RAPD analysis of genotypic groups of Trypanosoma congolense and other African trypanosome species

Abstract:

Oligonucleotide primers of arbitrary nucleotide sequences were used in PCR reaction to amplify genomic DNA from the four types of T. congolense: Tsavo-type, Savannah-type, Kilifi-type and West African riverine/ forest-type. Several primers produced significantly different RAPD patterns for the four types of T. congolense. Similarity indices imply that the Kilifi-type and Savannahtype T. congolense (SI; 0.453) are the most closely related evolutionarily among T. congolense whereas the West African riverine/forest-type and Savannah type T. congolense (SI; 0.405) are the most distantly related. RAPD patterns of the four types of T. congolense were also compared with those of other trypanosome species. Similarity indices of this comparison implies that T. evansi and T.b. gambiense (SI; 0.667) are the most closely related whereas Kilifi-type T. congolense and T. b. brucei (SI; 0.315) are the most distantly related. The results further indicate that the T. congolense genotypic groups may be as different as they are from any other trypanosome species studied in this work.