

## QTL mapping for the improvement of drought tolerance in cereal crops: An overview

Hafiz Muhammad Ahmad<sup>1,\*</sup>, Mahmood-Ur-Rahman<sup>1</sup>, Farrukh Azeem<sup>1</sup> and Qurban Ali<sup>2</sup>

<sup>1</sup> Department of Bioinformatics and Biotechnology, Government College University, Faisalabad, Pakistan

<sup>2</sup> Centre of Excellence in Molecular Biology, University of the Punjab, Lahore, Pakistan

Corresponding author: [hafizahmad90@yahoo.com](mailto:hafizahmad90@yahoo.com), [saim1692@gmail.com](mailto:saim1692@gmail.com)

**Abstract:** Cereals are annual grasses having starchy grains that are used as food. Drought is major stress that largely constrains the productivity of cereal crop in all over the world. Improving the cultivars against drought stress will increase crop yield as well as the cultivatable areas. Therefore, the development of cultivars having resistance against drought stress is a fundamental challenge for biologists to address future problems of food security. Identifying genomic regions responsible for drought tolerance will be helpful to develop the cultivars suitable for drought stress environments. Hence quantitative trait loci (QTL) mapping is a fundamental tool which aids to dissect the complex traits of drought stress. Significant work has been done in this direction by plant breeders and biologists. This review article narrates the cereal specific research on QTLs and enlightens the traits that have been considered responsible for drought tolerance. Moreover, it has also been discussed that how breeders have improved these traits in cereals by using a QTL mapping approach. The knowledge can help the plant breeders to expedite the release of cultivars that are resistant to drought stresses by quick and accurate accumulation of desirable alleles in breeding programs.

[Ahmad HM, Rahman MU, Azeem F, Ali Q. **QTL mapping for the improvement of drought tolerance in cereal crops: A review.** *Life Sci J* 2015;12(4s):102-108]. (ISSN:1097-8135). <http://www.lifesciencesite.com>. 14

**Keywords:** QTL mapping, Abiotic stress, Drought resistance, Molecular markers, Cereal crops

### Introduction

Crop production is inherently sensitive to variations in climatic conditions (Pasha *et al.*, 2015). Naturally, plants are simultaneously exposed to a combination of biotic and abiotic stresses that causes reduction in the crop yield (Ahmad *et al.*, 2015, Ramegowda and Kumar., 2015). Drought is a situation when the supply of available water is lower than the demand of plants, which ultimately lead to wilting or death of plant. In other words drought is an imbalance between soil water availability and evaporative demand (Tardieu *et al.*, 2011). Due to drought, a series of biochemical and molecular changes occur in plants that affect the plant growth and crop productivity, these changes appear in the form of morphological and physiological variations in plants (Sahoo *et al.*, 2014). Plants acquired various mechanisms during the course of their evolution to avoid drought as they do not have the ability to move and avoid drought. Responses to drought stress are commonly dependent on plant genotypes, plant species, age of plant, its developmental stage and the severity of drought (Ali *et al.*, 2011; Gall *et al.*, 2015). In order to improve the yield under water limited conditions, plants traits, i.e. leaf angle, leaf size and area, stomata size, abscisic acid accumulation, root density and its architecture, are the basic targets for plant breeders. Capacity for deep root growth and large xylem diameters in deep roots may also improve root acquisition of water (Comas *et al.*, 2013). On the basis of drought responses to plant physiology, plant

molecular biologists have discovered many genes that are involved in drought tolerance, including functional and regulatory genes, which protect the cell from drought and regulate the stress response (Mizoi and Shinozaki, 2013). Functional genomics has been used to understand the relationship between genome of an organism and its phenotype under different environmental conditions (Soda *et al.*, 2015). QTL mapping is a tool to separate the complex phenotypic traits into their components and is a source of understanding the genetic basis of plant traits under diversification selection during crop evolution (Bo *et al.*, 2015). The identification of QTLs affecting drought tolerance is a major step in understanding the genetic basis of plant response to water deficit conditions and for the development of drought tolerant cultivars. Through indirect manipulation of quantitative trait loci, improvement in crop yield is possible because QTLs can be used to control the heritable variability of the traits and physiological mechanisms that determine biomass production and partitioning (Nicholas *et al.*, 2008). Several efforts have been made to identify QTL for drought tolerance in crop plants by biologists, but due to the complex inheritance mechanism of drought tolerance, identified QTLs have been proven unstable across different environments. Further utilization of QTL information for marker-assisted breeding or candidate gene identification has become difficult due to complexity of inheritance mechanism. Quantitative trait loci (QTL) approach has helped to identify genomic

regions for the drought tolerance related traits including length, weight and thickness of root and shoot height, leaf rolling and osmotic adjustment under hydroponics (kato *et al.*, 2008) and other artificially created stress conditions (Cui *et al.*, 2008). The root-related characters have recently been used in breeding for tolerance to drought stress (Liu *et al.*, 2008). Identification of genetic factors involved in plant responses to drought stress provides a solid foundation to improve drought resistance. The discovery of genes from new germplasm resources has become extremely important for drought resistance. Localization of these genes that contribute to drought avoidance in a quantitative way will enable the exploitation of these genes in breeding through marker-assisted selection, and may lead to the discovery of genes and corresponding functions (Price *et al.*, 2002). Optimizing root architecture can lead to a significant yield advantage in water-limited environments (Manschadi *et al.*, 2010). Drought tolerance QTLs also influenced the plant growth under salt stress by reducing salt uptake (Sharma *et al.*, 2011) indicating that some QTL/genes may have pleiotropic effects on multi-stress tolerance. Present review has the aim to discuss the role of QTLs mapping approach for the improvement of drought tolerance in various cereal crops to enhance grain yield of these crops under water deficit conditions.

#### **1-QTL mapping for drought tolerance in wheat**

Wheat is a principal cereal crop occupying largest cropped area in the world. It is cultivated throughout the world including irrigated, arid and semi arid areas of the world (Raza *et al.*, 2015). Development of high yield cultivars with desirable combination of traits has always been the most important objective of wheat breeders (Ashfaq *et al.*, 2014). In dryland cropping system, drought is a major factor that reduces the grain yield as it causes physiological changes in plants, including osmotic adjustment, turgor pressure and reduction in leaf water potential (Shao *et al.*, 2008). Due to variability in timing and severity of drought stress, it is difficult to characterize the physiological and phenotypic traits required for screening and improving crop performance under drought stress.. It also has been observed during early days to flowering in wheat causes to avoid drought and abiotic stresses in rainfed areas (Raza *et al.*, 2015). Consequently, this difficulty has limited the use of a trait-based approach in plant breeding to enhance the drought tolerance of crops. The breeding of wheat varieties with improved yield and yield stability under water limited environments is a high priority for improving food supply and to ensure food security of rapidly increasing population (Ahmad *et al.*, 2014). Hence researchers are required to identify the traits which are responsible for plant

performance under water limited conditions i.e deep rooted plants, turgor pressure, leaf water potential and root architecture. Manschadi *et al.*, (2010) concluded that optimizing the root architecture can lead to a significant yield advantage in water-limited environments. The idea that drought tolerance is quantitatively inherited and controlled by several genetic loci has helped the researchers to investigate many QTLs for drought (Sayed *et al.*, 2012, Kalladan *et al.*, 2013). In wheat most of the work regarding drought tolerance has been done for the improvement of root architecture. A QTL has been reported for deep root ratio in hexaploid wheat (Hamada *et al.*, 2012), a QTL (QRl.ccsu-2B.1) for root length and for root dry weight (QRdw.ccsu-2A.1, QRdw.ccsu-2A.2.) on chromosome No 2B and 2A respectively (Gupta *et al.*, 2014). Similarly, Christopher *et al.*, (2013) found the QTLs (QRA.qgw-2A, QRA.qgw-3D, qRA.qgw-5D) for root angles and a QTL (qRN.qgw-1B) for root numbers. Moreover, QTLs for root anatomical traits, i.e xylem vessel characteristics have also been reported (Sharma *et al.*, 2010). Fine mapping is in progress in durum wheat for a major QTL on chr. 3B, that will influence the grain yield across a broad range of soil moisture regimes (Maccaferri *et al.*, 2008).

#### **2-QTL mapping for drought tolerance in maize**

Drought is an important abiotic stress constraint that causes significant yield losses in maize grown throughout south and south-east Asia. The most economical option to offset the damage caused by drought is to genetically incorporate tolerance in cultivars that are grown widely in the target agro-ecologies (Zaidi *et al.*, 2015). By development of drought related molecular markers it is now possible to recognize major quantitative trait loci (QTL) regulating specific drought responses (Lebreton *et al.*, 1994). Drought tolerance QTL studies in maize and the strategies for its uses in marker-assisted selection (MAS) in breeding programs have been reported by (Collins *et al.*, 2008; Tuberosa and Salvi, 2009). A genetic linkage map developed using RFLP markers was used to identify QTLs associated with drought-related traits. Twenty-two QTLs were detected, with a minimum of one and a maximum of nine for drought-related traits. Four QTLs were detected for osmotic potential on chromosomes 1, 3, and 9, together accounting for 50% of the phenotypic variance. Nine QTLs were detected for leaf surface area on chromosomes 3 and 9, with various degrees of phenotypic variance, ranging from 25.8 to 42.2% (Rahman *et al.*, 2011). Stay-green is a desirable character for crop production in maize. Wang *et al.*, (2012) detected three major QTLs for stay-green related traits in corn. Mano *et al.*, (2005) mapped QTL for adventitious root formation under waterlogged conditions on chromosome 4 and 8 in maize. Root

traits can be used to improve tolerance to abiotic soil stresses, such as drought and nutrient deficiency, by enhancing the metabolic efficiency of soil exploration (Lynch, 2013). Root cortical parenchyma reduces root respiration, and improves plant performance and yield under water deficit conditions in maize (Zhu *et al.*, 2010). In maize near isogenic lines, two major QTLs have been derived on chromosome bins 1.06 and 2.04 that influence root architecture and grain yield under different water regimes (Landi *et al.*, 2010). The genetic dissection of drought tolerance in maize was reported, which widely accounts for successful practical application of identified QTL in maize improvement programs (Truntzler *et al.*, 2010; Li *et al.*, 2011; Ali *et al.*, 2012). The reasons are manifold, including genetic complexity, influence of genetic background, epistasis, population-specific nature of identified QTL and involvement of donor lines that are not agronomically elite.

### 3-QTL mapping for drought tolerance in rice

Rice is the staple food of more than 60% of the world's population. Drought is the major source to reduce the rice production across Asia and sub-Saharan Africa. In the context of current and predicted water scarcity, increasing irrigation is generally not a viable option to alleviate drought problems in rice growing areas. Variation in intensity and severity of drought from season to season and from place to place requires cultivation of rice varieties with different levels of drought tolerance in different areas. Rice is highly sensitive to drought stress during the reproductive stage, when even moderate stress can result in drastic reduction in grain yield (O'Toole, 1982). The timing of drought: early season, mid-season, or terminal stage has a major influence on how much yield loss occurs. Therefore, poverty reduction strategies in drought prone areas must focus on stabilizing yields, that is, on breeding varieties with improved yield under drought stress as well as good response to irrigated conditions. The identification and introgression of QTL leading to high grain yield under drought have been considered to be the preferred breeding strategy to improve drought tolerance in rice. A lot of work has been done in this area to obtain the cultivars having resistance against drought. Srividhya *et al.*, (2011) discovered QTLs (qsl1.1) for shoot length and (qmr13.1 & qmr13.2) for root length on chromosome No.1 and 3 respectively having resistance against drought in rice cultivars. Uga *et al.*, (2008, 2010) reported a QTL for root anatomical traits i.e., root stele and xylem vessel diameter in rice. Similarly Mardani *et al.*, (2013) reported QTL (qGR-1 and qGR-4 present on chromosome No 1 & 4 showing the resistance against drought stress. Yue *et al.*, (2005) analyzed the QTLs for traits of plant water status and their relationships with root traits under drought.

Correlation and QTL correspondence between root traits and putative drought tolerance traits revealed that drought avoidance via thick and deep root traits was the main genetic basis of drought resistance in sandy soil condition, while drought tolerance may play more roles in the genetic basis of drought resistance in paddy soil condition. Lanceras *et al.*, (2004) investigated that the cumulative effects of QTL on chromosomes 3, 4, and 8 resulted in higher grain yield. These QTLs will be useful for rainfed rice improvement, and will also contribute to our understanding of the genetic control of grain yield under drought conditions at the sensitive reproductive stage.

### 4-QTL mapping for drought tolerance in pearl millet and sorghum

Pearl millet and *Sorghum bicolor* are an important source of food, feed, and biofuel. They are also termed as dryland cereals, often grown in areas with marginal rainfall. The growing instability of seasonal rainfall patterns and temperature conditions has prompted greater attention towards the genetic improvement of traits that maximize grain yield in water-limited environments. Post-flowering drought adaptation in sorghum is associated with the stay-green phenotype. Typically, QTL study includes an accurate phenotypic evaluation of an adequately large mapping population, its molecular profiling and a statistical analysis to test the association between a phenotype and a marker genotype. Significant progress has been made in mapping a number of QTLs for components of grain and Stover yield, as well as yield maintenance, under terminal drought stress conditions in pearl millet (Yadav *et al.*, 2004; Bidinger *et al.*, 2005). Recent genetic mapping research in pearl millet has mapped several QTLs for grain yield and its components under terminal drought stress conditions. Most importantly, a major QTL associated with grain yield and for the drought tolerance of grain yield in drought stress environments has been identified on linkage group 2 (LG 2) which accounts for up to 32% of the phenotypic variation of grain yield in mapping population testcrosses (Rattanet *et al.*, 2010). The results thus confirmed the effectiveness of the putative drought tolerance QTL on LG 2, but suggested that it may enhance drought tolerance by favoring a particular phenotype with adaptation to terminal stress (Bidinger *et al.*, 2005). Nodal root angle in sorghum influences vertical and horizontal root distribution in the soil profile and is thus relevant to drought adaptation. Mapping of four QTLs for nodal root angle (qRA) was performed in sorghum, in addition to three QTLs for root dry weight, two for shoot dry weight, and three for plant leaf area (Mace *et al.*, 2012). A QTL (qTLA3\_8) for flag leaf area was identified by Mace *et al.*, (2012),

which was important for resistant to drought stress in sorghum. Drought affects the Sorghum at post-flowering drought tolerance (stay green), pre-flowering drought tolerance stages (Kebede *et al.*, 2001). The identification of QTLs and markers for pre-flowering drought tolerance and lodging tolerance will help plant breeders in manipulating and pyramiding those traits along with stay green to improve drought tolerance in sorghum (Kebede *et al.*, 2001).

#### 5-QTL mapping for drought tolerance in barley

Barley is the fourth most important cereal after wheat, rice and maize in terms of area and production worldwide. Approximately 75% of barley global yield is used as feed, 20% as raw material for beverages and 5% as food (Sreenivasulu *et al.*, 2008). Barley is an important crop species and it is an ideal material for genetic studies because of its relatively simple genetic background (Costa *et al.*, 2001). Barley is widely adapted to adverse environmental conditions and displays much higher tolerance to different environmental stresses than its close relative wheat (Nevo *et al.*, 2012). Plant genotypes express an adequate range of variability under diverse environmental conditions for grain and biological yield (Ahmad *et al.*, 2012). Drought is one of the most important abiotic factors constraining barley production, causing complete grain failure in severely affected fields (Akash, 2013). Improving crop yield under water deficit environments is an urgent task for crop breeding worldwide. Drought tolerance is quantitatively inherited and controlled by several genetic loci and in barley and many QTLs have been reported for drought tolerance (Kalladan *et al.*, 2013). Peighambari *et al.*, (2005) detected several co-localized QTLs for different traits under drought stress conditions in barley. Fan *et al.*, (2015) reported many QTLs which are responsible for drought tolerance related traits in barley, i.e (QDT.TxFr.2H) and (QDT.TxFr.5H) present on linkage group 2H and 5H respectively. They also reported two QTLs responsible for proline content under drought conditions in barley (QPC-D.TxFr.3H) and (QPC-S.TxFr.3H) on linkage group 3H. A QTL conferring moisture content trait was also investigated by (Fan *et al.*, 2015) in barley. Huseynova, (2015) has confirmed the existence of a special locus associated with drought tolerance in the barley genotypes.

#### Conclusion

Due to the complex inheritance mechanism of drought tolerance, efforts made by plant breeders to identify QTL for drought tolerance in crop plants have not been proven fully fruitful due to the complex inheritance mechanism of drought tolerance. The reason is that identified QTLs have been proven

unstable across different environments. In some circumstances identified QTLs show adverse effects on grain yield. So, it is important to keep in mind that drought resistant traits should also contribute to yield stability under drought stress. There is a dire need to link the work of different researchers of this field to get the maximum benefit from their work by selecting the proper QTL on a specific linkage groups or chromosomes to reduce the loss caused by drought. The QTL mapping approach will also be helpful to save the time by accumulating the desirable alleles in breeding programs.

#### Reference

1. Ahmad HM, M Ahsan, Q Ali and I Javed. Genetic variability, heritability and correlation studies of various quantitative traits of mungbean (*Vigna radiata* L.) at different radiation levels. *Int Res J Microb.* 2012; 3(11): 352-362.
2. Ahmad HM, Rahman MU, Ali Q Awan SI. Plant cuticular waxes: a review on functions, composition, biosynthesis mechanism and transportation. *Life Sci J* 2015;12(4s):60-67.
3. Ahmad HM, SI Awan, O Aziz and MA Ali. Multivariate analysis of some metric traits in bread wheat (*Triticum aestivum* L.). *Eurp J Biotech and Biosci.* 2014; 1 (3): 18-21.
4. Akash MW. Development of SCAR markers for molecular tagging of drought tolerance QTL in barley. *Life Sci J* 2013; 10(12s).
5. Ali, Q., Ahsan, M., Tahir, M. H. N., Khaliq, I., Kashif, M., Elahi, M. & Anwar, M. (2012). An overview of genomics assisted improvement of drought tolerance in maize (*Zea mays* L.): QTL approaches. *African Journal of Biotechnology*, 11(65), 12839-12848.
6. Ali, Q., Ahsan, M., Tahir, M. H. N., Elahi, M., Farooq, J., & Waseem, M. (2011). Gene Expression and Functional Genomic Approach for abiotic stress tolerance in different crop species. *IJAVMS*, 5(2), 221-248.
7. Ashfaq S, HM Ahmad, SI Awan, SA Kang M Sarfraz and MA Ali. Estimation of genetic variability, heritability and correlation for some morphological traits in spring wheat. *J Biol. Agri and Healthcare* 2014;4(5):10-16.
8. Bo K, Ma Z, Chen J, Weng Y. Molecular mapping reveals structural rearrangements and quantitative trait loci underlying traits with local adaptation in semi-wild Xishuangbanna cucumber (*Cucumis sativus* L. var. xishuangbannanensis Qi et Yuan). *Theor Appl Genet.* 2015;128(1):25-39.
9. Christopher J, M Christopher, R Jennings, S Jones, S Fletcher, A Borrell AM. Manschadi, D

- Jordan, E, Mace, G Hammer. QTL for root angle and number in a population developed from bread wheats (*Triticum aestivum*) with contrasting adaptation to water-limited environments. 2013; *Theor Appl Genet.* 126:1563–1574.
10. Collins NC, Tardieu F, Tuberosa R. Quantitative trait loci and crop performance under abiotic stress: where do we stand? *Plant Physiol* 2008;147:469–486.
  11. Comas LH, Steven R. Becker, V Mark V. Cruz, PF. Byrne, and A David. Root traits contributing to plant productivity under drought. *Front Plant Sci.* 2013; 4: 442.
  12. Costa JM., Corey A, Hayes PM., Jobet C, Kleinhofs A, Kopsisch-Obusch, A Kramer, SF Kudrna, D Li, M, Riera-lazarazu, O Sato, K Szucs, P Toojinda, T Vales, MI Wolfe. Molecular mapping of the Oregon Wolfe barleys: a phenotypically polymorphic double-haploid population. *Theor. appl. Genet* 2001; 103: 415-424.
  13. Cui, K, J Huang, Y Xing, S Yu, C Xu and S Peng, “Mapping QTLs for Seedling Characteristics under Different Water Supply Conditions in Rice (*Oryza Sativa* L.) *Physiologia Plantarum* 2008; 132(1): 53-68.
  14. Fan Y, S Shabala, Y Ma, R Xu and M Zhou. Using QTL mapping to investigate the relationships between abiotic stress tolerance (drought and salinity) and agronomic and physiological traits. *BMC Genomics.*2015;16:43.
  15. Gall, HL, F Philippe, JM. Domon, F Gillet, J Pelloux and C Rayon. Cell wall metabolism in response to abiotic stress. *Plants* 2015; 4:112-166.
  16. Gupta PK, S Bharti, and H S Balyan. Quantitative trait loci analysis for some root traits in Bread Wheat (*triticum aestivum* l.) *Int. J. Agric. Sci.* 2014; 4 (7): 214-221.
  17. Hamada A, Nitta M, Nasuda S, Kato K, Fujita M, Matsunaka H, Okumoto Y. Novel QTLs for growth angle of seminal roots in wheat (*Triticum aestivum* L.). *Plant Soil.* 2012; 354:395–405
  18. Harris K, Subudhi PK, Borrell A, Jordan D, Rosenow D, Nguyen H, Klein P, Klein R, Mullet J. Sorghum stay-green QTL individually reduce post-flowering drought-induced leaf senescence. *J Exp Bot.* 2007;58(2):327-338.
  19. Huseynova M, SM Rustamova, MY Nasrullayeva, JA Aliyev. Screening of barley genotypes for drought tolerance using molecular markers. *Int J P Res.* 2015;1(3):88-92.
  20. Kalladan R, Worch S, Rolletschek H, Harshavardhan VT, Kuntze L, Seiler C, et al. Identification of quantitative trait loci contributing to yield and seed quality parameters under terminal drought in barley advanced backcross lines. *Mol Breed.* 2013;32(1):71–90.
  21. Kato Y, S Hirotsu, K Nemoto and J Yamagishi. Identification of QTLs controlling Rice Drought Tolerance at Seedling Stage in Hydroponic Culture,” *Euphytica* 2008;160( 3): 423-430.
  22. Kebede H, PK Subudhi, DT Rosenow, H T Nguyen. Quantitative trait loci influencing drought tolerance in grain sorghum (*Sorghum bicolor* L. Moench. *Theor. Appl. Genet.* 2001;103(2-3): 266-276.
  23. Lanceras JC, Pantuwan G, Jongdee B, Toojinda T. Quantitative trait loci associated with drought tolerance at reproductive stage in rice. *Plant Physiol.* 2004;135(1):384-99.
  24. Landi P et al. Characterization of root-yield-1.06, a major constitutive QTL for root and agronomic traits in maize across water regimes. *J. Exp. Bot.* 2010;61: 3553-3562.
  25. Lebreton C, V Lazić-Jančić, A Steed, S Pekić and SA Quarrie. Identification of QTL for drought responses in maize and their use in testing causal relationships between traits. *J. Expe. Bot.* 199;46(7): 853-865.
  26. Li Y, Yang M, Dong Y, Wang Q, Zhou Y, Zhou Q, Shen B, Zhang F, Liang X. Three main genetic regions for grain development revealed through QTL detection and meta-analysis in maize. *Mol Breed* 2011; doi:10.1007/s11032-011-9610-x.
  27. Liu, L., P. Mu, X. Li, Y. Qu, Y. Wang and Z. Li, “Localization of QTL for Basal Root Thickness in Japonica Rice and Effect of Marker-Assisted Selection for a Major QTL,” *Euphytica* 2008; 164(3):729-737.
  28. Lynch JP. Steep, cheap and deep: an ideotype to optimize water and N acquisition by maize root systems. *Ann Bot.* 2013;112:347–357.
  29. Maccaferri M et al. Quantitative trait loci for grain yield and adaptation of durum wheat (*Triticum durum* Desf.) across a wide range of water availability. *Genet.* 2008;178: 489-511.
  30. Mace SE, V Singh, EJV Oosterom, GL Hammer, CH Hunt, DR Jordan QTL for nodal root angle in sorghum (*Sorghum bicolor* L.Moench) co-locate with QTL for traits associated with drought adaptation. *Theor. Appl. Genet.* 2012; 124:97–109.
  31. Mano Y, Muraki M, Fujimori M, Takamizo T Varietal difference and genetic analysis of adventitious root formation at the soil surface during flooding in maize and teosinte seedlings. *Int. J. Crop Sci.* 2005a;74: 41–46.
  32. Manschadi AM, Christopher JT, Hammer GL, deVoil P. Experimental and modelling studies of drought-adaptive root architectural traits in

- wheat (*Triticum aestivum* L.). *Plant Biosyst.* 2010; 144:458–462.
33. Mardan Z, B. Rabiei, H. Sabouri, A. Sabouri. Mapping of QTLs for Germination Characteristics under Non-stress and Drought Stress in Rice. *Rice Sci.* 2013;20(6): 391–399.
  34. Mizoi J. and K. Yamaguchi-Shinozaki. Molecular approaches to improve rice abiotic stress tolerance. *Methods Mol Biol.* 2013;956:269-283.
  35. Nevo E, Fu YB, Pavlicek T, Khalifa S, Tavasi M, Beiles A. (2012) Evolution of wild cereals during 28 years of global warming in Israel. *Proc. Natl. Acad. Sci. USA*, 109:3412-5.
  36. Nicholas C. Collins, Francois Tardieu, and Roberto Tuberosa. Quantitative Trait Loci and Crop Performance under Abiotic Stress: Where Do We Stand? *Plant Physio.* 2008; 147:469–486
  37. O'Toole JC. Adaptation of rice to drought-prone environments. In *Drought resistance in crops with emphasis on rice*. Los Baños, Philippines: International Rice Research Institute;1982; 195–213.
  38. Pasha, MFK, HM Ahmad, M. Qasim, I Javed. Performance evaluation of zinnia cultivars for morphological traits under the Agro-climatic conditions of Faisalabad. *Eurp. J. Biotech. Biosci.* 2015; 3 (1): 35-38.
  39. Peighambari, SA., Yazdi-Samadi, B Nabipour, A Charmet, G Charmet. QTL analysis for agronomic traits in a barley doubled haploids population grown in Iran. *Plant. Science* 2005; 169: 1008-1013.
  40. Pettigrew WT. Moisture deficit effects on cotton lint yield, yield components, and boll distribution. *Agron J.* 2004;96(2): 377-383.
  41. Price AH, Townend J, Jones MP, Audebert A, Courtois B. Mapping QTLs associated with drought avoidance in upland rice grown in the Philippines and West Africa. *Plant Mol Biol.* 2002;48(5-6):683-95.
  42. Rahman H, S Pekic, V Lazic-Jancic, SA Quarrie, SM Shah, A Pervez, MM Shah. Molecular mapping of quantitative trait loci for drought tolerance in maize plants. *Genet Mol Res.* 2011; 10(2):889-901.
  43. Ramegowda V and M. Senthil-Kumar. The interactive effects of simultaneous biotic and abiotic stresses on plants: Mechanistic understanding from drought and pathogen combination. *J. P. Physiol.* 2015; 176: 47–54.
  44. Rattan S. YD Sehgal and V Vadez. Using genetic mapping and genomics approaches in understanding and improving drought tolerance in pearl millet. *J. Exp. Bot.* 2010; 62(2) 397–408.
  45. Raza MA, Ahmad HM, Akram Z, Ali Q. Evaluation of wheat genotypes for morphological traits under rainfed conditions. *Academ Arena* 2015;7(9):19-26.
  46. Sahoo, RK., M. W. Ansari, R. Tuteja and N. Tuteja. 2014. OsSUV3 transgenic rice maintains higher endogenous levels of plant hormones that mitigates adverse effects of salinity and sustains crop productivity. *Rice*, 7:17.
  47. Sarwar MH, MF Sarwar, M Sarwar, NA Qadri and S Moghal. The importance of cereals (Poaceae: Gramineae) nutrition in human health. *J. Cereals and Oilseeds* 2013;4(3): 32-35.
  48. Sayed MA, Schumann H, Pillen K, Naz AA, Leon J. AB-QTL analysis reveals new alleles associated to proline accumulation and leaf wilting under drought stress conditions in barley (*Hordeum vulgare* L.). *BMC Genetics.* 2012;13:61.
  49. Shao HB, Chu, LY, Jaleel CA, Zhao CX. Water-deficit stress-induced anatomical changes in higher plants. *C. R. Biol.* 2008.331, 215–225.
  50. Sharma PC, Sehgal D, Singh D, Singh G, Yadav RS. A major terminal drought tolerance QTL of pearl millet is also associated with reduced salt uptake and enhanced growth under salt stress. *Mol Breed.* 2011;27(2):207–22.
  51. Sharma S, Demason D, Ehdai B. Dosage effect of the short arm of chromosome 1 of rye on root morphology and anatomy in bread wheat. *J Exp Bot.* 2010;61:2623–2633.
  52. Soda, N., S. Wallace and R. Karan. Omics study for abiotic stress responses in plant. *Adv Plants Agric Res.* 2015; 2(1): 00037.
  53. Sreenivasulu N, Usadel B, Winter A, Radchuk V, Scholz, Stein N, Barley grain maturation and germination: metabolic pathway and regulatory network commonalities and differences highlighted by new MapMan/PageMan profiling tools. *Plant physiology*, 2008; 146(4):1738-1758.
  54. Srividhya, A. L. R. Vemireddy, P.V. Ramanarao, S. Sridhar, M. Jayaprada, G. Anuradha, and B. Srilakshmi. Molecular Mapping of QTLs for Drought Related Traits at Seedling Stage under PEG Induced Stress Conditions in Rice. *Amerc. J P Sci.* 2011; 2.190-201.
  55. Tardieu, FO, Granier C. Muller B. Water deficit and growth. Co-ordinating processes without an orchestrator? *Curr. Opin. Plant Biol.* 2011; 14, 283–289.
  56. Truntzler M, Barriere Y, Sawkins MC, Lespinasse D, Betran J, Charcosset A, Moreau L. Meta-analysis of QTL involved in silage quality of maize and comparison with the position of candidate genes. *Theor Appl Genet.* 2010; 121:1465–1482.

57. Tuberosa R, Salvi S (2009) QTL for agronomic traits in maize production. In: Bennetzen JL, Hake SC (eds) Handbook of maize: its biology, 1st edn. Springer, New York, pp 501–541.
58. Uga Y, Okuno K, Yano M. Fine mapping of *Stal1*, a quantitative trait locus determining stele transversal area, on rice chromosome 9. *Mol Breed*. 2010;26:533–538.
59. Uga Y, Okuno K, Yano M. QTLs underlying natural variation in stele and xylem structures of rice root. *Breed Sci* 2008; 58:7–14.
60. Wang Ay, Li Y and Zhang C. QTL mapping for stay-green in maize (*Zea Mays*). *Cand J P Sci*. 2012; 92: 249–256.
61. Yadav RS, Hash CT, Bidinger, FR, Devos KM, Howarth CJ. Genomic regions associated with grain yield and aspects of post-flowering drought tolerance in pearl millet across stress environments and testers background. *Euphytica* 2004;136, 265–277.
62. Yue B, Xiong L, Xue W, Xing Y, Luo L, Xu C. Genetic analysis for drought resistance of rice at reproductive stage in field with different types of soil. *Theor Appl Genet*. 2005; 111(6):1127-1136
63. Zaidi PH, Z Rashid, MT Vinayan, GD Almeida, RK Phagna, and R Babu. QTL mapping of agronomic waterlogging tolerance using recombinant inbred lines derived from tropical maize (*Zea MaysL*) germplasm. *PLoS One*. 2015; 10(4): e0124350. doi: 10.1371/journal.pone.0124350.
64. Zhu JM, Brown KM, Lynch JP. 2010. Root cortical aerenchyma improves the drought tolerance of maize (*Zea mays L.*) *Plant Cell Environ* 2010;33:740–749.

9/22/2015