

Phylogenetic relationship and population structure of the captive Eld's deer (*Panolia eldii*) in Thailand using genome-wide SNPs derived from restriction site-associated DNA sequencing

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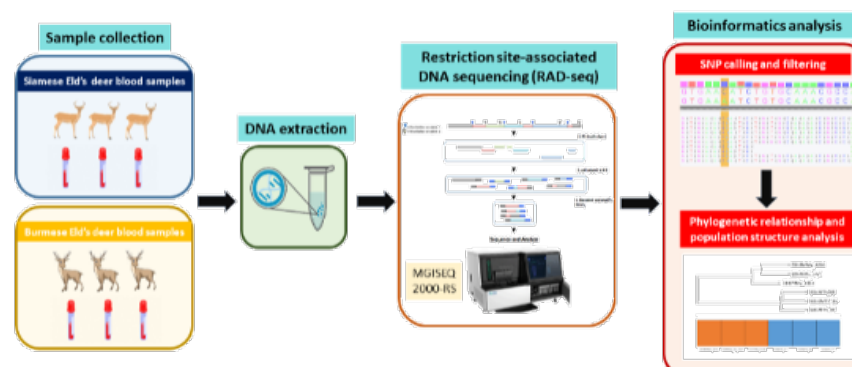
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Abstract: Eld's deer (*Panolia eldii*) is a medium-sized deer which was distributed across South and Southeast Asia. In Thailand, two subspecies, Siamese and Burmese Eld's deer, were found. According to the overexploitation and hunting, this species has experienced a dramatic decline and is classified as "endangered" in the IUCN Red List. Breeding of Eld's deer in captivity and controlled environment is an effective attempt to recruit the population size. However, the patterns of genetic diversity and population structure of Eld's deer in Thailand remain unknown. In this study, the restriction site-associated DNA sequencing (RAD-seq) was utilized to search for genome-wide single nucleotide polymorphisms (SNPs) of 6 captive individuals (3 Siamese and 3 Burmese Eld's deer). We obtained 1.27 million SNP loci. A set of 1,052 filtered SNPs was used to construct a UPGMA phylogenetic tree with 1,000 bootstrap replicates. The population structure was analyzed using 1000 iterations with the number of clusters (K) of 1-6. Our results revealed that Siamese and Burmese Eld's deer populations could be separated into two clusters, in which best fit K value = 2. Similarly, the phylogenetic tree was diverged into two clades and with a close relationship within subspecies. In conclusion, the large-scale SNP discovery by RAD-seq could be used for investigating the genetic variability of Eld's deer in captivity. This outcome provides insights into a well-designed breeding plan for avoiding inbred mating and restoring genetic diversity in the remaining population. It could be applied to construct effective founders for reintroducing into the wild.



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Graphical abstract:



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