

## ABSTRACT

### **Genetic and pathogenic variation of *Colletotrichum gloeosporioides* Penz., causing yam anthracnose in Dominica**

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A study utilizing up to 50 isolates of the yam anthracnose pathogen *Colletotrichum gloeosporioides* obtained from 11 yam varieties grown on 8 farms distributed across the agro-ecological zones of Dominica, was designed to investigate pathogenic and genetic variation in the pathogen population. The variation was based on measurements of genetic relatedness, pathotoxin activity evidenced by foliar necrosis and pathogen aggressiveness indexed by time to appearance of visible symptoms, leaf area damage and lesion number per unit area.

The pathogen aggressiveness studies differentiated the *C. gloeosporioides* population into several groups and the numbers and isolate composition varied with the yam varieties tested and the method used to assess pathogen aggressiveness. The number of groups identified when screening on individual yam types were 3 to 5 for the appearance of visible symptoms and 2 to 3 each for methods assessing leaf area damage and lesion number per unit area. When the data was analyzed as a means of all yam types, 3 groups were obtained for the method of time to appearance of visible symptoms and 2 for leaf area damage.

Notably, *C. gloeosporioides* isolates which induced visible symptoms fastest and caused the largest leaf area damage segregated together.

Utilizing random amplified polymorphic DNA's, the study on genetic relatedness delineated the pathogen population into 8 groups. Each group was associated only with the farm from which the isolates were obtained.

The pathogen toxins extracted from fungal exudates of 4 pathogen isolates tested were glycoproteins with sizes ranging between 14 to 25kDa. Toxin activity also varied with the fungal origin of the toxin. Toxins of isolates from *D. cayenensis/rotundata* was the only toxin that affected all *D. alata* yams assessed.

The pathogen aggressiveness study also segregated the yam varieties tested into 3 groups, which were assumed to reflect levels of resistance to anthracnose.

**Keywords:** anthracnose, *Colletotrichum gloeosporioides*, *Dioscorea* species, pathogen aggressiveness, toxin activity, DNA polymorphism.