The species of Tortricidae has a common name “leafrollers” owing to its larval habit of shelter-building by folding or rolling leaves of the food plant (Brown et al. 2008), and there are more than 11,300 species of leafroller moths in the world (Gilligan et al. 2018). Currently, the Tortricidae is divided into three subfamilies: Tortricinae, Chlidanotinae, and Olethreutinae. The genus Cerace belongs to the Tortricinae, and Cerace xanthocosma Diakonoff, 1950 is distributed in China and Japan. As an important economic pest, the larvae of C. xanthocosma feed on many plants such as Camellia, Symplocos, Acer, and Castanopsis (Liu and Li 2002).

The mitochondrial genome (or mitogenome) is a typically double-stranded and circular DNA molecule containing 37 genes (13 protein-coding genes (or PCGs), 22 transfer RNA genes (or tRNAs), and 2 ribosomal RNA genes (or rRNAs)) and a non-coding A+T-rich region (11,225 bp of 13 PCGs, 1462 bp of 22 tRNAs, 2170 bp of 2 rRNAs, and 383 bp of A+T-rich region) and one non-coding A+T-rich region (383 bp) is rela-
the main reason leading the differences in the size of mitogenomes among insect species (Dai et al. 2018).

The sizes of 22 tRNAs of *C. xanthocosma* mitogenome range from 62 to 71 bp, comprising 9.5% (1462 bp) of the complete mitogenome. The gene orientation and arrangement of tRNAs is *trnM-trnI-trnQ*, which is considered as a character derived from ancestral gene order *trnI-trnQ-trnM* (Boore 1999). Two rRNAs are 2170 bp in size. The larger one (*rrnL*) is located between *trnL*1 and *trnV*, while the smaller is located between *trnV* and A + T-rich region. This arrangement is also the same as the other sequenced lepidopterans.

Up to now, 28 complete mitogenome sequences belonging to 2 subfamilies (Tortricinae and Olethreutinae) of Tortricidae have been verified in GenBank. Phylogenetic analysis based on these complete mitogenome sequences was performed using Bayesian Inference (BI) method. *Eogystia hippophaecola* Hua, Chou, Fang & Chen, 1990 (Lepidoptera: Cossidae) was used as the outgroup. The result shows the sister relationship between Tortricinae and Olethreutinae with the placement of *C. xanthocosma* as the basal lineage of Tortricidae (Figure 1). It is noticeable that *Acleris fimbriana* Thunberg & Becklin, 1791 (Tortricinae) was clustered as the basal lineage of the two subfamilies, which means that Tortricinae may not be a monophyletic group and needs more data for the further study. In addition, two sequences of *Choristoneura occidentalis* (MG948539 and MG948541) were not clustered together, which also needs further study.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).
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