

S02-T3

A novel potato cyst nematode effector displays polymorphism linked to nematode (a)virulence and interferes with plant defense

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The esophageal glands of the potato cyst nematode *G. rostochiensis* are thought to be a major source for nematode effectors in plant parasitism. Nematode effectors are delivered into host cells through the oral stylet, what leads to the formation of a complex multicellular feeding site. Potato plants carrying *HI* resistance gene specifically recognize the effectors of *G. rostochiensis* pathotype Ro1. Disease signalling, which is activated by the *HI* gene, results in isolation of the feeding site in its early stage by ring of necrotic cells. We believe that an effector secreted by the esophageal glands of the nematode triggers such a strong and quick resistance response. Two lines of *G. rostochiensis* differing in their (a) virulence on *HI*-carrying potato were selected from single female crossings. Proteome and transcriptome analysis of both lines indicate presence of less than 2% polymorphisms. Our current study aims to identify these differences within the secretome of the virulent and avirulent nematode line early in the parasitic development. We constructed a cDNA library from the avirulent line of *G. rostochiensis* isolated from the susceptible potato roots 11 days post inoculation. Single run sequencing of 4000 clones generated a set of ESTs, which were clustered and translated into peptides *in silico*. In total 74 ESTs were predicted to encode a signal peptide for secretion. The clones, from which the ESTs originated, were fully sequenced. Primers designed on the predicted open reading frames were used for PCR amplifications on genomic and cDNA of both the virulent and avirulent line. Polymorphic amplicons are explored by studying differences on the population level, nematode *in situ* hybridization, *in planta* localization and subcloning of underlying genes into plant expression vectors for functional studies.