responsive QTLs conferring tolerance at various crop stages.

In wheat, QTLs associated with drought tolerance have also been mapped from RILs populations and identified for root architectural traits conferring tolerance at various growth and development stages. Two QTLs for seminal root angle and two for seminal root number have been identified from the double haploid populations that conferring tolerance under acute water deficit condition (Christopher, et al., 2013). Furthermore, six QTLs have also been mapped from the RILs population associated with drought tolerance mechanism on the various genomic locations of the mapping populations (Zhang, et al., 2013). In similar studies conducted by Malik et al. (2015), 4 QTLs have been identified on

the chromosome 2A of the wheat genome associated with relative water contents, photosynthesis and membrane stability when plants subjected to acute water deficit condition. The mapping populations developed using wild emmer wheat as a source of drought tolerance, three QTLs associated with yield and biomass were mapped on chromosome 1BL, 2BS and 7AS and these QTLs conferring tolerance under long-term water deficit condition (Merchuk-Ovnat, et al., 2016). Later, 13 QTLs associated with abscisic acid synthesis under water deficit condition have been identified on the various chromosomal locations of the wheat genome (Barakat, et al., 2015).

Maize production is globally affected by drought due to lack of the availability of drought tolerant cultivars. Therefore, identification of genes and QTLs conferring drought is important for development of drought tolerant maize cultivars using marker-assisted backcross breeding. In context to development of drought tolerant maize cultivars, the root architecture and root angle play significant role in the drought tolerant mechanism. Other QTLs associated with morphological and physiological traits under water deficit condition have been identified from on chromosome 1, 4, 5 and 10 (Almeida, et al. 2014). The Meta-QTLs using 36 recombinant inbred lines have been identified by Zhao, et al. (2018) for kernel length, grain yield, and 100 kernel weights under acute water deficit condition. In other studies, 34 candidate genes in the corresponding meta-QTL regions were found to be associated with the inflorescence development and drought resistance regulation (Zhao, et al. 2017).

4. Genomic-assisted breeding for drought stress tolerance

Development of drought tolerant crops cultivars using genomic-assisted breeding approaches are depends on the availability of donor source with having desirable QTLs and genes conferring tolerance at various crop stages. Screening of wild crop relatives,

landraces, germplasm and crop cultivars for desirable traits give strength to the molecular breeding for the development of resilient cultivars. In context to drought tolerant, number of genes, QTLs, meta-QTLs have been identified from wild crop relatives and landraces. Introgression of these QTLs and genes into crop cultivars through marker-assisted breeding has been implemented in several crop cultivars for the development of resilient crops. Drought is polygenic traits governed by many genes and QTLs at various growth and development stages of the crops. In rice, marker-assisted backcross breeding has been successfully employed for the drought tolerant rice cultivars. Cultivars like Sabitri and Nepalese are the successful example of the marker-assisted backcross breeding in the case of rice (Dixit, et al., 2017). Another example of the genomic-assisted breeding with respect to drought tolerant is MR Dhan 219 with higher yield potential under water deficit condition (Shamsuddin, et al., 2016). Major QTLs like *qDTY12.1* and *qDTY2.3* conferring drought tolerant have also been introgressed with significant yield advantages at reproductive stage of the development in to rice cultivars FUNAABOR-2 were achieved by Anyaoha, et al. (2019). Similarly in wheat, QTLs and traits associated with drought tolerance have been introgressed though genomic-assisted backcross breeding approaches. In case of wheat, the traits particularly governing high chlorophyll content, grain yield and deeper root system have been focused for introgression into major wheat cultivars like HD2733 and GW322 (Jain, et al., 2014). The other important QTLs like *Qyld.csdh.7AL* conferring tolerance under water deficit condition have been incorporated through marker-assisted backcross breeding in the wheat cultivars HUW234, HUW468, K307 and DBW17 (Gautam, et al., 2020). Like rice and wheat, several QTLs and genes involved in the drought tolerance mechanism have been identified and incorporated into maize

cultivars through genomic-assisted breeding (Shikha, et al., 2017). The important physiological traits governing drought tolerance mechanism in maize related to drought-responsive transcriptional factor have also been used in the development of drought tolerant maize cultivars (Shikha, et al., 2017).

CONCLUSION

Molecular markers based identification of genes and QTLs governing drought tolerant mechanism in the major cereal crops and their introgression into popular cultivars through marker-assisted backcross breeding have been practiced by several workers for the development of crops gives better response under water deficit condition. As drought is governed by multiple traits due to polygenic nature, so the chances for the development of drought tolerant crops cultivars are limited. Molecular breeding for the development of drought tolerant crop cultivars needs more exercise in the screening and identification of drought responsive traits and their cumulative pyramiding into a cultivars to achieve durable resistance. Future era of genomic wide association studies for the development of drought tolerant crops cultivars may also provide future to the breeders for development of drought resilient crops cultivars with yield potential.

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