Marker development of potato nematode resistance to *G. rostochiensis* pathogen Ro2/3 and Ro5

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Potato is the most important host for Potato Cyst Nematodes (PCN). PCN (*Globodera rostochiensis* and *Globodera pallida*) have become a major problem for potato producers by damaging the root and reducing yield. PCN are widespread in many countries, particularly Northern Europe. The number and range of pathotypes vary from country to country. Single dominant R genes have been reported in several wild types: *H1, Gpa2* from *S. tuberosum* ssp. *andigena* CPC1673, *GroV1* from *S. vernei* and *GroI* from *S. spegazzinii*. Quantitative resistances to *G. rostochiensis* also have been reported in S. *vernei*-Hybrids ((VTn)262.33.3, MPI 58.1642/4, MPI 65.346/19), *S. spegazzinii*, *S. kurtzianum* and *S. multidissectum*. The potato cultivars or breeding lines having the resistance from wild species have been crossed. Particularly, the resistances to *G. rostochienesis* pathotype Ro2/3 and Ro5 are important agronomic traits.

In 2003, the department of potato breeding produced tetraploid F1 population conferring resistance to pathotype Ro2/3 and Ro5, which is derived from *S. vernei*-hybrids. This population consisting of 252 progenies was derived from the cross between cultivar Oktan conferring the resistance to PCN *G. rostochiensis* pathotypes Ro1-5 and the extreme resistance to PVY and cultivar Ulme having the resistance to *G. rostochiensis* pathotypes Ro1 and Ro4, and the full resistance to wart disease. This population was propagated during 2003 and the resistance *G. rostichiensis* was evaluated with 4 to 6 replications for each line per pathotype in 2004. The resistance to pathotype 5 was evaluated in 252 progenies and the resistance to pathotype 2/3 was evaluated in 107 out of 252. According to the resistance evaluation, 62 selected lines and parents were used for Bulked Segregant Analysis and AFLP assay. 44 out of 512 primer combinations were selected and subsequently, these marker candidates were tested with all individuals of the whole population. Six markers among of 44 marker candidates were cloned and sequenced. In single marker regression analysis with data of resistance evaluation on 2004, the marker **A** was analyzed to explain over 30% and 39 % of phenotypic variance to both pathotypes Ro2/3 and Ro5. One STS marker **A-1** (268 bp) was successfully developed based on sequence data of marker **A** by co-segregating with AFLP marker **A**. Through sequence analysis, the marker **A** was found to share high sequence identity (95 %) with one EST sequence out of the potato EST databank, which is annotated to encode putative Mitogen-activated protein kinase in Arabidopsis according to blast annotation. In addition to STS marker **A-1**, two STS markers **A-2** (337 bp) and **A-3** (364 bp) were successfully developed by designing two forwards primers based on the homologous EST sequence. Marker identification with AFLP marker **A** was especially difficult in potato varieties, whereas the STS markers selected 11 out of over 200 tested potato varieties. The pedigree of some selected varieties indicate that the resistances to Ro2/3 or Ro5 originates from MPI65.346/19 or *S. vernei*-Hybrid (VTn)262.33.3. These developed STS markers could be feasible to marker assisted selection in the potato breeding.

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