

Current classification and diversity of Fusarium species complex, the causal pathogen of Fusarium wilt disease of banana in Malaysia

The re-emergence of the Fusarium wilt caused by *Fusarium odoratissimum* (*F. odoratissimum*) causes global banana production loss. Thirty-eight isolates of *Fusarium* species (*Fusarium* spp.) were examined for morphological characteristics on different media, showing the typical *Fusarium* spp. The phylogenetic trees of *Fusarium* isolates were generated using the sequences of histone gene (H3) and translation elongation factor gene (TEF-1 α). Specific primers were used to confirm the presence of *F. odoratissimum*. The phylogenetic trees showed the rich diversity of the genus *Fusarium* related to Fusarium wilt, which consists of *F. odoratissimum*, *Fusarium grosnichelii*, *Fusarium sacchari*, and an unknown species of the *Fusarium oxysporum* species complex. By using Foc-TR4 specific primers, 27 isolates were confirmed as *F. odoratissimum*. A pathogenicity test was conducted for 30 days on five different local cultivars including, *Musa acuminata* (AAA, AA) and *Musa paradisiaca* (AAB, ABB). Although foliar symptoms showed different severity of those disease progression, vascular symptoms of the inoculated plantlet showed that infection was uniformly severe. Therefore, it can be concluded that the *Fusarium oxysporum* species complex related to Fusarium wilt of banana in Malaysia is rich in diversity, and *F. odoratissimum* has pathogenicity to local banana cultivars in Malaysia regardless of the genotype of the banana plants.

Keyword: *Fusarium oxysporum*; *Fusarium odoratissimum*; Banana; Molecular characterization