

The choice of molecular marker methods for population genetic studies of plant pathogens

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SUMMARY

DNA markers have been used in many studies of fungal plant pathogens, and in particular in investigations of mating systems, gene flow, the establishment of epidemics and adaptation to host crops. Many aspects of population structure can be analysed by means of contingency tables, using χ^2 tests. Some extensions of such tests, with particular applications to plant pathology, are described. One test is applicable to situations where there is more than one level of subdivision of populations, while another is appropriate when there are two types of division, for instance by geographical area and by host crop. Furthermore, the χ^2 test offers a convenient way of combining information from several independent markers. Tests for the differentiation of subpopulations are based on certain underlying assumptions, and it is argued that the primary consideration in choosing a marker system should be whether or not it fits the appropriate genetic criteria. Other considerations, such as time, cost and difficulty, should be evaluated if two or more methods are capable of generating markers which fit the genetic assumptions adequately. Although a large number of markers should be examined in order to estimate the extent of population subdivision, it might only be necessary to use a few markers to test whether such subdivision exists. Likewise, only a few markers may be needed to distinguish clones of a pathogen in a partially sexual population. However, in all of these tests, these markers should be well characterized genetically. It is shown that an existing genetic fingerprinting system for the barley powdery mildew fungus, *Erysiphe graminis* f. sp. *hordei*, is suitable for identifying clones but not for describing the differentiation of subpopulations. It may be possible to use markers based on random amplified polymorphic DNA (RAPD) or on amplified fragment length polymorphism (AFLP) in quantitative research in population genetics of *E. graminis* f. sp. *hordei*.

Key words: Clones, *Erysiphe graminis* f. sp. *hordei* (barley powdery mildew), genetic fingerprinting, molecular markers, population structure.

WHY AND HOW ARE PATHOGEN POPULATIONS STUDIED?

Plants growing in a field or in a natural situation are exposed to several different species of pathogen. Each species exists as a population of many individuals between which there is almost invariably some genetic variation. The fact that plants are exposed to pathogen populations which are genetically diverse is an important consideration in disease control. Individual pathogens vary in their potential range of host species, ability to infect different genotypes of a plant species, adaptation to non-biological factors, such as temperature, and resistance to crop protection chemicals. Each of these factors might affect the course of a disease, whether as an infection of a single plant or as an epidemic in a crop or in a natural population of plants. For example, a pathogen population might evolve to become more virulent or aggressive on a

cultivar or to become resistant to a fungicide. Questions about the origin and maintenance of genetic variation are therefore important when trying to understand how varietal resistance or fungicide applications become less effective in controlling disease. By implications, such an understanding can help in the formulation of strategies for improving disease control (Brown, 1995a).

In the last decade, molecular genetics has had a major impact on population genetics. The range of questions that can be asked about a population, and the precision with which they can be answered, has increased enormously. This is as true for plant pathogens as for other organisms. Before the mid-1980s, the markers which are available for population studies were either morphological or pathological in nature, or were allozymes. The first two kinds required specialized knowledge of the organism in question, whereas the variation in plant pathogens which could be detected with allozymes was gen-