Mapping polygenic Potato Cyst Nematode (PCN) resistance in a tetraploid population of potato

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Introduction

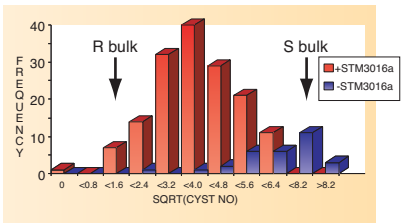
Potato cyst nematode (PCN) have become a major threat to potato production in the UK and mainland Europe.

We are engaged in a project whose aim is to genetically dissect one of the most useful sources of resistance to the PCN *Globodera pallida.* 'H3' resistance derived from *Solanum andigena,* is polygenic in its mode of inheritance and is effective against pathotypes Pa2/Pa3 of *G. pallida* which is prevalent in the UK.

We have used bulk segregant analysis (BSA) to target markers to a large effect QTL on linkage group IV. Our aim is to perform a thorough genetic dissection of this locus using a tetraploid potato population.

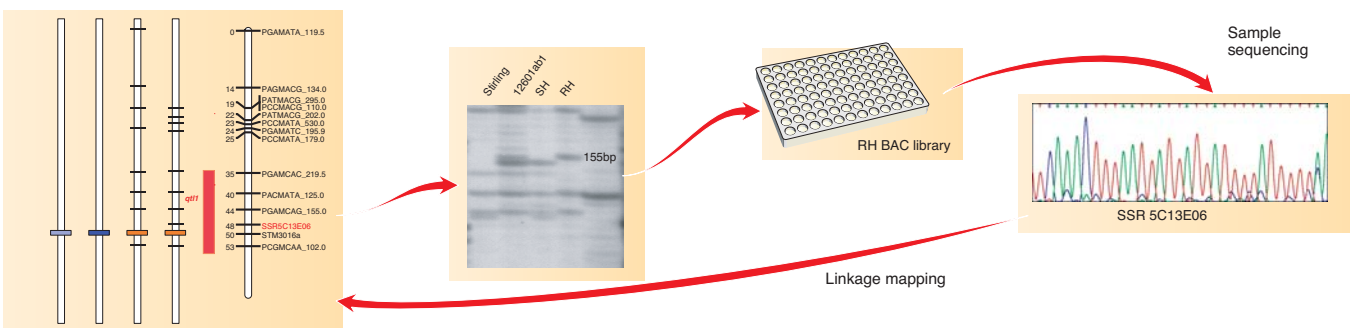
Bulk Segregant Analysis

Work was carried out using a tetraploid cross comprising c.300 F1 progeny between cv. Stirling and SCRI breeding clone 12601ab1. Previously we have shown that a major QTL for PCN resistance from the 12601ab1 is linked in coupling to a microsatellite marker (STM3016) on LGIV. A resistant bulk was constructed by selecting progeny possessing an SSR allele (STM3016a) linked in coupling to the resistance QTL and then selecting clones from these with the lowest cyst counts. A susceptible bulk was constructed by selecting the most susceptible plants from those lacking the STM3016a allele.



These bulks were subjected to AFLP analysis with 196 primer combinations. 12 AFLP markers tightly linked to this locus have been identified and these have been used to generate a linkage map of this locus.

Identification of markers linked to the LG IV PCN QTL



In our previous studies STM3016 was found to account for 21% of the variation for resistance to PCN. The AFLP marker PGAMCAG_155.0 identified by the BSA approach taken above, mapped closer to the QTL and was found to account for 35.1% of the variation for resistance. While this marker was derived from a tetraploid cross, a fragment of exactly the same size was generated from the diploid genotype RH for which we have previosuly constructed a BAC library. Based on the concept that co-migrating AFLPs are homologous fragments we used this and other markers screen the RH BAC library which we have pooled for PCR-screening using a multidimensional strategy (see poster by G.Bryan et al P516).

Identified BACs were subcloned and partially sequenced and the sequences used to develop codominant SSRs for mapping back onto the potato genetic map. One of the SSRs generated, 5C13E06 from a BAC supporting the amplification of PGAMCAG_155.0 mapped to the same region as STM3016 and the original PGAMCAG_155.0.

Conclusions

We have begun a detailed investigation of a large-effect QTL on LGIV affecting 'H3' resistance, derived from *S.tuberosum* ssp. *andigena.* Our studies have been greatly facilitated by use of an efficient bulking strategy using phenotypic and marker scores.

To date one SSR has been discovered and successfully mapped to this region on LGIV. Our goal is to perform a thorough genetic dissection of this region. We have started to establish the gene content of this region by subcloning and sequencing BAC clones and we plan to use these to develop SNP markers in the region. A similar bulking strategy has been used to identify cDNA AFLP fragments and the intention is to map these.
Also located on this region of LGIV is the Late Blight QTL which is present in the Stirling parent. Codominant markers which are found to be linked to this QTL will also be mapped.

Acknowledgements
We gratefully acknowledge the financial support of the Scottish Executive for Environment and Rural Affairs Department.