

Use of Crop Wild Relatives (CWRs) of Wheat in Disease Resistance Breeding

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Wheat (*Triticum aestivum* L.) is one of the three major cereal crops contributing 20% calories to the world population. The most serious constraints to wheat production are biotic stresses like rusts, blights, powdery mildew, bunts and smuts. Genetic or host plant resistance is the best way to control these diseases than use of chemical pesticides. Continuous search for novel genes is indispensable to counter the dynamic and rapidly evolving pathogen population. In case of some diseases like spot blotch, Karnal Bunt and Fusarium head blight development of resistant cultivars is not an easy task as the resistance to them found in the germplasm is not satisfactory and none of the commercial cultivars showed resistance. Hence, underutilized crop wild relatives prove to be valuable resource in the search for new disease resistance genes to combat wheat diseases.

Key Words: Fusarium head blight, Karnal bunt, Resistance genes

Introduction

Cereals are the major source of calories for the global human population. Wheat (*Triticum aestivum* L.) is one of the three major cereal crops contributing 20% calories to the world population. The most serious constraints to wheat production are biotic stresses like rusts, blights, powdery mildew, bunts and smuts. Genetic or host plant resistance is the best way to control these diseases than use of chemical pesticides. Through coordinated and concerted research efforts in development and release of resistant varieties, a check has been kept on the management of various diseases and insect pests over past four decades in the country and no epidemics of these occurred. However, new pathogens are always posing challenges and development of new and more virulent pathotypes result in breaking of resistance of popular wheat varieties. The expected onslaught of climate change is also a worrisome aspect and breeding strategies have to be reoriented to mitigate the biotic stresses. Leaf rust caused by *Puccinia triticina* and yellow rusts caused by *P. striiformis* f. sp. *tritici* are serious biotic stresses in the major wheat growing zones like North western plain zone, Northern hill zone and North Eastern plain zone. Stem rust caused by *P. graminis* f. sp. *tritici* is prevalent in hotter climates of Peninsular and Southern India. On the other hand, spot blotch caused by *Bipolaris sorokiniana* has also emerged as one of the most important diseases limiting wheat production

in warmer and humid regions of the world. Another important disease Karnal bunt (KB) caused by *Tilletia indica* has gained importance over the years in NWPZ as most of the varieties recommended for the zone are susceptible to KB. Karnal bunt is an impediment in export of wheat as many importing countries are having zero tolerance to it. Fusarium head blight (FHB) or head scab of wheat caused by *Fusarium graminearum* has also emerged as an important wheat disease worldwide in 21st century. Presently, FHB is a minor disease in India but can cause significant yield loss if rain occurs during mid anthesis.

Crop Wild relatives as Sources of Genes for Disease Resistance

Resistance genes present in current varieties can become obsolete in near future with the emergence of virulence against them. For instance, most of the Indian cultivars have the *Lr* genes *Lr1*, *Lr3*, *Lr9*, *Lr10*, *Lr13*, *Lr14a*, *Lr17*, *Lr19*, *Lr23*, *Lr24*, *Lr26*, *Lr28* and *Lr34*. Out of this *Lr1*, *Lr3*, *Lr10*, *Lr13*, *Lr14a*, *Lr17* and *Lr23* are native to cultivated wheat and have become ineffective due to evolution of new virulence in the pathogen population. Virulence has evolved even against some of the alien genes such as *Lr9*, *Lr19*, *Lr26* and *Lr28* (Niranjana *et al.*, 2017). *Yr* genes in Indian cultivars are *YrA*, *Yr2*, *Yr2KS*, *Yr2* (SKA), *Yr9*, *Yr18*, *Yr27*. Out of these break down of resistance is reported in *Yr9* (Tomar *et al.*, 2014). This suggests that continuous

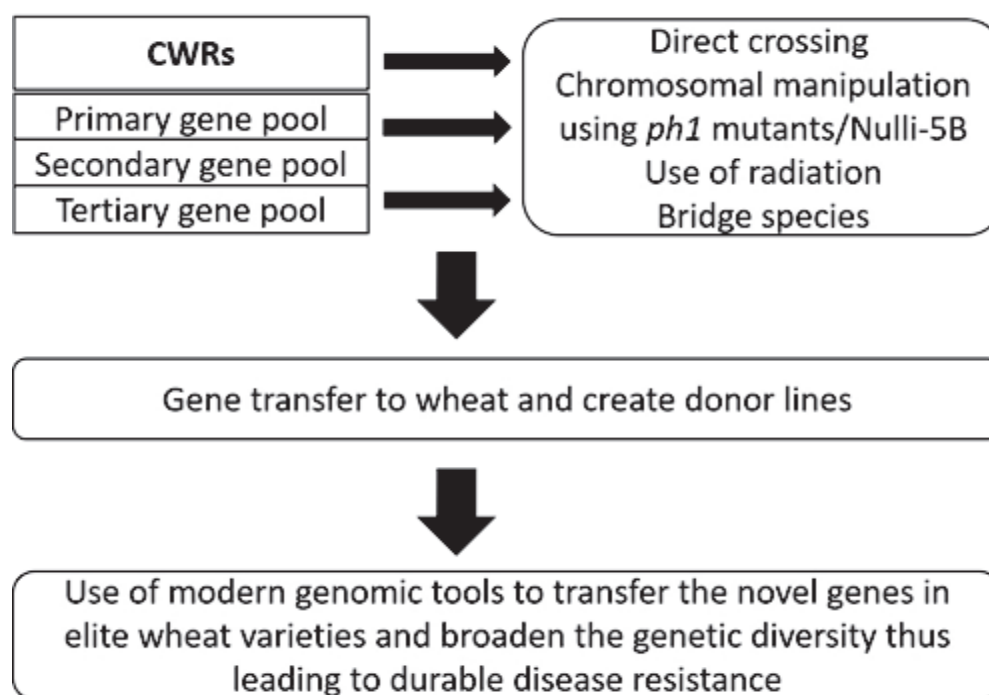
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search for novel genes is indispensable to counter the dynamic and rapidly evolving pathogen population. In case of some diseases like spot blotch, Karnal Bunt and FHB development of resistant cultivars is not an easy task as the resistance to them found in the germplasm is not satisfactory and none of the commercial cultivars showed resistance. Hence underutilized CWRs prove to be valuable resource in the search for new disease resistance genes to combat these diseases.

CWRs of wheat are known to possess high level of diversity for both biotic and abiotic stress tolerance and are excellent source for broadening the genetic base for resistance to rusts as well as emerging diseases like Karnal bunt, spot blotch and head scab. Some of the *Lr*, *Sr* and *Yr* resistance genes have been derived from related and distantly related species like *T. monococcum*, *T. dicoccoides*, *T. turgidum*, *T. spelta*, *T. timopheevi* and genera including *Aegilops*, *Agropyron*, *S. cereale*, *Thinopyrum* and *Elymus* (Naik et al., 2015). Resistance to Karnal bunt was identified in *S. cereale*, *Triticale*, several accessions of *Aegilops biuncialis*, *Ae. columaris*, *Ae. crassa*, *Ae. juvenalis*, *Ae. ovata*, *Ae. speltoides*, *T. uratu* and *Ae. squarrosa* (Warham 2009). Amphiploids synthesized from *T. durum* with *T. monococcum*, *T. boeoticum* and *Ae. squarrosa* crosses were screened for KB resistance (Multani et al., 1988). Several markers and quantitative trait loci (QTLs) for spot blotch resistance

have been mapped in wheat (Gupta et al., 2018) but none from CWRs. Similarly, in case of FHB limited sources of resistance known to *Fusarium* spp. causing head scab.

CWRs of wheat can be broadly classified as primary, secondary and tertiary. The primary gene pool of wheat comprises species having homologous genome as in wheat (A, B, D). This includes tetraploid species like *T. dicoccoides*, *T. dicoccum*, *T. durum*, *T. polonicum*; hexaploid species *T. aestivum*, *T. spelta*, *T. compactum*, *T. sphaerococcum* and diploid species with A and D genome like *T. urartu*, *T. monococcum*, *T. boeoticum* and *Ae. squarrosa*. Since their chromosomes are homologous to the cultivated types, they will easily undergo homologous recombination. The primary gene pool has been best utilized for crop improvement as it is relatively easy to transfer genes among them. The secondary gene pool comprises of species which has at least one homologous genome in common with the cultivated species. This includes species like *Ae. speltoides* (SS), *T. timopheevii* and *T. militinae* (AAGG), *Ae. cylindrica* (CCDD). Species included in the tertiary gene pool are distantly related species whose genome is unique from A, B or D genome. This includes species of *Secale* (RR), *Thinopyrum* (EE), *Hordeum* (HH). Despite being a hexaploid, bread wheat acts as an amphidiploid due to the presence of *Ph1* (*pairing homeologous*) locus



which prevents homeologous pairing between A, B, D genomes and promote homologous pairing. For transfer of genes from tertiary genepool homeologous pairing between wheat and alien genomes should be induced by the inactivation of *Ph1* gene. A single *Ph1* deletion mutant developed in hexaploid wheat cultivar Chinese Spring namely CS *ph1b* has been utilized for this purpose. Since *Ph1* locus is located on 5B chromosome nullisomics lacking 5B (Nulli-5B) chromosome could be utilized. Special strategies such as irradiation, bridge species and gametocidal chromosomes are also used. The availability of such natural diversity provides an excellent starting material for the betterment of wheat genetic base by conventional breeding techniques and chromosome engineering.

Future Prospective and Action Points

1. Development of wheat varieties from diverse parents and exploit genes from underutilized wild relatives of wheat in the breeding cycle which will broaden the genetic base of wheat varieties and prevent genetic erosion.
2. Pre-breeding efforts should be strengthened for the initial transfer of genes from CWRs as it is the trickiest part. Since sterility issues are evident only few progenies could be derived and cytogenetic stability of the introgression lines should be ensured before utilizing them in breeding cycle.
3. Availability of high-quality reference sequence of wheat opens wide vistas in utilization of genes from

CWRs. Fine mapping of the genes derived from wild relatives will lead to development of linked markers or better gene-based markers.

4. Once we develop a molecular map and identify the linked markers or gene-based markers they could be utilized in molecular breeding and ensure development of CWR derived elite varieties in a short span of time.

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