Identification of a candidate barley stem rust susceptibility gene determining the recessive nature of Rpg4-mediated Ug99 resistance in barley.

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The rpg4/Rpg5 locus in barley (Hordeum vulgare) provides recessive resistance against several wheat stem rust races (Puccinia graminis f. sp. tritici) including QQCI and the highly virulent race TTKSK (aka Ug99). Three genes required for wheat stem rust resistance (HvADF3, Rpg5, and HvRGA1) were identified in the ~70kbp rpg4/Rpg5 stem rust resistance locus using high-resolution mapping and virus induced gene silencing. The dominant rye stem rust resistance gene Rpg5 is predicted to have the typical R-gene domains including the nucleotide-binding site (NBS), leucine rich repeat (LRR), and serine/threonine protein kinase (STPK) domains. The Rpg5 gene appears to condition compatible or incompatible interactions with the wheat stem rust races QQCI and Ug99, because it is the only polymorphic gene correlating with resistance and susceptibility in the delimited rpg4/Rpg5 region. Sequence analysis of rpg5 susceptible alleles showed that they make up two groups. The group-1 susceptible lines contain an insertion/deletion region having a predicted functional protein phosphatase 2C gene (HvPP2C) in place of the Rpg5 STPK domain (Harrington, Steptoe, and Sm89010). The group-2 susceptible lines have an intact STPK domain but a predicted nonfunctional rpg5 allele due to a single cytosine insertion causing a frame shift mutation resulting in a premature stop codon (Golden Promise, OSU6, and MD2). Analysis of F1 progeny from crosses between Q21861 and group-1 and -2 susceptible lines segregated in 1:3 ratio (resistant:susceptible) when the HvPP2C gene is present but in a 3:1 ratio (resistant:susceptible) when the HvPP2C gene is absent. Thus, it appears that the previously identified Rpg5 dominant rye stem rust resistance gene also imparts rpg4-mediated wheat stem rust resistance and behaves as a dominant gene in the absence of the HvPP2C gene but as a recessive resistance gene in the presence of HvPP2C. The data suggests that components of rpg4 and Rpg5 resistance are not distinct and the difference in the dominant or recessive nature of resistance is due to the HvPP2C gene acting as a dominant susceptibility factor that suppresses rpg4/Rpg5-mediated resistance against the wheat stem rust races including Ug99.

Targeted re-sequencing of the wheat exome and the generation of public co-dominant single nucleotide polymorphism markers.


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The complex nature of the wheat genome has, until recently, resulted in a lack of single nucleotide polymorphism (SNP)-based molecular markers of practical use to wheat breeders. Recently, large numbers of SNP-based wheat markers have been made available via the use of next generation sequencing combined with a variety of genotyping platforms. However, many of these markers and platforms have difficulty distinguishing between heterozygote and homozygote indi-