Chinese Grey Shrike (*Lanius sphenocercus*) is an endemic species in Eastern Asia. It belongs to the compact group of gray shrikes and with two subspecies: nominate subspecies (*L. s. sphenocercus*) and south-west subspecies (*L. s. isabellinus*) in China. At present, most studied species are the groups that inhabit Europe and North America. Data on the biology, vocalization, and behaviour of Asian species of the group are scarce (Opaev 2014). Especially, the limited molecular data dampen the evolution and diversity studies in genus *Lanius*.

A naturally dead *L. s. sphenocercus* was collected at Hongjian NUR (39°04′N, 109°53′E), Shaanxi, China. The specimen (Voucher number: XWBL01) was preserved in 100% ethanol and stored at −20°C, and deposited in the animal specimens museum of Shaanxi Institute of Zoology, Xi’an, China. Genomic DNA was prepared in paired-end libraries, tagged and subjected to the high-throughput Illumina HiSeq2500 platform with 125bp paired-end strategy and yield 23,398,290 Paired-End Raw Reads with 126 bp in length. Clean reads were trimmed by removing regions with a Phred score of <10. Mapping against the complete mitogenome of *Lanius isabellinus* (GenBank: KP995437), high-quality reads were assembled using SOAPdenovo2 (Hahn et al. 2013). A total of 228,309 individual mitochondrial reads gave an average coverage of 1669.5×. Comparing with the *L. isabellinus*, annotations were generated in MITOchondrial genome annotation Server (MITOS) (Bernt et al. 2013).

The total length of *L. s. sphenocercus* mitogenome is 16,833 bp (GenBank: KU884610). The base composition of the entire mitogenome was 30.5% A, 25.4% T, 29.0% C and 15.1% G. There are 17 intergenic spacer regions, ranging in size from 1 to 10 bp (81 bp in total). Gene overlap involves 29 bp over 6 locations.

The typical ATG start codon is present in 12 of the 13 *L. s. sphenocercus* PCGs, nonstandard start codons (GTG) are found in *COI*. Open-reading frames of most *L. s. sphenocercus* genes end with AGG, TAA, AGA, or TAG, while *COII, COIII* and *ND4* have the incomplete stop codon (T). But, the function of *COI* with incomplete stop codon T should be further investigated. The phylogeny revealed that genetic distance of Laniidae and Corvidae was closer than other species. Compared to other three shrike species, *L. s. sphenocercus* occupy a separate status in the genus *Lanius*.
Disclosure statement
The authors declare no competing interests.

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