

ABSTRACT

Genetic variability within a population has a direct impact on the virulence because a highly variable gene pool allows them to adapt more quickly to environmental change and so increases their potential to produce new virulent variants. The purpose of this study is to identify the *Phytophthora* related to heart rot in pineapple as well as understand the genetic diversity. In total, 109 isolates were collected and molecular identification results showed that 98 isolates were identified as *Phytophthora nicotianae*, 4 isolates were identified as *Py. perillium*, 1 isolate of *Py. splendens*, 2 isolates of *Py. acantophoron*, 1 isolate of *Py. sp. Cal 2011*, 1 isolate of *Py. catenulatum*, and 1 isolate of *Py. myriotylum*. To understand the population genetics, nine simple sequence repeat (SSR) markers were used to obtain the genetic diversity data from 98 isolates of six populations. The data then analyzed using POPPR package in R environment. The phylogenetic tree constructed by MEGA revealed three major clades; the first and second clades were dominated by the isolates from pineapple plantation sites, and the third clade contained isolates from the non-pineapple sites. The allelic pattern analysis using Genalex software revealed the local alleles specific to Lampung and Blitar populations. The AMOVA of microsatellite genotypes data showed that the isolates had a low diversity among the population (6%) but high diversity within individual. This study also revealed that there was gene flow between the Central Lampung *P. nicotianae* population and Blitar population.

Key words: genetic variation, microsatellite, *Phytophthora nicotianae*, population structure