生态学报　2006 26 (2006(11)): 3572～3577　ISSN: 1004-616x　CN: 44-1063/R

研究论文

青藏公路对高原鼠兔种内遗传分化的影响

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收稿日期 2006-1-11 修回日期 2006-7-10 网络版发布日期: 2006-11-25

摘要　研究采用7个微卫星标记分析在青海省西大滩区域，位于青藏公路两侧的4个高原鼠兔（Ochotona curzoniae）种群的遗传变异情况。分别采用软件TFPGA和GENE POP 3.4计算各种群间的Nei’s标准遗传距离，基因分化系数（Fst）等参数，并对遗传距离进行UPGMA聚类分析。研究结果表明，公路同侧种群间平均遗传距离和基因分化系数分别为0.0808和0.0541；异侧种群间平均遗传距离和基因分化系数分别为0.1037和0.0705，公路东侧和西侧的两个种群分别聚为一类。青藏公路对分布于公路两侧的高原鼠兔种群间的基因交流产生了一定的阻隔效应，并导致种群间出现了一定程度的遗传分化。

关键词　高原鼠兔；遗传分化；微卫星；青藏公路
分类号　Q143,Q958

Effects of Qinghai-Tiber Highway on genetic differentiation of planteau pilka (*Ochotona curzoniae*)

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Abstract The plateau pika (Ochotona curzoniae), distributed largely coincides with the high alpine grassland of the Qinghai-Xizang (Tibet) Plateau of People’s Republic of China, is one of the dominant small mammals in the alpine meadow ecosystem. It has very important function in keeping the balance of the food chain on alpine meadow ecosystem. Four geographical populations of the plateau pikas (East-1 population, West-1 population, East-2 population and West-2 population) were selected from Xidatan area in Qinghai province. The populations of West-1 and West-2 were on the west side of Qinghai-Tibet Highway, while the other two populations were on the east side. Genetic variation and genetic differentiation among populations were assessed with seven microsatellite markers of North-American pika (Ochotona princeps) in order to study the effects of Qinghai-Tibet Highway on the genetic differentiation among plateau pika populations. TFPGA and GENEPOP 3.4 software were used to calculate all indices. Our results showed that the number of alleles detected per locus varied from 2.00～24.00.The polymorphism information content (PIC) per locus ranged from 0.3233 to 0.9189 comprising of highly-polymorphic two loci while the other five were medium-polymorphic. The observed and expected heterozygosity (Ho and He) of the seven loci varied between 0.3451～0.9912 and 0.4021～0.9236, respectively, and the mean value of Ho and He were 0.6068 and 0.5515, respectively. The results indicated that the genetic diversity of the plateau pika had medium-level. The average fixation index (F) was below zero, this indicated that heterozygote was excess in natural populations. Mean value of genetic differentiation index (Fst) of all loci was 0.0385, implied that 3.85% of the genetic variation were intrapopulation, while 96.15% of the variation were interpopulation. The genetic distance, genetic differentiation index and gene flow between populations on the same side of the road were 0.0808, 0.0357 and 7.2170, respectively. While between populations on the opposite side were 0.10

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37, 0.0443 and 5.4235, respectively. The results of the UPGMA cluster analysis showed that the two populations of the east side were clustered into one group and the other two populations of the west side were clustered into another one. These results implied that the road had played some barrier effect on the genetic interaction between plateau pikas that inhabited the two sides of the highway and therefore led to some genetic differentiation. However, because the duration of the effect was short, the level of genetic differentiation was still limited. And we assumed that the level of genetic differentiation between plateau pika that inhabited the two sides of Qinghai-Tibet Highway would get higher in the future.

Key words plateau pika _ genetic differentiation _ microsatellite _ Qinghai-Tibet Highway

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