

Linkage disequilibrium between alleles at highly polymorphic mini- and micro-satellite loci of *Theileria parva* isolated from cattle in three regions of Kenya.

Abstract

Theileria parva schizont-infected lymphocyte culture isolates from western, central and coastal Kenya were analysed for size polymorphism at 30 *T. parva*-specific variable number tandem repeat (VNTR) loci using a panel of mini- and micro-satellite markers. The mean number of alleles ranged from 3 to 11 at individual loci and 183 distinct alleles were observed in total, indicating high genetic diversity within the *T. parva* gene pool in Kenyan cattle. The frequency distribution of the length variation of specific alleles among isolates ranged from normal to markedly discontinuous. Genetic relationships between isolates were analysed using standard indices of genetic distance. Genetic distances and dendrograms derived from these using neighbour-joining algorithms did not indicate significant clustering on a geographical basis. Analysis of molecular variance demonstrated that the genetic variation between individual isolates was 72%, but only 2.3% when isolates from different regions were pooled. Both these observations suggest minimal genetic sub-structuring relative to geographical origin. Linkage disequilibrium was observed between pairs of loci within populations, as in certain Ugandan *T. parva* populations. A novel observation was that disequilibrium was also detected between alleles at three individual pairs of VNTR loci when isolates from the three regional meta-populations were pooled for analysis.