Molecular Characterisation of Bacterial Wilt Resistance in *Lolium Multiflorum* Lam.

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Introduction Italian ryegrass (*Lolium multiflorum* Lam.), a forage grass of prime importance throughout the world, is adversely affected by the pathogen *Xanthomonas translucens* pv *graminis*. Breeding for resistant cultivars is the only practicable means of disease control. However, the inheritance of bacterial wilt resistance is largely unknown. The aim of our research is to elucidate genetic control of bacterial wilt resistance using molecular technologies such as genetic linkage mapping and the analysis of quantitative trait loci (QTL).

Materials and methods A mapping population consisting of 306 F_1 progenies of a pair-cross between a susceptible and a resistant genotype of unrelated cultivars has been established. A high density genetic linkage map of dominant amplified fragment length polymorphism (AFLP) and codominant microsatellite markers has been constructed using a two way pseudo-testcross strategy (Grattapaglia & Sederoff, 1994).
Resistance to bacterial wilt of the mapping population was examined in greenhouse and field experiments by artificial inoculation using a well characterised bacterial isolate. Additionally, the susceptible and the resistant parental population was assessed in the field as reference. Disease progress was monitored using a score from 1 (no symptoms, plant is resistant) to 9 (plant is perishing and highly susceptible). The area under disease progress curve (AUDPC) as a measure of quantitative disease resistance was calculated according to the trapezoid rule (Jeger & Viljanen-Rollinson, 2001)

Results In the greenhouse, significant segregation for resistance was observed (mean disease score (MDS)=6.68, standard deviation (SD)=1.67). The skewed, bimodal frequency distribution of AUDPC disease values (Figure 1) indicates the resistance to be controlled by several genes rather than one single major gene.
In the field, the MDS of the mapping population was lower (MDS=2.76, SD=1.04) when compared to the greenhouse experiment, but differed significantly (P<0.05) from the MDS of the resistant and the susceptible reference population. Moreover, the results were supported by a high operative heritability of 77 % and field and greenhouse resistance data were highly correlated (r=0.67 P<0.01).

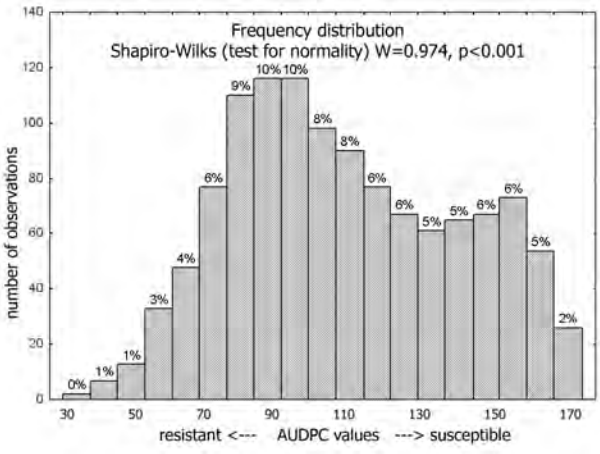

Figure 1 Frequency distribution of greenhouse AUDPC values for F_1 progenies

Conclusion Results of bacterial wilt resistance evaluation in the greenhouse and the field were highly correlated and indicate the resistance to be of quantitative nature influenced by major genes. The significant segregation for resistance within the mapping population and the genetic linkage map will serve as a valuable basis for QTL analysis and the identification of genomic regions associated with bacterial wilt resistance which are currently in progress.

References

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