Differentiation of field populations of the sugar beet cyst nematode based on a pathogenicity gene

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An improved investigation of intra- and interpopulation genetic variation is required to follow the epidemiology of the important sugar beet cyst nematode *Heterodera schachtii*, and design an effective control management with respect to specific properties of local populations.

The venom allergen like protein gene, *vap1*, is an essential pathogenicity gene of *H. schachtii* which is expressed during the initial period of root penetration and migration. The secreted effector protein interacts with the immune system of the host plant and thus is probably under strong selective pressure, so that the *vap1* gene is expected to exhibit high genetic variation among populations of *H. schachtii*.

In our study we aimed to develop and apply the genetic fingerprinting technique PCR-DGGE to resolve gene variants of *vap1*. From each individual of *H. schachtii* up to six variants of the gene were amplified by PCR which differed in DNA sequence and appeared as separate bands in DGGE. PCR-DGGE profiles from multiple cysts from a field reflected the relative distribution of *vap1* variants in the population. Populations from distant fields significantly differed in *vap1* allele frequencies. Significantly different *vap1* patterns among populations from selected sugar beet regions in Germany were detected. The concomitant differences in aggressiveness towards host plants will be investigated. Conclusions of our results with respect to spread of populations and selection of *vap1* gene variants will be discussed.