

Fine mapping of 5 resistance genes on introgressions of *Hordeum bulbosum* in barley with SNP markers

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Barley growing is threatened by plant diseases such as scald (*Rhynchosporium secalis*), leaf rust (*Puccinia hordei*) or the soil-borne virus complex of BaMMV, BaYMV-1 and -2, the latter of which is transmitted by the fungus *Polymyxa graminis*. Breeding of resistant varieties can minimize the yield losses. The wild *Hordeum* species *H. bulbosum*, which makes up the secondary gene pool of barley, is a source of resistance genes against these fungi and viruses. Interspecific crosses of *H. vulgare* x *H. bulbosum* resulted in different recombinant diploid barley progeny with dominantly inherited immunity against the two fungi and the virus complex, respectively. Two virus resistance genes, *Rym14*^{Hb} and *Rym16*^{Hb}, have been introgressed to the short arm of chromosome 6 (6HS) and the long arm of chromosome 2 (2HL), respectively. The gene *Rrs16*^{Hb}, which confers

immunity to *R. secalis*, was introgressed to the short arm of barley chromosome 4 (4HS). Two introgressions containing genes for resistance to *P. hordei* are present on chromosomes 2HL and 5HL, respectively. Mapping populations for the 5 resistance genes segregated in a 3:1 ratio of resistant to susceptible plants, suggesting a dominant monogenic inheritance of the different resistances. For the fine mapping of these genes SNP markers will be developed on the basis of sequence information generated by exome capture and the mapping populations genotyped with the Illumina VeraCode GoldenGate Genotyping Assay, Genotyping By Sequencing and Pyrosequencing. Finally, recombinant plants with reduced introgression sizes containing the resistance genes will be identified by marker-assisted selection for barley breeding.