



Sclerotinia sclerotiorum populations: clonal or recombining?

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Abstract

Sclerotinia sclerotiorum, a homothallic plant pathogen, undergoes sexual reproduction *via* haploid selfing (equivalent to clonal reproduction), and produces long-lasting surviving vegetative structures called sclerotia, enhancing clonal persistence and spread. Thus it is not surprising to detect clones of the species. Whether outcrossing can occur in the homothallic *S. sclerotiorum* remains unanswered. Early studies showed that *S. sclerotiorum* has a clonal population structure, consistent with its life history traits. However, recent studies using polymorphic and co-dominant molecular markers showed frequent genetic recombination, suggesting outcrossing. This review focuses on recent developments in population genetics studies related to detecting recombination, random association of alleles and dynamic mating type (*MAT*) alleles in *Sclerotinia*. Despite frequent reports of random association of alleles, the mechanisms for outcrossing in a homothallic species remain elusive. Recent intriguing findings are: the *MAT* genes in *Sclerotinia* are subject to inversion or deletion in every meiotic generation, the *MAT* gene deletion is related to ascospore dimorphism and mating type switching in *S. trifoliorum*, and ascospore dimorphism was also observed in *S. sclerotiorum*. Determining the nature of the dimorphic ascospores and their prevalence in relation to environmental cues could significantly advance our understanding how *S. sclerotiorum* populations behave in nature.

Keywords White mold · Genetic recombination · Outcrossing · Ascospore dimorphism · Mating type (*MAT*) alleles

Introduction

Sclerotinia sclerotiorum is a ubiquitous necrotrophic plant pathogen. It causes various diseases generally called white mold or stem rot on more than 400 plant species including many economically important crops (Boland and Hall 1994). Management of *Sclerotinia* diseases is difficult because resistance to *Sclerotinia* is inadequate or unavailable in many crop cultivars (Bolton et al. 2006). The pathogen produces

recalcitrant vegetative surviving structure sclerotia, but no other forms of asexual spores (Bolton et al. 2006). Sclerotia can germinate by means of mycelium or are induced to go through sexual processes by means of self-fertilization to produce apothecia with ascospores. However, its behavior in nature is more complicated than what is expected from laboratory observations, as indicated in many population genetics studies. Because of its microscopic nature and scarcity of observable morphological features, a better understanding of its behavior in nature relies on molecular population genetics studies.

Population genetics, a subdiscipline of genetics, is the study of genetic variation of populations and its change over time and space, and molecular population genetics is the study of genetic variations at molecular level (Casillas and Barbadilla 2017). Studying the changes and differences in genetic variation through mathematical modeling allows inference about the behavior of the populations and prediction of their evolutionary potential (Casillas and Barbadilla 2017). Even though uniform crops in monoculture are ideal environments for pathogen proliferation and disease outbreaks, agricultural practices such as crop rotation, deployment of resistant cultivars, and application of pesticides often impose

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