

Molecular phylogenetics and tribal classification of Japanese Pyraustinae and Spilomelinae (Lepidoptera: Crambidae)

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Supplementary material

Fig. S1. Bayesian inference phylotree of Japanese Pyraustinae and Spilomelinae. Nodes are labelled with posterior probability.

Table S1. Taxa sampled in the present study, along with current taxonomic placement, sample ID, and GenBank accession numbers.

Table S2. The primers used in the present study.

Table S3. The PCR amplification strategy for each gene.

Table S4. The base substitution models selected by ModelTest-NG. The Bayesian information criterion (BIC) is used as the criterion for model selection. Numbers in parentheses after the gene names represent one of the three codon positions.

Table S5. The base substitution models selected by Kakusan4. The Bayesian information criterion (BIC) is used as the criterion for model selection. Numbers in parentheses after the gene names represent one of the three codon positions.

Table S6. The revised list of Japanese Pyraustinae and Spilomelinae. Species are based on Jinbo (2021).

File S1. Photographs of adult, male and female genitalia of the sampled species.