

## **Abstract:**

Eighty nine *Exserohilum turcicum* isolates comprising 56 Kenyan, 26 German and 7 Austrian isolates were isolated from diseased maize plants and cultured on complete liquid medium to generate mycelium for DNA extraction. DNA extraction was done following the CTAB method, DNA purified using spermidin and fingerprinting conducted using Amplified fragment length polymorphism (AFLP) procedure. NTSYSpc, pop gene and Arlequin programs were used to analyze the data and to generate the dendograms. The number of amplified bands and polymorphism varied with the different primer combinations with primer combinations E-ACAfT -CCA, E-ACAfT -CAC, E-ACAfT -CGA, E-ACAfT -CTA revealing a high (79%) level of polymorphism. Cluster analysis of the 607 polymorphic bands from these primer combinations using UPGMA algorithms generated dendograms with 7 main AFLP groups with isolates from different localities grouping together with only two outliers. Pair wise similarity matrix derived with SIMQUAL program showed a wide variation in the AFLP fingerprint of the *E. turcicum* isolates. Nei's genetic distance matrix showed that the three populations of *E. turcicum* isolates differed genotypically with the Kenyan isolates being more genetically related to Austrian isolates (genetic identity of 0.9998) whereas the isolates from Germany and Austria were more diverse (genetic identity of 0.9978). This study showed that AFLP marker is useful in the study of genetic variation of *E. turcicum* and the pathogen has a high level of genetic diversity.