

EVOLUTION OF MATING TYPE (*MAT*) ALLELES AND GENETIC RECOMBINATION IN *Sclerotinia*

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The genus *Sclerotinia* contains both heterothallic and homothallic species. Examining the mating type (*MAT*) alleles provides an opportunity to study the evolution of mating systems. *MAT* alleles in three *Sclerotinia* species showed that all contain a repeat motif that mediates gene rearrangement. Inverted repeats of a motif previously found in both *S. sclerotiorum* and *S. minor* cause inversion of a part of the *MAT* locus, resulting in two alleles (inversion+ *MAT* and inversion-*MAT*), apparently without affecting their mating behavior (homothallic). Direct repeats of a 146-bp motif in *S. trifoliorum* cause deletion of *MAT1-2* genes, causing directional mating type switching (L allele, homothallic to S allele, heterothallic). Comparison of the *MAT* alleles suggests that an evolution from heterothallism to homothallism in *Sclerotinia* is the most parsimonious route.

Population genetics of *S. sclerotiorum* is the most extensively studied among *Sclerotinia* species. Early studies suggested a clonal genetic structure, consistent with homothallic feature of the species. However, recently more and more studies suggest existence of genetic recombination. Recombination is often inferred by the Index of Association (I_A or r_d) tests after clone correction. A significant I_A value renders rejection of null hypothesis of random mating. The recent introduction of Bayesian STRUCTURE analyses showed that many populations of *S. sclerotiorum* are subdivided. Such information of genetic subdivision was previously ignored in I_A analyses. Incorporating genetic subdivision in I_A tests lowers I_A significance levels, frequently rendering failure to reject the null hypothesis. Additionally, linkage disequilibrium decay was observed among markers located on the same chromosomes. These observations suggest that genetic recombination occurs in *S. sclerotiorum* populations more frequently than previously thought.