

# Spatial genetic homogenization of the only clade of the tick *Rhipicephalus microplus* in the Neotropics.

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## Abstract

This study addresses the variability of the mitochondrial cytochrome oxidase subunit I (COI) and 16S rDNA (16S), and nuclear internal transcriber spacer ITS2 (ITS2) genes in a set of purposely collected samples of the cattle tick, *Rhipicephalus microplus* (Canestrini, 1888) introduced in the Nearctic-Neotropical range (Mexico to Argentina), and in geo-referenced sequences from GenBank. The main aims of the study are (i) to provide evidence of the phylogeny of the tick in the region, as consequence of a single or several introductions, (b) to explore a possible impact of environmental traits, and (c) to check for the effect of geographical distance on genetic variability. We included published sequences of *Rhipicephalus annulatus* (Nearctic, Afrotropical and Mediterranean), *R. microplus* (Afrotropical, Asia), to fully characterize the Neotropical populations (total: 74 16S, 44 COI, and 49 ITS-2 sequences included in the analysis). Only clade A of *R. microplus* spread in the Nearctic-Neotropics. The K statistic, a measure of phylogenetic signal, supports low divergence rates of every tested gene in populations of *R. microplus* in the target region even under diverging environmental conditions. This test demonstrates that spatial distance and genetic variability are negatively correlated. The low variability of these genes may be due to (i) the recent introduction of the tick in the Neotropics, (ii) a high degree of panmixia because exchange of populations, and (iii) low environmental pressures, promoting a lack of genetic drift. These results have implications for the ecology and control of cattle tick infestations.

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