Marker Assisted Selection for Development of Drought Resistant Crops

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ABSTRACT: The most important environmental stress effecting field crops productivity is drought. In major crops the drought resistance is governed by genetic, genomic and molecular studies. These studies include identification of genes affecting drought resistance and their engineering in staple crops. Underlying drought resistance in crops elucidation of complex mechanisms enhance the drought resistance in new varieties development. The key tools of engineering and breeding drought resistance (DR) crops is to unreveal the complex mechanism of drought resistance through intensive and integrated studies in crop plants. DR is regulated by hundreds of genes, numerous small effect loci controlling physiological and morphological responses of drought. During the breeding process exploitation of information related to traits position which are governing the agronomical importance and linked molecular markers can be achieved by molecular assisted selection (MAS). Among the traits success of MAS depends upon factors such as degree of association between molecular marker and target gene, genetic base of trait, number of individual that can be analyzed, background of target gene in which it has to be transferred MAS inherited traits governed more importance in breeding programs leading to accelerating the breeding process. Recent advances in rice research, genomics, rice genome sequencing completion made it easy to identify and mapping large no of genes through linkage to DNA markers. For breeders to develop stress resistance, high yielding, better quality rice cultivars using of cost-effective DNA markers produced from fine mapped genes position for agronomic traits and MAS strategies. Plants response to drought stress in multiple ways by physiological and morphological changes adaptation controlled by diverse signalling cascade. Plants response to drought includes the gene activation for perception and transmission of drought stress and its signals. The foremost threat for global cereal production is drought due to change in climatic scenario's. To transfer, introgressive genes by following methods: MAS, MAI, MABC, MARS, MAGP, GWS, GS. Greater then 12 hundred QTL resulted from 50 interval mapping studies globally. Under drought stress and optimum moisture conditions maximum number of QTL's reported for thousand grain weight following grain yield. As marker assisted selection enhanced with feasibility and rapid progress for choosing the stress accumulated crop plants for selection accuracy. Regarding contributions recent development in functional genomics and genome mapping served as useful tool for molecular classification of complex trait like drought tolerance. The major challenge for improvement of DR crops in field trails is by biochemical and molecular basis. To unreveal the metabolic pathways and genes governing the drought tolerance using modern genomics and coupled phenotyping with genetic approaches. To improve the food security with variable and changing climate molecular breeding approaches like MABC have to be integrated into crop improvement programme. The physiologists and breeders at CIMMYT created a general model for drought adaptation of wheat that includes traits with a potential function in dry environments.

Keywords: QTL, Molecular Markers, Marker assisted selection, Drought Resistant Crops.

INTRODUCTION

A complex trait that affects the activity of various genes by triggering the wide physiological responses in plants is DR (Jena & Mackill 2008). The climate change with the increasing population, high death rate of different crops contributes the factors of water scarcity which shows the importance for improvement of water use efficiency (WUE) in agriculture. This is done by increasing the tolerance to drought through conventional breeding, genetic engineering to meet global needs of food. Stress adaptation is a major challenge for genetic improvement of DR. To improve WUE in plants, the physiological responses like decreasing leaf area, leaf abscission, leaf wilting, increased root growth by diverting nutrients to underground parts of plant, plant survival hormone ABA which is plant stress hormone induces closure of stomata to reduce water loss by transpiration. Environmental factors influence the genetic control to abiotic stress at various stages of plant growth (Francia

et al., 2005). In the current global climate change sustainable crop production is major challenge. Drought is one of the abiotic stress which had an negative impact on crop productivity. The severity of drought depends on several factors like occurrences and distribution of rainfall, moisture retaining capacity of soil, evaporation rate. Deficiency of soil moisture causes drought by 3 mechanisms, 1. Reduction of radiate use efficiency (RUE). 2. Decrease of canopy absorption of PAR. 3. Reduction of harvest index. The awareness of molecular regulation leads to study of drought stress responses especially translational and post translational machinery plays an important role in stress adaptation for immediate molecular process (Ghatak *et al.*, 2017). The genes for perception and transmission of stress signals include compatible solutes accumulation, cell structure stabilization by ROS (Francia *et al.*, 2005). To combat biotic and abiotic stress of climate change to increase the rice productivity marker assisted breeding (MAB). Enhances the improvement of introgression of single or multiple genes for single trait to multiple genes for multiple traits. MAS based on population size needed for introgressing more than two genes or QTLs. From different generation F3- F8 grain yield and genotyping data for 5 marker assisted breeding are analyzed for understanding the effect of genotyping and phenotyping on selection of better progenies in early generations (Kumar *et al.*, 2018). To identify and select mendelian components recent developments in molecular genetics provide the plant breeders as tools for both simple and complex agronomic traits. Markers and traits association was first reported by isozymes in maize, for application of MAS collection and use of high-quality phenotypic data is required. The construction of genetic maps was done with advent of abundant DNA based molecular markers. to establish marker trait associations (QTL). The marker technologies including with statistical and phenotypical technologies are critical. For population improvement MARS (Marker assisted recurrent selection) constitutes selection of individual based on phenotype of marker and randomly intermated to produce next generation. MARS also done by recombination among selected individual of segregating populations consisting of mosaic favorable chromosomal segments from their parents. In introgression of transgenes and conversions of simple and complex traits MAS become successful in maize. The third important food grain crop is maize in the world. the demand for maize is 50% from 558 million ton's in developing countries. For intensifying production in existing land, the maize is grown even under rainfed conditions. Hence to provide greater drought withstand and perform well in optimum conditioned, CIMMYT contributed many resources to increase the grain yield under water limited conditions (Ribaut & Ragot 2007). for improvement of polygenic traits there are number of MAS approaches of different types available, in tropical maize molecular assisted backcross selection (MABC) is used for improving grain yield under drought stress. The recurrent parent which is drought susceptible is crossed with donor parent, the resultant is repeatedly backcrossed with recurrent parent. This resulted at 5 target regions introgression of favorable alleles involved in expression of flowering traits and yield components for increasing grain yield, at water stress condition it also reduces asynchrony between male and female flowering. In only 4 generations 85% of non-target loci in recurrent parent is recovered by screening large segregating populations for 3-4 generations. The backcross population of BC-F3 derived evaluated by crossing with 2 testers under different water regimes. The mean yield of this is more than controlled hybrids. Under mild drought stress less than 50% of yield reduction is seen. This confirms that the drought tolerance genetic regulations depend on intensity of drought. This involves partial conversions that id presence of favorable alleles at non target loci for phenotypic selection. Selection of more genotypes of 10-20 in each marker assisted backcrossing are most efficient (Ribaut & Ragot 2007). We highlight the importance of drought tolerance, especially in a variable environment, and address recent advances in crop physiology for precise phenotyping and genomic approaches, such as the identification and cloning of QTLs and the identification of candidate genes associated with drought tolerance. Furthermore, new molecular breeding strategies such as marker-assisted recurrent selection (MARS), genomic selection (GS), and genome-wide selection (GWS) are explored as options for incorporating into crop improvement programmes for producing the next generation of drought-tolerant crops. The International Maize and Wheat Improvement Center (CIMMYT) has distributed advanced lines to rain-fed environments worldwide as a result, and it has been confirmed that PT crossing results in cumulative gene action in selected progeny, resulting in increased yield under drought conditions. Research problem dealing with understanding of physiological and genetic basis is important to address the complexity of plant drought response. The advantage is that recent improvement in crop physiology, provide breeders more knowledge and new tools for crop improvement by improving selection efficiency. The disadvantage is that if we fail to understand the seed yield stability molecular mechanisms, use of both traditional and modern genetics for crop improvement like drought tolerance is also hampered. The biosafety and expensive issue limit the use of molecular breeding.

A. Application of MAS in Agriculture

As number of genes are involved in expression of quantitative trait their manipulation is difficult due to its genetic complexity and small individual effect (Choudhary *et al.*, 2008), pearl millet (*Pennisetum glaucum* (L). R.Br). is a staple food for driest, hottest areas of sub tropics and tropics. As drought stress is severe in these regions an essential attribute to incorporate is stress tolerance in pearl millet. Recent research in breeding mapped several QTL for grain and stover yield per se and its maintenance under drought stress. For improving the stress tolerance of hybrid cultivar, the possible selection criteria is evaluation of

QTLS. The advantage of QTL based top cross hybrids is that the initial evaluation of hybrids with top cross pollinators which are bred from mapping population. Drought tolerant parent of mapping population similar to the progeny plant phenotype, in background of drought sensitive parent from introgression of QTL mapping population, H77/833-2, subsequent evaluations were based on test crossed hybrids for drought tolerance under terminal drought stress these QTL introgression lines had greater combining ability for grain yield and both yielded test cross hybrids with recurrent parent unrevealed in gradient and terminal drought stress. From drought tolerant parent of mapping population, the introgression line bred by MABC for drought tolerance is QTL × H77/833-2 (Serraj *et al.*, 2005). Genetic map development is used for detection and breeding of qtl for more traits like components of drought adaptation, grain and stover yield, terminal drought tolerance. The segregating population obtained by crossing H77/833-2 and PRLT2/89-33 and on linkage group 2 of this population QTL for drought tolerance is identified and mapped. These QTLS serves as a major target for MAS across variable terminal stress to improve the grain yield and grain stability on linkage group 2 the QTL also reduces transpiration rate and high rates on ABA in leaves for drought tolerant bajra lines. This QTL also tolerant to saline and alkaline conditions by decreasing NA+ accumulation in leaves of bajra. As compared to drought sensitive parent, 2 QTL NILS of drought tolerant parent (PRLT2/89-33) record higher yield at post flowering stages (Ghatak *et al.*, 2017).

B. Genetic Control of Physiological Traits for Drought Resistance
Physiological traits like membrane stability and osmotic adjustments (OA) also helps for development of DR crops. the OA is the accumulation of solutes under stress by decreasing osmotic potential for increasing water retention and turgor maintenance, OA also causes several advantages in crops like in pea increases the yield under drought stress condition along with increased plant development, root growth, root length density. Hence QTL mapping of OA and associated traits is done in several genotypes only under stress. Because, under stress solute accumulation takes place as a function of leaf desication. ABA is used as a preinvasive defencer and drought avoidance under stress condition but its genetic basis of ABA accumulation for morphological traits is unknown, WUE is studied in wheat and barley under drought stress condition with higher yields by reducing its size, leaf area. The difference in carbon isotope discrimination acts as indirect indicator for WUE among the genotypes (Hu *et al.*, 2014).

C. Breeding for DR Crops
The breeding techniques for developing DR crops are conventional breeding and MAS. Conventional breeding involved backcross strategy for increasing the yield potential and drought resistance where genetic variability analysis of various genotypes are done and introduced into cultivars the required characters. The drawback of conventional breeding is available of suitable genes for breeding and field environmental temporal variation. Whereas MAS is diploid for disease resistant crops. In this method the disease resistant donor genotypes introduced into high yielding with few disease resistant yielded superior cultivars with major QTLS. As, markers of RFLP, RAPD, Isozyme are more effective for development of drought resistant genotypes as they are independent of environment for expression. MAS application in DR genotype are still in progress and experiments are still carrying out (Kiriga *et al.*, 2016). Though phenotypic recurrent selection is used for improvement of complex traits in maize, it is rarely used due to long cycle path. With advancement of molecular markers and classification of traits into QTL's, a mosaic of chromosomal segments carrying the favorable alleles of various parents called an ideal genotype was identified. This ideal genotype not be attainable by MABC due to number of loci and relative contribution of parents. Hence MARS satisfy the need that is it involves the crossing population of several generations, multi trait selection indices. Therefore, the genetic gain for MARS is greater than MABC. For example, when 2 conditions water limited, well-watered conditions are taken for grain yield MABC improves one of the 2 traits whereas MARS improves both the traits. Two recombinant inbreeds grown in Michigan and Mexico in 1990-1994 at 8 locations under stress and non-stress to identify RAPD marker for drought resistance in common bean (*Fasciola's vulagaris*). They are screened with 600primers of which 50% are polymorphic. 70 primers which are polymorphic used for each population screening. Using multiple regression, one way variance analysis we found 4 RAPD in 1 and 5 RAPD markers in another population of stress and non-stress respectively for yield. MAS of sierra/AC1028 was effective under severe stress in Michigan and ineffective in Mexico. Using of RAPD markers in MAS increases the yield by 11% under stress and 8% under non-stress. The effectiveness of MAS is inversely proportional to heritability of the trait is revealed. MARS requires more genetic resources compared with MABC provided they may not be large when genetic background of markers are used for recovery of recurrent parents for MABC approach (Ribaut & Ragot 2007).

D. Genetic Control of root traits in Aspect of DR
Under stress conditions plants roots also play a vital role as productivity is maintained by them. With available ample water at a depth, small diameter of xylem vessels are good for water absorption. The source of genetic progress is genetic variability of soil exploration with effective root system. For selection of traits suitable to target environment QTL contributing to root trait considered either adaptive or constitutive methods. Though these methods are difficult to detect phenotype therefore more researchers choose the plant parts above the ground. Multiple genes are involved in control of root traits with their interaction as the root traits of drought tolerance in targeted environment have greater potential to MARS. Before MRRS programme QTL identified in green house condition must validated

on field for productivity improvement, MARS helps the breeders to select the combination of traits for above and below ground parts with molecular disequilibrium to QTL root trait together with gene are identified and assisted in breeding programme. The challenge is that use of molecular markers for increasing productivity to drought tolerance due to difficulty of detection phenotype with root variation (Hu *et al.*, 2014).

E. Genetics Involved in Drought Resistance

Leaf traits genetic control for drought resistance associated with mechanism used for evaluation of DR crops through QTL mapping the complex functional traits recognized due to availability of functional annotation with QTL studies and gene based markers development. morphological and physiological traits are used by plants as drought avoidance. For sugar content and osmotic adjustment plants have drought tolerance as genetic basis on leaf by QTL mapping to understand the genetic basis of gene expression in drought resistance detection of QTL for photosynthesis and WUE is important. As the ability of photosynthesis depends in stomata density and aperture but due to its unknown genetic variation it becomes harder for researchers in understanding genetic basis. The sensitivity and response of drought varies from plant to plant as repeated drought closes the stomata through increased environmental sensitivity changes. Another drought avoidance trait is leaf rolling which reduces the leaf area exposing to heat and water loss under water deficit conditioned which confers yield advantage (Hu *et al.*, 2014). Once through QTL mapping the gene controlling drought tolerance is identified, they can be incorporated into genetic population through genetic engineering (*Agrobacterium tumefaciens*) and hybridization by MAS (Oladosu *et al.*, 2019). The pyramided lines produced more grain yield advantage over recipient parent across generation and backgrounds as this lines are either a single gene or combination of genetic loci for grain yield. Based on analysis with QTL combinations the superior QTL classes from F3/BC1F3/BC2F3 with QTL X Background, QTL X QTL interaction where recognized by phenotype maintenance of its superiority of yield under RS stress (Reproductive stage), non-stress. The number of genotypes decreased from generations to generations with MAS breeding combining phenotyping and genotyping in early generation of 25 to 68% compared with traditional MAS (Kumar *et al.*, 2018).

RESULT AND DISCUSSION

For development of superior genotypes for drought tolerance using modern breeding approaches firstly select a target trait to be established to select grain yield under drought stress. Then phenotyping of source trait is done using sophisticated techniques like NIR, MRI, NMR. QTL is discovered and cloned for identification of drought tolerance genes.

The yield reduction in maize due to drought is severe in flowering time . Yield components are measured on equal no of plants/ family like kernel number, ear number, grain yield, 100 kernel wt. under severe stress 60% reduction of grain yield due to drought. The population which performed best under well watered conditions are subjected to more stress and no positive correlation exists between drought tolerant index and yield, using composite interval mapping QTL's for grain yield, ear number, kernel number are identified with phenotypic variance of less than or equal to 13%. Across drought environments the stable qtls are identified by evaluation of QTL environment interaction from CIMMYT, apart ado postal 6-641, 06600mexico, 2 QTL's of grain yield which is present on chromosome 1 and 10 coincide with 2 QTL's for kernel number which are stable . Molecular marker assisted selection which is simply called a MAS involves in selection of plants exhibiting expression of genes of interest in genomic regions by molecular markers, therefore for both grain yield and anthesis is silking at interval of 4 genomic regions are identified as only MAS with QTL involving In yield expression is not best strategy we take combination of best QTL's for different traits. Under drought and nonstress conditions 28 significant marker trait association recognized for yield related trait in japonica rice. Under severe drought stress to benefit the farmers with yield advantage of one ton per hectare introgression of 2 or more QTL's are required like qDTY 1.1, Qdty2.1, Qdty3.1. for rice drought varieties in Swarna – sub1, MR219, TDK1-sub1, IR64 sub1, Samba mahusuri from F3-F6/F7/F8 generation (Ribaut *et al.*, 1997). One of the successful example for MABC in rice is the Sabitri, by pyramiding of two QTL's (qDTY12.1, qDTY2.3) FUNAABOR-2 was made in MAGP study imparting drought tolerance at reproductive stage. Introgression of major effective genes like (qDTY1.1, qDTY2.2) developed for drought tolerance. In wheat QTL's introgression (GHD2733, GW322) under MABC governs chlorophyll content, 1000 kernal weight, grain yield, drought tolerance (Wani *et al.*, 2020). The future scope is in some major crops the integrated physiology, breeding approaches, genomics anticipated the initiation of acceleration in orphan crops which is important for food security in developing countries.

CONCLUSION

To study genetic and molecular basis of DR various approaches like engineering, breeding of DR crops are integrated. For developing multiple stress resistance plants gene pyramiding with number of relevant traits is required for breeding of these crops though the QTL have been identified by this method only some are successful due to environment change in field conditions or multiple stresses the use of molecular markers in both public and private maize breeding programmes increasing day by day with profound use of MARS in private sector. The exponential growth of genetic information generated challenge to MAS to integrate this information into specific biological contest and convert it into knowledge. The genetic improvement of quantitative traits can be easily done by MARS in plants and animals. Until the complex traits are classified MAS is restricted to gene of moderate to

large effect. As MAS is not only labour and cost effective but also less time consuming. Better understanding of drought traits is done by QTL analysis and molecular mapping. Even under analogues conditions the QTL of specific background is not significant to QTL of different backgrounds. In rice for physiological and yield traits 3 QTL's (RM8085, 112s and RM6836) using RIL's population (IR20 X Nootripathu) under drought stress. 10QTL's for physiological and productivity using back cross inbred lines (Swarna X WAB450),4QTL's for root length and root dry weight using BC2F2 population (OM1490 X WAB880-1-38-18-20-P1-HB). Using 21623 SNP markers with 180 rice landraces of Vietnam, GWAS studies conducted for drought response and recovery mapping.

Crop models can make a major contribution to a higher degree of integration by directly connecting physiological processes to complex crop phenotypes within the crop. The magnitude of source–sink relationships Likewise, Because of recent developments in genomics, it is now possible to not only conduct. However, large-scale and high-throughput marker genotyping are needed. Even sequence or re-sequence germplasm genomes collections, making it easier to identify QTLs and candidate genes linked to drought resistance.

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