



Review Article

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Genetic Improvement of Wheat for Biotic and Abiotic Stress Tolerance

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ABSTRACT

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The higher wheat grain production will be needed to meet the demand of ever growing population which can be achieved by increasing the productivity and reducing the losses caused by biotic and abiotic stresses. All the three rusts along with Karnal bunt and loose smut in favorable environments causing significant yield losses in wheat. The major abiotic stresses affecting wheat are heatstress and drought which has significant impact on wheat production, hence developing resistant/tolerant wheat cultivars is the most eco-efficient approach for management of biotic and biotic stresses therefore the genetics of resistance/tolerance is having prime importance for genetic improvement of wheat which is tried to review in this article.

Introduction

Wheat is a major staple food crop being consumed by 30 percent population of the world (Eversole *et al.*, 2014) and is grown in all the continents. Globally wheat is grown on 219.70 million hectares area with production of 755.2 mt (Source: USDA, 2017) while in India cultivated on an area of 30.60 million hectares with production of 98.61 mt, with highest ever productivity of 3.22 t/ha according to 3rd advance estimate (2017-18) of government of India. In India, wheat comes next to rice in terms of production and plays an important role in food security through a sizeable portion in the buffer stock, placing India to second largest producer of wheat in the world (Source: USDA, 2017). In India, sizeable area under wheat cultivation is

confined to northern states like Uttar Pradesh, Madhya Pradesh Punjab, Haryana, Gujarat, Rajasthan, and Bihar. Conversely, in view of growing population, we need higher grain yield in the future may be through increase in productivity and reducing the losses caused by abiotic and biotic stresses. The major biotic stress in wheat production includes diseases like rust, Karnal bunt, loose smut, powdery mildew and blast (Prescott *et al.*, 1986).

Among several pathogens damaging wheat crop, rust pathogens are the most prevalent. They are reported from all wheat growing countries (Roelfs *et al.*, 1992) and causes a severe damage to the wheat production worldwide. It includes leaf rust (*Puccinia triticina*), stem rust (*P. graminis tritici*) and

stripe rust (*P. striiformis*). All the rust pathogens are obligate parasite in nature and have specific host range. Severe epidemics have been reported by all the three rusts in favorable environments (Roelfs *et al.*, 1992) causing significant yield losses which were recorded in some counties. Losses due to rust diseases ranges from 15-20 percent worldwide, which accounts nearly 20-30 mt of grain yield (Hanson *et al.*, 1982).

In case of abiotic stress, wheat cultivars are affected by stress due to moisture, salt, temperature and micronutrient. Continued experience to high temperatures in rainfed areas of the globe, may lead to drought stress. Prolonged high temperature may leads to osmotic stress as rapid evaporation of water from soils resulting in higher salt concentrations. A meta-analysis of 1,700 published simulations (Challinor *et al.*, 2014) estimated a significant level of yield loss in wheat with each 2°C rise of temperature in temperate and tropical regions. Asseng *et al.*, (2015) reported that decrease in 6% for every °C rise in temperature in wheat production which is equivalent to a reduction of about 42 Mt globally. Therefore the major challenge of today's agriculture is to maintain crop productivity levels to mitigate the need of growing population under limited resources. Conventional breeding for improving stress tolerance in crop is not only time and labor consuming but involves multigene families that govern the molecular and physiological mechanisms. Hence molecular plant breeding has great role in the improvement of crops for stress tolerance.

Genetic basis of disease resistance

Wheat rust

In India, all the three types of rusts are known to be present in different agro-climatic regions. Yellow or stripe rust of wheat

(*Puccinia striiformis*) is more common in cooler areas of Northern India. Black or stem rust of wheat (*P. graminis* Pers. f. sp. *Tritici* Eriks & Henn.) is restricted to Peninsular and Central India (Joshi *et al.*, 1976). Among all the rusts, brown or leaf rust (*P. triticina* Eriks.) is widespread and affect the wheat crop where ever it is grown (Roelfs, 1992). The various adaptive range of this pathogen in different climatic conditions adds to its potential to predominant for the crop losses (Roelfs *et al.*, 1992). Leaf rust perhaps results in major losses due to more number of infection cycles in the favorable environment during crop growth and has potential to cause yield losses up to 50 percent, if infection starts at early growth stage (Huerta-Espino *et al.*, 2011). The commonly distributed pathotypes of leaf rust (*Puccinia triticina*) across the country are 12-4, 12-5, 12-7, 77-1, 77-2, 77-5, 77-9, 104A, 104-2 and 104-3, 162A, 162-1 and 162-2 whereas, in stem rust pathotype 21-1, 40A, 40-1, 40-2, 117-A, 117-1, 117-2, 117-3 117-4 117-5 and 117-6 have been frequently identified. Pathotype 77-5 and 40A for leaf and stem rust respectively were the most predominant in the country.

Genetic studies on leaf rust resistance started about a century ago. So far 79 leaf rust resistance (*Lr*) genes have been designated in wheat (McIntosh *et al.*, 2017). In India, from 1931 to 2015 about 120 new pathotypes have been reported in all three rusts of wheat. In leaf rust alone, 50 pathotypes have been reported in India during 1931-2011. Leaf rust resistance genes commonly exploited in Indian cultivars are *Lr1*, *Lr3*, *Lr9*, *Lr10*, *Lr13*, *Lr14a*, *Lr17*, *Lr19*, *Lr23*, *Lr24*, *Lr26*, *Lr28*, *Lr34* and *Lr46* (Bhardwaj *et al.*, 2010; Tomar *et al.*, 2014). Pathotype 77-5, most virulent and predominant in India and it knocks down most of the *T. aestivum* derived seedling leaf rust resistance genes (Tomar *et al.*, 2014). Virulent pathotypes have also evolved against several alien genes such as *Lr9* (Nayar *et al.*,

2003), *Lr19* (Bhardwaj *et al.*, 2005), *Lr26* (Nayar *et al.*, 1993) and *Lr28* (Bhardwaj *et al.*, 2010). *Lr24* is still effective in India, however, virulence for *Lr24* has already been reported in several parts of the world (Singh, 1991).

Similarly stem rust resistance genes *Sr2*, *Sr7a*, *Sr8a*, *Sr9b*, *Sr11*, *Sr13*, *Sr14*, *Sr21*, *Sr23*, *Sr24*, *Sr25*, *Sr28*, *Sr30*, *Sr31* and *Sr36* have been identified in bread wheat cultivars in India. Of the stem rust resistance genes, *Sr31* is effective against all the pathotypes in India, though emergence of Ug99 and its variants in several countries has made this gene vulnerable (Pretorius *et al.*, 2000). *Sr2* confers wide spectrum but moderate level of resistance at adult plant stage (Mishra *et al.*, 2011; Tomar *et al.*, 2014).

The resistance genes *Lr1*, *Lr3*, *Lr10*, *Lr13*, *Lr23*, and *Lr26* are race-specific commonly found alone or in combination in Indian cultivars e.g. bread wheats; NIAW34, GW322, HS420, HD2329, VL832 and A-9-30-1, PDW233, PBW34 and GW1189 (durum wheat) exhibit adult plant resistance against one or more virulent and prevalent pathotypes 12-2, 77-5 and 104-2 (Bhardwaj *et al.*, 2010). The wheat cultivars carrying gene *Lr13+* or *Lr13+Lr34+* combination showed adequate level of APR (Kulkarni *et al.*, 1980).

Till date 57 stem rust resistance (*Sr*) genes have been designated in wheat (McIntosh *et al.*, 2017) since genes *Sr2*, *Sr11*, *Sr31* and *Sr24* have been commonly used in Indian bread wheat cultivar; and *Sr2*, *Sr7b*, *Sr9e*, *Sr11* and *Sr12* in durum wheat (Nayar *et al.*, 2001; Bhardwaj *et al.*, 2011; Mishra *et al.*, 2011). While the most frequent stripe rust resistance genes are *Yr2*, *Yr9*, *Yr18* and *Yr27*. However, *Yr27* has been exploited commonly in some of the genotypes e.g. PBW343, HS490 and PBW373 (Anonymous, 2006).

Frequent evolution of virulent pathotypes forced the breeder to search for new sources of resistance. To enhance the diversity of resistance in cultivated varieties, secondary and tertiary gene pools of wheat are being exploited. The identification of molecular marker(s) linked to the trait of interest will be useful in speeding up the breeding programme. The knowledge of affectivity of introgressed resistance to different pathotypes helps the breeder to design the breeding programme. Therefore effective gene deployment based on prevalence of pathotypes in a target geographical area by pyramiding the resistance genes helps to minimize the yield loss. Developing resistant wheat cultivars is the most efficient, economical, and environment friendly approach for management of rusts. However, rust is a dynamic pathogen and there is a rapid evolution of new pathotypes which can overcome the resistance in wheat cultivars.

Karnal bunt

Karnal bunt of wheat is caused by *Neovossia indica* Mundkur (Syn. *Tilletia indica*), and first reported in India by Mitra (1931), was considered as a minor disease in the country till 1968. However, the outbreak of disease occurred during 1969-70 and since then in the Indian subcontinent Karnal bunt has become a serious disease of wheat. It causes significant yield losses and deteriorates the quality of grain (Fuentes-Dávila, 1995). Its control by fungicides is not effective mainly due to its soil, air and seed-borne nature. Therefore the most efficient method of disease control is developing resistant varieties.

Most of *Aegilops* spp. accessions were found to be resistant to Karnal bunt (Warham *et al.*, 1986; Chhuneja *et al.*, 2008). Resistance in synthetic hexaploid wheat has been derived from *Aegilops tauschii* and elite durum wheat cultivars and crosses of synthetic hexaploids

with bread wheat cultivars (Mujeeb-Kazi *et al.*, 2006). Fuentes-Dávila *et al.*, (1995) reported six resistance genes *Kb1*, *Kb2*, *Kb3*, *Kb4*, *Kb5*, and *Kb6* which can be effectively used in wheat breeding for disease resistance.

Loose smut

Loose smut, caused by the fungus *Ustilago tritici* (Pers.), is a seed-borne disease of wheat which is common and prevalent in all wheat-growing regions of the world (Nielsen and Thomas, 1996). There are eight resistance genes have been reported so far against loose smut of wheat which were designated as *Ut1*, *Ut2*, *Ut3*, *Ut4*, *Ut5*, *Ut6*, *Ut7* and *Ut8* (Kassa *et al.*, 2015).

Genetics of abiotic stress tolerance

Wheat is an important crop worldwide, providing 25%–50% of calorific needs of growing human population (Dixon *et al.*, 2009). However, there has been a decline in the rate of growth in world wheat production and yields for several years during the present decade due to various reasons. In past 50 years wheat production and productivity have been significantly improved through exploitation of genes for plant resistance to biotic stresses, dwarfness and photoperiod insensitivity (Reynolds and Borlaug, 2006). However, further increase in wheat productivity only possible through the genetic improvement of cultivated wheat for abiotic stresses mainly like terminal heat tolerance and drought tolerance or else photosynthetic ability is enhanced through manipulation of ribulose 1,5-bisphosphate carboxylase oxygenase (RUBISCO) (Reynolds *et al.*, 2011).

Major abiotic stresses

Factors that influence yield outputs are various biotic and abiotic stress constraints augmented by environmental factors which

adversely affect growth, metabolism, and yield. Drought, salinity, low and high temperatures, floods, pollutants, and radiation are the important stress factors limiting the productivity of crops (Lawlor and Cornic, 2002). There is sufficient genetic variation in the wheat gene pool that can be ensured for continued improvement of wheat adaptation to abiotic stress (Trethowan and Mujeeb-Kazi, 2008).

Heat stress

Wheat as a cool season crop, it has as an optimal growing temperature during reproductive stage of 15 °C and for every degree Celsius temperature above this optimum leads to reduction in yield of 3%–4% has been observed (Wardlaw *et al.*, 1989). However, it has been reported that the average worldwide temperature is increasing at a rate of 0.18 °C every ten years (Hansen *et al.* 2012). Thus, the likely impact of heat stress in wheat has recently attracted increasing attention (Moriondo *et al.*, 2011). Heat stress causes injury to cellular structure and disturbs various metabolic pathways, specifically photosynthesis, membrane thermostability, and starch synthesis related pathways (Larkindale *et al.*, 2002). Denaturation of proteins and increased levels of unsaturated fatty acids caused by heat stress disrupt water, ion, and organic solute movement across membranes, leading to increased cell membrane permeability, and in turn, inhibition of cellular function (Cossani *et al.*, 2012). Temperature can modify developmental and growth rates in plants. Similarly, heat stress affects agronomic traits at every growth stage, but the before flowering stage and anthesis period are comparatively more sensitive to high temperature compared to after flowering stages.

Heat tolerance is a quantitative trait, controlled by a number of genes/QTL

(quantitative trait loci). Over the last three decades' efforts have been made to reveal the genetic basis of heat tolerance. Langdon chromosome substitution lines were firstly used in mapping heat tolerance genes and associated genes were found on chromosomes 3A, 3B, 4A, 4B, and 6A in 1991 (Sun *et al.*, 1991).

Xu *et al.*, (1996) later reported that chromosomes 3A, 3B and 3D were associated with heat tolerance in wheat cultivar (cv) Hope. Using chromosome substitution lines between Chinese Spring and Hope, chromosomes 2A, 3A, 2B, 3B, and 4B of Hope significantly enhanced heat tolerance (Chen *et al.*, 2007). Collectively, chromosomes 3A and 3B appeared to harbor key genes controlling heat tolerance in wheat.

Exploration and utilization of novel genetic variation is the priority for genetic improvement of heat tolerance in wheat breeding programs. In a study of > 1200 Mexican wheat landraces collected from areas with diverse thermal regimes, a highly significant correlation between leaf chlorophyll content and thousand grain weight was observed and a group of superior accessions were identified (Hede *et al.*, 1999).

Populations of wild species frequently harbor high intra-species variation for tolerance traits that are superior to what is available in the modern cultivars. Indeed, *Triticum dicoccoides* and *T. monococcum* have been reported as potential sources of germplasms that can be used to enhance heat tolerance in bread wheat. Additionally, variable degrees of heat tolerance were observed in *Aegilops speltoides*, *Ae. longissima* and *Ae. Searsii* (Pradhan *et al.*, 2012). However, only a small portion of the reported genetic variation in heat tolerance has been utilized due to limitations of conventional breeding methods.

Drought stress

The term “drought” defined as the absence of rainfall / irrigation for a period of time in which the plant water content reduced enough to interfere the plant processes (Tuberosa, 2012). Adverse environmental factors, of which water scarcity represents the most severe constraint to agriculture, account for about 70 % of potential yield losses worldwide (Boyer, 1982). The most affected states in India are Rajasthan, parts of Gujarat, Haryana and Andhra Pradesh (Mitra, 2001). As drought persists, the conditions surrounding it gradually worsen and its impact on the local population gradually increases (Nath *et al.*, 2017). Developing crop cultivars with improved drought resistance is considered as a sustainable and an economically viable approach to enhance crop productivity and ensure food security for the growing human population (Blum, 1988; Bennett *et al.*, 2012).

Drought stress environments is complex, since each of these traits is controlled by many genes, each individual gene having a small effect (Blum *et al.*, 1988). The genetic analysis of Canopy Temperature Depression under drought has been carried out and QTL for CT were reported on chromosomes 1B, 2B, 3B, and 4A (Pinto *et al.*, 2008). Spielmeyer *et al.*, (2007) reported QTL for early shoot vigor on chromosome arm 6AS of wheat. Genetic variability for green flag leaf area (GFLA) has been reported detected on chromosome 2D, the trait exhibits moderate heritability and seems to be under additive genetic control (Verma *et al.*, 2004). GA-sensitive dwarfing gene Rht8 was shown to reduce plant height without affecting coleoptile length or early vigor so that efforts are being made for the development of semi dwarf wheat genotypes suitable for cultivation in drier environments (Rebetzke *et al.*, 2004). ABA is a stress hormone that accumulates in plant cells as a quick response to drought stress. Increased ABA makes the plant better

adapted to water stress conditions (Mizrahi *et al.*, 1974). Quarrie *et al.*, (1994) later reported a QTL for drought-induced ABA accumulation on 5A using single chromosome substitutions from a high ABA-genotype Ciano 67 into low ABA genotype Chinese Spring. Genetic variability for root traits has been reported in durum wheat the major QTL for seminal root traits were reported on 2AL, 7AL and 7BL chromosome arms through association mapping (Sanguineti *et al.*, 2007). Traits like canopy temperature depression, shoot vigor, stay green habit and stomatal conductance provides an improvement of wheat genotypes under both drought and heat stress. Seedling emergence, coleoptile length, GA-sensitive dwarf-ness, root vigor and architecture responsible for development of good wheat cultivars under drought stress.

In conclusion, application of chemical fungicides and pesticides can control pest and diseases to some extent but they are costly and environmentally undesirable measures while controlling abiotic stress cumbersome agronomic practice have to follow. The development resistant/ tolerant varieties based on its own defense mechanisms will be the most suitable approach for sustaining agricultural production and to improve environment and health. Understanding the genetics of resistance or tolerance is important so as to improve the efficiency of practical application of resistance genes/QTLs in wheat breeding program. The new technological development, like high-throughput DNA sequencing and microarray analysis, these advances facilitate the mapping and cloning of major genes and QTLs which eventually help in developing resistant/ tolerant cultivars of wheat for biotic and abiotic stress. Genomic information about both host plants and pests and pathogens should accelerate the rate of discovery of resistance genes. Transcript profiling techniques will allow the simultaneous

examination of thousands of genes, and can be utilized to study changes in gene expression that are transcriptionally regulated in different environmental conditions. Ahead of transcript profiling, genomics also facilitates the functional analysis of genes associated with resistance and susceptibility. Therefore understanding the genetic nature of biotic and abiotic stress resistance/ tolerance respectively is important to combat with upcoming problems of maintaining the crop productivity in changing environment.

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