High resolution mapping of virus resistance genes derived from *Hordeum bulbosum*

Julia Kretsch[1], Dragan Perovic[1], Antje Habekuß[1], Viktor Korzun[2], Klaus Oldach[2], Neele Wendler[2] and Frank Ordon[1]

[1]Julius Kühn-Institut, Institute for Resistance Research and Stress Tolerance, Quedlinburg
[2]KWS LOCHOW GMBH
E-mail of corresponding author: julia.kretsch@julius-kuehn.de

To prevent yield losses of barley due to viruses there are in general two approaches, i.e. control of vectors or breeding for resistance. The control of the aphid-transmitted *Barley yellow dwarf virus* (BYDV) is becoming difficult due to governmental regulations concerning insecticides. The use of chemicals to control the *Barley mild mosaic virus*/*Barley yellow mosaic virus* (BaMMV/BaYMV), transferred by soil-borne *Polymyxa graminis*, is not possible. As there is no complete resistance in the primary gene pool of *H. vulgare* against BYDV and the resistance against BaMMV/BaYMV may be overcome, search for new sources of resistance in *H. bulbosum*, the only member in the secondary gene pool of barley, is of prime importance. The *Hordeum bulbosum* introgression line 203S11 carries resistance against BaMMV/BaYMV (*Rym16*) and Ryd_{203S11}^{Hb} for tolerance against BYDV located on chromosome 2HL. After backcross with the barley cultivar 'Emir' two DH lines carrying the shortest introgression containing either *Rym16* or Ryd_{203S11}^{Hb} for BYDV tolerance were identified and characterized using a set of 31 molecular markers. Blasting sequences of these markers allowed anchoring the introgression to the physical map of barley. A size of 5 Mb for the Ryd_{203S11}^{Hb} locus and 2.2 Mb for the *Rym16* locus were calculated. Up to now, 320 F_2 plants carrying the Ryd_{203S11}^{Hb} were genotyped and out of these four recombinant plants were detected by using co-dominant flanking markers developed with help of the 50K Illumina chip array. In a next step, 1200 F_2 plants carrying the *Rym16* locus will be screened for recombinations in the target interval. Based on such recombinant plants, respective intervals will be saturated by using markers derived from the 50K Illumina chip array, as a basis for isolating respective genes via a map based cloning approach. A non-gridded BAC library will be used to identify candidate genes located in the *H. bulbosum* introgression fragment.