Estimating pathogen migration and population size

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Abstract

Understanding the dynamics of pathogen change is critical in developing long-term, sustainable disease management strategies. Many commonly used control methods, such as race-specific resistance, or fungicides, can fail due to pathogen changes. These changes can take place more easily within large populations, or the pathogen genotypes responsible for these failures can migrate from neighbouring populations. The latter is especially critical in an age where increased travel, coupled with reduced trade barriers, can increase pathogen movement beyond what was common in the past. Thus, better understanding of pathogen migration and the size of the underlying populations will assist in evaluating the longevity of disease control strategies. It is timely that modern tools, based on coalescence theory, have become more usable due to advances in computational ability, and they offer analyses that are more refined compared to what could be previously done. Our studies of *Phytophthora infestans*, the causal agent of potato late blight, have shown that large, sexually reproducing populations of the pathogen have replaced the older, clonal one in the Nordic region Here we show that additional analyses of these data is possible using the program 'migrate-n'. Whereas our previous analyses have shown, at best, one large population, the analyses from migrate-n have permitted estimation of population size and migration between the different Nordic countries. Different models, not necessarily nested, can also be compared using Bayes factors, and this allows testing of specific hypotheses, such as the existence of a single population vs. one that is subdivided. Testing for unidirectional migration is also possible within this framework.