High resolution mapping of the BaYMV/BaMMV resistance gene *rym*13

Lehmann, S.[1], Habekuß, A.[1], Perovic, D.[1], Stein, N.[2], Friedt, W.[3], Ordon, F. [1]

[1] Julius Kühn-Institute, Institute for Resistance Research and Stress Tolerance, Erwin Baur-Straße 27, 06484 Quedlinburg
[2] Leibniz-Institute of Plant Genetics and Crop Plant Research, Corrensstr. 3, 06466 Gatersleben
[3] Justus Liebig University Giessen, Department of Plant Breeding, Heinrich-Buff-Ring 26-32, 35392 Giessen
Email of corresponding author: Sandra.Lehmann@jki.bund.de

Barley yellow mosaic virus (BaYMV) and *Barley mild mosaic virus* (BaMMV) transmitted by the soil-borne plasmodiophorid *Polymyxa graminis* cause severe yield losses up to 50% in barley (*Hordeum vulgare* L.).

Because chemical measures are neither effective nor ecologically sound, the only way of preventing these yield losses is breeding for resistance.

The aim of this project is, therefore to isolate the resistance gene *rym13* located on chromosome 4HL via a map based cloning approach. This gene originates from the Taiwanese cultivar ´Taihoku A´, which turned out to be resistant against BaMMV, BaYMV, BaYMV-2, BaMMV-Teik and BaMMV-Sil.

For fine mapping a high-resolution mapping population comprising 5,181 F_2-plants of the cross ´Taihoku A` x ´Plaisant` corresponding to a resolution of 0.0096 % recombination was constructed. F_2-plants were analyzed with flanking markers WMS06 and HVM67 and the target interval between these flanking markers turned out to be 12.84 cM. Plants carrying a heterozygous recombination event within this interval were selfed in order to identify homozygous recombinants. For this purpose twelve plants per F_2-plant were analysed in F_3 with respective markers.

Using this approach, a set of 475 homozygous segmental recombinant inbreed lines (RILs) has been obtained and was used for marker saturation and phenotyping. For this purpose, plants were mechanical inoculated with BaMMV–ASL 1 in the climatic chamber, and were sown in BaYMV/BaMMV infested fields. The virus titer was estimated by DAS-ELISA. In addition, marker saturation was conducted in a first step by mapping flanking markers in published high density maps of barley. Using this approach the marker interval carrying *rym*13 was shortened to 1.42 % recombination. Further marker saturation will be conducted by exploiting the barley/rice/ Brachypodium/sorghum syteny and using NGS-data available in barley.