Strategies for fine mapping and isolation of resistance QTLs on Linkage Groups IV of Potato

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Introduction

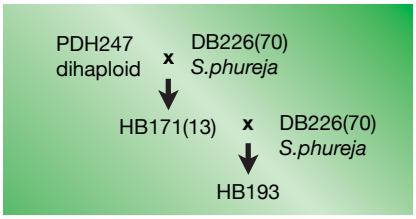
Potato is the world's most important non-cereal crop and *Phytophthora infestans,* the causal agent of Late Blight, is arguably it's most important pathogen. In the UK, a further major threat is due to *Globodera pallida* (Potato Cyst Nematode), resistance to which has not yet been effectively deployed in most potato cultivars. The cost, in both financial and environmental terms, is significant. The breeding of new potato cultivars with high levels of durable resistance, such as field resistance on Chromosome IV to both of these pests is considered the best strategy for sustainable potato production in the future.

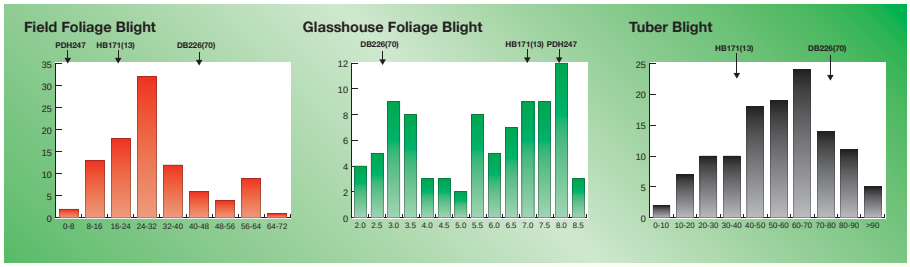
P. infestans devastation

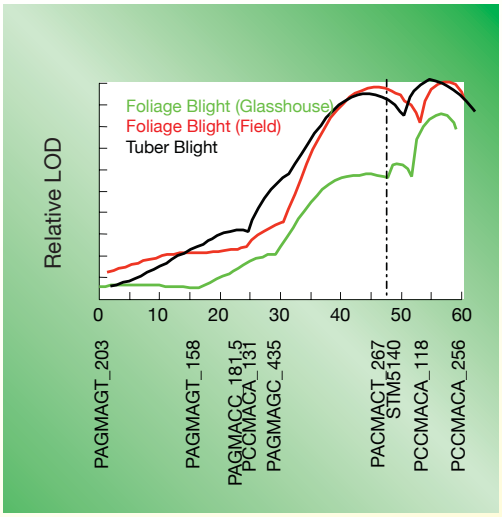
Globodera pallida

Late Blight Resistance

QTL Mapping has been carried out for both foliage and tuber blight using a backcross population derived from a resistant dihaploid *S.tuberosum* clone and a long-day-adapted *S.phureja* clone.





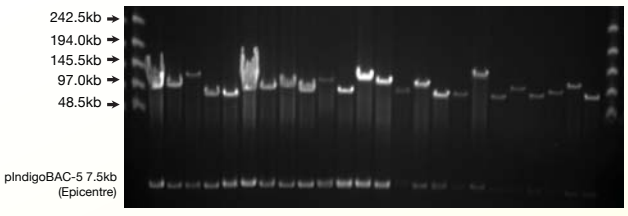


QTL and Linkage Mapping was carried out on 120 clones for which tuber and foliage resistance had previously been assessed. Results of Kruskal-Wallis analysis, interval mapping and graphical genotyping were all consistent with a large-effect QTL for blight resistance between two AFLP markers on Linkage Group IV which was identified by an SSR, STM5140. (Bradshaw et al 2006, TAG in press). Similar work is being carried out to look at *G. pallida* resistance.

BAC Library Construction

In an attempt to isolate the gene/genes of interest on Linkage Group IV, a Bacterial Artificial Chromosome (BAC) library has been constructed from the resistant parent, HB171(13) using a pIndigoBAC-5 vector (according to Hein et al, Biotechniques, 2005 38: 69-71).

2-week old leaf material for BAC library construction



Pulsed-field gel electrophoresis of 24 BAC clones

40,000 plus clones have been arrayed in 384-well plates with an average insert size of 100kb representing a coverage of 4 genome equivalents. Also, 160 pools of about 1,300 clones each were created, potentially giving us access to an additional 20-fold genome coverage as described by Isidore et al 2000, Functional Integrative Genomics 5, 97-103. Initially the arrayed clones will be screened with markers linked to the QTLs and other blight resistance genes on LGIV as well as R gene probes.

Acknowledgements

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