

Sequence of the mitochondrial control region, tRNA^{Thr}, tRNA^{Pro} and tRNA^{Phe} genes from the black rhinoceros, *Diceros bicornis*

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A DNA fragment containing the mitochondrial tRNA^{Thr}, tRNA^{Pro} and tRNA^{Phe} genes and the control region (D-loop) was amplified from East African black rhinoceros, *Diceros bicornis michaeli* total genomic DNA utilizing conserved primer pairs L15926 + H00651 (1). The fragment was digested with DpnII, PstI/DpnII and HindIII/DpnII separately, and cloned into both M13mp18 and M13mp19. The nucleotide sequences of cloned fragments were determined using dideoxynucleotide chain termination method (2). The segment of tRNA^{Thr} gene corresponds to human mitochondrial DNA from site 15927 to site 15953. Multiple insertions, almost all of which occur at the loop region are required for alignment with the human sequence (3, 4). The tRNA^{Pro} gene was easily aligned with the human gene with two single-base deletions, and they are 78% identical to each other (3). The 1200 bp length control region was aligned with that of human through introduction of insertions and deletions. The major feature of the rhinoceros control region is a tandem repeat sequence located upstream approximately 300 bp from tRNA^{Phe} gene. The structure of the repeat sequence is shown in Figure 1. This repeat sequence has not been observed in the human, cow and mouse control region (3–5). The tRNA^{Phe} gene was also easily aligned with that of human with two single-base deletions both of which occur at loop region. The identity of the two genes is 71% (3). The deduced cloverleaf structures of mitochondrial tRNA^{Pro} and tRNA^{Phe} are shown in Figure 2.

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5' (CGCACACACA)₂(CGCATATACA)₉(CGCACACACA)
(CGCATATACA)₂(CGCACACACA) 3'

Figure 1. The structure of tandem repeat sequence in the mitochondrial DNA control region from the East African black rhinoceros, *Diceros bicornis michaeli*.

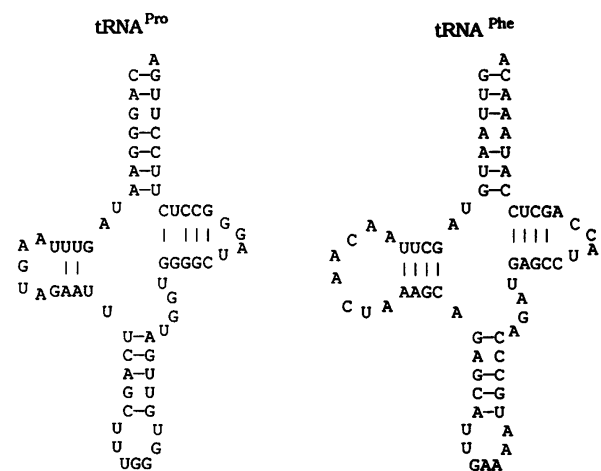


Figure 2. Proposed cloverleaf structures of *Diceros bicornis michaeli* mitochondrial tRNAs as inferred from gene sequences. A Watson-Crick base pair in a stem region is indicated by a dash.

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