

Pathogenicity for onion and genetic diversity of isolates of the pathogenic fungus *Colletotrichum gloeosporioides* (Phyllachoraceae) from the State of Pernambuco, Brazil

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ABSTRACT. Onion anthracnose, caused by *Colletotrichum gloeosporioides*, is one of the main diseases of onions in the State of Pernambuco. We examined the pathogenicity of 15 *C. gloeosporioides* strains and analyzed their genetic variability using RAPDs and internal transcribed spacers (ITS) of the rDNA region. Ten of the strains were obtained from substrates and hosts other than onion, including chayote (*Sechium edule*), guava (*Psidium guajava*), pomegranate (*Punica granatum*), water from the Capibaribe River, maracock (*Passiflora* sp), coconut (*Cocos nucifera*), surinam cherry (*Eugenia uniflora*), and marine soil; five isolates came from onions collected from four different regions of the State of Pernambuco and one region of the State of Amazonas. Pathogenicity tests were carried out using onion leaves and bulbs. All strains were capable of causing disease in leaves,

causing a variable degree of lesions on the leaves; four strains caused the most severe damage. In the onion bulb tests, only three of the above strains caused lesions. Seven primers of arbitrary sequences were used in the RAPD analysis, generating polymorphic bands that allowed the separation of the strains into three distinct groups. The amplification products generated with the primers ITS1 and ITS4 also showed polymorphism when digested with three restriction enzymes, *DraI*, *HaeIII* and *MspI*. Only the latter two demonstrated genetic variations among the strains. These two types of molecular markers were able to differentiate the strain from the State of Amazonas from those of the State of Pernambuco. However, there was no relationship between groups of strains, based on molecular markers, and degree of pathogenicity for onion leaves and bulbs.

Key words: *Allium cepa*; Anthracnose; Molecular markers