Micro- and minisatellite-expressed sequence tag (EST) markers discriminate between populations of *Rhipicephalus appendiculatus*.

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**A B S T R A C T**

Biological differences, including vector competence for the protozoan parasite *Theileria parva* have been reported among populations of *Rhipicephalus appendiculatus* (Acari: Ixodidae) from different geographic regions. However, the genetic diversity and population structure of this important tick vector remain unknown due to the absence of appropriate genetic markers. Here, we describe the development and evaluation of a panel of EST micro- and minisatellite markers to characterize the genetic diversity within and between populations of *R. appendiculatus* and other rhipicephaline species. Sixty-six micro- and minisatellite markers were identified through analysis of the *R. appendiculatus* Gene Index (RagI) EST database and selected bacterial artificial chromosome (BAC) sequences. These were used to genotype 979 individual ticks from 10 field populations, 10 laboratory-bred stocks, and 5 additional *Rhipicephalus* species. Twenty-nine markers were polymorphic and therefore informative for genetic studies while 6 were monomorphic. Primers designed from the remaining 31 loci did not reliably generate amplicons. The 29 polymorphic markers discriminated populations of *R. appendiculatus* and also 4 other *Rhipicephalus* species, but not *R. zambeziensis*. The percentage Principal Component Analysis (PCA) implemented using Multiple Co-inertia Analysis (MCaA) clustered populations of *R. appendiculatus* into 2 groups. Individual markers however differed in their ability to generate the reference typing using the MCaA approach. This indicates that different panels of markers may be required for different applications. The 29 informative polymorphic micro- and minisatellite markers are the first available tools for the analysis of the phylogeography and population genetics of *R. appendiculatus*.

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