

Genotypic variation of *Phytophthora infestans* within and between fields in the Nordic countries

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SUMMARY

In this study, we have investigated the population structure of *Phytophthora infestans* in Denmark, Finland, Norway and Sweden. We tested the hypothesis: (i) Sexual reproduction of *P. infestans* is common in the Nordic countries and (ii) no predominant clonal lineages of *P. infestans* exist in the region.

Isolates of *P. infestans* were collected using stratified sampling with country, field and disease foci as the different sampling strata. The sampling was done in both conventional and organic potato fields during 2008. Only single lesion leaflets, randomly chosen from different plants in different disease foci in each field were collected. The leaflets were dried and later DNA was extracted using a CTAB-based protocol. Seven microsatellite markers were used to determine the genotypic variation in the sampled material.

A stratified sampling approach makes it possible to calculate the level and distribution of genetic/genotypic in the different sampling levels. This will give an indication if and to what extent sexual recombination is contributing to the population structure. It will also enable studies on the spread of the pathogen within and between fields. The results show a high genotypic variation in the Nordic countries since most of the genotypes were found only once and very few clones were found among the collected isolates. The major part of the genotypic variation was observed within the fields, with little differentiation between the fields.

The results strongly suggest that sexual reproduction of *P. infestans* does occur frequently in the Nordic countries and that oospores are an important inoculum source.

KEYWORDS

Phytophthora infestans, SSR, population, oospores

