further investigate the events that lead to this fusion, we coupled a protocol for genome complexity reduction with the Illumina platform, to sequence at 40X coverage a bulk of seven RH lines carrying or missing the *scs* gene. The sequences identified in the first (positive) bulk but not in the second (negative), were considered to represent the *scs* region. These 3.2 K differential pair-ends sequences were then extended to 1–5 Kb in size, employing the publicly available 50X survey sequences of *Aegilops tauschii*. Furthermotr, these extended sequences were assembled with DNAStar into 556 contigs spanning 1.2 Mb with an N50 of 3Kb. This gapped sequence was then anchored to the scaffold RH map, pin-pointing the *scs* locus to an interval of just eight genes. The result of coupling Illumina sequencing, Wheat Zapper synteny analysis, and RH populations is discussed here in relation to the evolutionary importance of the *scs* region and its map based cloning.

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 QCCJ 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 QCCJ 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 F_2 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-