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REVIEW PAPER

QTL MAPPING FOR CROP IMPROVEMENT AGAINST ABIOTIC STRESSES IN CEREALS

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ABSTRACT

Quantitative trait loci (QTL) approach is the source for plant breeders to scrutinize the complex traits like drought, temperature, salinity stress tolerance, etc. into their components as they largely affect the crop productivity. Agricultural production can be enhanced by incorporating the tolerance against these stresses. In this review article, we will discuss the progress made by various researchers in the area of QTL mapping for the improvement of abiotic stress tolerance in cereals. The knowledge may be helpful for plant breeders to accelerate the release of abiotic stress resistant cultivars by reducing selection time of desirable traits and to incorporate the precise and accurate alleles in breeding programs.

Keywords: QTL mapping, abiotic stress, drought stress, salinity stress, heavy metal stress, heat stress.

INTRODUCTION

Development of resistant cultivars against environmental stress is the main task for plant breeders. As in nature, plants have to face various environmental stresses simultaneously that cause the reduction in the productivity and significant economic loss to cereal crops (Sanghera *et al.*, 2011; Ramegowda and Kumar, 2015). Abiotic stresses like salinity, drought, heavy metals, water lodging, submergence, shattering, high and low temperature largely affect the crop productivity by reducing the fertility near flowering and seed growth stages. It has been estimated that abiotic stresses causes to reduce 70% yield in agricultural crops throughout the world. Due to abiotic stresses, a series of molecular and biochemical modifications take place in plants which lead to generate morphological and physiological changes (Sahoo *et al.,* 2014). Many functional and regulatory genes have been identified by plant breeders (Mizoi and Yamaguchi-Shinozaki, 2013) which are up or down-regulated in response to abiotic stresses. Generally, plants response to abiotic stresses varies depending upon plant species, genotypes, age, stress intensity and timing of stress application (Gall *et al.,* 2015).

QTL mapping: importance and procedure: QTL mapping is statistical procedure used to distinguish the complex plant traits into their components (Ahmad *et al.,* 2015; Yao *et al.,* 2016). It controls the heritable variations in crop plants (Collins *et al.,* 2008). It is also helpful to learn the genetic architecture of plants to improve them for desirable traits during the course of their evaluation (Bo *et al.*, 2015). This approach also dissect the physiological and genetic elements affecting source sink relationship under abiotic stress (Welcker *et al.*, 2007). In the field of agriculture, evolutionary biology and medicines, QTL mapping is being intensively used to find the precise location of the interested regions/genes. Functional genomics is an important tool to find the correlation between phenotype and genome of an organism subjected to diverse environmental conditions (Soda *et al.,* 2015). To identify the abiotic stresses resistant QTLs, a lot of work has been done by plant biologists but identified QTLs proved unstable across different environmental conditions due to their complex inheritance mechanism of abiotic stress tolerance. In this review, we will illustrate the various major and minor QTLs identified in different crops for different abiotic stresses that may help the researchers to find the desirable QTLs according the abiotic stress they are dealing with.

To carry out the QTL analysis, two basic things are required, (i) two or more strains of genetically different organism and (ii) availability of molecular markers (SSRs, SNPs, RFLPs, etc.) to distinguish between these strains. By crossing the strains, heterozygous (F1) individual is obtained and then these heterozygous individuals are crossed in different ways to obtain maximum diversity. QTLs can also be performed by using hybrid population, pedigree and sibships (Svishcheva, 2007) domesticated and wild relatives of crops (Pandey *et al.*, 2008). Molecular markers genetically linked to the interested traits will segregate more frequently with trait value on the other hand unlinked markers will not show considerable association (**Figure-1**). Major objective of this analysis is to find the fact that phenotypic differences are due to few loci with large effects or many loci with smaller effects. Most of the phenotypic variations in quantitative traits are due to few loci with great effect and less due to large loci with lower effect (Maki-Tanila and Hill, 2014). In mapping QTLs, sample size is also an important factor because low sample size may fail to detect the exact effects of QTLs (Svishcheva *et al.,* 2012; Belonogova *et al.,* 2013).

QTLs for drought stress: A condition in which the requirement of water increases than the supply in plants is termed as drought. Among abiotic stresses, drought stress is a major source that has limited the crop productivity worldwide in arid and semi-arid environments (Bita and Gerats, 2013; Noreen *et al.,* 2017). Drought is a major threat to crop productivity (Hussain *et al.,* 2015). At cellular level drought causes physiological and biochemical disorders i.e. electrolytic leakage through cell membrane. So the cell membrane stability in the presence of stresses like drought or high temperature may indirectly indicate the ability of plant to withstand periods of stress (Ahmad *et al.,* 2015).

It is difficult to characterize the drought related physiological and phenotypic traits due to inadequate understanding about the mechanism of drought tolerance. However crop yield can be enhanced in water limited environments by optimizing the root architecture because large root system is less affected by water deficient conditions (Manschadi *et al.,* 2010). Improving water use efficiency, uptakes of available water, reduces water loss from plant surfaces by reducing leaf area or control of stomatal conductance (Abbate *et al.,* 2004), abscisic acid content (Reynolds and Tuberosa, 2008), relative water content, adjusting osmotic, penicale and leaf water potential (Jongdee *et al.,* 2002) and altering the flowering time may enhance the yield under drought conditions (Reynolds and Tuberosa, 2008).

A large variation in timing and severity of drought stress has made it complex to screen for the improvement of crop production under drought conditions. That's why traits based approaches to enhance the crop performance under water limited environments remained low due to complexity in genetic makeup of plants. Evidence shows that some QTLs have pleotropic effects on multi stress tolerance because in some cases drought related QTLs also influenced the plant growth under salt stress (Sharma *et al.,* 2011). So it is important to identify specific genes from new germplasm resources that are tolerant to multiple stresses. By exploiting the functions of genes that are responsible for drought will enable the plant biologists to use them in plant breeding programs to get drought resistant cultivars (Price *et al.,* 2002; Ahmed *et al.*, 2011). Root architecture plays a vital role to avoid terrestrial plants from drought because, for deep rooted plants, it is easy to absorb more water from deep soil layers (Rich and Watt, 2013; Uga *et al.,* 2015). Investigation that mechanism of drought tolerance is quantitatively inherited and controlled by various genetic loci has lead the plant breeders to the development of several drought related QTLs (Sayed *et al.,* 2012; Kalladan *et al.*, 2013).

QTLs for water deficient conditions have been studied in almost all cereals, regarding the factors controlling drought stress. QTLs for water-use-efficiency and deep root ratio in wheat were investigated by (Spielmeyer *et al.,* 2007; Hamada *et al.,* 2012). Three QTLs for root angle (QRA.qgw-3D, QRA.qgw-2A and qRA.qgw-5D), and a QTL for number of roots (qRN.qgw-1B) were mapped in wheat (Christopher *et al.,* 2013). QTLs for root length (QRl.ccsu-2B.1), dry weight of roots (QRdw.ccsu-2A.2 and QRdw.ccsu-2A.1) on chromosome 2B and 2A respectively in wheat were studied (Bharti *et al.,* 2014). QTLs related to drought tolerance in wheat were investigated in wheat which were associated with net photosynthetic rate (QPn2AC), cell membrane stability (QCMSa2AC), relative water content (QCMSa2AC) (Malik *et al.,* 2015).

QTLs for water use efficiency have been investigated in maize (Landi *et al.,* 2007), sorghum (Harris *et al.,* 2006), brassica (Hall *et al.,* 2005), barley (Teulat *et al.,* 2002), rice (Steele *et al.,* 2007; Laza *et al.,* 2010) and pearl millet (Yadav *et al.,* 2004; Bidinger *et al.,* 2007). QTLs for seedling root growth in rice were also reported (Atkinson *et al.,* 2015). Three QTLs (*qtl*RWC1, *qtl*WC-2, *qtl*ELWL) were studied in cotton that were associated to excised loss of water and relative water content under drought stress (Saleem *et al.* 2015). Mace *et al.* (2012) mapped a QTL (qTLA3-8) for leaf area in sorghum. Adaptation of drought stress after flowering is correlated with stay green phenotypes. Post-flowering drought tolerance QTLs linked with stay green traits have been mapped by (Haussmann *et al.,* 2002; Thomas and Ougham, 2014) in different crops. Four major QTLs having characteristics of stay green Stg1, Stg2, Stg3 and Stg4 were mapped in sorghum. Stg1 and Stg2 were found on chromosome 3 of sorghum (Harris *et al.,* 2006; Xu *et al*., 2012). Stg3 was located on chromosome 2 while Stg4 was mapped on chromosome 5 (Harris *et al.,* 2006).

QTLs for high and low temperature stresses: Extreme temperature situations either high or low, both severely damage the plant structure and physiology. Due to global warming, elevated temperature has become the major abiotic stress and plants are needed to adjust with these stresses to survive (Hall, 2010). In many areas of the world, heat stress is an important cause to reduce the economical yield of agricultural crops (Wahid *et al.,* 2007). High temperature disturbs many cellular and developmental processes in plants. It reduces fertility rate, lower the grain production and quality in agricultural crops (Barnabás *et al.,* 2008). Goulas *et al.,* (2006) reported that heat stress has also lead to change in plant metabolism and gene expression.

High temperature causes to early abortion in tapetal cells leading the pollen mother cells toward mitotic phase and finally goes to PCD yield to pollen sterility (Parish *et al.,* 2012). To overcome the heat related stresses, plant biologists have mapped many QTLs in various important crops. In order to improve the crop productivity of rice under high temperature, Vijayalakshmi *et al.,* (2010) reported many QTLs that were related to senescence under high temperature stress. Similarly, Zhao *et al.,* (2016) reported an important QTL on chromosome 9 in Indian rice cultivar that explained up-to 50% phenotypic variation which was related to heat tolerance and amylose content. In bread wheat, QTLs for heat tolerance were mapped by using different heat related traits such as decrease in canopy temperature (Pinto *et al.,* 2010), senescence (Vijayalakshmi *et al.,* 2010) and discrimination of carbon isotopes (Rebetzke *et al.,* 2008). Four QTLs (Qhr1; qhr3-1qhr4-3qhr8-1) associated to heat tolerance at flowering stage in rice were reported by Ye *et al.,* (2012 & 2015).

Two minor QTLs (qHTSF1.1 and qHTSF4.1) controlling the spikelet fertility under high temperature conditions were mapped in rice by (Ye *et al.,* 2012 & 2015). High temperature decreases spikelet fertility and disturb membrane stability so keeping these traits in mind, Talukder *et al.,* (2014) investigated QTLs (qHTSF1.1, qHTSF4.1) related to spikelet fertility in high temperature.

Like high temperature stress, cold stress also imparts many physiological, biochemical events in agricultural crops (Thomashow, 1999). It also delay seed germination and seedling growth, and non uniform maturity causes to disturb plants biological functions by chilling and freezing injuries (Andaya, 2003; Manangkil *et al*., 2013). Due to chilling stress plant traits such, as stay green leaf, leaf area, shoot weight and nitrogen contents are affected (Jompuk *et al.,* 2005). Root conductivity (RC) is an important trait that can be used as an indicator to map quantitative trait loci (QTLs) of cold tolerance in cereals *(*Xiao *et al*., 2014). Cold tolerance can be controlled by controlling biological mechanism taking place in plants, i.e cold sensing, transcriptional regulations and post-transcriptional modifications (Zhang *et al.,* 2008; Sanghera *et al.,* 2011). Different researchers have explained the molecular and cellular mechanism of chilling temperature however its genetic mechanism is not understood yet (Pandey *et al.,* 2009).

Among cereals rice is most affected cereal by cold stress so by broadening the rice gene pool through introducing cold tolerance traits and its related genes in wild rice, its production can be enhanced (Xie *et al*., 2012). QTLs for cold tolerance at seedling and booting stage have been reported in rice (Lou *et al.,* 2007; Shinada *et al.,* 2014). Mamun *et al.,* (2006) reported nineteen QTLs for cold tolerance in rice that were present on chromosome No.3 and 8. Reinheimer *et al.*, (2004) mapped a frost tolerance QTL (QFr-H1) in barley. Low temperature related QTLs have mapped in lentil (Kahraman *et al.,* 2004), maize (Hund *et al*., 2005; Presterl *et al.,* 2007; Revilla *et al.,* 2016), ryegrass (Zhang *et al*., 2009) and Sorghum (Knoll and Ejeta, 2008) faba bean (Sallam *et al.,* 2016). QTLs (qCTB7) and (qCTB8) related to low temperature tolerance at booting stage in rice were mapped (Zhou *et al.,* 2010; Kuroki *et al.,* 2007). Most of the cold tolerant QTLs identified in cereals were linked with avoidance mechanism. However two QTLs related to cold tolerance at seedling stage (qCTS11-1) & (qSCT-11) were mapped and associated to cold induced wilting tolerance and recovery of growth after cold stress in rice (Andaya, 2003), (qSCT-3-1) (Kuroki *et al.,* 2007) and a QTL (*qCTS8.1) by* (Wang *et al.,* 2011) qCTS12, qCTS4 by (Andaya and Tai, 2006). Germination in low temperature conditions is one of the most important traits in seedling development under direct sowing of rice (Satoh *et al.,* 2016).

Many QTLs have been identified and evaluated for low temperature germination ability i.e qLTG3-1, (*qLTG11.1*) (Wang *et al.,* 2011) and qCtss11. Four QTLs related to germination factors were evaluated by (Satoh *et al.,* 2016) and reported that qLTG3-1; qLTG3-2 and qLTG11-1 enhanced the germination under cold stress while the QTL qLTG1-1 delayed germination under cold climatic conditions. In maize, six QTLs on chromosome 4,5,6,7, and 9 were mapped that were associated to germination at low temperature and primary root length in this crop (Hu *et al.,* 2016). Due to low temperature male sterility is induced at reproductive stage and badly affects the production of important crops. So two QTLs (qCTR5 & qCTR12) were detected on chromosome 5 and 12 of maize genome which control this trait at reproductive stage (Koumoto *et al.,* 2016). The major QTLs detected, named *4A-1*, was located on the long arm of chromosome 4 (Barrero *et al.,* 2015).

QTLs for salinity stress: Soil Salinity is one of the major abiotic stresses that reduce the yield of cereal crops. Excess amount of soluble salts present in soil solution adversely affect plant metabolic activities (Lutts *et al.,* 1995). About 830 million hectares area is affected by salinity worldwide (Rengasamy, 2006). Salinity tolerance is a complicated trait having various components. They can be understood by genome wide association studies (Kumar *et al*., 2015). To improve the crop production under saline conditions QTL mapping is an important approach to enhance the productivity (Gimhani *et al.,* 2016). It provide good understanding about the understanding of genetic control of salinity tolerance (Turki *et al.,* 2015). Newly developed high yielding cultivars are more sensible to slat stress (Tiwari *et al.,* 2016).

Salinity effects agricultural crops in many ways i.e reduces germination rate (Kamyar, 2011), eliminate seedling survival (Lutts *et al.,* 1995), damages chloroplast structure (Yamane *et al.,* 2008), diminish photosynthesis rate and reduces grain yield (Asch *et al.,* 2000). Adverse effect of salinity can be minimized by improving antioxidant machinery and photosynthesis rate (Tuteja *et al.* 2013), eliminating Na+ ion contents of tissues (Xue *et* *al*., 2009) and water soluble carbohydrates and chlorophyll contents (Siahsar and Narouei 2010). Salinity is controlled by various genes which are expressed at different developmental stages of plants. So by understanding the mechanism of salinity tolerance crop loss due to salinity stress can be minimized (Tuteja *et al*., 2013). Significant variability has been studied in yield and other yield related traits in different plants under salt stress. Hence the productivity of agricultural crops can be improved by discovering and incorporating salt tolerant genes in genetic makeup (Kumar *et al.,* 2015).

QTL mapping approach may be helpful to improve the salt tolerant traits in agricultural crops (Hossain *et al.,* 2015). Many major and minor salt tolerant QTLs have been identified by plant biologists which are being used in breeding programs (Flowers *et al*., 2000; Shavrukov *et al*., 2010; Sbei *et al.,* 2014). However the efficiency of these QTLs is low due to relative lower heritability and factors effecting gene expression. QTLs for salinity tolerance in rice were reported (Hossain *et al.,* 2015; Kumar *et al.,* 2015; Tiwari *et al.,* 2016) Similarly, salt resistant QTLs in barley cultivars were also reported (Xue *et al.,* 2009; Sbei *et al*., 2014). Sodium (Na+) and Potassium (K+) related QTLs in various cereals have been reported (Koyama, 2001). Various salt ion concentration i.e Na+,K+, Cl- QTLs on reproductive stage of leaf tissues in rice genotypes were also reported (Ammar *et al.,* 2009; Pandit *et al*., 2010). Low Na+ tolerance QTLs were investigated in barley (Mickelson, 2003), in rice (Lian *et al*., 2005) and in seedling stage of maize (Wang *et al*., 2012). Dubcovsky *et al*., (1996) reported that a locus "*kna1*" present on chromosome 4D of wheat controls K+/Na+ ratio in leaves and is associated with high salt tolerance.

A QTL for Na+ exclusion have been mapped by (Lindsay *et al.,* 2004; James *et al*., 2013) on chromosome 2A in wheat. Ren *et al.,* (2005) and James *et al.,* (2006) reported sodium tolerant QTLs (OsHKT1;5 and TmHKT1;5-A) in rye and wheat (TaHKT1;5-D). Pandit *et al.,* (2010) find the QTL (qNaSH8.1) that was controlling sodium content under high salinity conditions in rice. Ahmadi and Fotokian (2011) reported a QTL (qNar/Kr5) associated to sodium and potassium ratio in rice roots. Potassium and sodium concentration in plant tissues is also an important factor regarding the salinity of plants, keeping this in view Xu *et al.,* (2012) investigated two QTLs qSKC9; qSNC9) on chromosome 9 of rice that were controlling K+ and Na+ concentration. Recently two salinity tolerance QTLs (QST.TxFr.7H & QS1wd, YG.4H) were investigated (Ma *et al.,* 2015).

A QTL with the characteristic of Na+ exclusion in wheat organs was reported by (Genc *et al.,* 2010). Cl^- uptake and its accumulation is a polygenic trait and a QTL(5A; *barc56/gwm186*) controlling the concentration of Cl^- was mapped by (Genc *et al*., 2014) in wheat. During their work on wheat salinity tolerance, James *et al.,* (2006) find two QTLs (TaHKT1;5-D & TmHKT7-A2) that were linked with sodium tolerance and its accumulation in shoots of wheat respectively. Quantitative trait loci (QTLs) for P deficiency tolerance had been identified in rice (Wissuwa *et al*., 1998; Wang *et al.,* 2014). Ten salinity tolerance QTLs (qSFW-1a-CK, qSFW-1b-CK, qRK-1-CK, qSN-1-CK, qSDW-3-CK, qSTR-4-CK, qSNK-6-CK, qSDW-7-CK, qSNK-9-CK, qRNK-9-CK) were detected by (Anh *et al.,* 2014) on rice chromosome 1,3,4,6,7 and 9. A salt tolerance QTL (*Saltol* QTL) was reported in rice by (Ganie *et al.,* 2016).

QTLs for heavy metal stress: Presence of heavy metals adversely affect the crop productivity along with health risks to animals and human beings which are fed by these crops (Stitt and Hurry, 2002; Goulas *et al.,* 2006) . The excess amount of heavy metals exert harmful effects on plant cells due to their toxicity, reduces crop yield and increases health problems for the consumers of these crops (Appenroth, 2010). So the harmful effects of these metals can be minimized by understanding the mechanism of metal tolerance and their accumulation in contaminated soils. Identification of heavy metal stress tolerant genotypes will make the researchers enable to enhance the crop yield in contaminated soils and reduce the soil pollution as well. Here are some examples of QTLs detected for metal tolerance in cereals. Zhang *et al.,* (2008) detected arsenic tolerance QTLs in rice cultivars with characteristics of low straw and high grain yield.

Similarly Aluminum stress related QTLs have been detected in wheat (Raman *et al.,* 2005), oat (Wight *et al.,* 2006), rye (Matos *et al*., 2005), barley (Wang *et al.,* 2007), rice and sorghum (Magalhaes, 2004; Magalhaes *et al*., 2007; Caniato *et al*., 2007), soybean (Xue *et al.,* 2007) and maize (Ninamango-Cárdenas *et al.,* 2003). An Al tolerance QTL (SbMATE) was reported by (Magalhaes *et al*., 2007) in sorghum genotypes. QTLs for nickel tolerance were reported in *S. vulgaris* (Bratteler *et al*., 2006) and wild cabbage (Burrell *et al.,* 2012). QTLs resistant to boron accumulation were observed in wheat (Schnurbusch *et al.* 2007), rice (Ochiai *et al*., 2008; de Abreu Neto *et al*., 2017) and maize (Ducrocq *et al.,* 2008). QTLs for zinc content has been reported by (Wahid *et al*., 2007), in seeds of been. Filatov *et al*., (2007) and (Frérot *et al*., 2010) analyzed the cross between *C. perraea* and *C. halleri* that were grown in zinc polluted soils and identified five QTL regions related to zinc concentration. QTLs related to heavy metal tolerance through phytoremediation in cereals were reported by Verbruggen *et al.,* (2013).

Ding *et al.,* (2011) reported ten QTLs (qLAC1, qSAC1a, qSAC1b, qLAC5, qSAC5, qKAC5, qKAC7, qLAC8, qBAC9a, qBAC9b) in maize plants that were present on different chromosomes and showing resistance to arsenic concentration. Cadmium (Cd) is a toxic element, and rice is known to be a leading source of dietary Cd for people who consume rice as their main caloric resource (Sun *et al.,* 2016). To overcome the Cd toxicity in rice crop, Yan *et al.,* (2013) found a shoot cadmium accumulation resistant QTL (scc10) and three grain cadmium accumulation resistant QTLs (gcc3, gcc9 & gcc11). Three QTLs (HvMATE, HvAACT1 & Bot1) controlling boron toxicity in barley have been reported by (Furukawa *et al.,* 2007; Sutton *et al*., 2007; Wang *et al.,* 2007) respectively.

QTLs for water lodging and submergence stress: Water lodging is a condition when excess amount of available water covers only root system of plants instead of all plant or stem. Lodging causes to displace the plant stem from upright position permanently. Lodging has been very serious problem in cereals *(*Verma *et al.,* 2005) and due to sever lodging whole crop field is compressed causing huge loss to the crop production (Crook and Ennos, 1995). Lodging stress causes to reduce the production and quality of cereals by breaking or bending of stem (Zhang *et al.,* 2016). Lodging can be divided into two categories; (1). Stem lodging: This is caused by bending or breakage of lower culm internodes. This type of lodging is dependent to tensile strength of inter node, diameter of stem wall and its thickness. (2) Root lodging; this loading is caused by disturbance of plant root system and culms of crown (Berry *et al.,* 2003; Piñera-Chavez *et al.,* 2016).

Lodging can be minimized by selecting proper variety, suitable sowing time, deep drilling, sustaining soil fertility (Sterling *et al.,* 2003). High nitrogen also causes to increase plant height, increase lower internode length, increases fresh weight of areal parts which may lead to lodging so optimal use of nitrogen may reduce this stress (Pinthus, 1967). Lodging stress can be minimized by reducing plant height and producing semi dwarf cultivars but this trait may also affect the biomass production and have negative effects on yield related components (Keller *et al*., 1999). Deficiency of GA decreases self weight of above plant parts which results in lodging resistance cultivars (Okuno *et al.,* 2014). Culm and stem strength is very important feature for improving cereal cultivars against lodging stress (Okuno *et al.,* 2014) so for the improvement of lodging resistance major focus should be given for the improvement of this trait (Zhang *et al.,* 2013) because stem, culm thickness, length, and strength are directly correlated with lodging resistance (Zhang *et al.,* 2013).

Basal internodes with short length and hard basal culm may also be lodging resistant. QTLs for lodging resistance were reported in many cereal crops like barley (Backes *et al.,* 1995; Hayes *et al.,* 1993), rice, oat (De Koeyer *et al.,* 2004) and maize (Flint-Garcia *et al.*, 2003). A water lodging resistant QTL (lrt5) was mapped in rice under typhon conditions by Ishimaru *et al.*, (2008). Despite other abiotic stresses traits, only a little work has done for the improvement of lodging resistance in cereals. So by characterizing the resistant genes this trait can be improved and yield can be enhanced in cereals.

A stress condition where the water covers areal parts along with root system of plants is termed as submergence. Submergence stress is more dangerous as compared to lodging because too much water at any developmental stage may cause crop injury and yield loss. First effect of this stress is deprived seedling growth, less germination percentage with poor crop establishment when rainfall occurs few days following seedling (Ismail *et al.,* 2012; de Melo *et al.,* 2015). Previously more emphasize was given to the lodging resistance while this stress remained uncharacterized (Abiko *et al.,* 2012; Thirunavukkarasu *et al*., 2013). Toojinda (2003) reported submergence QTL (SUB1) in rice. From the fine mapping of this QTL a cluster of submergence genes (SUB1A, SUB1B, and SUB1C) were reported (Xu *et al.,* 2006). Further experiment confirmed that high degree of submergence tolerance in rice can be achieved by SUB1A (Septiningsih *et al*., 2008; Sarkar and Bhattacharjee, 2011; Singh *et al.,* 2014). Campbell *et al.,* (2015) recently reported a submergence related QTL (Subtol6) in maize on chromosome 6.

QTLs for shattering stress: Like other environmental factors, shattering also causes huge yield loss in cereal crops. Main factors involved in shattering are high or low temperature, excess or lower availability of water, pest pathogen attack (Zhou *et al.,* 2010). The other source of grain shattering is abscission layer (Ji, 2006). The degree of shattering depend upon the morphology of abscission layer. In wheat abscission layer associated genes (sh2, sh4, and sh-h) have been mapped on chromosome 1,3 and 7 respectively (Oba *et al.,* 1995; Fukuta and Yagi, 1998). Kernel shattering is the important trait which can affect shattering in wheat. It has been reported that chromosome 2B, 3B and 7A have agronomic regions which are associated with kernel shattering (Zhang and Mergoum, 2007). Konishi *et al.,* (2006) mapped a QTL (qSH1) in rice that was resistant to seed shattering at maturity. A pod shattering resistant QTL (qPDH1) was mapped in soybean by (Funatsuki *et al.,* 2012). Lin *et al.*, (2012) reported that a gene (sh1) is a universal shattering resistant gene present in sorghum, rice and maize crops.

In past years shattering resistant genes sh4 (Li, 2006; Lin *et al.,* 2007), qSH1 (Konishi *et al.,* 2006), OsCPL1 (Cheng *et al.,* 2016), SHAT1 (Hofmann, 2012 and Cheng *et al.,* 2016), and SH5 (Yoon *et al.,* 2014) have been characterized in rice. Lee *et al.,* (2016) detected QTLs (qSh1 and qSh6) pertaining to breaking tensile strength and abscission layer, on chromosome 1 and 6 of rice. Kwon *et al.,*(2015) in his study confirmed the roll of these genes (qSH-4 and sh-h) in rice for shattering resistance. Recently, Cheng *et al.,* (2016) reported four important QTLs (qSH1JCQ, qSH3JCQ, qSH6JCQ, and qSH11JCQ) they also confirmed that QTL *qSH1JCQ* may cause significant decrease in expression of shattering related genes (*qSH1*, *OsCPL1*, *Sh4*, *SH5*, and *SHAT1*). Two shattering resistant QTLs (*qSRI.A06 and qSRI.A09)* were mapped in rapeseed (Liu *et al.,* 2016). In addition to rice shattering genes, the wheat Q gene was studied to have effects on the compaction wheat ears (Simons *et al.*, 2006).

Table.1 Important QTLs identified for abiotic stress tolerance in cereals.

Sr. No.	Crop	Abiotic stress/ Plant Trait	QTL/Gene	Linkage group/ Chromosome No	References
1	Wheat	Root angle	QRA.qgw-2A	2A1	Christopher *et al.,* 2013
2	Sorghum	Leaf area	qTLA3-8	SBI-08-II	Mace *et al*., 2012
3	Wheat	Root angle	QRA.qgw-3D, qRA.qgw-5D	3D 5D	Christopher *et al.,* 2013
4	Wheat	Number of roots	qRN.qgw-1B	1B	Christopher *et al.,* 2013
5	Wheat	Root length	QRl.ccsu-2B.1	Chromosome-2B	Bharti *et al.,* 2014
6	Wheat	Root dry weight	QRdw.ccsu-2A.1, QRdw.ccsu-2A.2	Chromosome-2A, Chromosome-2A	Bharti *et al.,* 2014
7	Wheat	Net photosynthetic rate	QPn2AC	2A	Malik *et al*., 2015
8	Wheat	Cell membrane stability	QCMSa2AC	2A	Malik *et al*., 2015
9	Wheat	Relative water content	QCMSa2AC	2A	Malik *et al*., 2015
10	Rice	Heat tolerance at flowering stage	Qhr1 *qhr3-1* *qhr11-1*	Chromosome-1 Chromosome-3 Chromosome-11	Cao *et al.,* 2003
11	Rice	Low temperature tolerance	qCTB8	Chromosome-8	Kuroki *et al.,* 2007
12	Rice	Heat tolerance at flowering stage	qhr3-1 qhr4-3 qhr8-1	Chromosome-3 Chromosome-4 Chromosome-8	Ye *et al*., 2012
13	Rice	Cold tolerance	qSCT-3-1	Chromosome-3	Zhang and Xie, 2014
14	Rice	Spikelet fertility under high temperature conditions	*qHTSF1.2*, *qHTSF2.1*, *qHTSF3.1* *qHTSF4.1* *qHTSF6.1* *qHTSF11.2*	Chromosome-1 Chromosome-2 Chromosome-3 Chromosome-4 Chromosome-6 Chromosome-11	Ye *et al.,* 2015
15	Wheat	Spikelet fertility under high temperature	qHttmd.ksu-6A QHttmd.ksu.1D	Chromosome-6A Chromosome-1D	Talukder *et al.,* 2014
16	Wheat	Plasma membrane damage under high temperature	QHtpmd.ksu.2B	Chromosome-2B	Talukder *et al.,* 2014
17	Barley	Frost tolerance	QFr-H1	Chromosome arm 2HL	Reinheimer *et al*., 2004
18	Rye	Na Tolerance	OsHKT1;5, TmHKT1;5-A	Skc1, Nax2	James *et al.,* 2006; Ren *et al*., 2005
19	Wheat	Na Tolerance	TaHKT1;5-D	Kna1	James *et al.,* 2006; Ren *et al*., 2005
20	Rice	Na content under high salinity	qNaSH8.1	Chromosome-8	Pandit *et al.,* 2010
21	Rice	Na+/K+ ratio in roots	qNar/Kr5	Chromosome-5	Ahmadi and Fotokian, 2011
22	Rice	K+concentration Na+concentration	qSKC9, qSNC9	Chromosome-9 -do-	Wang *et al.,* 2012
23	Wheat	Na Tolerance Shoot Na accumulation	TaHKT1;5-D, TmHKT7-A2	Kna1, Nax1	James *et al.,* 2006
24	Wheat	Na+ exclusion	HKT1	Chromosome-2A	Genc *et al.,* 2010
25	Barley	Salinity tolerance	QS1wd,YG.4H, QS1wd.YG.7H	4H, 7H	Ma *et al.,* 2015
26	Maize	Arsenic concentration	qLAC1,	Chromosome-1	Ding *et al.,* 2011

			qSAC1a,	-	
			qSAC1b	-	
			qLAC5,	Chromosme-5	
			qSAC5,	-	
			qKAC5	-	
			qKAC7	Chromosome-7	
			qLAC8	Chromosome-8	
			qBAC9a,	Chromosome-9	
			qBAC9b	-	
27	Rice	Shoot cadmium accumulation	scc10	Chromosome-10	Yan *et al.,* 2013
28	Rice	Grain cadmium accumulation	gcc3,	Chromosome-3	Yan *et al*., 2013
			gcc9,	Chromosome-9	
			gcc11	Chromosome-11	
29	Barley	Boron toxicity tolerance	Bot1	N/A	Sutton *et al.,* 2007
30	Barley	Aluminum toxicity tolerance	HvMATE	Alp	Furukawa *et al.,* 2007
31	Barley	Aluminum toxicity tolerance	HvAACT1	Alp	Wang *et al.,* 2007
32	Sorghum	Al Tolerance	SbMATE	AltSB	Magalhaes *et al*., 2007
33	Rice	Cold tolerance	qSRS1,	1	Cheng *et al.,* 2012
			qSRS7,	7	
			qSRS11a	11	
			qSRS11b	11	
34	Rice	Heat Tolerance	qSF4,	4	Cheng *et al.,* 2012
			qSF6	6	
35	Barley	chlorophyll fluorescence	QFv2H	2H	Siahsar and Narouei, 2010
36	Barley	Chlorophyl content under salinity	QCh7Ha	7H	Siahsar and Narouei, 2010
			Qch2Ha	2H	
37	Barley	water soluble carbohydrate	QWSC2H	2H	Siahsar and Narouei, 2010
38	Rice	Break tensile strength	qSh1	Chromosome1	Lee *et al.,* 2016
			qSh6	Chromosome1	

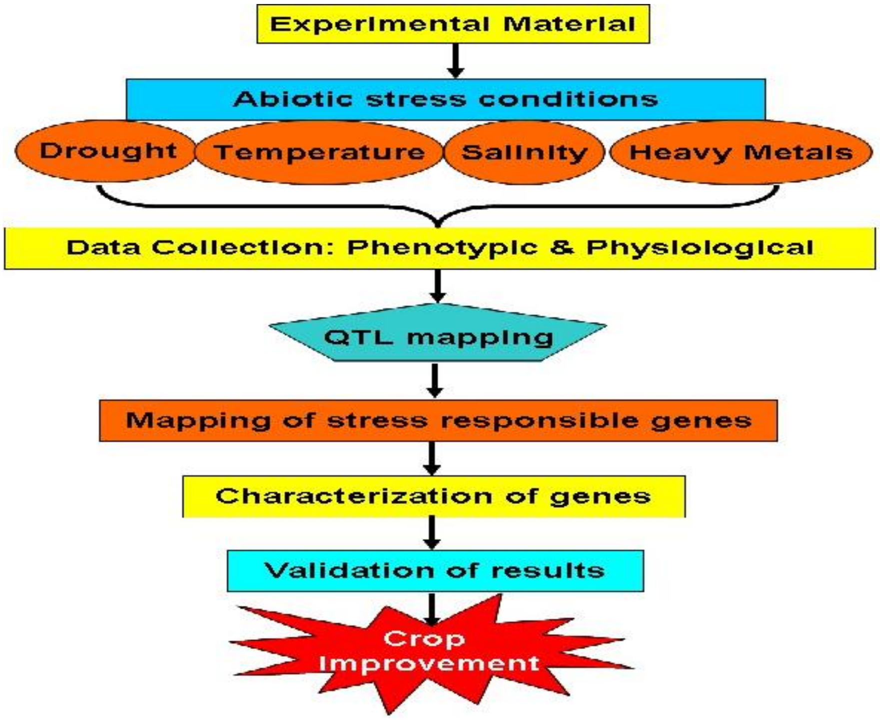

Figure-1: Schematic diagram of use of QTLs for crop improvement.

Conclusions: A lot of work has been done in the field of quantitative traits loci (QTL) mapping by plant breeders but it is needed to link this work to achieve the fruitful results. Main problem in QTL approach is that its effect varies during the change in environment. Recently, QTLs detected on the bases of high density genetics maps has increased the understanding about the genetic control of abiotic stresses in cereals and other agricultural crops. This approach helps to discover the resistant genes and to understand the mechanism of plant adaptation under stress conditions.

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