RESEARCH ARTICLE

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Phylogeography of red muntjacs reveals three distinct mitochondrial lineages

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Abstract

Background: The members of the genus *Muntiacus* are of particular interest to evolutionary biologists due to their extreme chromosomal rearrangements and the ongoing discussions about the number of living species. Red muntjacs have the largest distribution of all muntjacs and were formerly considered as one species. Karyotype differences led to the provisional split between the Southern Red Muntjac (*Muntiacus muntjak*) and the Northern Red Muntjac (*M. vaginalis*), but uncertainties remain as, so far, no phylogenetic study has been conducted. Here, we analysed whole mitochondrial genomes of 59 archival and 16 contemporaneous samples to resolve uncertainties about their taxonomy and used red muntjacs as model for understanding the evolutionary history of other species in Southeast Asia.

Results: We found three distinct matrilineal groups of red muntjacs: Sri Lankan red muntjacs (including the Western Ghats) diverged first from other muntjacs about 1.5 Mya; later northern red muntjacs (including North India and Indochina) and southern red muntjacs (Sundaland) split around 1.12 Mya. The diversification of red muntjacs into these three main lineages was likely promoted by two Pleistocene barriers: one through the Indian subcontinent and one separating the Indochinese and Sundaic red muntjacs. Interestingly, we found a high level of gene flow within the populations of northern and southern red muntjacs, indicating gene flow between populations in Indochina and dispersal of red muntjacs over the exposed Sunda Shelf during the Last Glacial Maximum.

Conclusions: Our results provide new insights into the evolution of species in South and Southeast Asia as we found clear genetic differentiation in a widespread and generalist species, corresponding to two known biogeographical barriers: The Isthmus of Kra and the central Indian dry zone. In addition, our molecular data support either the delineation of three monotypic species or three subspecies, but more importantly these data highlight the conservation importance of the Sri Lankan/South Indian red muntjac.

Keywords: Phylogeography, Archival DNA, Muntjac, Southeast Asia, Species complex

Background

The number of recognized deer species has increased in recent decades, and it continues to do so due to rare discoveries of new forms in the wild, increased molecular efforts and the careful reexamination of museum collections. For example, the genus Muntiacus has increased in the number of named species through discovery of the Gongshan muntjac (*Muntiacus gongshanensis*) from the wild in 1990 [1], the Putao muntjac (*Muntiacus*

putaoensis) from Myanmar, described based on molecular comparisons [2] and the Bornean Yellow muntjac (Muntiacus atherodes) described from museum skulls and skins in 1982 following a reappraisal of the muntjac taxa described previously from Borneo [3].

The genus *Muntiacus* Rafinesque (1815) comprises an undefined number of species and subspecies all native to South, Southeast and East Asia. Although muntjacs are studied for their dramatic variation in chromosome numbers [4, 5], taxonomic concordance within this genus has not been achieved yet, due to lack of molecular studies combined with, in some cases, limited morphological or ecological differences. Although the genus

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