The streaked rosefinch *Carpodacus rubicilloides* is a true finch species and it commonly occurs in southwest China and the Himalayas. In this paper, we described the whole mitochondrial genome of the Streaked Rosefinch. The entire mitochondrial sequences were determined using long-range PCR and conserved primer walking approaches. The results demonstrated that the whole mitochondrial genome of *C. rubicilloides* was 16,805 bp in length with 53.9% A + T content; the genome harbored the same gene order as that of other passerine birds, including 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes, and 1 non-coding control region. The control region (D-loop) of *C. rubicilloides* was located between tRNA-Gln and tRNA-Phe with 1228 bp length. Phylogenetic analysis indicated that the genome of *Carpodacus* species clustered within a clade and is closer related to other *Fringillidae* species than *Anatidae* species. These mitochondrial data are potentially important for the further studies on molecular evolution and conservation genetics in true finch species.
supported by high bootstrap values at most nodes (Figure 1). The phylogenetic tree revealed that four Carpodacus species clustered in a clad and were closer related to Fringillidae species than Anatidae. All the clades were consistent with the traditional morphology-based taxonomies and recent molecular taxonomies (Gill and Donsker 2018). Currently, most of Carpodacus species are poorly known about their natural history and genetic information (Xiao et al. 2017; Gill and Donsker 2018), and only three complete mitochondrial genomes of Carpodacus species have released in Genebank (Figure 1). The additional complete mitochondrial genome of the Streaked Rosefinch could provide fundamental information for further molecular phylogenetic studies on Carpodacus species.

Disclosure statement
No potential conflict of interest was reported by the authors.

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