

Review

Potentials of molecular based breeding to enhance drought tolerance in wheat (*Triticum aestivum* L.)

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The ability of plant to sustain itself in limited water conditions is crucial in the world of agriculture. To breed for drought tolerance in wheat, it is essential to clearly understand drought tolerant mechanisms. Conventional breeding is time consuming and labor intensive being inefficient with low heritability traits like drought tolerance. Recent progress made in the field of genomics enabling us to access genes linked with drought tolerance has enhanced our understanding of this complex phenomenon. The purpose of this review paper was to briefly overview the accomplishments in molecular breeding for drought tolerance in wheat. Thus, by knowing the genetics of drought tolerance and identifying quantitative trait loci (QTLs) linked with DNA markers will help wheat breeders to develop high yielding drought tolerant cultivars.

Key words: *Triticum aestivum* L, drought tolerance, QTLs, marker assisted selection (MAS).

INTRODUCTION

Wheat (*Triticum aestivum* L) is a cereal of choice in most countries of the world. Constant efforts are therefore needed to boost its production to keep the pace with ever increasing population. But unfortunately, these efforts are seriously being hampered by a number of abiotic stresses among which is drought (Boyer, 1982). According to Pfeiffer et al. (2005), 50% of wheat production area is affected due to drought worldwide. Drought leads to abnormal germination and poor crop stand (Harris et al., 2002; Kaya et al., 2006). Furthermore, drought prevailing at various critical growth stages like flowering and grain filling greatly reduce crop yield and due to that reason, its importance have been realized at the global level. Thus, developing drought resistant cultivars has been the objective of plant breeders and plant biotechnologists.

Considerable efforts have been made in the past to develop drought tolerant cultivars of wheat through conventional breeding. But with little success due to quantitative (polygenic) nature of drought tolerance which

is more influenced by external environmental conditions than by the genetic component (El-Jaafari, 1999; Krishnamurthy et al., 1996; Ingrams and Bartels, 1996; Zhang, 2004).

The recent progress in the field of genomics is astonishing providing breeders new tools for crop genetic improvement with reference to drought tolerance (Cattivelli et al., 2008) This review paper therefore analyses how genomic based approaches can contribute to the accelerating release of drought tolerant wheat cultivars.

DROUGHT TOLERANT MECHANISMS

Drought tolerance is the ability of plant to sustain itself in limited water supply (Ashley, 1993). As aforementioned, drought tolerance is a complex polygenic trait, therefore a number of factors come in to play making the plant to sustain drought. Drought affects the plant at the cellular, tissue and organ levels (Beck et al., 2007) and drought tolerant plants tackle the injurious effects of drought by initiating various defense mechanisms which should be understood in order to breed for drought tolerant cultivars

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(Chaves and Oliveira, 2004; Zhou et al., 2007). Drought tolerant mechanisms can be morphological, physiological or molecular (Bohnert et al., 1995; Farooq et al., 2009).

Morphological mechanisms include; drought escape which is the ability of plant to complete its life cycle before the onset of drought season (Mitra, 2001), drought avoidance which is the plant's ability to retain the water by increasing the uptake of water and reducing its loss through reduced transpiration which is made possible by long and thick root network as well as leaf and stomatal characteristics (Blum, 1988; Turner et al., 2001; Iznaloo et al., 2008; Agbicodo et al., 2009).

Among the physiological mechanisms, osmotic adjustment (OA) is perhaps the most crucial factor which allows the cell to decrease osmotic potential and maintain the turgor and the plant is able to sustain itself in decreased water supply (Blum, 2005; Farooq et al., 2009; Taiz and Zeiger, 2006).

The role of abscisic acid (ABA) a stress hormone cannot be overlooked. Under water deficit environment, ABA induces the closure of stomata and thus reducing water transpiration (Turner et al. 2001). Glucosiness (a waxy covering over the cuticle) is also considered to be a reliable parameter leading to increase in water use of efficiency in wheat plant thus providing a mechanism of drought tolerance (Richards et al; 1986).

The molecular mechanisms involve activation of a cascade of genes which ultimately make the plant desiccation tolerant (Agarwal et al., 2006; Umezawa et al., 2006)

MAPPING QTLs FOR DROUGHT TOLERANCE IN WHEAT

As aforementioned, conventional breeding strategies like selection and hybridization have met with little success in breeding for drought tolerance in wheat. The genomic based approaches provide excellent opportunities to search and map quantitative trait loci (QTLs) for drought tolerance. This is due to our increased understanding of gene structure and function at the cellular and molecular level (Gosal et al., 2009). Various QTLs for drought tolerance in wheat are summarized in Table 1.

Earlier, Quarrie et al. (2005) conducted mapping of QTLs for drought tolerance in hexaploid wheat which were located on chromosomes 1A, 1B, 2A, 2B, 2D, 3D, 5A, 5B, 7A, and 7B.

Double haploid populations serve as a permanent source of mapping QTLs. Dashti et al. (2007) used 96 doubled haploid lines of wheat to analyze QTLs for drought tolerance. They found drought tolerant indices for QTL effects ranged from 13 to 36%. Recombinant inbred lines developed from crossing drought resistant and drought susceptible lines were used to produce mapping populations for QTL analysis regulating yield under drought (Tuberosa et al., 2002).

MAPPING QTLs THROUGH MARKER ASSISTED SELECTION (MAS) IN WHEAT

Marker assisted selection (MAS) refers to selection based on DNA markers linked to QTLs. The DNA markers are very powerful. Once these are identified, their mapping on the chromosome in relation to QTLs is carried out. Thus, presence of QTLs for drought tolerance can then be tracked by careful monitoring of these DNA markers (Thoday, 1961; Everson and Schaller, 1955). Various DNA markers like restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), and simple sequence repeat (SSR) have been used to tag QTLs for drought stress in wheat (Quarrie et al., 2005). Application of microsatellite markers in wheat for tagging QTLs for disease resistance, grain protein contents, and yield have also been documented by a number of scientists (Fahima et al., 1998; Huang et al., 2000; Del Blanco et al., 2003; Huang et al., 2003; Prasad et al., 2003).

Kirigwi et al. (2007) used simple sequence repeat (SST)/expressed sequence tag (EST) marker for mapping QTL on chromosome 4A for grain yield and yield components in wheat. The markers associated with the QTL were *XBE637912*, *Xwmc89*, and *Xwmc420*. Thus, the DNA markers closely linked with QTLs conferring drought tolerance would greatly enhance the selection efficiency (Cattivelli et al., 2008).

CANDIDATE GENES AND FUNCTIONAL GENOMICS

A candidate gene is one which is associated with the function and development of any trait. There has been a growing interest to map and sequence the candidate genes with known or proposed function determining QTLs associated with drought tolerance (Byrne and McMullen, 1996; Gutterson and Zhang, 2004; Nguyen et al., 2004).

The technologies of microarrays and DNA chips are being successfully employed to quickly monitor or predict the expression of millions of genes and search the genomes of target crops (Schena et al., 1996; Lemieux et al., 1998). The technology of microarray becomes more useful when coupled with EST analysis (Sreenivasulu et al., 2007). EST markers are available for rice and efforts for developing EST markers for wheat are in progress (Goff, 1999). In short a dedicated effort is what is required to isolate and develop EST markers for drought tolerance to be able to get full potential of microarray technology.

TRANSGENIC DROUGHT TOLERANT WHEAT

In recent years, introducing drought tolerant genes from different sources into drought susceptible plants has

Table 1. Summary of QTLs associated with drought tolerance in wheat^a

Cross	Trait	QTL Mapping	Number of QTL	Reference
Chinese Spring x Ciano 67	ABA concentration	DHL*	1	Quarrie et al. (1994)
Songlen x Cobdor 4/3Ag14	Osmoregulation under drought	RIL*	1	Morgan and Tan (1996)
Trident x Molineux	Yield interaction with water supply and hot conditions	DHL	1	Kuchel et al. (2007)
Durum x Wild emmer	Various morpho-physiological traits	RIL	many	Peleg et al. (2009)
Seri M82 x Babax	Various productivity and physiological traits	RIL	many	McIntyre et al. 2010; Suzuky Pinto et al., 2010.

*DHL= doubled haploid; RIL= recombinant inbred lines; ^aSimilar studies reported in the text were not included in this table.

Table 2. List of recently produced transgenic wheat with drought tolerant genes.

Gene	Mechanism of tolerance	Reference
<i>DREB1A</i>	Regulatory control	Pellegrineschi et al. (2004).
<i>HVA1</i>	Protective proteins	Sivamani et al., 2000; Bahieldin et al., 2005
<i>mtID</i>	Mannitol as osmoprotectant	Abebe et al. (2003)
<i>P5CS</i>	Osmoprotectant	Kavi Kishor et al., 1995; Sawahel and Hassan, 2002;
<i>TaLTP1</i>	Lipid transfer protein	Jang et al. (2004).

become one of the promising avenues for plant genetic engineers. A transgenic approach involves the structural modification in traits by transferring genes from one species to another (Ashraf, 2010). A number of genes conferring drought tolerance from different sources have been incorporated in wheat making it transgenic (Table 2).

Most of these transgenic lines have been tested in the laboratory. Their full scale utilization in the field would provide important information for continued exploitation of transgenic work. Nonetheless it is expected that transgenic approach will have an increased role in the future as far as the mapping and engineering of QTLs for drought tolerance is concerned (Cattivelli et al., 2008; Ashraf, 2010).

CONCLUSION

Drought is a major cause of yield losses of wheat in the world. Applications of conventional selection based breeding are limited due to complex nature of drought stress and drought tolerance. The molecular based tools would ultimately help us to identify potential candidate genes and valuable QTLs for drought tolerance and their effective utility in marker assisted breeding (Tuberosa

and Silvio, 2006; Taishi et al., 2006; Fleury et al., 2010). The integration of these novel approaches with conventional system of crop genetic improvement should provide exciting results to breed for drought tolerance in wheat in the near future (Khan and Iqbal, 2011).

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