

Summary

Population-level genetic tools to study the epidemiology of potato cyst nematodes (PCN) are needed to evaluate their adaptive potential and validate management strategies. The effector gene *vap1* is essential in early infection by PCN. We expected high allelic variation due to diversifying selection. A technique was developed specifically to amplify *vap1* fragments of PCN, and electrophoretically separate variants in a denaturing gradient (DGGE). Sequenced gene variants differed in intron as well as exon regions. Siblings were more similar in *vap1* pattern than juveniles from different cysts. Nearly all juveniles analysed had unique patterns with up to ten or five *vap1* variants for *Globodera pallida* or *G. rostochiensis*, respectively. Patterns differed significantly among populations, with similarities increasing from between-species, within-species to within-pathotype comparisons. In conclusion, the method is suitable to determine the similarity of heterogeneous PCN populations for studies on their temporal change and spread.