Phytophthora infestans in the Andes: Unraveling the Mysteries

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The late blight pathogen, *Phytophthora infestans* Mont. de Bary, has a global distribution on potatoes and tomatoes, and is believed to have originated in Central Mexico (Goodwin et al, 1992). Elsewhere, populations contain only a subset of the genetic diversity found in Mexico and, until recently, consisted of only one mating type. Since the early 1980s, the A2 compatibility type has been detected in Europe (Hohl and Iselin, 1984), and new genotypes have since appeared in many countries (Drenth, 1994; Fry, 1996; Goodwin, 1997; Shattock and Day, 1996). The development of a variety of molecular markers has greatly helped tracking the movements of the pathogen around the world (Goodwin, 1997). Using these tools, two major migrations were documented (Goodwin, 1997). Several authors (Andrivon, 1996; Brommonschenkel, 1988; Tooley et al. 1989) have suggested the possibility of other migrations from Mexico to South America.

Much of the discussion about the origins and migrations of *P. infestans*, recently reviewed by several authors (Andrivon, 1996; Fry et al. 1993; Goodwin et al. 1993) is based primarily on what is known about isolates from potato. This is largely because late blight is an economically important disease on potatoes in the Temperate Zone, where most of the research on the pathogen has been carried out, and where there appear to be few alternative hosts. *P. infestans* on tomato has also received much attention, but the dynamics of the pathogen population on this host are not clear. Studies have shown that some genotypes of the fungus infect potato and tomato equally (Fry et al 1991; Goodwin et al. 1995; Legard et al. 1995; Brommonschenkel, 1988) suggesting no host specialization or divergence. Other studies, however, indicate clear genetic differentiation of the populations from the two crops (Brommonschenkel, 1988; Goodwin and Fry, 1992; Koh et al. 1994; Lebreton and Andrivon, 1998; Oyarzun et al. 1998.).

Very little attention has been paid to the possible role that other less important crops and wild species play in the dynamics of the host pathogen population. In Central and South America, many alternative hosts exist in the same geographical environment as potatoes. Many non-cultivated species show resistance, but little interest has been taken in the pathogen growing on these plants in the wild. Disease severity was assessed on seven wild hosts in Mexico, but genetic analyses of the pathogen were not carried out (Rivera-Peña, 1990). Matuszak et al., 1994, included some isolates from wild species in a study on metalaxyl resistance in Mexico and found that they showed a similar frequency of resistance and sensitivity to isolates from cultivated species, suggesting that they formed part of the same population. In Ecuador, however, recent isolations from *Solanum brevifolium* and *S. tetrapetalum* have revealed the presence of the A2 mating type (Oyarzun et al. 1998), whereas only the A1 mating type has been found on potato and tomato (Forbes et al.1997; Oyarzun et al.1998). These A2 isolates are very different from all those from potato and tomato which have been reported to date (Forbes et al. 1998). It is not known how or when the A2 compatibility type arrived in Ecuador. Many other Solanaceous plants are also hosts of *P. infestans* in Ecuador, but little is known of the pathogen populations attacking these.

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In this study, we present information from recent studies in which we have begun to characterize these populations genetically and phenotypically. Some preliminary data were presented (Erselius et al 1998). From the extended data we present now, we address a few important questions. What role do these populations play in disease of domesticated crops (and vice versa)? What can we learn about the species in general (historical movements, genetic diversity, host specificity)? What are the consequences for taxonomy of the pathogen?

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