A Glucanase Gene Cosegregates with a QTL for Crown Rust Resistance in *L. Perenne*

H. Muylle
Centre of Agricultural Research, Belgium

J. Baert
Centre of Agricultural Research, Belgium

E. Van Bockstaele
University of Ghent, Belgium

I. Roldán-Ruiz
Centre of Agricultural Research, Belgium

The XX International Grassland Congress took place in Ireland and the UK in June-July 2005. The main congress took place in Dublin from 26 June to 1 July and was followed by post congress satellite workshops in Aberystwyth, Belfast, Cork, Glasgow and Oxford. The meeting was hosted by the Irish Grassland Association and the British Grassland Society.

Proceedings Editor: D. A. McGilloway

Publisher: Wageningen Academic Publishers, The Netherlands

A glucanase gene cosegregates with a QTL for crown rust resistance in *L. perenne*

H. Muylle[1], J. Baert[1], E. Van Bockstaele[1,2] and I. Roldán-Ruiz[1]
[1]Department of plant genetics and breeding, Centre of Agricultural Research, Caritasstraat 21, 9090 Melle, Belgium;[2] Faculty of Bioscience Engineering, University of Ghent, Coupure Links 653, 9000 Gent, Belgium. Email: h.muylle@clo.fgov.be

Keywords: *Lolium*, crown rust, STS marker, candidate gene approach

Introduction An important disease in *Lolium* spp. is crown rust caused by the fungal pathogen *Puccinia coronata*. In order to study the genetic background of crown rust resistance in *L. perenne,* a mapping study was carried out and is discussed below. To identify genomic regions or genes involved in resistance, STS markers are extremely useful. This candidate gene approach was applied in the present study.

Material and methods In order to study the genetic background of crown rust resistance in *L. perenne,* an F_1 population segregating for crown rust resistance was created by crossing a resistant and a susceptible parent. The parents were heterozygous plants chosen among breeding materials. Phenotypic analysis was done as described by Adams *et al*. (2000). Mapping and QTL studies were performed using AFLP, SSR, STS and RFLP markers and using Joinmap3.0 and MapQTLv4 (Van Ooijen & Voorrips, 2001).

STS markers were developed from a cDNA library constructed from leaf tissue. 130 cDNAs were sequenced. 58 cDNA sequences showed interesting homologies with DNA sequences with known gene function. For 44 cDNA sequences, it was possible to design primer pairs that span an intron at the genomic DNA-level.

Results Phenotypic analysis revealed that resistance was oligogenic in this segregating F_1 population. Mapping studies using AFLP, SSR, STS and RFLP markers resulted in a genetic map of 833 cM. QTL analysis revealed 4 genomic regions involved in crown rust resistance explaining 45 % of the variance in the population.

Out of the developed STS marker set, one marker, showing homology to a glucanase gene, could be mapped in the F_1 population segregating for crown rust resistance. It coincides with a QTL on LG1 explaining 6.4 % of variance for crown rust resistance in this population.

Conclusion With the candidate gene approach, we could map a STS marker, showing homology to glucanase genes, in a genomic region involved in crown rust resistance. Glucanase genes are known to be involved in defence responses of the plant against biotic stress. Expression profiling will have to confirm these results.

References

Adams, E., I. Roldán-Ruiz, A. Depicker, E. Van Bockstaele & M. De Loose, 2000. A maternal factor conferring resistance to crown rust in *Lolium multiflorum* cv. 'Axis'. Plant Breeding 119: 182-184.

Van Ooijen, J.W. & R.E. Voorrips, 2001. Joinmap® 3.0, software for the calculation of genetic linkage maps. Plant Research International, Wageningen, The Netherlands.