Genetic diversity of 45 C. capsici isolates in Thailand was studied based on colony growth rate, surface mycelium, colony color, mass conidial color, conidial and appressoria size in relation to three different levels of location including within farm, within districts in western area, and within Thailand. Cluster analysis based on colony growth rate, surface mycelium, colony colors, and mass conidial colors divided the 45 isolates into 16 groups. However when the data was combined with conidia and appressoria data, the isolates were not be able to group indicating a large genetic diversity based on variation of conidia and appressoria size. Based on the clusters of the isolates, there was no correlation to geographic location.

Eleven isolates of C. capsici were inoculated on nine chilli genotypes derived from four cultivated species of Capsicum: C. annuum, C. baccatum, C. chinense and C. frutescens using microinjection on red fruit, the host reaction was assessed nine days after inoculation. A set of disease scales were developed based on % lesion size in relation to fruit size; and assigned disease scores from 0 to 9. Three pathotypes, PCC1, PCC2 and PCC3 were identified according to differential qualitative infection of the fruit of the C. chinense genotypes ‘PBC932’ and ‘C04714’. PCC1 was the most virulent pathotype that infected all genotypes whereas; PCC3 was the least virulent pathotype that infected only the genotypes of C. annuum and C. frutescens. Quantitative infection occurred in all chilli genotypes except for genotypes of C. baccatum where no infection occurred, thus demonstrating various levels of aggressiveness of isolates within pathotypes.