

Mapping resistance to Late Blight in two *S. verrucosum* populations

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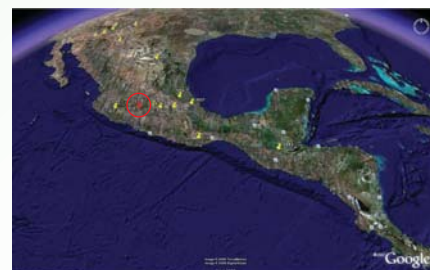
Introduction

Late blight, caused by the oomycete pathogen *Phytophthora infestans* (Mont.) de Bary, is one of the most devastating diseases in potato worldwide. The use of resistance genes from wild species is generally accepted as a more effective and economical way to control this disease compared with chemical management.

Solanum verrucosum is a wild diploid potato species from Mexico which confers

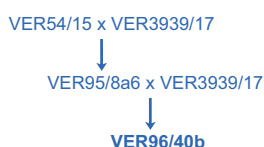
resistance to different isolates of *P. infestans*. *S. verrucosum* is easily crossable with different South American species and as such it is an ideal candidate for use in diploid breeding programmes.

We have mapped this resistance in an intraspecific cross (Ver 96/40) and also an interspecific cross (Ver 01/32). Both populations were generated using the same resistant parent Ver54/15.



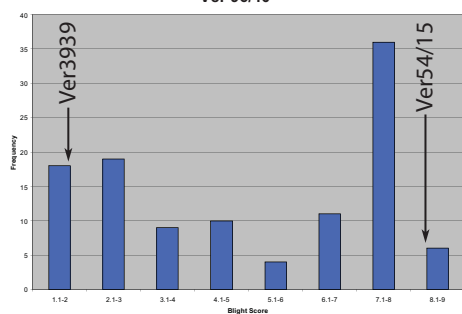
Ver 96/40

A quantitative Trait Locus (QTL) of large effect was identified on Linkage Group IX. A chromosome specific RFLP marker, TG328, was mapped on this population to the middle of LGIX, close to this QTL. This marker is linked to the QTL for blight resistance derived from *S. mochiquense* (Smilde *et al.* TAG (2005) 110: 252-258).



Marker	Map Position	Parental Origin	%Variation Explained
E38M48_105	0	B	0
P14M42_208	3.314	M	0
P18M44_295	12.453	M	10.9
P18M41_100	30.681	M	20.8
E38M51_110	39.377	B	7.1
STM1021_177	45.927	B	10.8
STM1021_175	47.446	P	0
P13M42_182	54.912	P	0
TG328/HpaII	57.261	M	28.9
P18M51_221	59.207	M	32.1
P16M51_269	68.453	M	15.8
E38M51_236	77.863	P	0
P12M32_325	88.937	P	0

Ver 96/40



Ver 01/32

Two major QTLs were identified – one on Linkage Group VIII and one on Linkage Group IX.

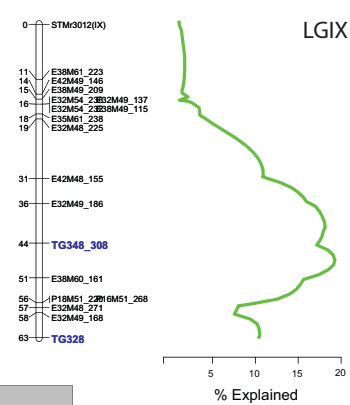
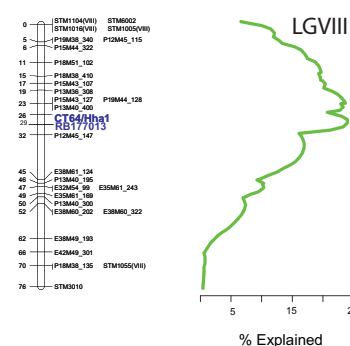
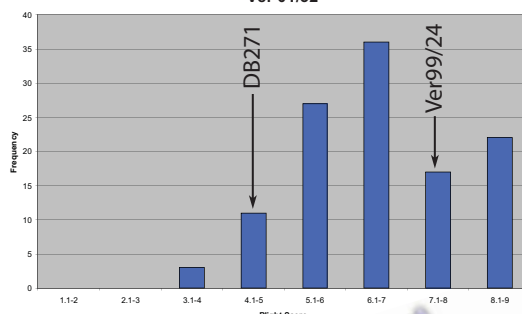
The LGVIII QTL maps close to the RB/B1b1 resistance gene derived from *S. bulbocastanum*.

A marker, RB177013, was developed from a length polymorphism between resistant and susceptible BACs (Junqi Song *et al.* PNAS 2003 100 9128-9133) and this was mapped to the middle of LGIX along with a chromosome specific RFLP marker, CT64 (Edwin van der Vossen *et al.* Plant Journal (2003) 36 867-882).

The LGIX QTL maps close to blight resistance derived from *S. okadae*. A chromosome specific RFLP marker, TG348, was mapped on this population to the distal end of LGIX, underneath the QTL.



Ver 01/32



Conclusions

We plan to carry out allele mining using RB/B1b1 orthologues in order to fine map the region around the LGVIII locus. To elucidate the resistance specificity of the locus mapped to LGVIII and to compare it to RB/B1b1, we will utilize effectors including the recently profiled *lpiO* and its variants that have been demonstrated to be recognised by *Rpi-b1b1* (N.Champouret *et al* 5th Solanaceae Genome Workshop 2008).

Although both populations were generated using the same resistant parent, it is not clear why the QTLs on LGIX map to different regions of the chromosome. Further work will be carried out to clarify this including allele mining using orthologues derived from *S. okadae* and *S. neorossi*.

