



Utilization of Wild Relatives for Insect Resistance Breeding in Cereals

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Introduction

Diseases and insect pests are key biotic constraints leading to low yields in cereal production worldwide. Insect pests in particular destroy approximately 14% of all potential food production, including rice, wheat and sorghum, despite the application of greater than 3,000 million kilograms of pesticides per year (Pimentel, 2007). Losing crops to insect pests constitutes a great limitation to recognition of food security worldwide. Host plant resistance through crop breeding remains the keystone of an integrated pest management strategy to minimize losses and impact on grain quality. Wild relatives on account of being growing under natural conditions without any artificial selection have constantly been exposed to varied stresses in the past and as a result have evolved various resistance genes to tackle them. They therefore possess sufficient variability to act as donor for various insect resistance traits. An in-depth account of wild relatives of important cereals as wheat, rice and sorghum that have been identified and utilized in recent past as donor of resistant traits have been discussed.

Wheat

The species belonging to primary, secondary, and tertiary gene pools of *Triticeae* species (*Aegilops*, *Agropyron*, *Elymus*, *Hordeum*, *Leymus*, *Secale*, *Thinopyrum*, and *Triticum*) are rich source of genes for improvement of traits pertaining to biotic and abiotic stress tolerance and quality improvement. Introgression of alleles from nearly 52 related species have already been done for improvement of wheat for different traits. Wheat crop is affected by various insects during different stages of development causing significant grain yield loss. Beside use of pesticides which not only increases the cost of cultivation but also causes environmental pollution, development of host plant resistance is a sustainable approach to pest management where genes from related wild species can be used to breed tolerance against insect attack. Resistance against insect attack have been found in a number of related species of wheat. A large number of insects causes yield loss in wheat both in field as well as under storage. Few of the most significant amongst them includes green bug (*Schizaphis graminum*), aphids as *Diuraphis noxia*, *Rhopalosiphum padi L.* and *Sitobion avenae*, Hessian fly (*Mayetiola destructor*), cereal cyst nematode (*Heterodera avenae*) and mite (*Aceria tosichell*). It was found that *Aegilops tauschii* possess Cre3 locus controlling resistance to cereal cyst nematode and resistance genes against Hessian fly infestation while *Aegilops*



variabilis serves as donor for nematode resistance genes. *R. padi* resistant twenty-one accession from six *Aegilops* species and one accession from *Triticum araraticum*, a tetraploid species of wheat were further screened for aphid resistance and it was found that out of all the accession screened, *Aegilops neglecta* accession showed antibiotic effect against colonization by *D. noxia* and *S. avenae*. According to various publications resistance to aphid *R. padi* was conferred by *T. araraticum*, *A. tauschii* and *Triticum boeoticum*, to *S. graminum* was controlled by genes present in *A. tauschii* and *T. turgidum* and higher level of resistance to *S. avenae* was conferred by *T. araraticum* and *T. dicoccoides*.

Rice

Genus *Oryza* of the gramineae family constitutes a total of 24 species. Out of these 24 species *O. sativa* L. and *O. glaberrima* are the only cultivated species of genus *Oryza* while the remaining 22 are wild species distributed worldwide. Depending on the ease of transfer of genes to their cultivated counterparts, the wild species are divided into three complexes i.e., *O. sativa* complex, *O. officinalis* complex and *O. meyeriana* and *O. ridleyi* complex (Morishima and Oka, 1960). Later these complexes were renamed as the primary, secondary and tertiary gene pool of rice. Wild species of rice are a rich source of economically valuable traits on account of being grown in diverse climate and lack of artificial selection. Brown plant hopper is one of the most devastating insect affecting rice cultivation worldwide. A total of 30 brown plant hopper resistant genes have been identified and out of these more than a dozen are contributed by crop wild relatives. Resistance to brown plant hopper have been conferred by genes present in *O. punctata*, *O. minuta*, *O. officinalis*, *O. eichingeri*, *O. latifolia* and *O. australiensis*. While *O. officinalis*, *O. eichingeri* have valuable genes for white backed plant hopper and green leaf hopper resistance. The most distantly related wild species, *O. meyeriana*, *O. longiglumis*, *O. granulata*, *O. coarctata* and *O. ridleyi* have most valuable genes for stem borer. Many valuable genes for brown plant hopper tolerance in rice have been identified and tagged (Jena, 2010) viz., *Bph6*, *bph11*, *Bph13*, *14*, *15* have been identified in *O. officinalis* and tagged with suitable markers. While *Bph20*, *Bph21* identified and tagged in *O. minuta*, *Bph12* in *O. latifolia* and *Bph10*, *Bph18* in *O. australiensis*. Tagging of these genes with specific markers makes their transfer into elite lines much easier and will subsequently reduce the problem of linkage drag associated with wide hybridization. Four resistance genes including *Bph14* from *O. officinalis* and *bph29* from *O. rufipogon* have already been cloned and introgression of brown plant hopper resistance from wild to elite lines is also being performed simultaneously.

Sorghum

Resistance level to stem borer and sorghum shoot fly is reported to be low to moderate in sorghum germplasm (Sharma et al., 2003). There is therefore an immediate need to look for alternative resistance genes providing high level of resistance in wild relatives. High level of shoot fly resistance has been reported in *Sorghum purpureosericeum* and *S. versicolor*. Sorghum midge (*Stenodiplosis sorghicola*) resistance was reported in some Australian species of sorghum. Odors from the panicles of *S. halepense* were found to be more attractive to the females of sorghum midge compared to the odors from *S. stipoides*, *S. angustum*, *S. brachypodum*, *S. nitidum*, *S. macropsermum*, *S. laxiflorum* and *S. amplus*.



The hybrids derived from *S. bicolor* ssp. *Verticilliflorum* race *virgatum* was found to possess high level of resistance to green bug (*Schizaphis graminum*) and resistance to green bug (biotype E) was also discovered in *S. halepense*. Another study was conducted in which 17 wild relatives of sorghum were screened for resistance to shoot fly (*Atherigona soccata*) in order to identify alternate resistance genes. Under multi choice conditions in field, Stiposorghum, Parasorghum and Heterosorghum were although preferred for oviposition but they showed low deadheart formation and did not suffered any damage. One accession each of Chaetosorghum (*S. macrospermum*) and Heterosorghum (*S. laxiflorum*) also suffered very low intensity of shoot fly damage. Non preference for oviposition was shown by *S. exstans*, *S. matarankense* and *S. stipoideum*. Therefore, these wild relatives with different resistance mechanisms can be used as a source of alternate genes to enhance the levels and broaden the basis of resistance to shoot fly, *A. soccata*. Spotted stem borer is yet another destructive pest of sorghum and levels of resistance to this insect is of low to moderate level in sorghum germplasm. Wild relatives of sorghum were screened to identify resistant sources to this pest and also to investigate the mechanism of resistance. High level of resistance against stem borer was displayed by heterosorghum, parasorghum and stiposorghum while Chaetosorghum, *S. halepense* and four wild races of *S. bicolor* subsp. *verticilliflorum* were found to be susceptible. Although egg laying was observed on all evaluated accession under no choice condition but Stiposorghum and Para□sorghum were less preferred for oviposition when compared to control, IS 2205. Stiposorghum showed no appearance of dead hearts while in Para□sorghum, very few deadhearts were formed. Although *Heterosorghum* was highly preferred for oviposition and showed about 82% dead heart formation, but the recovered larvae died within a month of emergence. Therefore, both antixenosis and antibiosis was reported to be the mechanism of resistance against *C. partellus* in sorghum wild relatives.

Conclusion

It is therefore clear that wild relatives are a gigantic source of insect pest resistance genes. The need of the hour is to tap these genes present in wild relatives by mobilizing them into the adapted germplasm by means of pre breeding activities. Once present in adapted germplasm these genes can help in dealing with enhanced insect susceptibility of modern germplasm one of the most potent problem of commercial plant breeding now a days.

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