Poster 59. Haplotype analysis of the leaf stripe resistance locus Rdg2a in different barley genotypes.

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Leaf stripe disease on barley is caused by the seed-transmitted hemi-biotrophic fungus *Pyrenophora graminea* (anamorph *Drechslera graminea*). Race-specific resistance to leaf stripe is controlled by two known *Rdg* (*Resistance to Drechslera graminea*) genes, the *H. spontaneum*-derived *Rdg1a*, mapped to chromosome 2HL, and *Rdg2a*, identified in *H. vulgare* and mapped on chromosome 7HS and cloned in the resistant cultivar Thibaut. The *Rdg2a* locus contains a gene cluster of three sequence-related coiled-coil, nucleotide-binding site, and leucine-rich repeat (CC–NB–LRR) encoding genes. However, only one gene conferred resistance to isolate Dg2, against which *Rdg2a* is effective, when the susceptible cultivar Golden Promise was transformed with the *Rdg2a* candidates. The high level of sequence similarity between the three genes most likely contributed to significant rearrangements during evolution, probably derived from unequal crossing-over resulting in sequence exchange between paralogs and in the generation of recombinant genes, as well as in expansion/contraction of gene copy number. To examine the haplotype variation at the *Rdg2a* locus, the sequencing of the allelic *Mrdg2a* (*Morex rdg2a*) locus of the Dg2-susceptible cultivar Morex was carried out and revealed large rearrangements including two deletions that generated an *Rdg2a*-homolog gene. This gene most likely derived from an un-equal crossing-over between the *Rdg2a* ancestor(s) and its paralog *Nbs2-Rdg2a*. PCR analyses performed with informative markers at eight loci within the *Rdg2a* locus identified eight different haplotypes. The Thibaut haplotype was observed to be largely conserved in Dg2-resistant barley cultivars. The resequencing of the *Rdg2a* gene in barley genotypes showing the same Thibaut haplotype or the same resistant phenotype revealed high sequence similarity to Thibaut *Rdg2a*, demonstrating the widespread conservation of the gene. Nonetheless, some sequence variation were identified in at least two barley genotypes that were verified for possible differences, with respect to *Rdg2a*, in the range of resistance specificities towards different leaf stripe isolates.

Poster 60. Identification of a novel major leaf rust resistance QTL in the Swiss winter wheat cultivar Forno.

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Leaf rust (*Puccinia triticina*) is a major wheat disease which can cause significant yield losses globally. Rapidly evolving pathogen races increase the demand for more durable and race-nonspecific resistance genes. So far only four (*Lr34*, *Lr46*, *Lr67*, and *Lr68*) such durable leaf rust resistance genes have been identified. The identification and characterization of new sources of durable leaf rust resistance is important to ensure food security in the future. We earlier identified two major leaf rust resistance loci on chromosomes 1BS and 7DS in the Swiss winter wheat cultivar Forno. The resistance on chromosome 7DS was conferred by a single gene named *Lr34* that encodes ABC transporter gene.

In this study we further characterized the second resistance locus on chromosome 1BS, named *QLrP.sfr-1BS*. This locus initially explained 28–32% of the phenotypic variance using 240 recombinant inbred lines (RILs) of the cross 'Arina/Frono'. We grouped these 240 RILs into the following categories: *+QLrP.sfr-1BS/–Lr34*, *–QLrP.sfr-1BS/+Lr34*, *+QLrP.sfr-1BS/+Lr34*, *–QLrP.sfr-1BS/–Lr34*, each having 21, 26, 22, and 18, lines respectively. The selected lines were phenotyped for the three traits, area under disease progress curve for the percentage of leaf area infected infection type, and leaf tip necrosis (LTN). The average length of LTN of only the *QLrP.sfr-1BS* group was significantly lower than the group having *Lr34*, indicating that unlike *Lr34*, *QLrP.sfr-1BS* is not associated with LTN. The groups only containing either *QLrP.sfr-1BS* or *Lr34* showed the same level of resistance, whereas the group containing both *QLrP.sfr-1BS* and *Lr34* show significantly higher level of resistance, demonstrating an additive effect of the two genes. A genetic linkage map for chromosome 1BS spanning a distance of 190 cM was constructed using SSRs and RFLP markers. Composite interval mapping detected *QLrP.sfr-1BS* with a LOD score of 17, flanked by markers wmc230 and gwm18. By adding