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ANCESTRAL RANGE RECONSTRUCTION IN THE AMERICAN DEER DIVERSIFICATION

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One of the major goals of historical biogeography is to use phylogenetic methods to infer the evolution of species geographic ranges. Capreolinae (Mammalia: Cetartiodactyla: Cervidae) includes south-american cervids, mooses, reindeers, roe deers etc., in a total of 23 species distributed into four tribes (Capreolini, Alceini, Odocoileini and Rangerafini). The most accepted diversification hypothesis of Capreolinae suggests an Asiatic origin, followed by colonization of North America through Bering Strait and its arrival to South America after formation of the Panama land bridge during the Great American Biotic Interchange. We tested this hypothesis by estimating ancestral ranges using probabilistic modeling. We generated a time-calibrated molecular phylogeny of Cetartiodactyla using all mitochondrial data available in GenBank and kept 23 species of Capreolinae for our analysis. We used BioGeoBEARS package in R to infer the ancestral range and compared the fit of two models: DEC (that consider dispersion and extinction) and DEC+J (that add founder-event parameter to DEC model). The ancestral range reconstruction supports the original hypothesis of Asia-North America-South America colonization. However, our results suggest that the origin of Odocoileini took initially place in South America, and its diversification could be related to a recolonization event, mediated mainly by dispersion process from South to North. These results are quite surprising, suggesting an alternative evolutionary history from that considered until now, and show that there is much of the natural history of American deer diversification to be elucidated.