

**Title: Characterization of the Genetic Diversity and Pathogenicity of Colletotrichum Kahawae using Random Amplified Polymorphic Dna(Rapd)Analysis**

**Author: Owaka, Margaret**

Coffee is a small shrub which is a source of a stimulating beverage. It ranks as one of the world's major commodity crops and is the major export product of many countries including Kenya. Economic production of Arabica coffee in Kenya is greatly hindered by the Coffee Berry Disease (CBD) caused by *Colletotrichum kahawae*. Since the release of the resistant Ruiru 11 in 1985, efforts have been devoted to the improvement of the genetic base of resistance, but this has, faced the problem of possible pathogen variation. A good understanding of CBD pathogen diversity could lead to the development of cultivars with sufficient disease resistance. This study was aimed at determining the genetic and virulence diversity of *Colletotrichum kahawae*; and their correlation with coffee growing regions and interaction with coffee varieties. Infected berries were obtained from three coffee growing regions in Kenya (Western, Central and Eastern regions). Arabica varieties in these regions include SL 28, SL 34, K7, and the resistant Ruiru 11. At each location, diseased berries were randomly sampled from susceptible and resistant plants in marginal and upper coffee zones. In locations where both resistant and susceptible varieties were grown, a larger proportion of the berries were obtained from the resistant varieties to increase the chances of obtaining different pathotypes. A total of

**Abstract:** 34 single conidia isolates were obtained and subjected to variation analysis using DNA banding patterns. The RAPD analysis revealed 5 distinct groups of isolates of which one representative isolate was selected and used to inoculate coffee differentials with known resistance / susceptible reactions. The varieties included Rume Sudan, Catimor, K7 and SL 28 (susceptible). Seedlings were individually scored for disease symptoms developed and mean grade of infection computed. The mean grade data was then used to perform Analysis of Variance (ANOVA) using the random effects model. The results were used to determine the correlation between molecular polymorphism and diversity in virulence. The variety x isolate interaction effects although significant ( $p < 0.05$ ) did not conclusively reveal the existence of races because the isolate effect was not significant. The Tukey tests revealed that variation was due to main effects of varieties. Rume Sudan was highly resistant with a mean grade of 4.75. The variety is known to carry two resistant genes on R- and k- loci. Catimor (mean grade = 7.66) showed medium resistance. It is also known to carry resistant genes on the dominant T- locus. K-7, with recessive gene on k- locus, showed medium resistance with a mean grade of 9.97. SL 28, with no known resistant genes was highly susceptible with a mean grade of 11.75. The growing regions had no influence on the genetic and virulence diversity since *C. kahawae* isolates from all regions were pathogenic on the coffee cultivars tested. All the isolates were significantly ( $p < 0.05$ ) more aggressive on coffee cultivar SL28, followed by K7 and Catimor in that order. Rume Sudan showed high resistance to all the isolates tested

irrespective of the region. It is concluded that variation in *Colletotrichum kahawae* population is largely due to differences in aggressiveness of the isolates. There is no conclusive evidence of the existence of races. More biochemical and molecular markers for Pathogenisity should be screened on large sample of isolates across coffee growing regions using large number of primers.