

**Title** *Colletotrichum*: Host specificity and pathogenicity on selected tropical and subtropical crops  
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#### **Abstract**

*Colletotrichum* and its teleomorph *Glomerella* are considered as a 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 almond, avocado, citrus, mango, papaya, passiflora, strawberry and tamarillo. It is also common to find a single species infecting multiple hosts such as *C. gloeosporioides* on avocado, strawberry, apple, peach, papaya and other hosts. The ability to cause latent or quiescent infections has grouped *Colletotrichum* as one of the most important post-harvest pathogens. Identification of *Colletotrichum* species responsible for disease is vital for implementing effective control strategies and for breeding for resistance. Traditional methods based on morphology, vegetative compatibility, and various molecular techniques, are used for identifying *Colletotrichum* populations on various hosts cultivated in close proximity. Crossinfection potential was evident between two species, *C. gloeosporioides* from almond (Israel), apple (USA), avocado (Israel) and mango (Israel), and *C. acutatum* from anemone (Israel, Australia), apple (USA), peach (USA) and strawberry (Israel), on a variety of hosts in artificial inoculations. Molecular analyses, including ITS sequencing is reliable for taxonomic identification of *Colletotrichum* taxa, whereas repetitive DNA elements, A+ T-rich DNA and apPCR are used for determining subpopulation diversity within species. Subpopulations within *C. acutatum* and *C. gloeosporioides* have been characterized, however, their taxonomic status is unclear. *C. boninense* has recently been identified as a diverse new species infecting multiple fruit crops.