

Chapter

Genes for Different Abiotic Stresses Tolerance in Wheat

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Abstract

In the recent past years, global warming and climate change have drastically affected the agricultural crop productivity grown in tropical and subtropical areas globally by appearing to several new biotic and abiotic stresses. Among the abiotic stresses, heat, drought, moisture, and salt stresses are most prevalent. Wheat is the most common and widely used crops due to its economic and social values. Many parts of the world depend on this crop for food and feed, and its productivity is highly vulnerable to these abiotic stresses. Improving tolerance to these abiotic stresses is a very challenging assignment for wheat researchers, and more research is needed to better understand these stresses. The progress made in understanding these abiotic stress tolerances is due to advances in three main research areas: physiology, genetic, and breeding research. The physiology research focused on the alternative physiological and biochemical metabolic pathways that plants use when exposed to abiotic stresses. Identifying genes contributing to particular stress tolerance is very important. New wheat genotypes having a high degree of abiotic stress tolerance are produced through marker-assisted breeding by making crosses from promising concerned stress-tolerant genotypes and selecting among their progeny using gene-specific markers.

Keywords: climate change, abiotic stress, wheat, physiology, genetic, marker assisted breeding, phytohormones

1. Introduction

Wheat is the second most important cereal crops of the world occupying about 220 million hectares area (mha) with a production of 716 million tons of food grain with a productivity of 3.2 tons per hectare [1]. It is extensively grown in Asia particularly in China and India. In India its production is enhances after the green revolution of late 1960s followed by another green evolution during 1980s. During these two green revolutions, the rate of annual growth in wheat production globally was ~3%, but in recent years it is declined to <0.9% due to appearance of new biotic and abiotic stresses. Although currently, the global wheat production has been able to meet the current demand and consumption, but we will have to enhance production and achieve the targets of at least ~858 Mt to meet the demand in 2050, as against current global production of 763 Mt. It comprises amounts to at least ~15% desired increase in global wheat production (1.5% annual increase)

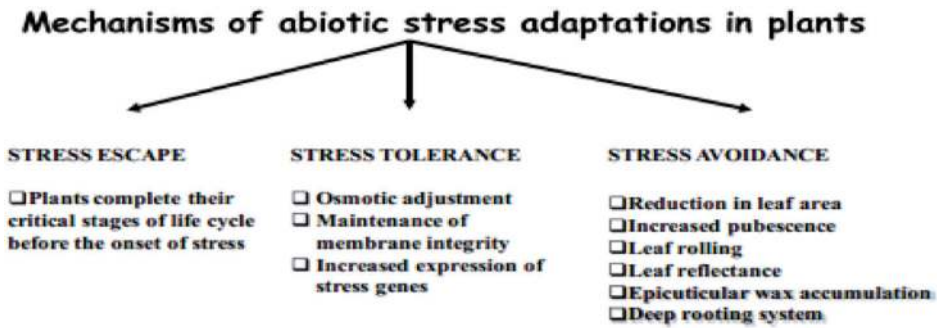


Figure 1.
Abiotic stress adaptive mechanism and their associated traits in plants heat stress tolerance.

during the next three decades to feed the global human population, which is estimated to reach ~9.7 billion in 2050 (<https://population.un.org/wpp/>). It is quite challenging to achieve this target production despite of shrinkage in arable land due to urbanization, and the probable negative impact of climate change. Due to its significant contribution to global food security, it is very much essential to improve its production and productivity to feed the ever increasing population on limited cultivated land. However, the most remarkable environmental concern in agriculture is the increase of global temperature. With regard to global climate models, the mean ambient temperature is predicted to increase by 1–6°C by the end of twenty-first century [2]. Such increase of global temperature may have a significant influence on agricultural productivity in accordance with the severity of the high temperature, drought, salinity, water logging, and mineral toxicity stresses (**Figure 1**).

2. Heat stress tolerance

High temperature-induced heat stress is expressed as the rise in air temperature beyond a threshold level for a particular period which is sufficient to cause injury or irreparable damage of crop plants in general [3]. The heat stress situation is become more intense when soil temperature increases due to increase in air temperature associated with decline in soil moisture. It negatively affects the yield attributing traits and ultimately results in reduction in wheat productivity. Some indicators of heat stress effects in wheat are illustrated in **Figure 2**. Wheat is very sensitive to heat stress particularly in some physiological growth stages. It has been estimated that reduction in global wheat yield falls by 6% for each 1°C of further temperature rise [4]. The low latitudes showed a distinct increase in simulated yield variability with higher temperature than that observed at high latitudes. This greater relative yield decline was due to the higher reference temperature [5]. The effects of heat stress on plants are very complex resulting in alteration of growth and development, changes in physiological functions, and reduced grain formation and yield.

Heat stress leads to changes in plant water relations, reduction of photosynthetic capacity, decreases of metabolic activities and changes of hormones, production of oxidative reactive species, promotion of ethylene production, reduction of pollen tube development, and increases of pollen mortality [1] in wheat. During the period from 1880 to 2012, the Earth’s system warmed by 0.85°C [6]. This warming period will be continue and is predicted to rise between the range of 1.5–4.0°C in the future [7]. The changes in climatic factors like temperature, precipitation, CO₂, weather

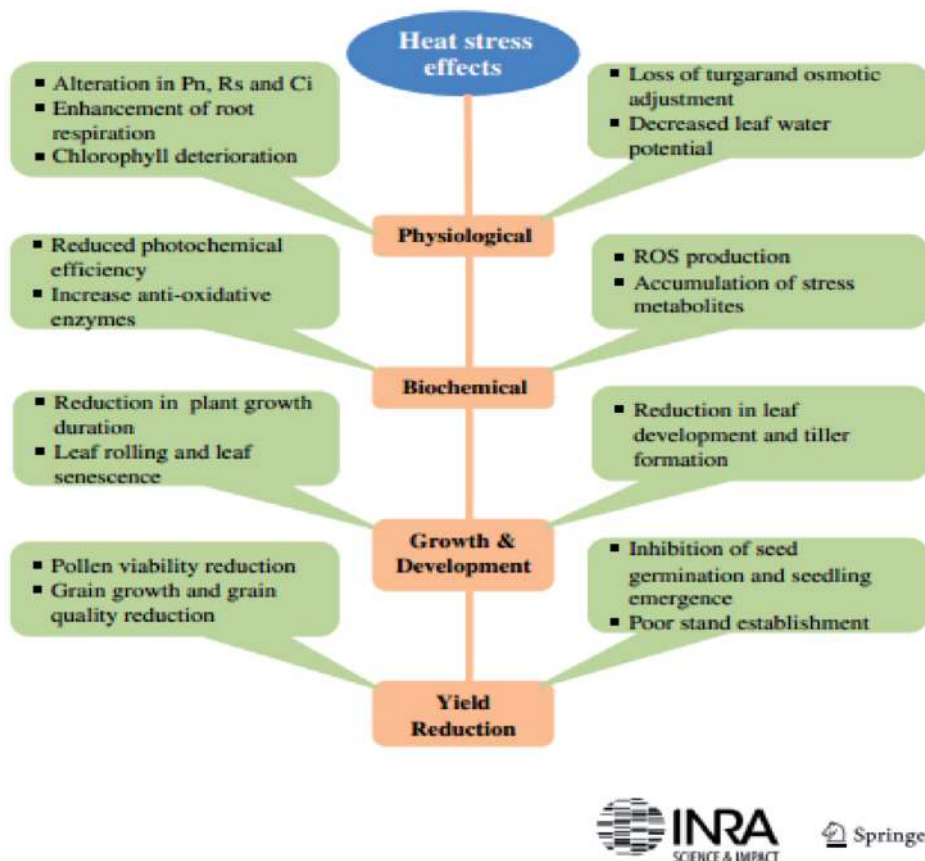


Figure 2. Major effects of heat stress on plants growth and development. Pn, Rs, and Ci indicate photosynthesis, stomatal conductance, and intercellular CO₂ concentration respectively.

variability, and soil moisture deficit would have positive or negative effects on crop system which will appear in its production level. The deleterious impacts of climate change on crop production are challenging the food security of the world and it is predicted that sustaining wheat production will be impacted more by increasing temperature. High temperature affects crops in different ways including poor germination and plant establishment, reduced photosynthesis, leaf senescence, decreased pollen viability, and consequently production of less grain with smaller grain size. Degree of such effect varies depending on the crops, cultivars, phenological stages, sowing dates and management practices. Some other adaptation measures are related to surface cooling by irrigation, antioxidants defense [8] and osmoprotectants [3, 5] minimize the effects of heat stress. However, development of heat-tolerant wheat varieties and generation of improved pre-breeding materials for any breeding program in future is crucial in meeting the food security [9]. Proteomic and transcriptomic data are important to identifying genes and proteins that respond to environment, and affects yield and quality of wheat.

2.1 Genetic management

Breeding is a strategy for genetic manipulation of crop and its adaptation response under changing environment. Therefore, it requires the evaluation of genetic diversity of existing germplasm for the selection and induction of stress inducible genes/QTLs of genetic resources for developing new varieties in the production systems.

Sl. no.	Traits/QTL	Phenotypic variance (%)	Linked marker (position in cM)	Physical position (Mbp) ^d	References
I. Agronomic traits					
1. Grain yield					
a.	Q.Yld.aww-3B-2	22	XWPT8021-Xgwm0114B (190.7)	802.3	—
2. Thousand grain weight					
a.	Q.tgw.iwbr-2A	23.7	Xgwm12280.8	(174.41)	—
b.	QHthsitgw.bhu-7B	20.3	Xgwm1025-Xgwm745 (144.1)	ND	[12]
c.	2A (36.1) ^c		224,948 F 0-9:T > A-9:T > A-kukri_c22235_1549 (21–24)	ND	[13, 14]
3. Grain weight per spike					
a.	Q.tgws.iwbr-2A	28.9	Xgwm497.1 (41.61)	684	—
b.	Q.gws.iwbr-2A	19.9	Xgwm122 (171.41)	80.8	—
4. Grain number per spike					
a.	Q.lgns.iwbr-2A	23.16	Xgwm372 (149.01)	203.3	—
b.	Q.gns.iwbr-2A	20.04	Xgwm448 (166.51)	154.4	—
5. Kernel number per spike					
a.	QHknm.tam-2B	21.6	Xgwm111.2 (36.9)	786.6	[15]
6. Kernel weight per main spike					
a.	QHkwm.tam-3B	19	Xwmc527 (89.8) 540.2		[15]
b.	QHkwm.tam-3B	21.2	Xwmc326 (123.6)	778.7	[15]
7. Single kernel weight of main spike					
a.	QHskm.tam-1A	22.6	Xcfa2129 (43.2)	513.7	[15]
b.	QHskm.tam-2A	21	Xgwm356 (129.5)	670.6	[15]
II. Physiological traits					
1. Grain filling duration					
a.	QHgfd.iwbr-5A	22	X1079678 F 0 (107.5)	ND	[16]
b.	QHthsigfd.bhu-2B	20.2	Xgwm935-Xgwm1273 (385.3)	ND	[12]
2. Ear emergence time					
a.	Q.Eet.aww-7A-2	39	XPPDD1-XWPT0330 (35)	63.5	—
3. Canopy temperature: grain filling					
a.	Q.Ctgf.aww-3B	21	XWPT-8021-Xgwm0114B (192.7)	802.3	—
4. Canopy temperature depression					
a.	QHtctd.bhu-7B	19.8	Xgwm1025-Xgwm745 (144.1)	ND	[12]

Table 1.
List of major and stable QTL for heat tolerance-related traits in wheat.

2.1.1 Stable QTLs for heat stress-related traits

Recent advances in molecular science play an important role to understand the complexity of stress response mechanisms under heat stress conditions and emphasized on the knowledge of molecular pathways and protective mechanisms to breed heat stress tolerant plants. Heat tolerance is obviously a polygenic trait, and the molecular techniques also help in analyzing the genetic basis of plant thermo tolerance. QTL mapping and subsequent marker-assisted selection made it possible to better understanding the heat tolerance in plants [10]. Recently several QTLs for different yield component traits have been identified which can be used for developing heat tolerance in wheat. For example, QTLs for heat tolerance has been identified for grain weight and grain-filling duration, senescence-related traits and canopy temperature. Besides others recognized QTLs present on chromosomes 2B, 5B and 4A in wheat under heat stress conditions [11]. The electrolyte leakage is an indication of reduced cell membrane thermo stability (CMT) which reflects the performance of wheat genotypes under heat shock. Genotypes generating heat shock proteins (HSPs) can withstand heat stress as they protect proteins from heat-induced damage. It has been also suggested that the abundance of small heat shock protein and superoxide dismutase during milky-dough stage plays a vital role in the biosynthesis of starch granule, and this will help to develop heat-tolerant wheat cultivars containing high grain quality. A large number major and stable QTLs were reported (**Table 1**), which included for agronomic traits and for physiological traits showing $\geq 20\%$ phenotypic variances. These QTLs may prove useful for improvement of such traits using marker assisted selection (MAS).

2.1.2 Biotechnological approach for improving heat tolerance

Genetic engineering and transgenic approaches can diminish the adverse effects of heat stress by improving heat tolerance mechanisms [17]. It involves the incorporation of genes for heat tolerance into the desired plants [18]. However, the complexity of the genomic pattern makes it difficult to research for genetic modification in wheat. Prolong exposes to heat stress leads to increases in production of protein synthesis elongation factor (EF-Tu) in chloroplast which is associated with heat tolerance in wheat. The constitutive expression of EF-Tu in transgenic wheat protected leaf proteins against thermal aggregation, reduced thylakoid membranes disruption, enhanced photosynthetic capability, and resisted pathogenic microbes infection [19], hence the wheat genotypes having more EF-Tu showed better tolerance to heat stress as compared to genotypes with less EF-Tu [20]. Recently, it have been found that many transcription factors (TFs) involved in various abiotic stresses and engineered to improve stress tolerance in crops [21].

3. Drought stress tolerance

Drought stress can be simply defined as a scarcity of water which leads to dramatic changes in morphological, biochemical, physiological, and molecular features [22]. All of these changes hamper plant growth and crop production. Negative impact of drought stress appears at any growth stage and level of adverse effects depends on stage specific stresses and local environment. Therefore, genotypes may be tested for their drought tolerance at different particular growth stages. Severity of drought induced damage on plants depending on plant genotype and growth stage. Some genotypes may show tolerance to drought at germination or seedling stage, but these may be very sensitive to drought at the flowering stage or vice versa. Globally, more than 50% of the wheat cultivated land is exposed to periodic drought which causes

losses up to 9–10% in production. Furthermore, decrease in precipitation and increasing evaporation as a consequence of global warming may be expected to increase in frequency of drought and its severity in the future. Therefore, understanding the drought induced damages in wheat plants and approaches to improve drought tolerance is crucial to increase wheat productivity. Drought stress imposes damaging effects on several plants physiological processes occur in its different growth stages such as germination, vegetative growth, reproductive, and maturity. Under such stress conditions plant restricts the photosynthesis, respiration, transpiration, uptake and transportation of water and nutrient and translocation of assimilates. Drought stress damages the cell membrane structure, disorganization of ultra-structural cellular components and disruption of its properties, enzyme activities and anion and cationic imbalance are some of the major reasons for disturbing plant physiological processes. Drought stress usually leads to the production of reactive oxygen species (ROS). Hydrogen peroxide (H_2O_2), superoxide (O_2^-), singlet oxygen ($^1\text{O}_2$), and hydroxyl radicals (OH^-) are the most common species which are generated due to iron-catalyzed Fenton reaction due to the activities of lipoxygenases, peroxidases (POX), NADPH oxidase, and xanthine oxidase. The ROS in any form causes substantial damage to cell components and can cause cell death [23]. Plants have a very much evolved antioxidant defense system to rummage and keep up a reasonable degree of ROS to keep cells from oxidative harm. Under cell antioxidant defense system, it has some nonenzymatic antioxidants (ascorbic acid, AsA; glutathione, GSH; phenolic compounds; alkaloids; non protein amino acids; and α -tocopherols) and some antioxidant enzymes (super oxide dismutase, SOD; catalase, CAT; ascorbate peroxidase, APX; glutathione reductase, GR; monodehydroascorbate reductase, MDHAR; dehydroascorbate reductase, DHAR; glutathione peroxidase, GPX; and glutathione-S-transferase, GST) which work coordinately to eliminate ROS in an efficient way. Biotechnological approaches also helpful in enhancing the antioxidant system to confer oxidative as well as abiotic stress tolerance. Performances of drought-affected plants are remarkably improved by exogenous application of osmolytes, hormones, antioxidants and signaling molecules.

3.1 Genetics of drought tolerance

Drought stress tolerance is a complex trait influenced by genetic with many quantitative trait loci (QTLs) and environmental factors. Genetic analyses of drought tolerance have been studied through the development of molecular markers and genome sequencing in wheat. Such analyses include several approaches, e.g., QTL-mapping, association-mapping, genome-wide analyses and expression analysis aim to identify QTL or gene-related traits for drought stress tolerance. Revealing the genetic basis underlying the drought tolerance in wheat requires a phenotypic and genetic variation of relevant traits in large populations with dense genetic maps. The genetic basis of drought tolerance is due to polygenic inheritance, where each gene has small effect with high GXE interaction, hence low-heritability. Furthermore, the genetic independence of drought tolerance at different developmental stages makes the detected QTL less useful in crop improvement. Therefore, several QTLs have been discovered for drought tolerance-related traits, but a limited number of QTLs are genetically characterized or cloned and incorporated in breeding programs. Identifying stable QTL with large-effect that controls many drought tolerances-related traits at different developmental stages would be a great effort for crop improvement, but has not been found.

3.1.1 Quantitative trait locus (QTL) of drought tolerance

Quantitative trait loci (QTL) are location from where some genes influence a phenotype of quantitatively inherited trait. Genetic variations of a crop can be

clarified through QTL mapping (polygenes). Mapping of QTL allows the estimation of the places, quantity, level of effects for the phenotype, gene activity pattern and important genomic regions. Multi-environmental field conditions are commonly used to evaluate the genotype performance [24, 25] using a different type of bi-parental population, e.g., recombinant inbred line (RIL) population, doubled haploid (DH) population [26, 27] or advanced backcross [28]. Different DNA molecular markers have been used to genotype the populations and identify QTL [26, 29]. Recently, a high-density genetic SNP map [28] (SNP array or genotyping by sequencing (GBS)) have been used to genotype the population [27]. Numerous QTLs have been identified for grain yield on chromosomes one, three and six, grain number per spike on chromosome two, three and six and spikelet number for each spike on two, five and six. Such major QTL controlling grain yield can be utilized in marker-helped determination rearing for yield improvement under dry spell pressure. QTL studies using a biparental mapping population have also discovered the genetic factors of other physiological and adaptive traits (**Table 2**), e.g., leaf chlorophyll content, leaf waxiness and leaf rolling in wheat, transpiration efficiency, water-use efficiency, biomass, leaf area, and growth rate-related traits in wheat. Meta-QTL (MQTL) analysis on drought tolerance in wheat has revealed QTLs for, photosynthesis, soluble carbohydrates, water status, carbon isotope discrimination, canopy temperature, coleoptiles vigor and stay-green.

QTL investigation is so basic to target characteristics and for doing this a couple of stages are required. Initially, phenotypic evaluation of reasonably huge population for markers which are polymorphic is required. Besides, genotyping of the population is noteworthy. Thirdly, there is a prerequisite for quantifiable examination to distinguish the loci that are influencing the target trait. Several studies have been done and recognized >1200 QTLs for various characteristics conveyed over every one of the 21 chromosomes engaged with dry season resilience. Most extreme number of QTLs has been accounted for agronomic attributes, trailed by physiological qualities and root characteristics. Among agronomic qualities, most extreme QTL are known for thousand grain weight (TGW) trailed by grain yield and different attributes recorded under dry season conditions just as should be expected conditions. Among physiological qualities, most extreme number of QTLs are accessible for SPAD/chlorophyll content (82 QTL) trailed by water-dissolvable starches (76 QTL), coleoptile length (68 QTL). Among the root characteristics, greatest number of QTL is known for root length. Just 70 of these detailed QTL are major (clarifying ~>20% PVE), and just 19 QTL (counting 14 QTL for agronomic qualities, 5 for physiological attributes) are steady QTL utilized for QTL examination. The root attributes display high QTL × environment interaction, which recommends non accessibility of stable QTL for these characteristics. Fourteen stable major QTL were accounted for five agronomic attributes, with phenotypic fluctuation for individual QTL extending from 19.60% (grain yield QTL qGYWD.3B.2) to 45.20% (1000-grain weight QTL on 3B). These QTL can be utilized for development of dry spell resistance utilizing marker assisted selection (MAS). Two of the five QTL for grain yield that respond to dry season/heat stress cover a specific Mega QTL; these two QTL are found one each on chromosomes 4A and 7A [39] in areas, which likewise harbor QTL for the accompanying 14 qualities, which add to seedling rise, grain yield and reception to dry spell conditions: (1) days to heading, (2) days to development, (3) remain green propensity, (4) biomass, (5) shelter temperature; (6) carbon isotope separation, (7) coleoptile energy, (8) grain filling, (9) plant stature, (10) portion number, (11) spike thickness, (12) 1000-bit weight, (13) water-solvent sugars and (14) grain yield. Two other QTL for kernel width/thickness proportion on chromosome 5A cover a MQTL on 5A which represent to QTL for plant stature, spike weight and TGW [39]. The four stable major QTL for dry spell resilience incorporate two QTL for grain yield and two

Traits	Chromosome	Reference
Grain yield	1B, 1D, 3B, 4A, 6D, 7D	[30]
Grain weight per spike	1B, 1D	[31]
Thousand grain weight	1B, 1D, 2A, 2B, 3A, 3B,4A, 4D, 6A, 6D, 7B, 7D	[32]
Grain number (m ⁻²)	1B, 5A, 5B, 7D	[33]
Grain number per spike	1A, 2A, 2B, 3A, 6B	[33, 34]
Harvest index	1B, 2D, 4BS, 5A	[32]
Spike number per plant	1A, 2A, 2B, 2D, 4B, 5A,7B	[32]
Spikelet compactness	1A, 1B, 2B, 5A, 5B, 6A,6B, 7A	[32]
Spikelet number per spike	1B, 1D, 2B, 3B, 4B, 5A, 6B, 7D	[32]
Sterile spikelet number per spike	7A	[32]
Fertile spikelet spike per spike	2A	[32]
Spike length	2B, 7A, 7B	[32]
Biomass	1B	[32]
Shoot biomass	4B	[35]
Spike length	2B, 7A, 7B	[32]
Physiological traits		
Leaf area, growth rate, transpiration efficiency, water-use efficiency	2A, 2D, 3A, 4B, 6A	[36]
Stomatal density, index, aperture area, length; guard cell area and length	2B, 4AS, 5AS, 7AL, 7BL;1BL, 4BS, 5BS, 7AS	—
Stomatal conductance, net photosynthetic rate	5A, 6B	[33]
Root length	2D, 4B, 5D, 6B	[35]
Root biomass	2D, 4BS	[35]
Metabolite traits		
Abscisic acid (ABA)	1B, 2A, 3A, 4D, 5A, 6D,7B	[37]
Jasmonic acid (JA), salicylic acid (SA), ethylene	6A	[38]

Table 2.

The detected quantitative trait loci (QTLs) for agronomic, physiological and metabolite traits in wheat using bi-parental mapping populations.

QTL for kernel width/thickness proportion. In an ongoing report, after broad field tests directed under pressure conditions in India, Australia and Mexico, a fundamental impact yield QTL (QYld.aww-1B.2) was fine-mapped to 2.9-cM locale relating to 2.2-Mbp genomic area containing 39 predicted genes (Tura et al., 2020). This QTL could be exploited in wheat breeding. The QTL for TGW, which is a significant segment of grain yield and have high heritability as well as stability, can be exploited for development of grain yield under water stress. Four QTL for days to heading and days to maturity may likewise be exploited utilizing MAS. Five significant and stable QTL for three physiological characteristics (SPAD/chlorophyll content, stem save assembly and water-solvent starches) each clarified PV running from ~20 to ~60% (**Table 3**). These attributes add to grain filling/advancement and thus to grain yield. The markers related with QTL for these characteristics are additionally acceptable possibility for marker assisted selection (MAS).

Sl. no.	QTL/trait	PVE %	Linked marker (position in cM)	Physical position (Mbp)	References
I. Agronomic traits					
1. Grain yield					
	a. qGYWD.3B.2	19.6	Xgpw7774 (97.6)	16.2	—
	b. 4A	20	Xwmc420 (90.4)	538.2	—
	c. 4A-a	23.9	Xgwm397 (6)	708.6	[11]
	d. Qyld.csdh.7AL	20.0	Xgwm332 (155.9)	681.6	[40]
	e. 6D	26.6	2,265,648 F 0-60:A>G- 60:A>G-RAC875_ c57371_238 (73)	ND	[14]
2. 1000 grain weight					
	a. 2A	36.1	2,264,948 F 0- 9:T > A-9:T > A-Kukri_ c22235_1547 (21.0-24.0)	ND	[14]
	b. 3B	45.2	Xbarc101 (86.1)	34.3	[41]
	c. QTgw-7D-b	21.9	XC29-P13 (12.5)	ND	[42]
3. Days to heading					
	a. QDh-7D.b	22.7	XC29-P13 (12.5)	ND	[42]
	b. QHd.idw-2A.2	32.2	Xwmc177 (46.1)	33.7	[29]
	c. 5D	21.4	1,126,619 F 0- 21:A > T-21:A > T-wsnp_ Ex_c1278_2449191 (162)	ND	[43]
4. Kernel width/thickness ratio					
	a. qWTR-5A-1	33.09	Xwmc74-Xgwm291 (61)	702.5–698.1	[44]
	b. qWTR-5A-2	23.59	Xgwm291-Xgwm410 (71)	698.1	—
5. Days to maturity					
	a. QDm-7D.b	22.7	X7D-acc/cat-10 (2.7)	ND	[29]
II. Physiological traits					
1. Stem reserve mobilization					
	a. QSrm.ipk-2D	42.2	Xgwm249a (142)	141.1	[45]
	b. QSrm.ipk-5D	37.5	Xfbb238b (19)	ND	[45]
	c. QSrm.ipk-7D	21	Xfbb189b (338)	ND	[45]
2. Water-soluble carbohydrates					
	a. QWsc-c.aww-3A	19	Xwmc0388A (64.9)	208	—
3. SPAD/chlorophyll content					
	a. Qchl.ksu-3B	59.1	Xbarc68 (67.2)	76.1	[46]

PVE shows phenotypic variation explained; c means position of linked flanking marker was given if either the second marker or its sequence was not available; ND explain the physical position of QTL could not be determined due to lack of linked marker sequence information.

Table 3.

A list of major and stable QTL (PVE ranging from 19 to 59%) for agronomic and physiological traits identified under drought/water stress.

3.1.2 Genomics analyses of drought tolerance

As of late, genome-wide investigations fuse genome-wide association study (GWAS) and genomic selection (GS) has been used to grasp the inherited multifaceted nature and breed for drought tolerance. GWAS approaches can be utilized with huge quantities of SNPs that produce a high-thick guide in an enormous and various assortments that give an elective way to deal with distinguish explicit qualities while the GS can be utilized in both bi-parental and different populaces. A predetermined number of studies have concentrated on physiological attributes, e.g., leaf green region, leaf water substance and water-soluble carbohydrates with around 12 MTAs have been distinguished. Chromosome 1A was found to contain a significant genomic region for physiological attributes, for example, water-dissolvable starches. Recently, utilized the most recent wheat genome sequences to physically map the most consistent and significant genomic regions that related with numerous agronomic and physiological attributes under drought stress in wheat. For example, the physical region of 1A was as a highly significant region for grain weight, flag leaf area and flag leaf width.

4. Salt stress tolerance

Globally, over 20% of the cultivable land is influenced by salinity. Because of environmental change and anthropogenic exercises, the salt influenced region is tended to increase day by day. A saline soil is commonly characterized as one in which the electrical conductivity (EC) of the saturation extract in the root zone surpasses 4 dS m^{-1} (roughly 40 mM NaCl) at 25°C and has a exchangeable sodium of 15%. It has been assessed that overall 20% of all out developed and 33% of irrigated agricultural lands are influenced by high salinity. Salt affected soils currently constitute 6.74 million ha in various agro ecological regions, the zone is probably going to increment to 16.2 million ha by 2050. Abiotic stresses (including salinity) are responsible for more than 50% yield reduction [47]. In opposite, because of fast increment of worldwide population, food production ought to be expanded by over 70% by 2050 [48]. Wheat (*Triticum* spp.) positions first on the world's grain production. Wheat is expended as staple food by over 36% of world population. Wheat gives almost 55% of the carbohydrates and 20% of the food calories consumed globally. The productivity of wheat is frequently unfavorably influenced by salt stress. The yield of wheat begins to decay at $6\text{--}8 \text{ dS m}^{-1}$ [49].

4.1 Effect of salinity on growth: two phases of the growth response

In saline soil plant development is restrained by two reasons. To begin with, it decreases the plant's capacity to take up water, and this prompts more slow development. This is the osmotic stress or water-deficiency impact of salinity. Second, it might enter the transpiration stream and in the end harm cells of leaves includes in the transpiration prompts further reducing development. This is the salt-specific or ion-excess effect of salinity. The two impacts give rise to a two-stage development response to salinity (Figure 3). The outline shows the development reaction to salt that is included step by step.

Phase 1: The primary period of the development reaction results from the impact of salt present in the soil solution lessens leaf development and less significantly, root development [50]. The cell and metabolic processes included are in common to dry season influenced plants. Neither Na^+ nor Cl^- develops in developing tissues at concentrations that hinder development: meristematic tissues are

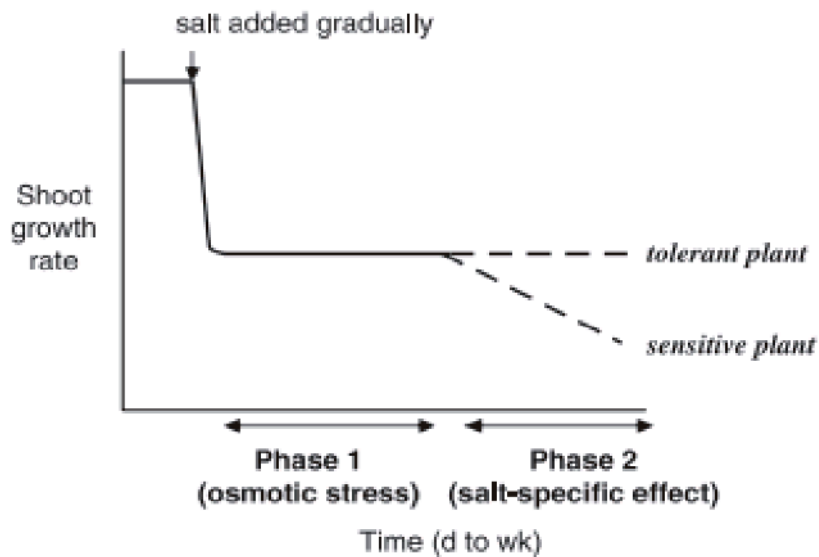


Figure 3.

Schematic outline of the two-stage development reaction to salinity for genotypes that differ in the rate at which salt arrives at harmful levels in leaves. For annual species, the time scale is d or wk., depending upon species and salinity level. For perennial species, the timescale is months or yr. During stage 1, development of the two genotypes is decreased in light of the osmotic stress of the saline solution outside the roots. During stage 2, leaves in the more sensitive genotype die and decrease the photosynthetic limit of the plant. This applies an extra impact on development [50]. In the event that salt is included one stage, the development rate dives to zero or below and takes 1–24 h to recover to the new consistent rate, contingent upon the level of the osmotic shock [51].

taken care of to a great extent in the phloem, from which salt is viably avoided and quickly elongating cells can accommodate the salt that shows up in the xylem inside their extending vacuoles.

Phase 2: The second phase of the development reaction results from the toxic effect of salt inside the plant. The salt taken up by the plant moves in old leaves: proceeded with transport into transpiring leaves brings about extremely high Na^+ and Cl^- concentrations, and the leaves become die. The reason for injury is presumably the salt burden surpassing the capacity of cells to compartmentalize salts in the vacuole. Salts would then develop quickly in the cytoplasm and inhibit enzyme activity. On the other hand, they may develop in the cell walls and get dried out the cell. The rate of leaf death is crucial for survival of the plant. In the event that new leaves are ceaselessly created at a rate more prominent than that at which old leaves die, there will be sufficient photosynthesizing leaves for the plant to produce flowers and seeds, in spite of the fact that in decreased numbers. In any case, if old leaves die more rapidly than new ones create, the plant may not get by to produce seed. For an annual plant there is a competition against time to initiate flowers and form seeds, while the leaf region is as yet sufficient to supply the important photosynthates. For perennial species, there is a chance to enter a state like to dormancy and survive under the stress. Salt stress not just prompts the decrease of harvest yield yet it additionally influences the metabolic processes in plants through disability of water potential of cells, ion toxicity, take-up of fundamental mineral supplements, membrane integrity and function. NaCl is the most dissolvable and across the board salt and collection of sodium particle (Na^+) in plant tissues is one of the most hindering impacts of saltiness. The take-up of fundamental micronutrients, for example, potassium (K^+) and calcium (Ca^+) from soil is restrained by higher centralization of Na^+ [52]. K^+ is required for development or improvement of plants and for keeping up high K^+/Na^+ ratio in shoot which is the significant technique received by plants to adapt up to salt stress. K^+ and Na^+ however having

comparative compound properties, both have distinctive physiological effect on plant development. Under salt pressure, hyperosmotic and hyperionic (particle harmfulness) stresses happen because of low water potential of soil and abundance sodium particle amassing inside the plant. Ionic stress is additionally connected with nourishing irregularity. Salt stress additionally causes diminished germination rate, decreased development, altered reproductive behavior and diminished yield. Modified enzymatic movement, disturbed photosynthesis, oxidative pressure, disrupted biomembrane structure and function, harm of ultrastructural cell components, and hormonal imbalance are a few explanations behind diminishing generally speaking development and improvement of plants under salt pressure.

4.2 Mechanisms of salt tolerance

Salt tolerant is a polygenic trait directed by multiple factors/genes. There are various systems for salt resilience helps in decreasing Na^+ gathering in the cytoplasm by restricting Na^+ section into the cell, effectively moving Na^+ out of the cell, and compartmentalizing Na^+ into the vacuole. High-affinity potassium transporters (HKTs) are most active at level of plasma membrane and act as Na^+/K^+ symporters as well as Na^+ particular uniporter. Significant two subfamilies of HKTs: HKT1 and HKT2 are being investigated phylogenetically [53]. HKT1 are only permeable to Na^+ but HKT2 are penetrable to both Na^+ and K^+ . The group of HKTs having a place HKT/Trk/Ktr-type K^+ transporter superfamily are found generally in microorganisms and plants. In numerous plants, Na^+ and Cl^- are avoided by roots and water is taken up from the soil. This avoidance at higher salinities is kept up by halophytes. For example, sea grain grass, *Hordeum marinum*, avoids both Na^+ and Cl^- until at least 450 mM NaCl. Receptive oxygen species (ROS), made during the stress causes chlorophyll degradation and membrane lipid peroxidation. Malondialdehyde (MDA) is one of the final products of peroxidation of polyunsaturated fatty acids in the cell layers. The increase in free-radicals causes the overproduction of MDA which is the most notable marker of the oxidative stress. Plants accumulate different kind of metabolites on introduction to stressful conditions. The enormous changes under abiotic stress are showed up by soluble sugar, proline, phenolic compounds, chlorophyll substance, K^+/Na^+ , shoot-root biomass proportion, etc. Total soluble sugar is an essential part of carbohydrate metabolism. It shows a close connection among photosynthesis and plant productivity and reflects the ability of grains to use assimilates. Proline is the fundamental amino acid act as excellent osmolyte and besides fill in as metal chelator anti-oxidative defense molecule and signaling molecule.

Thereby it maintains concentration of ROS in normal range and prevent oxidative burst in plants. Phenolic compounds also show important role in neutralizing the free radicals, quenching singlet oxygen and decomposing peroxides. Different approaches have been adopted to improve plant performance under salt stress; introduction of genes, screening of better performing genotypes, and crop improvement through conventional breeding methods which are often not so successful and not suitable due to time consuming or reduction of plant vigor with the succession of time. Uses of exogenous phytoprotectants, seed priming, nutrient management, and application of plant hormones are convenient for improving plant performances. These approaches are being also popular for stress management practices including the salt stress.

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4.3 HKT-type transporters and genes response to salinity

Class 1HKT genes are involved in regulating transport of Na⁺ in higher plants. Several HKT1 genes including HKT1; 1/2-like, HKT1; 3-like, HKT1; 4-like, and HKT1; 5-like, have been identified and mapped to wheat homologous chromosome groups 2, 6, 2 and 4 respectively. Among these, Nax1 in chromosome 2AL co-segregated with sodium transporter gene HKT1; 4-A2, which was shown to control Na⁺ unloading from xylem in roots and sheaths. Nax2 was mapped to the distal region of chromosome 5AL that is homologous to a region on chromosome 4DL containing Kna1 [54]. Based on synteny and phylogeny analysis with Nax2, TmHKT1; 5-A significantly reduced leaf sodium content and increased durum wheat grain yield by 25% compared to lines without the Nax2 locus. Furthermore, decreased expression of TaHKT1; 5-D, which is homoeologous to TmHKT1; 5-A and underlies Kna1 locus in bread wheat, caused by target-specific RNA interference-induced silencing (RNAi) led to an accumulation of Na⁺ in leaves, strongly suggesting that TaHKT1; 5-D should be the candidate gene of Kna1.

Class 1HKT genes are engaged with managing transport of Na⁺ in higher plants. A few HKT1 genes including HKT1; 1/2-like, HKT1; 3-like, HKT1; 4-like, and HKT1; 5-like, have been recognized and mapped to wheat homologous chromosome groups 2, 6, 2 and 4 respectively. Among these, Nax1 in chromosome 2AL co-segregated with sodium transporter gene HKT1; 4-A2, which was appeared to control Na⁺ emptying from xylem in roots and sheaths. Nax2 was mapped to the distal region of chromosome 5AL that is homologous to an region on chromosome 4DL containing Kna1 [54]. In view of synteny and phylogeny investigation with Nax2, TmHKT1; 5-An altogether decreased leaf sodium content and expanded durum wheat grain yield by 25% contrasted with lines without the Nax2 locus. Besides, diminished articulation of TaHKT1; 5-D, which is homoeologous to TmHKT1; 5-An and underlies Kna1 locus in bread wheat, brought about by target-explicit RNA obstruction actuated hushing (RNAi) prompted a collection of Na⁺ in leaves, firmly proposing that TaHKT1; 5-D ought to be the applicant quality of Kna1. A major mechanism in salinity tolerance of wheat is Na⁺ exclusion mediated by HKT genes. AtHKT1 is regulated by small RNA and DNA methylation. Moreover, DNA methylation also participates in the response of TaHKT1; Transcription factors such as AtAB14 and OsMYBc were shown to regulate HKT genes in plants, offering more candidate targets for enhancing salinity tolerance.

4.4 Genes involved between salinity response and other environmental and developmental signals in wheat

When there is high concentration of salt in plant system, the activation of complex physiological responses such as phytohormone signaling pathways and developmental signals starts to adapt the stress; therefore it is essential to identify the environmental and developmental signals. First of all an attempt was performed by looking at phytohormones, as most phytohormones are regulatory factors of both developmental process and stress response. For example, the wheat gene

TaAOC1, encoding cyclase involved in jasmonic acid synthesis, was induced by high salinity. Constitutive expression of TaAOC1 in both wheat and Arabidopsis restricted root growth, but enhanced salt tolerance and Jasmonic acid content. It indicates the different branches of metabolic pathway participate in a single process but controlled by different mechanisms. Light is an essential factor that positively affects the development and growth of plants. TaGBF1, a blue light specific responsive G-box binding factor, was prompted after exposure to salt. TaGBF1 caused salt affectability and advanced light blue interceded photomorphogenesis, indicating that it was a typical segment of the blue light and salt stress responsive signaling pathways. Curiously hereditary examination recommended that the job of TaGBF1 because of salt depended on AB15, a key part of ABA signaling pathway. The extensive studied has been done for the identification of salt tolerant QTLs. The available studies led to identification of ~500 QTL (excluding those involved in digenic

Sl. no.	Traits	QTL/locus	PVE %	Linked marker	Physical position (Mbp) ^a	References
	Na ⁺ exclusion	Kna1	—	Xwg199, Xabc305, Xbcd.402, Xpsr567, Xpsr375	390.2	[55]
	Na ⁺ exclusion	Nax1	38	Xgwm312, Xwmc170	709.0– 711.5	[56]
	Dry weight of plumule at germination	Qpdwg-4D.1	19.8	Xfbb226– Xfba177	ND	[57]
	Na ⁺ exclusion	QNax. aww-7AS	41	Xwmc083– Xcdo595	89.9	[58]
	Booting	QB.uabcs-2D	23.6	Xcdo1379		[59]
	Ear emergence time	QEet. uabcs-2D	27.1	Xcdo1379	ND	
	Flowering	QFl.uabc-2D	26.7	Xbcd102a	ND	
	Maturity	QM.uabc-2D	28.9	Xcdo137	ND	
	Ear length	QEL.uabc-2D	21.5	Xbcd102a	ND	
	Seedling shoot fresh weight	3B-1	19.2	wPt-798,970– wPt-8303	ND	
	Na ⁺ exclusion value	qSNAX.7 A.3	18.79	AX-95248570– AX-95002995	700.6	[60]
	3rd leaf Na ⁺ and K ⁺ concentration and K ⁺ /Na ⁺ ratio	4B	18, 20, 27	Xm564	657.1	[61]
	3rd leaf Na ⁺ concentration	3B	18	Xm551	701.9	
	K ⁺ μmol/g dry weight	QK.asl-5A	28.2	Vrn-A1	587.4	[62]

PVE: phenotypic variation explained; “–“explain PVE% not available; ND shows physical position of QTL could not be determined due to lack of linked marker sequence information.^aPosition of one flanking marker was given if either the second marker or its sequence was not available.

Table 4.

A list of major QTL/loci (PVE of ~>20%) for plant traits under salt stress condition in bread and durum wheat.

epistatic interactions and QTL \times treatment interactions); these QTL are spread over all the 21 wheat chromosomes and could prove useful resource for MAS intended at improving salt tolerance in wheat. The phenotypic variance (PV) explained by individual QTL ranged from 8.4% to 38.0%, and only a dozen major QTL have been reported (**Table 4**). The traits used for QTL analysis included Na⁺ exclusion/content, K⁺ content and K⁺/Na⁺ ratio, etc., both at the seedling and adult plant stages. Since several studies in different plant systems including wheat have demonstrated that Na⁺ concentration is not necessarily associated with salinity tolerance, other additional mechanisms (tissue tolerance and osmotic adjustment) may also be examined in future in order to breed for salinity tolerance in bread wheat. It has been studied that bread wheat exhibit low rates of Na⁺ transport, which leads to high K⁺/Na⁺ ratio in leaves. A high K⁺/Na⁺ discrimination provides tolerance to salinity stress. The extensive studied has been accomplished for the ID of salt open minded QTLs. The accessible examinations prompted identification of ~500 QTL (barring those associated with digenic epistatic collaborations and QTL \times treatment communications); these QTL are spread over all the 21 wheat chromosomes and could demonstrate valuable asset for MAS expected at improving salt resilience in wheat. The phenotypic difference (PV) clarified by individual QTL extended from 8.4% to 38.0%, and just 12 significant QTL have been accounted (**Table 4**). The qualities utilized for QTL investigation included Na⁺ rejection/content, K⁺ substance and K⁺/Na⁺ proportion, and so forth., both at the seedling and grown-up plant stages. Since a few investigations in various plant frameworks including wheat have exhibited that Na⁺ fixation is not really connected with saltiness resilience, other extra components (tissue resistance and osmotic alteration) may likewise be analyzed in future so as to raise for saltiness resistance in bread wheat. It has been contemplated that bread wheat show low paces of Na⁺ transport, which prompts high K⁺/Na⁺ proportion in leaves. A high K⁺/Na⁺ segregation gives resilience to saltiness stress.

5. Pre-harvest sprouting (PHS) tolerance

Germination of wheat inside the grain ear head before reap is called pre-gather sprouting (PHS). Exposure of prolonged precipitation and high humidity after the grain has matured and before it very well may be collected can prompts pre-harvest sprouting (PHS), which can be thought of as an premature germination. Germination can start as a wheat seed retains moisture and swells. A noticeable sign of PHS incorporates kernel swelling, germ discoloration, seed-coat parting, and the root and shoot emergence.

5.1 Effect of preharvest sprouting in wheat quality

Pre-collect growing in bread wheat (*Triticum aestivum* L.) is a setback that happens everywhere throughout the world to varying degrees. The issue happens when high humidity goes with precipitation on standing full grown wheat crops before harvest, and seeds in the spike sprout. As the outcome of this, wheat qualities as well as quantity are affected, diminishing healthy benefit and yield. Changes in sugar content, total protein and composition of amino acids joined by enzymatic activities are the explanations behind the degradation in quality and yield. Many early wheat scientists reported that pre-harvest sprouting is negatively correlated with yield, seed viability, seedling vigor, flour yield and baking quality. Pre-harvest sprouting results in lower yields due to decreased test weights, and it limits end-use applications for wheat due to decreased grain quality. Reduced grain quality,

coupled with decreased yields, can result in substantial financial losses to farmers and food processors. Products made from germinated seeds can be spongy, soggy, off-color and of inferior quality [63]. Sprouted seed baked to Compact interior and smaller volume breads due to higher α -amylase activity results in starch degradation, hence producing lower quality of bread that is below the accepted standards of consumers. Numerous early wheat researchers revealed that pre-harvest sprouting is negatively correlated with yield, seed suitability, seedling force flour yield and preparing quality. Pre-harvest sprouting outcomes in lower yields because of diminished test weight and it limits end-use applications for wheat because of diminished grain quality. Diminished grain quality, combined with diminished yields, can bring about significant financial losses to farmers and food processors. Items produced using germinated seeds can be spongy, soggy, off-color and of inferior quality [63]. Germinated seed baked to Compact inside and smaller volume breads because of higher α -amylase activity brings about starch degradation, thus creating lower quality of bread that is underneath the acknowledged norms of customers.

5.2 Mechanism of preharvest sprouting resistance

Pre-harvest sprouting is controlled by genetic factors, environmental conditions and their interactions. The protection from germination is fundamentally connected with an adequate level of kernel dormancy. Pre-harvest sprouting depends significantly on (1) hereditary attributes like kernel coat, protecting structures of spike and straightness of spike, (2) natural conditions like temperature and precipitation, and (3) agronomic perspective like fertilization. The main considerations next to conditions influencing the resilience to PHS are seed dormancy, seed coat penetrability and color, α -amylase activities, endogenous hormones levels, genes and QTLs. Dormancy was seen as the fundamental internal factor which lead to the wheat resistance from PHS [64–66]. The seed coat permeability is the essential guaranteeing divider which could increase the wheat PHS resilience. The seed coat color additionally assumes a critical activity in PHS. All around, white wheat varieties have higher germination rates than the red ones [67]. Cultivars having red kernels are more impervious to growing than white ones. Accordingly, red kernel shading is consistently used as an indicator of sprouting resistance in wheat. The α -amylase viewed as one of the significant elements that influence wheat germination rate, cold versatility and production. Some extraordinary endogenous factors like gibberellic acid (GA), abscisic acid (ABA) and indole acetic acid (IAA) could in like manner impact PHS through a wide scope of ways. PHS is a quantitative characteristic compelled by various genes. Viviparous-1 (Vp-1) has been recognized as the main gene that coordinated seed germination and dormancy. Some different genes were also regarded to participate in embryos maturing, seed dormancy and germination through system guideline with Vp-1 to control PHS. QTLs for dormancy and PHS were found in different materials through molecular markers. During kernel development, the Vp-1 gene expressed in cytoplasm subsequent to flowering controlled seed dormancy at the transcriptional level, advanced the seed development and checked the outflow of germination-related genes [68]. There were numerous allelic variety of Vp-1 gene in various grain crops, however the anticipated protein of Vp-1 was monitored with four DNA binding regions A1, B1, B2, and B3. Three alleles Vp-1A, Vp-1B, Vp-1D of Vp-1, situated on 3A, 3B and 3D homologous chromosomes in wheat, separately, have been identified [66, 69]. Numerous investigations additionally centered on the allele's variety of Vp-1 to clarify how Vp-1 managed the resistance to PHS. Six alleles of Vp-1A, namely Vp-1Aa, Vp-1Ab, Vp-1Ac, Vp-1Ad, Vp-1Ae and Vp-1Af, were found in 81 wheat cultivars and advanced lines [69]. Six alleles of Vp-1B named Vp-1Ba, Vp-1Bb, Vp-1Bc, Vp-1Bd, Vp-1Be and Vp-1Bf were

likewise found in wheat [69, 70]. However, no alleles of Vp-1D were found in wheat. The wheat varieties with alleles of Vp-1Ab and Vp-1Ad were regarded to have low germination index (GI) and strong PHS tolerance [69]. However, the wheat varieties with the allele Vp-1Ba have higher germination index and more sensitive to PHS than the other five ones, which even positively influenced on the decrease of germination rate [69, 70]. More than 47 investigations on QTL interval mapping for PHS resistance and related characteristics including ~40 distinct population derived from bread wheat (including synthetic wheat), durum wheat and *T. monococcum* have so far been conducted. QTL for PHS tolerance have been recognized utilizing the following parameters: PHS index, grain color, falling number, germination index, seed dormancy and alpha amylase activity (**Figure 4**).

Maximum numbers of QTL have been accounted for PHS index followed by seed dormancy, germination index, falling number, alpha amylase activity and grain color. About ~250 QTL were distinguished, among them just 29 QTL were major and stable across environments; these QTL are conveyed on 11 unique chromosomes (1B, 3A, 4A, 5A, 6A, 2B, 3B, 4B, 7B, 2D, 3D and 7D); the most noteworthy PV explained by an individual QTL range from 23% to 78.3%.

Chromosomes from homoeologous groups 3 and 4 together conveyed 17 of the 29 significant and stable QTL. The PHS and the germination index (a measure of dormancy) have regularly been utilized for estimation of tolerance against PHS. PHS index is a simple to score parameter and reliable, with the goal that it has been widely used. The QTLs because of seed dormancy, which is characterized as the powerlessness of practical seeds to develop under conditions great for germination is additionally connected with PHS tolerance. The QTL for PHS tolerance, present on the long arms of chromosomes of homoeologous group 3, have regularly been accounted for to be related with genes for red grain color, which contributes to coat-imposed dormancy. A significant stable QTL for PHS (QPhs.ccsu-3A.1; 24.68–35.21% PV) was accounted [71–80]. The utilization of markers related with this QTL in MAS brought about significant level of PHS tolerance, which was tragically connected with red grain color.

In wheat markets, especially in Southeast Asia and Middle East, Africa and North America, there is a consumer preference for white grain. Along these lines, endeavors were later made to deliver white-grained PHS-tolerant wheat genotypes;

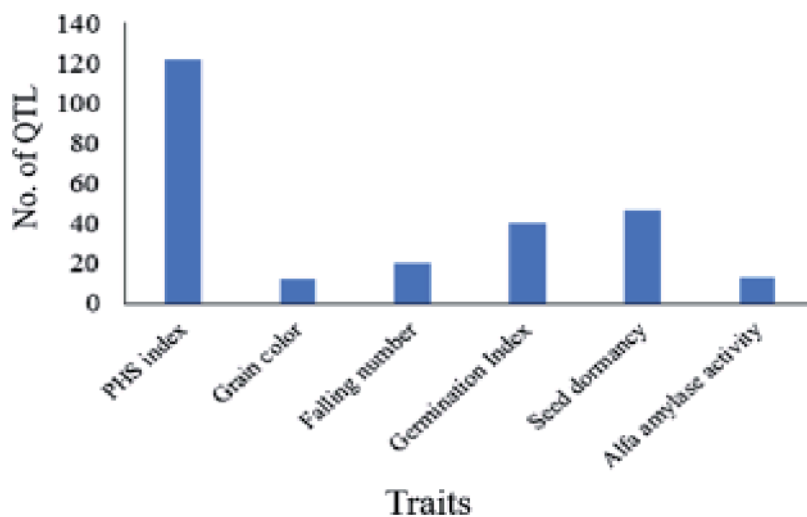


Figure 4. Number of QTL for five different traits associated with pre-harvest sprouting tolerance reported in the 47 studies in wheat.

Sl. no.	Traits/QTL	PVE (%)	Linked marker	Physical position (Mbp) ^c	References
	FN/5A	26.4	Xpsr1194–Xpsr918b	ND	[81]
	α-AA/5A	30.0	Xpsr1194–Xpsr918b	ND	[81]
	SD/4AL (33–77.2)		Xcdo795/Xpsr115		[82]
	PHS/QPhs.ccsu-3A.1 (78.3)		Xwmc153–Xgwm155	701.7–702.9	[71]
	SD/QPhs.ocs-3A.1 (23.0–44.8)		Xbarc310/Xbcd907	7.1	
	GI/QGi.crc-3B	27.0	Xbarc77–Xwmc307	430.1–783.5	[83]
	SI/QSi.crc-3B	24.0	Xbarc77–Xwmc307	430.1–783.5	[83]
	FN/QFn.crc-3B	33.0	Xbarc77–Xwmc307	430.1–783.5,	[83]
	GI-14/QPhs.dpivic-3D.1	26.0–43.0	Red Grain Color RGC -wms1200	ND	[84]
	VI/QPhs.dpivic-4A.1	21.0	Xbarc170–Xgwm269c	605.7–607.8	[84]
11.	PHS/QPhs.pseru-3AS	31.26–44.96	Xbarc12–Xbarc321	11.7–15.4	[85]
	QPhs.dpivic.4A.2	27.78–39.84	Xgwm637–Xgwm937	617.4	
	PHS/2DS	25.73–27.50	Xgwm261–Xgwm484	19.6–48.1	[86]
	GI/QGI.crc-4B	28.2–66.6	Xwmc349	640.9	[87]
	PHS/QSI.crc-4B	6.2–26.9	Xwmc349	640.9	[87]
	PHS/QPhs.cnl-2B.1	24.0	Xbarc55–Xwmc474	133.5–172.6	—
	GC/QGc.ccsu-3B.1	15.28–40.42	Xgwm938–Xgwm980	ND	[88]
	PHS/QPhs.ccsu-6A.1	12.01–29.47	Xgwm1296–Xgwm1150	ND	[88]
	PHS/QPhs.caas-3AS.1	11.8–27.7	Xbarc294–Xbarc57	7.9–10.3	[89]
	GI/QGi.crc-4A	27.6–58.1	—	ND	[90]
	PHS(SI)/QSi.crc-4A	10.5–32.1	—	ND	[90]
	PHS(SI)/QSi.crc-7B	11.8–20.5	—	ND 1/2	[90]
	FN/QFn.crc-7D	13.2–20.6	—	ND	[90]
	PHS, SD/Qphs.pseru-4A	17.2–26.5	GBS_212432–GBS_109947	ND	[91]
	QPhs.spa-4B	35.0–60.0	Xwmc617b–Xwmc48a	15.7–98.7	[92]
	QPhs.spa-7D2	14.0–47.0	Xbarc76–Xcfa2257a	634.0	[92]
	GI/3AS	21.6–41.0	KASP-222	7.2	[93]
	qPHS.sicau-3D	8.65–42.47	AX-94415259	562.5–5	[94]

Table 5.

A summary of the major and stable QTL for pre-harvest sprouting/dormancy-related traits in wheat.

for this purpose, major and stable QTL on chromosomes of group 4 and different chromosomes were suggested. SSR markers are accessible for practically all major and stable QTL (**Table 5**); these SSR markers have been utilized for introgression of a QTL for PHS/dormancy to derive lines with high degree of PHS tolerance related with golden grains.

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