MAPPING POLYGENIC POTATO CYST NEMATODE RESISTANCE IN DIPLOID AND TETRAPLOID POPULATIONS OF POTATO

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Introduction

The potato cyst nematode (PCN) species *Globodera pallida* has become a major threat to potato production in the UK and mainland Europe in recent years. We are currently performing a detailed genetic analysis of two of the most useful sources of resistance to *G. pallida*, 'H3' resistance from *Solanum tuberosum* ssp. *andigena* and resistance derived from the wild species *S. vernei*. These resistances are of particular interest as they are polygenic in their mode of inheritance and confer resistance to pathotypes Pa2/Pa3 of *G. pallida*, which are highly prevalent in the UK.

We have used bulk segregant analysis (BSA) to target AFLP markers to QTL contributing to resistance in tetraploid potato populations. We have generated a dense linkage map of a diploid potato clone segregating for components of *S. vernei*-derived resistance. For H3, we are targeting a large-effect QTL on linkage group IV, and our goal is to perform a thorough genetic dissection of this locus, by saturating it with markers and by developing improved statistical methods for QTL analysis in tetraploids.

S.vernei-resistance

Bulk segregant analysis in 12288af23 x Stirling F1 population

Bulk segregant analysis using 100 AFLP primer combinations was performed on a tetraploid population (12288af23 x Stirling) comprising 231 plants. Bulks were constructed using the 20 most resistant and susceptible plants.

Three AFLPs showing linkage to a resistance QTL were detected. PCR primers designed to each AFLP sequence were applied to the parents of the G87 x I88 diploid population. Primers against marker VRN1837 detected a 3-bp length polymorphism (see below), heterozygous in G87, allowing it to be mapped to LG V, close to an SSR (LERNALX). The three AFLPs detected by BSA explained 15-20% of the phenotypic variation in cyst counts.

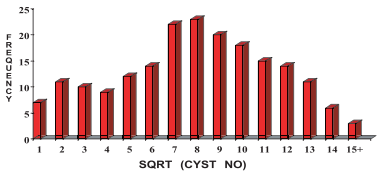
Mapping of VRN1837

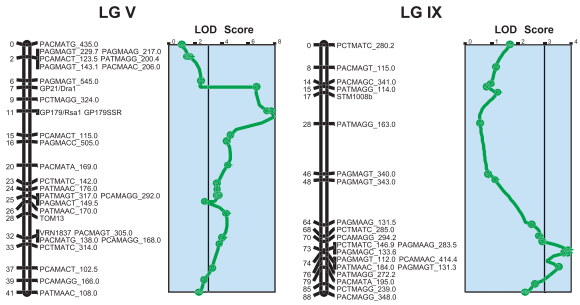
Application of PCR markers to germplasm carrying *S.vernei*-derived resistance

Primers directed against marker VRN1636 gave a single product with 12288af23 and no visible product with Stirling. Of 23 tetraploid potato breeding lines tested, only 4 generated this fragment (12288af23, 12385ab6, 14969ac9 and 15119ac5). These are all known to be descended from crosses involving PCN resistant *S. vernei* accessions and containg resistance to *G. pallida*.

QTL mapping in diploid population PDH538 x IVP48

A diploid population comprising 138 F1 clones segregating for *S. vernei*-derived resistance to *G. pallida* was also used to analyse this complex source of resistance. The dihaploid clone PDH538 (an 'ex-*S. vernei*' tetraploid) was crossed with PCN susceptible *S. phureja* clone IVP48. This population was scored for cyst number using a replicated canister test, and analysed with 20 AFLP primer combinations and 16 SSRs. A map of the PDH538 parent comprising ~380 markers was constructed using JOINMAP. These markers included VRN1837 and LERNALX, evaluated on the 12288af23 x Stirling population. The analysis suggests the existence of two QTL for PCN resistance on linkage groups V and IX. The QTL on linkage group V is centred near the VRN1837 and LERNALX markers, arising from BSA of the tetraploid population. The linkage map and the approximate positions of the two QTL detected are shown below.

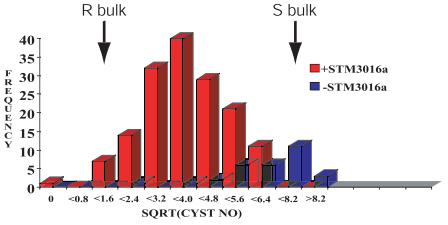




'H3' resistance

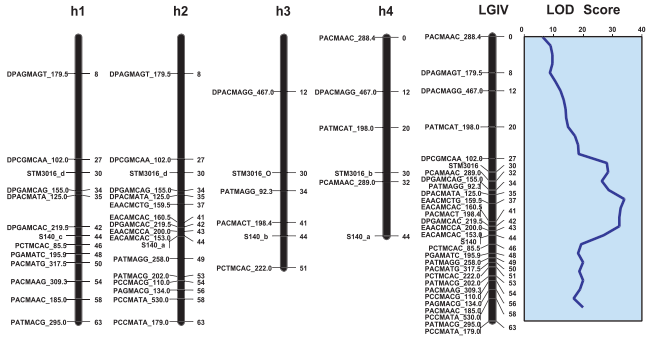
Bulk segregant analysis in Stirling x 12601ab1 population

For analysis of H3 resistance we have used an F1 population derived from a cross between the cultivar Stirling and the breeding clone 12601ab1. This population comprises c.300 individuals. Previously we have shown that a major QTL for PCN resistance from the 12601ab1 parent is linked to a microsatellite marker (STM3016) on LG IV. 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 ~200 primer combinations. To date, 12 AFLP markers tightly linked to this locus have been identified and these have been used to generate a linkage map of this locus (see below).



Use of bulks selected using both phenotypic and linked marker data has been very effective in targeting AFLPs to this locus. The duplex markers (e.g. P19M49) close to STM3016 explain more of the phenotypic variance (~30%) than the simplex ones, which is expected as the resistance allele at this locus is known to be present in two copies. Our goal is to perform an exhaustive genetic analysis of this locus by obtaining more linked SSRs from BAC clones in the region, and by developing more sensitive statistical methods for mapping and QTL detection.

Linkage map and QTL plot of 12601ab1 LG IV



Conclusions

1. We have detected two QTL in a diploid population segregating for PCN resistance, derived from the wild species *S.vernei*. One of these QTL is also detectable in a tetraploid population segregating for *S.vernei*-resistance. Interestingly, these QTL appear to be in similar locations to those (Gpa5 and Gpa6) reported by Rouppe van der Voort et al. (Theor. Appl. Genet. 101:1122-1130). This work is now published in Theor. Appl. Genet. 105:68-77.

2. We have performed a detailed investigation of the H3 source of resistance derived from *S. tuberosum* ssp. *andigena*. A large-effect QTL is found on LG IV and a smaller one has been detected on LG IX. Our goal is to fully characterise this region genetically with a view to the eventual cloning of PCN and late blight QTL at this locus. Our studies have been greatly facilitated by use of an efficient bulking strategy.

Acknowledgements

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