

## CHARACTERIZATION OF LRR MOTIF AT THE LOCUS GRO 1 IN SOLANUM WILD SPECIES

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The LRR (Leuchin Rich Repeats) motif of Gro 1-4 gene, responsible for resistance to *Globodera rostochiensis* race Ro1, is thought to be the protein/protein interaction site responsible for nematode race specific recognition. Its structure is determined by the succession of eleven leucine rich modules, each determining an hairpin structure, organized in a horseshoe shape.

This resistance gene is present in a *Solanum tuberosum*-*Solanum spegazzini* diploid hybrid (P40) and was assigned to short arm of chromosome 7 (Barone et al., 1990). Paal et al. (2004) have definitively cloned and sequenced 10 different genes organized in a cluster at locus Gro 1, all of which have LRR motives very similar to that of Gro 1-4.

Using sequence information available at EMBL/GenBank/DDBJ databases (accession numbers AY196151-AY196163) we have designed two primerpairs whose target area is the LRR motif of Gro 1-4 gene. These primers were used to amplify and then sequence the major part of the LRR coding sequence of Gro1 gene in 16 wild species. The alignment of sequences was compared to the consensus sequence of Gro1-4 gene from GenBank. In total 405 SNPs were found, varying from 11 SNPs in *S. demissum* to 36 in *S. stoloniferum*, *S. jamesii* and *S. fendleri*. Obtained sequences were then translated and multialigned. Polymorphisms were classified regarding to the position of amino acid substitutions and to the nature of amino acids involved. 218 Single Peptide Polymorphisms (SPPs) were found, varying from 6 SPPs in *S. demissum* to 17 in *S. stoloniferum* and *S. fendleri*. The non synonymous/synonymous substitution ratio (Ka/Ks) was calculated in comparison to the LRR sequence of Gro 1-4 gene from GenBank. For most species it was very different from 1, suggesting that this gene is under selective pressure. In particular, *S. phureja* (IVP 35) and *S. jamesii* (JAM1) have Ka/Ks ratio minor than 1, suggesting that these genes were under conservative selective pressure. On the other hand *S. tarijense* (TAR 1), *S. chacoense* (CHC1) and *S. hougasii* (HOU1) have Ka/Ks ratio major than 1, suggesting in these cases the trait is under a selective pressure that induces variability.

In general these genes are highly variable in solvent exposed amino acids responsible for selective protein-protein recognition, with most (45%) of 191 substitutions being non conservative. On the other hand consensus residues of LRR motif, that are the ones responsible for the proper packing of the hydrophobic core, are very conserved with only 30 substitutions, the 80% of which being conservative.

### References

- Barone et al. 1990 *Mol. Gen. Genet.* 224, 177-182  
Paal et al. 2004 *Plant J.*, v. 38, no. 2, p. 285-297