Genetic relatedness among twenty six Fusarium species isolated from soils in six different Land Use Types (LUTs) across a land use gradient was evaluated using Random Amplified Polymorphic DNA (RAPD) assay. The six LUTs were horticulture, maize, napier grass, fallow/shrub land, planted forests as well as indigenous forests. Six primers were used in this assay. Amplification products were examined and presence or absence of each size class of bands was scored as 1 and 0, respectively. The resulting matrix was used to compute Jaccard’s similarity coefficients and Unweighted Pair Group Method with Arithmetric mean (UPGMA) cluster analysis using computer package NTSYS-pc. Jaccard’s similarity coefficients ranged from 0.257 to 0.583 among the Fusarium species studied indicating high genetic diversity. The UPGMA cluster analysis grouped the 26 Fusarium species into two main clusters with the first cluster comprising of 17 species with genetic similarity values ranging from 26.2 to 58.3 %. The second cluster comprised of 9 species with genetic similarity values ranging from 29.5 to 56.34 %. Fusarium avenaceum and F. nygamai depicted the highest