Genome-wide association study of resistance to late blight based on JKI prebreeding potato clones (Solanum tuberosum)

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Despite decades of research, late blight, caused by the oomycete *Phytophthora infestans*, still causes high yield losses in potato cultivation. Particularly organic farming suffers badly because *P. infestans* can be controlled by copper only. For this reason, JKI is running a long-termed pre-breeding programme with a focus on polygenic resistance, which we believe is the only sustainable approach to fight late blight in potato.

To locate the resistance of this valuable gene pool, 161 pre-breeding clones and 39 varieties were tested for their foliage blight reaction using a detached leaf assay and for tuber resistance using a tuber slice test. In parallel, DNA samples were genotyped using Genotyping by Sequencing (GBS).

The reference genome has been the *S. tuberosum* group 'Phureja' clone, which was sequenced in 2011. After filtering for minor allele frequency (5 %) and missing values (30 %), 28,055 SNPs were used for the genome-wide association study (GWAS).

First results show that QTL of this gene pool for foliage blight resistance are located on chromosomes 9 and 11 ($log_{10}(p)>5$). QTL for tuber blight resistance were identified on chromosome 11. In the following two project years, results will be confirmed by additional data.