

### **INTISARI**

*Penyakit pasca panen yang disebabkan oleh *Colletotrichum* spp. menyebabkan kerugian besar. Spesies *Colletotrichum* sulit dibedakan jika hanya dilihat dari morfologinya. Penelitian ini mengkaji isolat *Colletotrichum* yang berasosiasi dengan antraknosa buah tropis menggunakan analisis multi-genetik dan potensi infeksi silang masing-masing isolat antar buah tropis. Sampel buah apel, alpukat, jeruk, pisang, mangga, pepaya, dan jambu biji dikumpulkan dari pasar di Daerah Istimewa Yogyakarta dan sekitarnya. Buah yang terkena antraknosa diisolasi sehingga menghasilkan 15 isolat. Morfologi koloni dan konidia kemudian dikarakterisasi dan dikelompokkan dengan UPGMA. Tujuh isolat perwakilan dipilih untuk identifikasi molekuler. Analisis multi-genetik dilakukan dengan menggabungkan sekuens ITS, gapdh dan tub2. Hasil analisis multi genetik mengelompokkan isolat terpilih menjadi empat spesies. Isolat dari pisang, alpukat, pepaya dan jeruk termasuk dalam kompleks spesies *gloeosporioides*, antara lain *C. siamense*, *C. asianum*, dan *C. gloeosporioides*. Isolat dari apel, jambu biji, mangga dan jeruk termasuk dalam spesies kompleks *acutatum*, yaitu *C. sloanei*. Uji potensi infeksi silang menunjukkan keragaman luas dalam patogenisitas isolat. Uji infeksi silang pada penelitian ini menunjukkan bahwa *C. siamense* dapat menyebabkan antraknosa pada pisang, apel, jeruk dan alpukat, *C. asianum* dapat menyebabkan antraknosa pada alpukat, pepaya dan jeruk, *C. gloeosporioides* dapat menyebabkan antraknosa pada jeruk dan apel, *C. sloanei* dapat menyebabkan antraknosa pada apel, jambu biji, jeruk dan pepaya.*

*Kata kunci: Antraknosa buah tropis, *Colletotrichum* spp., Infeksi silang, analisis multi- genetik.*

## ABSTRACT

Postharvest disease caused by *Colletotrichum* spp. caused major losses. The species of *Colletotrichum* are difficult to distinguish if only seen from their morphology. This study investigated *Colletotrichum* isolates associated with tropical fruits anthracnose using multi-genetic analysis and the cross infection potency of each isolates among tropical fruits. The fruit samples of apple, avocado, citrus, banana, mango, papaya, and guava were collected from the market in Special Region of Yogyakarta, and its surrounding area. The fruits affected by anthracnose subjected to isolation, resulting in 15 isolates. Morphology of colony and conidia then characterized and clustered with UPGMA. The seven representative isolates were selected for molecular identification. Multi-genetic analysis was used by combining ITS, gapdh and tub2 sequence genes. The results of multi-genetic analysis clustered the selected isolates into four species. Isolates from banana, avocado, papaya and citrus belonged to gloeosporioides species complex, including *C. siamense*, *C. asianum* and *C. gloeosporioides*. Isolates from apple, guava, mango and citrus belonged to acutatum species complex, including *C. sloanei*. The potency of cross-infection test revealed the board diversity in pathogenicity of the isolates. Cross-infection test in this study showed that *C. siamense* could cause anthracnose on banana, apple, citrus and avocado, *C. asianum* could cause anthracnose on avocado, papaya and citrus, *C. gloeosporioides* could cause anthracnose on citrus and apple, *C. sloanei* could cause anthracnose on apple, guava, citrus and papaya.

Keywords: Tropical fruits anthracnose, *Colletotrichum* spp., cross-infection, multi-genetic analysis.