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Mitogenomics of the mountain tapir (Tapirus pinchaque, Tapiridae, Perissodactyla, Mammalia) in Colombia and Ecuador: Phylogeography and insights into the origin and systematics of the South American tapirs

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Abstract We sampled 45 Andean mountain tapirs (Tapirus pinchaque) from Colombia and Ecuador and sequenced 15 mitochondrial genes (two rRNA and 13 protein coding genes)...

Introduction An important first step in protecting groups of similarly structured organisms is to place them into discrete taxa. Once a species is recognized we monitor its overall fitness and develop conservation plans towards its benefit.

T. pinchaque (Roulin 1829) is the smallest of the four living tapir species—having an average shoulder height of 0.90 m, body length of 1.8 m and weight of 150 kg.

This tapir is currently classified as an endangered species in the IUCN Red List (IUCN 2011) at the global level and it is also enclosed in Appendix I in CITES.

The origin of tapirs in South America and the role played by T. pinchaque in this origin are very controversial topics. Hershkovitz (1954) analyzed morphological characters and concluded that the ancestor of T. pinchaque was the first tapir form to enter South America prior to the formation of the Panamanian Isthmus more than 3–4 MYA.

Haffer (1970) introduced a different hypothesis on the origin of the tapirs of South America taking into account morphological and biogeographical considerations. He considered the ancestor of T. pinchaque to be the first form which colonized the Northern Andes during its last rising within the Pliocene.

Ashley et al. (1996) used mitochondrial COII sequences to determine that the ancestor of T. bairdii diverged from the ancestor of the two strictly South American tapir species around 19–20 MYA.

Recently, Cozzuol et al. (2013) claimed the existence of a new tapir species. They compared Cyt-b gene sequences of four Amazon tapir individuals (two from Brazil and two from Colombia) with 45 Cyt-b gene sequenced from Thoisy et al. (2010).

We sequenced the mitochondrial genomes of 45 T. pinchaque individuals sampled throughout six populations of Colombia and Ecuador. These two countries harbour more than 98% of the living mountain tapirs.

The main aims of the present work are as follows: (1) To determine mitochondrial diversity levels in T. pinchaque; (2) To determine levels of genetic differentiation between T. pinchaque populations to provide new results testing for the possible existence of subspecies within mountain tapirs (sensu Hershkovitz, 1954); (3) To analyze possible historical demographic changes throughout the evolution of T. pinchaque; (4) To determine spatial genetic structure in T. pinchaque; and (5) To contribute with new data to our understanding of speciation in the Tapirus genus.

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Section snippets

Material and methods

Out of 80 T. pinchaque samples from Colombia and Ecuador we selected 45 (high-quality DNA) for mitochondrial DNA sequencing. Additionally, 17 samples of T. terrestris, 13 samples of T. bairdii and 7 samples of T. indicus were also sequenced.

Genetic diversity

The maximum likelihood estimate of Transition/Transversion was 2.37 (Ln = -26,308.12). For a GTR model, the maximum likelihood estimate of the gamma parameter for sites rates was 0.2037 (+ G; five categories) (Ln = -25,481.66).

The genetic diversity level for the global T. pinchaque sample analyzed for the 15 mitochondrial genes concatenated showed 21 different haplotypes with Hd = 0.904 ± 0.003 (high genetic diversity) and pi = 0.0041 ± 0.0003 (low-medium genetic diversity) (see Table 5). The genetic ...

Genetic diversity, heterogeneity, demographic changes and absence of spatial structure in T. pinchaque

Our nucleotide diversity values for T. pinchaque (pi = 0.004 ± 0.0003) are considerably lower than estimates for T. terrestris reported by other studies. Ruiz-García et al. (2015) estimated a value of pi = 0.0114 ± 0.0003 for a wide geographical sample of T. terrestris.

The overall sample of T. pinchaque has about three times lower genetic diversity than T. terrestris for mitochondrial genes. However, T. pinchaque presented a higher nucleotide diversity than T. bairdii (pi = 0.0025 ± 0.0005; Ruiz-García et al. ...

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