

研究论文

大鸨(*Otis tarda*)两个亚种的遗传多样性与系统分化

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摘要 大鸨(*Otis tarda*)为中国 I 级重点保护动物, 分为两个亚种, 即指名亚种(*Otis tarda tarda*)和东方亚种(*Otis tarda dybowskii*)。研究从代表母系遗传特征的mtDNA控制区和代表双亲遗传特征的核微卫星两方面对两个亚种的遗传多样性与系统分化进行了分析。指名亚种mtDNA控制区3段序列(CtrIaL/CtrIioH、L438/H772和LCR2a/HCR8)的单倍型数、J、 δ 和K都明显高于东方亚种, 更显著高于松辽平原西北部繁殖区。东方亚种3个微卫星(Otmic08、Otmic16和Otmic26)的等位基因数、Ho和He明显低于指名亚种。因此东方亚种的遗传多样性都明显低于指名亚种, 甚至低于Madrid种群。两个亚种存在于不同的系统分支, 证实了两个亚种的系统关系, 欧洲指名亚种存在更多的系统分支。

关键词 [大鸨东方亚种](#); [大鸨指名亚种](#); [遗传多样性](#); [系统分化](#)

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The genetic diversity and phylogenetic differentiation analysis on two subspecies of *Otis tarda*

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Abstract *Otis tarda* is listed as a first-rating protected bird in China, which has two subspecies, *O. t. tarda* and *O. t. dybowskii*. The genetic diversity and phylogenetic differences between the two *Otis tarda* subspecies were analyzed by the mtDNA control region method that on behalf of the maternal genetic character and the microsatellite method that on behalf of parental genetic character. The number of haplotype, J, δ and K of *O. t. tarda* are higher than those of *O. t. dybowskii* among three sequences of mtDNA control region (CtrIaL/CtrIioH、L438/H772 and LCR2a/HCR8), and significantly higher than the population in the northwest of Songliao Plain. The numbers of alleles, Ho and He of *O. t. dybowskii* are lower than those of *O. t. tarda* among three microsatellites (Otmic08, Otmic16 and Otmic26). Therefore, the genetic diversity of *O. t. dybowskii* is obviously lower than that of *O. t. tarda*. The two subspecies are located at two phylogenetic branches, which confirmed that the phylogenetic relationship between two subspecies. Moreover, *O. t. tarda* has much more phylogenetic branches than *O.t. dybowskii*.

Key words [Otis tarda dybowskii](#) _ [Otis tarda tarda](#) _ [genetic diversity](#) _ [phylogenetic differentiation](#)

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