
Kota R.1, E.S. Lagudah1, R. Mago1, H. McFadden1, P.K. Sambasivam1, W. Spielmeyer1, L. Tabe1; B. Keller2, S.G. Krattinger2, L.L. Setter2; S. Herrera-Foesel3, J. Huerta-Espino3, R.P. Singh3; H. Bariana4, R. Park4, C. Wellings4; S. Cloutier5; Y. Jin6

Abstract

Two broad categories of resistance genes in wheat have been described. One group represents the so called seedling resistance or the ‘gene for gene’ class that often provides strong resistance to some but not all strains of a rust species. The other category referred to as adult plant resistance provide partial resistance that is expressed in adult plants during the critical grain filling stage of wheat development. A few seedling rust resistance genes have been cloned in wheat and other cereals and are predominantly from the nucleotide binding site/leucine rich repeat class which is associated with localized cell death at the pathogen entry site. Until recently, the molecular basis of race non-specific, partial and slow rusting adult plant resistance genes were unknown. Gene products that differ from known plant resistance genes were revealed from the recent cloning of the Yr18, Yr36 and Lr34 adult plant genes in wheat. The available range of diverse resistance gene sequences provide entry points for developing gene-based markers and will facilitate selection of germplasm containing unique resistance gene combinations.

Keywords

seedling resistance, adult plant resistance, cloned resistance genes

Resistance to wheat rusts caused by Puccinia graminis (stem rust), P. triticina (leaf rust) and P. striiformis (stripe rust) has relied on genes from cultivated wheat as well as those introgressed from close and distant relatives. The majority of genes belong to the so called seedling resistance group, sometimes referred to as major R genes, and a few are of the adult plant resistance category. Six rust resistance genes in wheat have been cloned. Three of these genes, Lr1, Lr10 and Lr21 (Huang et al. 2003; Feuillet et al. 2003; Cloutier et al. 2007) confer seedling resistance to leaf rust of which Lr1 and Lr10 provide resistance to a limited range of pathotypes. No virulence for Lr21 has been confirmed (see McIntosh, these proceedings). All three genes encode for proteins with nucleotide binding sites and leucine rich repeats (NB-LRR), which represent the largest class of known resistance genes in plants to date.

The other three cloned genes, Yr18, Yr36 and Lr34 are of the adult plant rust resistance class; Yr18 and Yr36 confer stripe rust resistance and Lr34 leaf rust resistance. These genes provide partial resistance and are race non-specific. Yr36 encodes a protein with a kinase and ‘START’ (lipid binding) domain and the resistance is expressed at high temperatures (Fu et al 2009). A single gene confers Yr18 and Lr34 resistance and encodes an ATP Binding Cassette (ABC) Transporter (Krattinger et al. 2009).

No stem rust resistance gene in wheat has been cloned. However, in barley two stem rust resistance genes, Rpg1 and Rpg5 that encode a protein kinase and NB-LRR fused with a kinase, respectively, have been cloned (Brueggemann et al 2002; 2008). The expectation is that many more of the wheat R genes encode NB-LRR genes. A number of candidate NB-LRR genes have been reported for wheat R gene loci and these include genes for resistance to stem rust. By virtue of the fact that the aforementioned genes have been cloned, their DNA sequences provide ideal templates for deriving gene-based markers for marker assisted selection. Given the abundant representation of NB-LRR sequences in plant genomes, primer combinations targeting conserved domains in these gene sequences have been used to derive resistance gene analogs (RGA). Such RGAs are located on all wheat chromosomes (McFadden et al. 2006), and serve as candidate gene markers in attempts to identify R genes that co-localize with the RGAs. Progress in the RGA mapping approach is reliant on the level of precision mapping of R genes in wheat segregating families.

Of particular significance is the observation that the molecular bases of the APR genes identified so far differ from the seedling R genes. This lends support to a different mechanistic process for broad spectrum disease resistance associated with some APR genes. Cloned APR gene sequences could be used as probes to characterize the large gene pool of wheat as part of allele mining strategies. Furthermore, completely different APR genes are likely to be revealed as related sequences or gene
family members of Yr18/Lr34 and Yr36 are non-existent at some of the other APR gene loci currently under investigation.

Ultimately combining multiple resistance genes with an additive effect and preferably with different defense mechanisms will ensure more durable resistance. As progress is made in cloning additional genes the questions that need to be addressed are:

What gene combinations provide optimal effects? What strategies can best ensure the rapid transfer of 4-5 rust resistance genes into a single cultivar bearing in mind that breeders have other additional traits to select for?

Will developing gene cassettes with multiple genes, e.g. APR genes, on a single T-DNA inherited as a single locus be helpful?

Finally, nothing is known about the molecular basis of suppressors of rust resistance present in the wheat genome which includes suppression of resistance to race Ug99 and its derivatives. Additional research investment is needed in this area.

References


