

Genetic Diversity Among Isolates of *Colletotrichum kahawae* Causing Coffee Berry Disease

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ABSTRACT

Monoconidial isolates of *Colletotrichum kahawae* Wailer and Bridge sp. nov (1993), the causal agent of Coffee Berry Disease (CBD) were subjected to genetic analysis using pathogenicity tests, protein, isozyme and Random Amplified Polymorphic DNA (RAPD) markers. Two non-pathogenic species *C. acutatum* and *C. gloeosporioides* commonly found colonising the coffee plant were included in the analysis for comparison. Pathogenicity analysis revealed significant variations ($P = 0.01$) among isolates for aggressiveness (main effects) and virulence (interaction effects).

Buffer soluble proteins, separated on a 10% polyacrylamide gel and stained with silver nitrate not only revealed genetic differences between pathogenic and non-pathogenic species (for proteins with molecular weights of 57 KD and 127 KD) but also among the pathogenic isolates (for proteins of 111 KD). A total of 13 enzyme systems were also assayed and 21 loci were resolved. All enzymes systems distinguished *C. kahawae* from *C. acutatum* and *C. gloeosporioides* but were all monomorphic with respect to *C. kahawae* isolates except esterase. Of special interest was the observation that isolates obtained from resistant host variety Ruiru 11 had the EST 1 locus in a homo- or heterozygous state while isolates obtained from susceptible host varieties such as SL 28 and St 34 lacked the locus. Benomyl resistant strains produced an overlapping presence of the EST 1 locus although they were obtained from susceptible hosts. Polymorphism was further detected between the pathogenic and non-pathogenic species by all the 48 decamer oligonucleotide primers screened for RAPD markers. However, among the pathogenic *C. kahawae* isolates, only 3 primers detected polymorphism.