

## Wehner

### Breeding for priming triggered leaf rust resistance in barley

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Leaf rust (*Puccinia hordei*) is one of the most important diseases of barley (*Hordeum vulgare* L.) leading to yield losses up to 60%. Resistance genes *Rph1-Rph25* are known in barley but most of these have been overcome meanwhile. But, priming of barley may offer an opportunity to enhance resistance to *P. hordei*. By quorum sensing of bacterial communities N-acyl homoserine-lacton (AHL) is produced, which is known to induce systemic resistance. The present study therefore aims at the detection of genomic regions involved in priming capacity of barley which is one of the most important cereal crops, worldwide.

A diverse set of 200 spring barley accessions were treated with bacteria, i.e. repaired *Ensifer meliloti* natural mutant *expR+ch* overexpressing AHL and transformed *E. meliloti* carrying the lactonase gene *attM* from *Agrobacterium tumefaciens* which inhibits AHL production. After three bacterial inoculations, plants were infected with *P. hordei* strain I-80 at the three leaves stage. 12 days after infection scoring of the leaf area diseased and the infection type was conducted. Results of two experimental replications revealed significant effects ( $p < 0.001$ ) of the bacterial treatment indicating a positive effect of priming on *P. hordei* resistance. Based on the observed phenotypic differences and 23,417 filtered SNPs derived from the Illumina 9k iSelect chip and genotyping by sequencing, 21 quantitative trait loci (QTL) involved in priming-efficiency were identified by genome wide association studies. Experiments will be repeated once to validate QTL regions and develop molecular markers facilitating marker assisted selection of priming efficient accessions in barley breeding.

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