



## Genetic diversity of *Phytophthora capsici* (Pythiaceae) isolates in Anhui Province of China based on ISSR-PCR markers

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**ABSTRACT.** *Phytophthora capsici* is a plant pathogenic oomycete that damages numerous crops worldwide. Consequently, interest in research on the genetic structure of this species has grown in recent decades. However, there is little information about *P. capsici* in eastern China. We investigated the genetic diversity of *P. capsici* isolates from three large regions of Anhui Province in eastern China based on ISSR-PCR technology. Thirteen random primers were screened and used to amplify DNA from 51 samples. We obtained 158 reproducible ISSR fragments, of which 90% were polymorphic, revealing a high degree of polymorphism among the isolates. Genetic similarity coefficients among all the isolates ranged from 0.56 to 0.94, with a mean of 0.84 based on the ISSR data, indicating a high level of genetic variation in these *P. capsici* isolates. Cluster analysis using UPGMA indicated that the Anhui isolates were divided into seven groups according to the DNA fingerprints, although there was no correlation between the ISSR group and geographic origin. Isolates from the same location showed no clustering based on the year of sampling. AMOVA partitioned variability among (13.6%) and within populations (86.4%). The gene flow among populations ranged from 2.804 to 4.937, with a mean of 3.545, indicating highly frequent gene exchange. Genetic distances

and genetic differentiation were negatively correlated with geographic distances. These results lead us to suggest that this pathogen has considerable evolutionary potential, which will enable it to adapt to and overcome management strategies over time.

**Key words:** *Phytophthora capsici*; Genetic diversity; ISSR-PCR; Anhui