Diversity and Phytophthora: a threat to forests, crops and traditional laboratory research - Mini Review

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Abstract

Genetic sequencing is revealing the tremendous diversity of Phytophthora in fields, forests, nurseries, waterways as well as during asexual growth. The overall diversity and plasticity is impressive and this review highlights recent work and future perspectives concerning genetic diversity and this important genus.

Review

The genus Phytophthora arose amidst intense controversy alongside our modern understanding of microorganisms and disease in the mid-1800 [1]. Even after it was established as a bona fide genus, it was misclassified as a fungus and it took many years to establish the diploid nature of the thallus; an important factor as the genus is illuminated via genetic sequencing. Phytophthora are highly successful terrestrialized aquatic organisms that share an evolutionary ancestry with brown algae and diatoms and this minireview discusses recent advances in understanding of genetic diversity within the genus.

Studying Phytophthora is a challenge. There are very few genetically defined morphological characters, isolates often spontaneously change in culture (more on this below) and valuable genetic techniques (e.g. transformation, in vitro crosses) are notoriously difficult. Lower-cost DNA sequencing is providing an unprecedented view of diversity within the genus; setting the stage to radically change how we categorize, quarantine and investigate these important pathogens. For example, Dr Marco Thines makes a compelling case that the classification of Phytophthora as a genus is erroneous as it contains a polyphyletic assemblage of organisms inclusive of the downy mildews (Peronospora) and to be fixed will require splits into multiple novel monophyletic genera [2].

Species and Species Hybrids

Unambiguous species identification is increasingly important and prior to genetic sequencing, identifying an unknown Phytophthora was deceptively simple as it relied on spore measurements and possibly host preference. Unfortunately, spore shape and production are highly variable and often have little to do with shared ancestry and host preference is often complex. DNA sequencing and molecular phylogeny have proved very helpful to organize many species but are less helpful for closely related species such as Phytophthora andina and Phytophthora infestans [3]. Although gene sequencing is not yet a panacea for species identification, in conjunction with host preference, spore morphology and mating preference, sequencing has catalysed the description of many new species. In addition, sequencing has revealed interspecific hybrids attacking a variety of important hosts; in some cases with host ranges beyond either of the proposed parent species [4]. How the hybrids are formed is a mystery, but clearly, interspecific hybridization provides many new possibilities for Phytophthora and there is much to learn concerning hybrids and their evolution.

Individual Isolates

Phytophthora strains are notoriously unstable. Isolates from diverse species are known to spontaneously change in culture to lose virulence and pathogenicity. Although variability has been reported for individual strains of various Phytophthora species – it is only with the help of molecular tools that the underlying genetic changes are being revealed.

A recent genome project for the vegetable pathogen Phytophthora capsici provides a glimpse of the genomic variation possible during asexual in vitro growth [5]. The genome project produced a high-quality reference genome (available at http://genome.jgi-psf.org/Phyca11/Phyca11.home.html), a dense Single Nucleotide Polymorphism (SNP)-based genetic linkage map, and extensive characterization of large-scale asexual genomic changes known collectively as loss of heterozygosity (LOH). LOH describes a phenomenon where variable length tracts of the diploid nuclear genome convert to one or the other haplotype making the previously heterozygous region homozygous. P. capsici maintains a huge complement of genetic variation in the form of heterozygous SNP sites (≈1 every 200 bp) and more than half of the 20 568 SNP markers placed on the genetic linkage map were impacted by LOH in at least one of the sexual progeny or clonally derived copies of the parent isolates [5]. In total, LOH affected more than 30% of the P. capsici genome and was
associated with a mating type switch (A2 to A1) and loss of pathogenicity [5]. How LOH occurs is not known but recent studies of asexually derived isolates of the taro pathogen *Phytophthora colocasiae*, the potato/tomato pathogen *Phytophthora infestans* and the downy mildew of spinach pathogen *Peronospora farinosa* indicate LOH is common and provides a powerful mechanism for genome reorganization (Kurt Lamour, unpublished data).

**How to Study a Moving Target?**

As species are refined, hybrids discovered and the plasticity of individual strains revealed, it is becoming increasingly clear why *Phytophthora* has been (and will continue to be) a challenge to study. One student aptly described maintaining *Phytophthora* in culture as ‘trying to hold water in your hand’. One strategy we are using to ‘hold it’ is to treat *Phytophthora* as an obligate organism and to study the genetic diversity of *Phytophthora* within the context of the infected plant. This is only recently feasible and we expect genome sequencing and large-scale genotyping to play a prominent role in the future of understanding these fascinating organisms.

**References**


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