Characterization of Fusarium proliferatum and Fusarium verticillioides based on species-specific gene and microsatellites analysis

ABSTRACT

Fusarium species are known to cause various diseases on plantations including fruits and vegetables. The most common Fusarium that can cause plant diseases are Fusarium proliferatum and Fusarium verticillioides. Ear rot disease on maize, wilt disease on cucurbits and fruit rot disease on tomato as well as banana are example of diseases caused by these two species. The objectives of this study were to identify F. proliferatum and F. verticillioides based on species-specific primers and polymerase chain reaction (PCR) amplification and to evaluate the genetic diversity of both species based on microsatellite markers. Fifty isolates of Fusarium species that were previously collected throughout Malaysia from different hosts were identified by using species-specific PCR amplification. Twenty-nine isolates were identified as F. proliferatum and 21 isolates were identified as F. verticillioides based on species-specific primer. The genetic diversity of all the fungal isolates was evaluated by using microsatellite analysis with six established primers. Five out of six primers amplified polymorphic bands with the most effective primer showing high polymorphism were (AG)7C and (TCC)5 meanwhile one primer (TTTC)4 gave negative result with no band amplified. The phylogenetic tree that was constructed showing two different clades distinguished between F. proliferatum and F. verticillioides.

Keyword: Fusarium proliferatum; Fusarium verticillioides; Microsatellite; Species-specific gene