Colletotrichum: host specificity and pathogenicity on selected tropical and subtropical crops

S. Freeman, S. Horowitz-Brown, L. Afanador-Kafuri, M. Maymon, D. Minz

Acta Horticulturae 975: 209-216: 2013.

Abstract

Colletotrichum and its teleomorph Glomerella are considered major fungal plant pathogens worldwide. They cause significant economic damage to fruit crops in tropical, subtropical and temperate regions. Several Colletotrichum species or biotypes are known to cause disease in a single host such as C. acutatum and C. gloeosporioides on apple, avocado, mango, papaya, passiflora, strawberry and tamarillo. It is also common to find a single species infecting multiple hosts such as C. gloeosporioides on apple, avocado, mango, papaya, peach, strawberry, and other hosts. Cross-infection potential was shown for two species, C. gloeosporioides from limonium and C. acutatum from strawberry, when inoculating peach, pear, mango, nectarine and strawberry. Molecular analyses including species-specific PCR amplification and ITS sequencing was reliable for identification of Colletotrichum isolates infecting apple, avocado, mango, papaya, passiflora, peach, strawberry and tamarillo fruits. Sub¬populations within C. acutatum, C. gloeosporioides and C. boninense were characterized using ITS sequence analysis, while the latter appears to be a diverse and emerging new species infecting multiple fruit crops.