

# A VIEW FROM SPACE TO ANALYZE THE GENETIC STRUCTURE OF *Sclerotinia sclerotiorum*

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*Sclerotinia sclerotiorum* is a menace to agricultural crops worldwide not only because of its polyphagous nature but also due to its capacity to thrive well in different environments. The ubiquitous occurrence of white mold in both temperate and tropical climates led researchers to hypothesize that the genetic structure of the pathogen population varies according to climate pattern. Several studies were conducted in the past three decades aiming at investigating variability of *S. sclerotiorum*. Overall, it seems that populations from different parts of the globe have similar genetic structure: clonality seem to predominate, but clonality is not strict and the occurrence of variants within clones is frequently reported. Additionally, there is evidence of outcrossing for some local populations. The mycelial compatibility groups play a role structuring the *S. sclerotiorum* populations. They probably work as distinct evolutionary lineages within which isolates can randomly mate. Apparently, these well adapted lineages persist in the field allowing for recurrent epidemics of white mold. Disease control will remain a major challenge, mainly in areas where many crop cycles of a particular host or alternated cultivation of different susceptible hosts can be conducted year-long and where individuals resistant to fungicides occur in the population.

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