Population Biology

Sclerotinia sclerotiorum Populations Infecting Canola from China and the United States Are Genetically and Phenotypically Distinct

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Accepted for publication 25 February 2013.

ABSTRACT

Attanayake, R. N., Carter, P. A., Jiang, D., del Río-Mendoza, L., and Chen, W. 2013. *Sclerotinia sclerotiorum* populations infecting canola from China and the United States are genetically and phenotypically distinct. Phytopathology 103:750-761.

Genetic and phenotypic diversity and population differentiation of Sclerotinia sclerotiorum isolates infecting canola from China and the United States were investigated. Genetic diversity was assessed with eight microsatellite markers and mycelial compatibility groups (MCGs). Phenotypic diversity was assessed with sensitivity to three fungicides, production of oxalate and sclerotia, growth rate, and virulence on two canola cultivars. No shared MCGs or multilocus haplotypes were detected between the two populations, and populations differed significantly (P < 0.001). Recombination was detected in both populations but was greater in the Chinese population. A polymerase chain reaction detection assay showed that ~60% of the isolates were inversion-plus at the mating type locus. The two populations differed significantly (P < 0.05) for all of the phenotypic traits except for sensitivity to fungicide fluazinam and virulence. Isolates in the Chinese population were unique in several aspects. Despite the phenotypic differentiation, heritabilities of the phenotypic traits were similar for both populations. Significant correlations were found among five phenotypic traits. Cross resistance to benomyl and iprodione was detected. Virulence was not significantly correlated with any other phenotypic trait and had the least heritability. However, both populations were equally virulent on either a susceptible or a moderately resistant canola cultivars.