

AN INTEGRATIVE APPROACH TO DELIMITING SPECIES IN TICKS USING MOLECULAR, BIOLOGICAL AND MORPHOLOGICAL EVIDENCE

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Species delimitation is a major goal in systematic biology because accurate knowledge of species boundaries is a prerequisite for evolutionary, ecological and epidemiological studies of living organisms. The use of different lines of evidence not only is necessary to formulate robust hypotheses about the specific status of a group of organisms, but also provide a source of information to prevent erroneous conclusions due to inconsistency among different characters sets. Phenetic distinguishability, genetic divergence and reproductive isolation can be used simultaneously to infer species boundaries. In the particular case of hard ticks (Acari: Ixodidae), systematic studies integrating cross-mating experiments, comparison of multiple gene sequences and morphological analysis have been instrumental to perform significant taxonomic reassessment of some species with sanitary and economic relevance. For example, morphological, biological (cross-mating trials) and genetic evidences have shown that the taxon previously recognized as *Amblyomma cajennense* is formed by six different species, and the reinstatement of *Rhipicephalus* (*Boophilus*) *australis* as a valid species different from *Rhipicephalus* (*Boophilus*) *australis* as a valid species different from *Rhipicephalus* (*Boophilus*) *microplus* was carried out based on the analysis of genetic divergence, experimental crosses and morphological dissimilarities.