

Supplementary files

First Record of *Osphyia* (Melandryidae: Osphyinae) from Chinese Mainland Based on Morphological Evidence and Mitochondrial Genome-Based Phylogeny of Tenebrionoidea †

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Figure S1 Phylogenetic tree of Tenebrionoidea produced from BI analysis based on 13 PCGs (PP values indicated in each clade)

Table S1 Distribution information of the *Osphya* species in the Oriental and eastern and southern Palearctic regions.

Species	Distribution	Longitude	Latitude	Source
<i>Osphya formosana</i> Pic, 1927	China: Taiwan	121.29578	24.99511	[14]
<i>Osphya trilineata</i> Pic, 1910	China: Taiwan	121.29578	24.99511	[10]
<i>Osphya orientalis</i> (Lewis, 1895)	Japan, Miyanoshta	139.06054	35.23929	[5]
	Japan, Nikko	139.54738	36.79846	[5]
<i>Osphya albofasciata</i> Champion, 1916	India: Assam, Patkai Mts.	95.99960	27.00004	[7]
<i>Osphya harmandi</i> Pic, 1926	India: Sikkim	88.48946	27.21889	[13]
	India: Darjeeling District	88.27189	27.02923	[13]
<i>Osphya dissimilis</i> Champion, 1922	India: Uttarakhand, Uttar pradesh	79.06097	30.14047	[9]
<i>Osphya nigriventris</i> Champion, 1920	India: Uttarakhand, Uttar pradesh	79.06097	30.14047	[8]
<i>Osphya nigroapicalis</i> Pic, 1921	India.	88.27189	27.02923	[11]
<i>Osphya nilgirica</i> Champion, 1916	India: Nilgiri Hills	76.76198	11.37447	[7]
<i>Osphya rufa</i> Pic, 1927b	Vietnam: Chapa	103.96834	22.50462	[15]
<i>Osphya superba</i> Pic, 1927	Vietnam: Chapa	103.96834	22.50462	[15]
<i>Osphya melina</i> Champion, 1916	Myanmar: Tenasserim, Victoria Point.	98.55190	9.99258	[7]
<i>Osphya sinensis</i> sp. nov.	China: Hubei, Shennongjia, Dajiuhu, Luoyanghe	110.13778	31.57722	This study
	China: Hubei, Shennongjia, Dajiuhu, Dongxi	110.12194	31.53944	—
	China: Hubei, Shennongjia, Muyu, Yanjiawan	110.43417	31.47722	—

Table S2 The best partitioning schemes and models for the Maximum Likelihood (ML) method

Partitions	Models	Genes
P1	GTR+F+I+G	atp6
P2	TIM+F+I+G	atp8
P3	GTR+F+I+G	cox1,cox2
P4	GTR+F+I+G	cox3
P5	GTR+F+I+G	cytb
P6	GTR+F+I+G	nad1
P7	TIM+F+I+G	nad2
P8	TIM+F+I+G	nad3
P9	GTR+F+I+G	nad4L
P10	GTR+F+I+G	nad4,nad5
P11	TIM+F+I+G	nad6

Table S3 The best partitioning schemes and models for the Bayesian Inference (BI) method

Partitions	Models	Genes
P1	GTR+I+G	atp6_pos1,cytb_pos1
P2	GTR+I+G	atp6_pos2
P3	GTR+G	atp6_pos3,atp8_pos3,nad3_pos3
P4	GTR+I+G	atp8_pos1,nad6_pos1
P5	GTR+I+G	atp8_pos2,nad2_pos2,nad3_pos2
P6	GTR+I+G	cox1_pos1,
P7	GTR+I+G	cox1_pos2
P8	GTR+I+G	cox1_pos3
P9	GTR+I+G	cox2_pos1, cox3_pos2
P10	GTR+I+G	cox2_pos2
P11	HKY+G	cox2_pos3
P12	GTR+I+G	cox3_pos2
P13	GTR+G	cox3_pos3,cybt_pos3
P14	GTR+I+G	cytb_pos2
P15	GTR+I+G	nad1_pos1
P16	GTR+I+G	nad1_pos2
P17	GTR+G	nad1_pos3
P18	GTR+I+G	nad2_pos1
P19	HKY+G	nad2_pos3
P20	GTR+I+G	nad3_pos1
P21	GTR+I+G	nad4L_pos1,nad5_pos1
P22	GTR+G	nad4L_pos2
P23	GTR+I+G	nad5_pos3,nad4L_pos3,nad4_pos3
P24	GTR+I+G	nad4_pos1
P25	GTR+I+G	nad5_pos2,nad4_pos2,
P26	GTR+I+G	nad6_pos2
P27	HKY+G	nad6_pos3