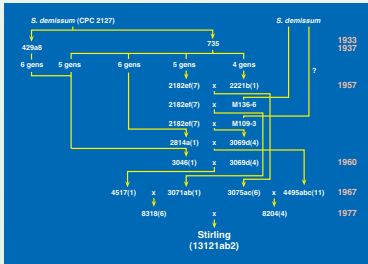


A genetical analysis of resistance to late blight in the foliage and tubers of potato cultivar Stirling

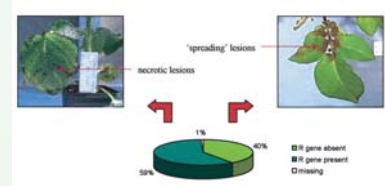
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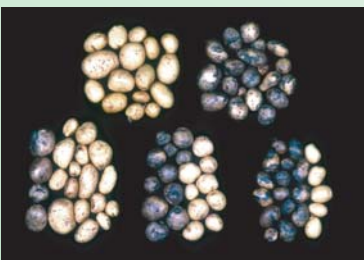
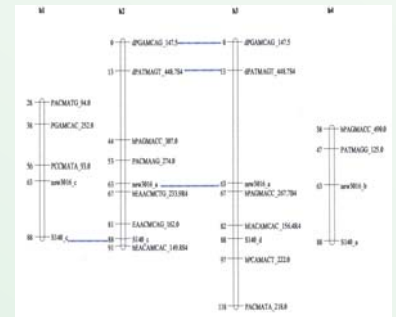
← The SCRI bred blight resistant cultivar Stirling traces back to crosses made with *Solanum demissum* in 1932 and 1937.

Initially breeding for resistance concentrated on major dominant R genes. Stirling has a single copy of one such gene which maps to linkage group XI, and is most likely to be R7. However, by the 1950s it was clear that R genes, either singly or in combination, do not provide durable resistance.

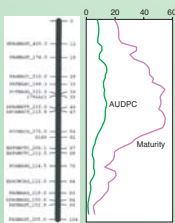


← Breeders therefore started to exploit quantitative field resistance by using complex races of blight compatible with the R genes present in their germplasm, a strategy that has continued to this day.

There is a QTL for foliage resistance at 76 cM on linkage group IV. Stirling has alleles on homologous chromosomes 2 and 3 which together give greater resistance than either allele alone. Segregation at this locus explains 32% of the variation in foliage blight scores in the 227 offspring from the cross 12601ab1 x Stirling.



← Resistance is required in the tubers as well as in the foliage because the one does not guarantee the other, and susceptible tubers can be infected by spores produced over a relatively long period of time from the slowly spreading sporulating lesions of a leaf-resistant cultivar. The two alleles at the QTL on linkage group IV also confer resistance in the tubers and their segregation explains 14% of the variation in scores.



← Resistance to late blight has long been associated with late maturity. Stirling has a single copy of a gene for early maturity at 36 cM on linkage group V. Segregation at this locus explains 54% of the variation in maturity scores made in field trials in 1999 and 2000. The gene is also associated with susceptibility to late blight in both foliage and tubers, explaining 20% and 26% of the variation, respectively. These associations are removed by analysing the residuals from the linear regression of blight scores on maturity.

Conclusion

Regression of foliage and tuber blight scores on both maturity and the two alleles at the QTL on linkage group IV accounts for 56% and 40%, respectively, of the variation seen in the 227 offspring from the cross



Acknowledgements

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