Introduction

The A2 mating type has now been identified in many parts of Europe and an increase in P. infestans genetic diversity is apparent. Large imbalances in mating type frequency have been observed with the A2 mating type comprising between 50 and <1 percent of the population. Such anomalies are poorly understood but will clearly affect the prevalence of the long-lived population. Such anomalies are poorly understood but will clearly affect the prevalence of the long-lived population. Changes in population structure were monitored over this period and will be examined in the context of existing disease management.

Materials and methods

Isolates were collected in 1996, 1999 and 1997 (Fig. 1). An ideal sample consisted of 3 diseased leaves from each of 5 plants within a focus. Mating type and metalaxyl sensitivity tests were carried out on agar plates and SSR analysis was performed. In most cases multiple isolates were obtained from each outbreak and the population structure was examined (Fig. 3). An ideal sample consisted of 3 diseased leaves from each of 5 plants within a focus. Mating type and metalaxyl sensitivity tests were carried out on agar plates and SSR analysis was performed. In most cases multiple isolates were obtained from each outbreak and the population structure was examined (Fig. 3).

Results

Mating type

As reported previously, the frequency of the A2 type in 1996-97 was 19%. However in 2003 the A2 type was only recovered from one of 39 sites and the frequency was only 2%. In 2004 amongst over 450 isolates from 86 sites only a single A2 isolate was found. This is in contrast to England and Wales were recent evidence suggests an increase in the A2 mating type to over 30% (British Potato Council Right Against Blight. David Cooke and David Shaw (unpublished data). Detailed analysis of SSR data will shed light on whether the A2 genotypes remain present in the population.

SSR genotype diversity and frequency

SSR data from over three sampling periods was examined to consider the combinations of different alleles at all five SSR loci. Each unique combination represents a different P. infestans genotype and the number of genotypes and their frequency over each time period are presented (Fig. 5). Forty seven different genotypes were observed amongst 708 isolates. Five of the six most prevalent genotypes were sampled over all three periods but 37 genotypes were unique to a single sample period. Many combinations were found at a very low frequency typically at only a single sample site.

Conclusions

This study indicates that the frequency of the A2 mating type has declined between 1995-2004. This suggests that the risk of oospores as a source of primary inoculum is also decreasing. The reasons for the decline are, however, not clear and the SSR data indicates that the population remains very diverse. The diversity in each outbreak supports the absence of oospore-borne inoculum but further analysis in the context of Euclablight and BPCFab from GB samples is needed to complete the picture.

Acknowledgements

We thank all those who provided samples and the Scottish Executive Environment and Rural Affairs Department (SEERAD) for funding the project.