Genetic diversity and pathogenicity differentiation of *Sclerotinia sclerotiorum* on rapeseed (*Brassica napus L.*) in Anhui Province, China

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**ABSTRACT.** The pathogenicity of 47 isolates of *Sclerotinia sclerotiorum* from oilseed rape (*Brassica napus L.*) in Anhui, China, was tested by detached leaf inoculation using the susceptible rape cultivar Wanyou-14. All isolates were pathogenic to the cultivar and could be grouped into 3 categories based on the lesion length on the leaves tested: weak pathogenicity type, intermediate pathogenicity type, and strong pathogenicity type. This suggested that there was differentiation in the pathogenicity among the strains tested of *S. sclerotiorum*. Additionally, the intraspecific DNA polymorphisms among 47 strains of *S. sclerotiorum* were investigated by screening 40 pairs of inter-simple sequence repeat (ISSR) primers. Unweighted pair-group method with arithmetic average cluster analysis of these ISSR data distinguished all strains from each other and revealed considerable genetic variability among them. These strains were classified into 7 clusters according to their branching in the dendrogram, and partial
correlation was observed between the genetic polymorphisms and the pathogenicity of \textit{S. sclerotiorum} strains.

\textbf{Key words:} \textit{Sclerotinia sclerotiorum}; Oilseed rape; Pathogenicity; Inter-simple sequence repeat (ISSR); Genetic diversity