Phylogeographic approaches have been defined as “explicit genealogical inquiries...into spatial and temporal dimensions of microevolution”\(^1\). This interdisciplinary area of study intersects with other fields of study, such as genetics, ecology, evolution, and paleontology. Phylogeography initially was described as a discipline to bridge the work of population geneticists and systematists\(^2,3\). Although first recognized in 1987, the discipline began in the late 1970s when animal mitochondrial DNA and restriction enzymes were used to infer evolutionary relationships of closely related organisms\(^1\). The use of mitochondrial DNA was revolutionary because of desirable qualities such as its rapid evolutionary rate, homoplasy, neutrality, compact nature, and maternal inheritance in animals\(^1,2,4\). As the number and types of genetic markers have expanded with the sequencing of single copy nuclear DNA and, more recently, whole-genome sequencing, opportunities to test phylogeographical hypotheses have increased\(^3,5\). Additionally, the adoption of statistical testing in phylogeography, including maximum likelihood approaches, Bayesian inferences, and various statistics for hypothesis testing, has allowed for quantification of the uncertainty, or error, of conclusions\(^6,7\). Similarly, the development of coalescent theory in the 1980s allowed for a statistical framework and modeling of stochasticity to generate genealogies that reflect random processes like genetic drift\(^4,8\). The combination of these methods allow for objective and efficient testing of phylogeographic hypotheses.

Because phylogeography is interdisciplinary, the methods are used in a wide array of research areas, including linguistics, conservation, and species histories over geological time\(^9,11\). In plant pathology, phylogeography has been used to answer questions regarding origins of plant pathogen introductions, the number of introductions, and epidemiological histories\(^12,14\). However, phylogeographic approaches do have constraints. First, strong phylogeographic methods rely on robust appropriate experimental designs. In plant pathology, this includes adequate sampling of introduced and potential source populations of pathogens\(^8\). This can be difficult when the source of an organism is not known at the time of study, as was the case with *Discula destructiva*\(^15\). Additionally, tools for assigning introduced genotypes to sources are complex due to stochasticity and unknown demographic factors like the number of individuals that are introduced and the probability that the pathogen will establish in an area\(^8\). Simple models sometimes do not capture the complexity of evolutionary history appropriately. Secondly, although microsatellite markers are still the most widely used genetic markers, arguably, the markers generally are not used in phylogenetics. Mutation rates of microsatellites can vary by locus, the evolution of microsatellites is not well understood, and the simple models developed for these markers do not capture the complexity of microsatellites, so their use in phylogenetic reconstructions has been considered dubious by some\(^16-20\). In contrast, single site polymorphisms (SNPs), which can be used in multilocus sequencing of nuclear DNA, can also be modeled in phylogenetic and phylogeographic reconstructions\(^21,22\). As SNPs continue to be used more widely due to lower costs and greater technological advances related to their discovery in non-model organisms compared to other markers, phylogeographic hypotheses can be tested in more species. Despite the constraints of various phylogeographic approaches that have been developed to test hypotheses, phylogeography remains a powerful discipline with tools that can answer a range of questions in a wide array of research areas.

**4:10pm | November 18, 2019 | Johnson 343 | Plant Pathology 515 Fall 2019**
References: