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昆虫学报, undefined 年, undefined 月, 第 undefined 卷, 第 undefined 期,
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题目: 马鸡属鸟类的系统发育关系

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摘要: The phylogenetic relationships of the avian genus *Crossoptilon* were studied by comparing mitochondrial control region (D-loop) and *cyt b* gene nucleotide sequences, with the *Lophophorus impejanus* and *Lophura swinhoii* as the outgroups. Using the synthesizing characters of morphology, ecology and biogeography to combine with Maximum (MP), Maximum Likelihood (ML) and Bayesian trees, we found that: ① *C. crossoptilon* and *C. harmani* were closely related and *C. harmani* was relatively primitive; ② *C. auritum* and *C. mantchuricum* had a close relationship and *C. auritum* was relatively primitive; ③ the genus *Crossoptilon* could originate in the boundary region of Sichuan, Yunnan and Tibet. One branch remained near the center of origin and diverged into *C. crossoptilon* and *C. harmani*; the other branch spread towards north China and diverged into *C. auritum* and *C. mantchuricum* [*Acta Zoologica Sinica* 51(5): 898 – 902, 2005].

关键词: 马鸡属 线粒体 控制区 细胞色素b 系统发育

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