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## Investigation on genetic diversity in subgenus *Eospalax* of *Myospalax* genus using cytochrome b gene sequences of Gansu province

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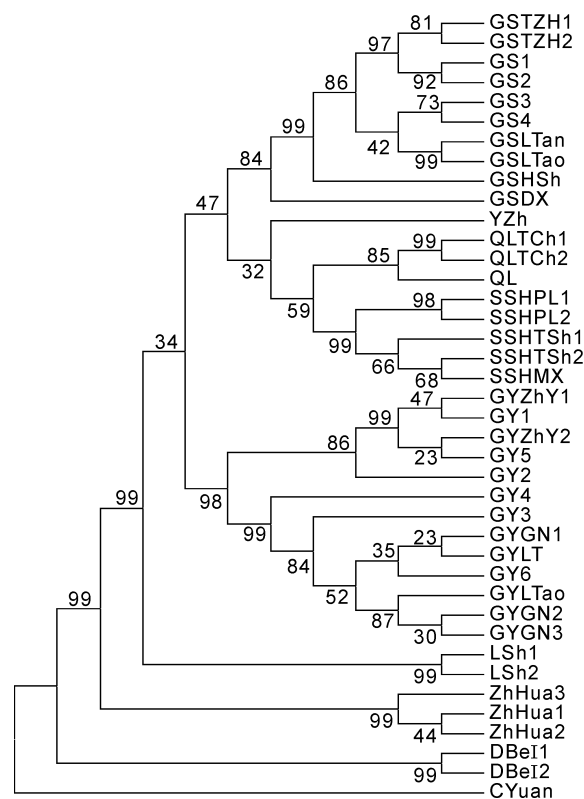
**Key words** : subgenus *Eospalax*, Cytochrome b gene, genetic diversity, conversion and transversion, phylogenetic

**Introduction** Complete sequences of cytochrome b gene were generated for 21 species of subgenus *Eospalax* of *Myospalax* in 11 different places of Gansu province, other sequences were acquired from GenBank. Five Gansu species include Qin ling zokor (*Eospalax rufescens*), Gansu zokor (*M. cansu*), Bailey's zokor (*M. baileyi*), Rothschild's zokor (*M. rothschildi*), and Smith's zokor (*M. smithi*). The phylogenetic tree was constructed from the 43 near-complete cytb sequences. The result illustrated the origin and evolution of subgenus *Eospalax* from molecular level firstly in Gansu province.

**Materials and methods** Twenty one liver samples were collected from five subgenera of *Eospalax* in our experiment from eleven places in Gansu province. (1) Total genomic DNA was extracted from the liver samples, treated using a procedure modified from *Hagelberg and Clegg* (1991). (2) PCR and Sequence Analysis: primer A L7: 5-ACCAATGACATGAA-AAATCATCGTT-3', H6: 5-TCTCCATTTCTGGTTTACA AGAC-3' for complete mitochondrial cyt b gene.

**Results** (1) Sequence Analysis: Twenty one complete sequences of cytb on the other for 5 species of zokors were obtained, the alignment of cytb sequences is 1143 nucleotides long, nucleotide insertion and deletion was not found. Nine groups of the 43 sequences were found more than 386 polymorphic sites. The content of A, G, C, T is this the highest concentration of T base pairs (31.2%), followed by A (30.8%), C third (25.8%), the lowest content of G (12.4%). There are different content of A, G, C, T in the third codon position, contents in the third position change at the rate of T (19.2% to 30.7%), C (24.3% to 44.2%), A (41.4% to 44.5%) and G (0.8% to 3.6%), significantly higher than that position 1 and 2. Eighty percent conversion and transversion occurred in the third codon position. Levels of homoplasmy measured for C-T, T-C substitutions are the highest in the third position, and the lowest in the first position. (2) Phylogenetic Reconstruction: A phylogenetic tree constructed from the 43 near-complete cytb sequences of 5 five species in the subgenus *Eospalax* is shown in Figure 1. According to the three indices (geographical position, heredity and evolution, difference of species), suggests that different zokors and areas form different short branches, which one branch may include different species.

**Conclusions** (1) the Grassland zokor and Northeast zokor are the old ancient species in the *Myospalax* genus, the Chinese zokor is in the second and the others are in one evolution branch. (2) There are two big evolution branches in the Subgenus *Eospalax* of Gansu, one is Bailey's zokor branch and the other is the big branch that consists of Smith's zokor, Gansu zokor and Qin ling zokor. (3) In the Bailey's zokor branch, the Bailey's zokor distributed in the Hexi Corridor deserted zone first diverged from the others.



**Figure 1** The most parsimonious tree of Complete cytb gene sequence data of mtDNA.