



## Complete mitochondrial genome of Cabot's tragopan, *Tragopan caboti* (Galliformes: Phasianidae)

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**ABSTRACT.** Cabot's tragopan, *Tragopan caboti*, is a globally threatened pheasant endemic to southeast China. The complete mitochondrial genome of Cabot's tragopan was sequenced. The circular genome contains 16,727 bp, encoding a standard set of 13 protein-coding genes, two ribosomal RNA genes, and 22 transfer RNA genes, plus the putative control region, a structure very similar to that of other Galliformes. As found in other vertebrates, most of these genes code on the H-strand, except for the NADH dehydrogenase subunit 6 (*nad6*) and eight tRNA genes (Gln, Ala, Asn, Cys, Tyr, Ser(UCN), Pro, Glu). All protein-coding genes initiated with ATG, except for *cox1*, which began with GTG, and had a strong skew of C vs G (GC skew = -0.29 to -0.73). One extra 'C' nucleotide was found in the NADH dehydrogenase subunit 3 (*nad3*). All the tRNA gene sequences have the potential to fold into typical cloverleaf secondary structures. Conserved sequences in three domains were identified within the control region

(D-loop). These results provide basic information for phylogenetic analyses among Galliform birds, and especially *Tragopan* species.

**Key words:** Mitochondrial genome; Cabot's tragopan; Phasianidae; *Tragopan caboti*; Galliformes