

(P05)

Identification of Molecular Markers Linked to Columbia Root Knot Nematode Tuber Resistance in Potato Breeding Lines

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The Columbia root knot nematode (CRKN), *Meloidogyne chitwoodi* Golden et al., is a major pest in Pacific Northwest potato production areas. Both roots and tubers are attacked, leading to decreases in yield and quality. We aim to identify single nucleotide polymorphisms (SNPs) linked to tuber resistance using a genomics and bulked segregant analysis approach. CRKN resistance from wild diploid species *Solanum bulbocastanum* accession SB22 was introgressed into tetraploid potato breeding material. Screening identified selection PA99N82-4 to be root and tuber resistance to CRKN. Segregating populations were generated by crossing PA99N82-4 with susceptible selections. DNA was sequenced from six resistant and six susceptible segregating genotypes on an Illumina HiSeq2000, and the resulting sequence data was combined into resistant and susceptible pools. Pooled sequence data was aligned to the SB22 genome, and SNPs were subsequently called. Over 800,000 SNPs differentiated the resistant and susceptible pools such that the resistant pool matched SB22, but the susceptible pool was different. A panel of 50 SB22 genome contigs with high SNP density was chosen to further validate linkage to CRKN resistance in a mapping population. Markers with tight linkage to CRKN resistance will be useful for marker-assisted selection. The set of candidate loci will also be interrogated in order to identify candidate resistance genes.

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Stability Analysis of Resistance to *Phytophthora infestans* of Potato Genotypes, using the AMMI Model

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Late blight caused by *Phytophthora infestans* is one of the main constraints for potato production worldwide. The disease is usually controlled by frequent application of fungicides. However, growing resistant cultivars can reduce the number of costly applications and their environmental hazards. The objective of this study was to assess biological stability of resistance to *P. infestans*. Potato genotypes were tested for field late blight resistance over a period of two years, with artificial inoculation of two *P. infestans* strains. The experimental fields were located in southern Brazil. Nine clones derived from crosses involving B3 population (International Potato Center, CIP), and nine check cultivars were evaluated. After the appearance of the first symptoms, the disease severity was recorded visually as percentage of foliage affected at 4- to 5-day intervals until the susceptible control (Agata) had reached 100% infection. Severity data was used to calculate the relative area under the disease progress curve (rAUDPC). The interactions genotype x year (G x Y), genotype x strain (G x S), and G x (Y x S) were analyzed using the AMMI model. The stability of resistance was also estimated by calculating the coefficient of variation (CV) of the rAUDPC for each genotype across environments. According to the AMMI model, potato genotypes originated from the B3 population, C2572-2-06, C2557-2-06, and the Eliza cultivar ranked moderate stability and partial resistance to late blight infection. CIP392.617.54 and C2551-2-06 genotypes showed high levels of resistance associated with low CV, and were considered to be the most stable genotypes.