A transcriptome-based approach for development of molecular markers for bacterial wilt resistance in perennial ryegrass (*Lolium perenne* L.)

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Bacterial wilt is a severe disease of major forage grasses such as perennial ryegrass (*Lolium perenne* L.), inducing considerable yield losses. The disease is caused by the gammaproteobacterium *Xanthomonas translucens pv. graminis* (*Xtg*) which occludes xylem vessels and causes wilting symptoms and necrosis of the leaves. The overall purpose of this study is directed to the development of selection markers for bacterial wilt resistance for directly use in plant breeding programs. Hence, a BC1 mapping population (n=286) segregating for bacterial wilt resistance was used for phenotyping of host susceptibility by (I) standardized artificial dip-inoculation with *Xtg* and visual observation (II) a DNA-based real-time PCR assay for *in planta* determination of bacterial proliferation. Thence, a next generation based massive analysis of cDNA ends (MACE) transcriptome profiling is currently performed by using infected and non-infected plants for (I) identification of closely linked markers (II) elucidating host defense responses.

Therefore bulks of 10 unambiguously defined resistant and susceptible phenotypes were sequenced for a differential analysis of transcriptional profiling. Various bioinformatical tools facilitate the detection of differential SNPs and transcripts that were exclusively expressed in the resistant bulk (ETRs). Selection of marker candidates is thereby highly focused on over-expressed ETRs. Bulks of resistant vs. susceptible genotypes were used for detection of polymorphic and informative markers. In a second approach transcriptomic data will be used for the characterization of disease resistance mechanism and for the potential prediction of the major QTL *LpXtg1* affecting resistance to bacterial wilt in *Lolium perenne* L..