

# Improve Root System Architecture: An Opportunity to Cereal Crop Improvement In Climatic Change Conditions

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## Abstract

To keep pace with the increasing population and world food supply requirements under the unpredicted conditions of climate change, improved root systems in staple crop plants will be essential. An improvement in root architecture is an effective strategy to increase crop yield. With the aid of novel molecular biology methods, continuing progress on root genetic research has been achieved in cereals. Root is the foundation of crop development, which absorbs most nutrients and water. The use of fertilizer changed dramatically in the twentieth century, but excess nutrients have involved in many environmental problems. Nitrogen use efficiency (NUE) for cereal production is approximately 33% worldwide. Nitrogen pollution is now claiming the next major threat to our planet after biodiversity loss and climate change. Drought, heat & salinity are the most severe abiotic stresses limiting crop productivity in the world, and poses a serious threat to the sustainability of crop yields in rainfed agriculture. Acquisition of more water from soil is a mechanism for drought & high temperature tolerance in rice, wheat and maize. Improving the understanding of the interaction between root function, nitrogen use efficiency and stress tolerance in crop could have a significant impact on global food security. A number of genes related to root morphological characteristics and physiological functions have been identified or cloned, which opened an opportunity for further improvement of cereal crops productivity. The over expression of noble transcription factors and genes results in more roots and higher grain yield. Therefore, improving root system with deep root and high water uptake & improve nutrient use ability would be the key to developing cereal crops suitable for water-saving farming system more sustainable solution than relying on fertilizer application alone.

**Key words:** Root architecture, Nutrient use efficiency, Drought stress, Heat stress, Salt stress, Transcription factors

## 1. Introduction

Wheat is one of the important food crop, more than half of the world's population is dependent on wheat. The increasing population and urbanization have been posing a high pressure for increase in food production (Zhang, 2007). To meet the demand of food for increasing population, raising the yield ceiling of wheat remains a priority task for researchers. As an important organ of wheat plant, root performs vital functions: acquisition of resources and anchorage of wheat plant. In addition, root systems serve the secondary functions, such as propagation, synthesis of growth regulators, storage (Fitter, 2002). Roots sense and response to abiotic and biotic stresses, and communicate with the shoot via signalling pathway. Drought causes water deficit that limits plant growth and survival because root water uptake from the soil is insufficient to meet the transpiration requirements of the plant. Water deficit stress reduces leaf cell turgor, canopy area, and photosynthetic source size, thus negatively affect biomass accumulation and overall crop yield (Chaves *et al.*, 2003). An effective drought adaptation mechanism is used to reduce water loss during transpiration, which helps in soil moisture conservation and allows plants to maintain an adequate water level to sustain critical physiological and biochemical processes (Chaves *et al.*, 2003). However, a reduction in transpirational water loss often leads to a decline biomass accumulation because decrease in carbon assimilation. Transpiration and CO<sub>2</sub> uptake occur through stomata, the pores bordered by a pair of guard cells (Hetherington and Woodward, 2003). Alteration of stomatal aperture in relation with the environment is a well-understood procedure that has been linked functionally to drought tolerance and water use efficiency (WUE; Nilson and Assmann, 2007; Kim *et al.*, 2010). However, it is unclear how these environment stresses regulate the developmental determinants and what are the consequences of

altered stomatal density with reference with heat & drought tolerance.

The root is an important organ in nutrients and water uptake. Optimizing root system architecture (RSA) can overcome yield limitations in crop plants caused by limited water or nutrient (Werner *et al.*, 2010). Roots can regulate not only stomatal conductance, and also affect the posture of leaf blade and photosynthesis rate under soil impedance, nutrient, drought and salt stresses. It is well known that the functions of absorption and support of root system are an important guarantee for biological yield. Therefore, root traits have been claimed to be critical for increasing yield under soil-related stresses (Lynch, 2007). Root morphology and physiology are closely associated with the growth and development of above-ground part of plant (Yang, 2011). Root researches have been paid more and more attentions in recent years. With the aid of novel molecular biology methods, continuing progress on root genetic research has been achieved in wheat. A number of genes related to root morphological characteristics and physiological functions have been identified or cloned, which opened an opportunity for further improvement of wheat crop.

## 2. Various transcription Factors & Genes Regulate Root Physiology during Environmental Stress:

### **DRO1 Gene:**

The root system is a vital plant organ owing to its involvement in water absorption, nutrient acquisition, anchorage, propagation, storage functions, secondary metabolite synthesis, and accumulation (Saini *et al.*, 2013). Accumulated evidence indicates that improved root architecture is an efficient strategy for drought avoidance (de Dorlodot *et al.*, 2007). Higher expression of *DEEPER ROOTING 1 (DRO1)* increases root angle and facilitates root growth in a more downward direction in rice (*Oryza sativa*). Introducing *DRO1* into a shallow rooting rice cultivar leads to a deeper root system, enhanced drought tolerance, and stable grain yield (Uga *et al.*, 2013). Statistical data show that increased biomass and increased yield in maize (*Zea mays*) in the American Corn Belt can be attributed to improved root architecture (Hammer *et al.*, 2009). To keep pace with the increasing population and world food supply requirements under the predicted conditions of climate change, improved root systems in staple cereal crop plants specially wheat will be essential.

### **ARF Gene:**

Root growth and differentiation are inextricably linked to plant hormones (Overvoorde *et al.*, 2010; Vanneste and Friml, 2009). Auxin, as one class of important phytohormones, attracts extensive

attention because of its involvement in almost every aspect of plant growth and development, including embryogenesis, organogenesis, tissue patterning, and tropisms (Quint and Gray, 2006). Indole-3-acetic acid (IAA) is an important natural auxin, responsible for root architecture and plant development at various stages (Benkova and Bielach, 2010; Overvoorde *et al.*, 2010; Lewis *et al.*, 2011; Lavenus *et al.*, 2013). Auxin response factors (ARFs) are transcription factors (TFs) that specifically bind to TGTCTC-containing auxin response elements (AuxREs) located in the promoters of primary/early auxin response genes and mediate responses to auxin (Guilfoyle and Hagen, 2007). *ARF* (Auxin Response Factor) genes belonging to a large gene family involved in hormone signalling are highly specific to selected cell and tissue types or developmental programmes in Arabidopsis and rice (Wilmoth *et al.*, 2005; Wang *et al.*, 2007; Qi *et al.*, 2012).

Previous research suggests that *AS2/LOB* genes play crucial roles in root initiation and development. *In vitro*, ARF7 binds to AuxREs in the promoters of two *AS2/LOB* genes in Arabidopsis, and ARF7 and ARF19 play a positive role in regulating lateral root formation via direct activation of *LBD/ASLs* (Okushima *et al.*, 2007; Feng *et al.*, 2012b). This approach can also be applied in wheat *via* genetic transformation mediated transgenic development.

### **TaMOR gene:**

Past researcher demonstrate that overexpression of transcription factor gene *MORE ROOT (TaMOR)* from wheat (*Triticum aestivum* L.) results in more roots and higher grain yield in rice (*Oryza sativa*). *TaMOR*, encoding a plant-specific transcription factor belonging to the ASYMMETRIC LEAVES2/LATERAL ORGAN BOUNDARIES (*AS2/LOB*) protein family, is highly conserved in wheat and its wild relatives. According to Li *et al.*, 2016 tissue expression patterns indicated that *TaMOR* mainly localizes to root initiation sites. The consistent gene expression pattern suggests that *TaMOR* is involved in root initiation. Researcher discovered a *MORE ROOT (TaMOR)* gene series in wheat containing a typical *AS2/LOB* domain. *TaMOR* are highly conserved in both nucleotide and amino acid sequences. They are involved in auxin signalling in the initiation of both lateral and crown roots. Overexpression of *TaMOR* leads to more lateral roots in Arabidopsis, and *TaMOR*-overexpressing rice plants have larger root systems and increased grain yields. Furthermore, *TaMOR* can interact with *TaMOR*-related protein (*TaMRRP*) on the cell membrane. *TaMOR gene* is a promising candidate for root improvement and grain yield enhancement in crops. The knowledge is provided for future researchers to solve food grain deficiency

by overexpressing *TaMOR* gene various wheat genotypes.

### **NOX Gene:**

Reactive oxygen species (ROS) have been shown to be toxic but they function as signalling molecules. NADPH oxidases (NOXs) are key enzymes of ROS generation and thus play crucial roles in a variety of biological processes (Torres and Dang 2005; Bedard and Krause 2007). However, in plants only NOX5-like type NOXs were found, even their multiple forms exist in different species (Wang *et al.*, 2013). The plant NOXs, also named as respiratory burst oxidase homologs (RBOHs), are proposed to be major ROS producers in plants under normal and stress environment (Foreman *et al.* 2003; Sagi and Fluhr 2006). Therefore, various plant NOXs were identified in dicots crops like *Solanum tuberosum* (Yoshioka *et al.*, 2003), *Arabidopsis thaliana* (Sagi and Fluhr 2006), *Medicago truncatula* (Marino *et al.*, 2011) and in monocots like *Zea mays* (Nestler *et al.*, 2014). In *Arabidopsis*, ten members of NOXs were reported as AtRBOHA–J, respectively (Sagi and Fluhr 2006). In rice, nine typical NOXs were reported (Wong *et al.*, 2007; Wang *et al.*, 2013). AtRBOHD and AtRBOHF reported to be involve in functioning disease resistance (Chaouch *et al.*, 2012) and salt stress tolerance (Xie *et al.*, 2011). Evans *et al.*, (2005) found that AtRBOHJ functions in salt stress tolerance. Recently, it was reported that AtRBOHH and AtRBOHJ play essential roles in pollen tube tip growth via Ca<sup>2+</sup> activated ROS production (Kaya *et al.*, 2015). In maize, the expression of the four NOX genes, induced by ABA treatment, implying in the function of plant stress tolerance (Lin *et al.* 2009). In rice, the expression of NOX-encoding genes showed unique stress-response characteristics (Wang *et al.*, 2013). In wheat roots, NOXs ameliorate the oxidative stress induced by nickel (Hao *et al.*, 2006). Overall, NOXs participate in the plant immune response (Yoshioka *et al.*, 2011), root hairs growth (Nestler *et al.*, 2014) and pollen tubes (Wudick and Feijo´ 2014; Kaya *et al.*, 2014, 2015), abscisic acid (ABA)-mediated stomatal closure (Zhang *et al.*, 2009; Shi *et al.*, 2012), apoptosis (Tewari *et al.*, 2012), tapetal programmed cell death (PCD) and pollen development (Xie *et al.*, 2014), control of cell differentiation and proliferation (Cano-Domínguez *et al.*, 2008), and seed after ripening (Muñer *et al.*, 2009) in higher plants. The ancient forms of NOXs also exhibit important roles. As the major producer of ROS during cell growth, plant development, and stress responses, the increasing evidence also show that plant NOXs participate in a number of signalling pathways (Zhang *et al.*, 2014), like Ca<sup>2+</sup>-dependent protein kinases and hormone-signalling transduction cascades (Zhang *et al.*, 2014). Thus, NOXs may serve as molecular ‘house’ during ROS-mediated

signalling in plants, therefore, crucially involve in plant stress response, normal growth and development. Although these studies in *Arabidopsis* have led to an understanding of the biochemical properties and physiological functions of NOXs, there has been no systematic study of the evolution and functional divergence of the NOX gene family, especially in Plants. As reported in past years, NOX is responsible for root hair growth (Nestler *et al.*, 2014) it will be boon for food security issues. By dense growth of root hair NUE & WUE is increased due to large surface area & indirectly it will help crops to win war with environmental stress especially high temperature and drought stress.

### **3. Conclusion and Future Prospectus:**

Although knowledge on wheat root is increasing and has given an insight into mechanisms of root development, it remains unclear what root traits should be taken into wheat breeding programs. There are difficulties that hampered progress of root genetics: research efforts devoted to the root system have been much less than to the above ground part. Lacking stable and credible morphological data makes it difficult to perform genetic research on wheat root traits. However, many methods are still time-consuming and laborious, and largely influenced by the complex underground environments. Root sampling procedures are often destructive. It is impossible to sample intact root system from plants in field environments. Root Improvement through genetic engineering have provided a new and convenient method in which the whole root system could be extracted from the plants for molecular analysis for stress resistance. But this *in vitro* culture system could not completely mimic the environments of wheat field, thus the information obtained in this system usually do not exactly reflect root feature under natural conditions. For identifying and screening the root traits, more facilitated and effective methods, especially the large-scale screening techniques for root measurement in paddy field are urgently required. Quantitative trait loci (QTL) mapping is a major approach for investigating complex genetic traits such as root. To cope with this problem, association mapping (meta-analysis) as a promising method was introduced to genetic dissection of complex traits. Using association mapping, it is possible to locate QTLs with better precision than using a mapping population.

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