

Summary

Pathogenic variability of 183 isolates of *Colletotrichum gloeosporioides* isolated from forage *Arachis pintoi* was determined on four CIAT accessions of *A. pintoi* (17434, 18744, 18748, 22160) and the original accession from which each of the isolates was obtained. These isolates were collected from four locations in Colombia: Carimagua, Caquetá, Palmira, and Popayán.

Pathogenic specialization was observed for the first time indicating the presence of physiologic races among these isolates on accessions of *A. pintoi*. The genetic diversity of 91 of these isolates was measured by random amplified polymorphic DNA (RAPD) restriction fragment length polymorphism (RFLP) analysis.

Results showed that there were at least five lineages of *C. gloeosporioides* among the isolates studied.

Detailed analysis of molecular data indicates that some isolates of the pathogen had probably been introduced from one location to another through vegetative materials. Caquetá area had the highest diversity of *C. gloeosporioides* isolates infecting this forage legume. Some isolates of *C. gloeosporioides* isolated from infected *A. pintoi* are also pathogenic to *S. guianensis*, and some which originated from accessions of *S. guianensis* can infect *A. pintoi*.