Genetic fingerprinting of sugar beet cyst nematodes based on pathogenicity gene *vap1* for epidemiological studies

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Heterodera schachtii, the sugar beet cyst nematode (SBCN), is a crucial pest in sugar beet production (Schmidt, 1992). Nematode management involves combinations of crop rotations, host plant resistance, cropping practices, chemical and biological control, all of which may have specific genotype-level interaction with the plant parasitic nematodes (Castagnone-Sereno, 2002; Blok, 2005). Knowledge on the epidemiology and genetic variability of *Heterodera schachtii* populations is important to preserve the durability of resistant sugar beet varieties (Plantard and Porte, 2004). The use of resistant cultivars may change gene frequencies, and consequently reduce the efficacy of the resistance.

The objective of our study was to develop a genetic fingerprinting technique based on variation of the pathogenicity gene *vap1* to investigate the genetic variability among nematode populations of different regional origin. Soil samples were collected from four sugar beet fields in each of four regions in Germany (Peine/Hildesheim, Söllingen, Göttingen, Rheineland). Cyst nematodes were extracted from the soil and reared on *Brassica napus* cv. NK-fair under controlled condition. The propagated cysts were extracted from the soil and ten cysts from every population were taken for DNA extraction by nematode lysis buffer (Holterman et al, 2009). The *vap1* genes were amplified by PCR using a novel primer set. Gene variants occurring in each population were separated by denaturing gradient gel electrophoresis (DGGE). The resulting patterns of bands were compared by using the GelCompar II 6.5 software.

Substantial variation among the samples was detected. However, populations from the same region did not show a consistent pattern, so that significant differences were not observed among regions.
Our plan is to investigate the genetic variability among individual juveniles and cysts of each population to compare the variation within and between populations from distant fields. Moreover, in greenhouse experiments the virulence /aggressiveness of *Heterodera schachtii* populations for different host plants will be determined and related to the observed genetic differences.