

Vegetative compatibility and genetic analysis of *Colletotrichum lindemuthianum* isolates from Brazil

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ABSTRACT. The causal agent of common bean anthracnose, *Colletotrichum lindemuthianum*, has considerable genetic and pathogenic variability, which makes the development of resistant cultivars difficult. We examined variability within and between Brazilian pathotypes of *C. lindemuthianum* through the identification of vegetative compatibility groups (VCGs) and by RAPD analysis. Two hundred and ninety-five *nit* mutants were obtained from 47 isolates of various pathotypes of the fungus collected from different regions, host cultivars and years. In complementation tests, 45 VCGs were identified. Eighteen RAPD primers were employed in the molecular analyses, producing 111 polymorphic bands. Estimates of genetic similarities, determined from the Sorence-Dice coefficient, ranged from 0.42 to 0.97; the dendrogram obtained by cluster analysis revealed 18 groups of isolates.

RAPD and VCG markers presented high genotypic diversity. The number of significant associations ($P = 0.05$) between RAPD, VCG and pathogenicity markers ranged from 0 (VCG) to 80% (pathogenicity). The test of multilocus association (r_d) for RAPD markers was significantly different from zero ($P < 0.001$), suggesting linkage disequilibrium. However, the results for VCG markers show the presence of recombination mechanisms. In conclusion, RAPD markers and VCGs were useful for detecting genetic variability among isolates of *C. lindemuthianum*. We found considerable diversity among isolates from the same geographic origin within a short interval; this suggests rapid evolution. There is a need for further studies to elucidate the population structure of this pathogen in agro-ecosystems.

Key words: Anthracnose; Common bean; RAPD analysis; Vegetative compatibility group; *nit* mutants