

Taxonomy and morphology of Chinese butterflies 4 - Heliconiinae: Argynniini: *Issoria* HÜBNER, [1819] subgenus *Kuekenthaliella* REUSS, 1921

(Lepidoptera, Nymphalidae)

by

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Abstract: The *Issoria* subgenus *Kuekenthaliella* REUSS, 1921, taxa from the Himalayas and the Tibetan Plateau, are revised based on studies of genital morphology in both sexes, mitochondrial COI gene fragments, and nuclear EF1-alpha gene fragments. Both, *Issoria wui* **stat. nov.** (= *Kuekenthaliella gemmata wui* HUANG, 1998) and *I. baileyi* (HUANG, 1998) **stat. rev.**, are confirmed as separate species from *I. gemmata* (BUTLER, 1881) through molecular analysis of nu-DNA EF1-alpha sequences. *I. wui zhenjuni* **subspec. nov.** is described from NW Yunnan. *I. baileyi rongxarensis* **subspec. nov.** is described from the Rongxar Valley of the Mt. Everest area. *I. baileyi songi* **subspec. nov.** is described from NE Tibet and SE Qinghai. *Issoria baileyi milarepa* KOCMAN, 1999 is removed from synonymy with *I. baileyi* (HUANG, 1998). All previous subspecies of *I. eugenia* (EVERSMANN, 1847) from the Tibetan Plateau and the Himalayas are confirmed to be subspecies of *I. altissima* (ELWES, 1882).

Introduction: The large-sized *Issoria lathonia* (LINNAEUS, 1758) and *I. issaea* (DOUBLEDAY, [1847]) are not treated in this paper. The small-sized species treated herein were grouped by REUSS (1921) in the subgenus *Kuekenthaliella* REUSS, 1921. DE MOYA et al.'s (2017) molecular study of 4307 bp from COI, WG, GAPDH, RPS5, and EF1-alpha genes revealed significant divergence among the four clades of *Issoria* HÜBNER, represented by *I. eugenia* (EVER., 1847) (subgen. *Kuekenthaliella* REUSS), *I. hanningtoni* (ELWES, 1889) (subgen. *Prokuekenthaliella* REUSS, [1927]), *I. smaragdifer* (BUTLER, 1895) (subgenus undefined), and *I. lathonia* (L.) (subgen. *Issoria* HÜBNER). Our study incorporating additional *Kuekenthaliella* taxa and *I. baumannii* (REBEL & ROGENHOFER, 1894), based on 1814 bp of COI and EF1-alpha genes, supports this conclusion, showing four distantly divergent sub-clades within *Issoria* HÜBNER: *I. baumannii* (REBEL & ROGE.) belongs to subgen. *Prokuekenthaliella* REUSS, while the *Kuekenthaliella* taxa form a closely clustered sub-clade that warrants recognition as a distinct subgenus.

For a long time, two taxonomic problems of the subgen. *Kuekenthaliella* REUSS have remained unsolved: one concerns the relationship between *I. eugenia* (EVERSMANN, 1847) and *I. altissima* (ELWES, 1882); the other concerns the status of *I. baileyi* (HUANG, 1998) and *I. gemmata wui* (HUANG, 1998).

In a locality on the eastern slope of the Mila Pass, ♂ specimens resembling *I. eugenia* *genia* (FRUHSTORFER, 1903) were found flying together with those resembling *I. altissima* (ELWES) (Fig. 44). Similarly, in a western locality (Rongxar Valley of the Mt. Everest area), a few small *I. altissima* (ELWES)-like specimens were found flying with normal *I. altissima mackinnonii* (DE NICÉVILLE, 1891) specimens (Fig. 19). As shown in Fig. 51, these extreme forms connect the traditional *I. eugenia* (EVERSMANN) and *I. altissima* (ELWES). Molecular work on both mt-DNA and nu-DNA fragments reveals no divergence among all populations of this species complex within the Tibetan limit. However, the nominotypical subspecies of *I. eugenia* (EVERSMANN) from Siberian areas shows a small but clear divergence in the molecular phylogeny, and this gap is confirmed by a small yet clearly defined difference in ♂ genitalia, where the true *I. eugenia* (EVERSMANN) has a markedly broader valva.

HUANG (1998: 235) noted the remarkable differences (in size and apical process of valva) in ♂ genitalia between *I. baileyi* (HUANG) and *I. gemmata wui* (HUANG) and observed that the two taxa are nearly sympatric at Duoxiongla Pass, which is only 4300 m high and does not form a barrier to isolate these two taxa. Such a distribution pattern can be explained by the two taxa sharing identical niches, thus being unable to coexist indefinitely in the same locality. However, from a critical perspective, it could also be explained by geographical variations within a single species (TUZOV & BOZANO, 2017), despite their differences in ♂ genitalia, the stability and taxonomic value of which have never been tested in this genus. Further field work in recent years has led to new discoveries, including a new population of *I. baileyi* (HUANG) found west of *I. gemmata* (BUTLER), exhibiting an equally small size and the same genitalia as in the eastern populations of *I. baileyi* (HUANG). Nevertheless, there remains no sympatric record within this small complex [*I. gemmata* (BUTLER), *I. baileyi* (HUANG), and *I. gemmata wui* (HUANG)], making molecular analysis necessary. This analysis concluded that not only is *I. baileyi* (HUANG) a valid species, but *I. wui* (HUANG) **stat. nov.** also deserves full species status.

Abbreviations:

SHNU: Biological laboratory of Shanghai Normal University, Shanghai, P.R. China.

CHH: Collection of HAO HUANG, Qingdao.

CSK: Collection of KUI SONG, Xining.

CWZJ: Collection of ZHEN-JUN WU, Fuzhou.

TL: Type locality.

Method. Two fragments of the nuclear EF1-alpha gene (1053 bp) and the 'Jerry-Pat2' fragment of the mtDNA COI gene (761 bp) were analyzed to infer phylogenetic relationships.

DNA extractions were conducted by Beijing Tsingke Biotech Co., Ltd. (Beijing, China). The primers used are shown in Tables 1-2. Sequence matrices were aligned by Cluster W and edited manually using MEGA 11 (TAMURA et al. 2021). Construction of the phylogenetic tree was performed by Maximum likelihood (ML) method using IQ-TREE as implemented in the web online server (TRIFINOPOULOS et al. 2016), with branch support values evaluated based on 1000 replicates for SHaLRT and ultrafast bootstrap. The substitution model was set to "Auto" for the combined analysis of different genes. In addition to the material sequenced in this work, some *Issoria* examples with their genes obtained from NCBI GenBank were also included in the molecular analysis.

Table 1. Forward and reverse primers names in this study

Gene	Forward primers	Reverse primers	References
COI part2	Jerry	Pat2	SIMON et al., 1994; YI et al. 2017
EF1-alpha part1	ef135	ef684	KANDUL et al., 2004
EF1-alpha part2	ef51.9	efrcM4(r)	CHO et al., 1995

Table 2. Primers sequences in this study

Primers	Sequences	Annealing temperature
Jerry	CAACATTTATTTTGATTTTTT	48-52
Pat2	TCCATTA CATATAATCTGCCATATT	48-52
ef135	CAAATGYGGTGGTATYGACAAACG	55
ef684	TCCTTRCGCTCCACSTGCCAYCC	55
ef51.9	CAR GAC GTA TAC AAA ATC GG	50
efrcM4(r)	ACA GCV ACK GTY TGY CTC ATR TC	50

The mitochondrial COI gene sequences of the *Issoria* specimens examined in this study have been deposited in GenBank under accession numbers PV774412- PV774423. Additionally, the two fragments of the EF1-alpha sequences are available under accession numbers PV786779- PV786794 and PV786795- PV786810.

All sequenced specimens are associated with voucher numbers, which are clearly indicated in dark red within the relevant figures.

Genus *Issoria* HÜBNER, [1819]
Subgenus *Kuekenthalia* REUSS, 1921

Molecular phylogeny: NuDNA phylogeny based on EF1-alpha fragments (Fig. 72) reveals relatively deep divergences between *I. baileyi* (HUANG, 1998), *I. wui* (HUANG, 1998) **stat. nov.** and *I. gemmata* (BUTLER, 1881). However, the relationships between the traditional subspecies of *I. eugenia* (EVERSMANN, 1847) remain unresolved, apparently due to the limited sequence data of this DNA fragment. Similarly, these relationships are unresolved in the mtDNA tree based on the COI fragment. To solve this problem, additional sequences from more gene fragments need to be included in future analyses. For the present study, an effective approach is to analyze the combined data of COI and EF1-alpha genes, which shows (fig. 73) that all traditional subspecies of *I. eugenia* (EVER.) cluster into a single clade, with *I. eugenia eugenia* (EVER.) appearing as a more distantly divergent basal node. Therefore, all Tibetan subspecies of *I. eugenia* (EVERS.) could be separated from *I. e. eugenia* (EVER.) at the species level and combined with *I. altissima* (ELWES, 1882) into a single species. This conclusion is further supported by morphological evidence [e.g., the wider valva in *I. eugenia* (EVER.)] and the zoogeographical isolation between Siberian and Tibetan fauna.

I. baileyi (HUANG) and *I. wui* (HUANG) **stat. nov.** cluster together but show considerable genetic divergence. They are not considered conspecific because: 1) there is a deep genetic gap between them in the nuDNA tree; 2) they do not cluster together in the mtDNA COI tree to form a monophyletic clade - instead, *I. baileyi* (HUANG) clusters with *I. gemmata* (BUT.); 3) both species exhibit geographical variations that are relatively consistent in adult size and genitalia morphology; 4) they show nearly sympatric distribution at Duoxiongla despite remarkable differences in genitalia.

It is noteworthy that a DNA sample of *I. baileyi* (HUANG) collected from Mila Pass (hhk08; marked in pink on the trees) shares identical mt-DNA COI sequences with sympatric *I. altissima* (ELWES) from the same locality, potentially indicating hybridization between these two *Issoria* species. However, nuclear DNA (nuDNA) analysis of the same specimen reveals sequences identical to those of other *I. baileyi* (HUANG) specimens.

Genitalia morphology: ♂ genitalia show some individual variation, except for the development of an inner process of the valva, which consistently distinguishes the *I. gemmata* (BUT.) complex from the *I. eugenia* (EVERS.) complex. The two complexes are sympatric at many localities but occupy different biological niches. However, no consistent differences were found in ♀ genitalia between any species, except for measurements of structures. The size of ♂ genitalia, height of the costa of the valva, and appearance of the apical process of the ampulla serve as diagnostic characters for species separation within the *I. gemmata* (BUT.) complex.

Subspecies concept: Due to the short length of the DNA fragments, subspecies relationships cannot be resolved by such limited molecular phylogenetic data. This study follows the subspecies concept proposed by HUANG (2024). When a concentrated range consisting of immediately connected localities contains individuals that are >95% diagnosable from those in another clearly defined and limited range, the populations from these two ranges are considered different subspecies, with transitional populations omitted from definitions. Under this classification, intermediate populations that are <95% diagnosable from others remain unnamed and may be assigned to the closest subspecies or treated as transitional populations. If we adopted a stricter concept requiring all populations to be included in subspecific taxa with >95% diagnosability, no subspecies would remain and all geographical variation would be disregarded. To establish a meaningful classification of geographical variation, certain transitional populations must be excluded from taxonomic delineation. Otherwise, no subspecific differentiation would be recognized within this continental species.

***Issoria eugenia* (EVERSMANN, 1847)**

***Issoria eugenia eugenia* (EVERSMANN, 1847)** (figs. 31, 45, 57, 61, 63-64)

Argynnis eugenia EVERSMANN, 1847: 68 (TL: in provincia Irkuzkiensis).

Argynnis eugenia var. *montana* BANG-HAAS, 1906: 127 (TL: Altai-Gebirge).

Issoria eugenia: WARREN, 1956: 384.

Issoria eugenia eugenia: LANG, 2012: 94, record from Altay, Xinjiang, pl. IX, fig. 3 for 1 ♂ from Xinjiang.

Material. 1 ♂ (CHH), W Mongolia, 1700 m, 27.VII.2010, ex. coll. KRUPITSKY; 1 ♂ (CHH), Russia, Permsky Krai, 22.VII.1991, ex. coll. KRUPITSKY.

Remarks. The mtDNA phylogeny, based on the COI fragment, does not cluster this taxon with the remaining Chinese subspecies of *I. eugenia* (EVERSMANN) from the Tibetan Plateau. Specifically, these subspecies do not form a monophyletic clade. Similarly, the nuD-

NA phylogeny, reconstructed using EF1-alpha fragments, also fails to support the monophyly of the traditionally defined *I. eugenia* (EVERSMANN).

The combined phylogenetic analysis places *I. eugenia eugenia* (EVERSMANN) in a clade with the other subspecies of *I. eugenia* (EVERSMANN), but it appears as a distantly divergent lineage at a basal node. Given these findings, this taxon is best treated as distinct from the other Chinese subspecies at the species level. This conclusion is further supported by morphological evidence (e.g., the wider valva in ♂ genitalia) and its remote zoogeographical isolation.

***Issoria eugenia vega* (CHRISTOPH, 1889)** (outside China)

Argynnis Eugenia (v.) *Vega* CHRISTOPH, 1889: 298 (TL: middle flow region of Lena river, Russia).

Material. None.

Remarks. Although this taxon was not included in the analysis, its wing morphology and distribution pattern undoubtedly place it within *I. eugenia* (EVERSMANN).

***Issoria altissima* (ELWES, 1882)**

***Issoria altissima altissima* (ELWES, 1882)** (figs. 16, 18, 54, 58-59, 62-64, 70)

Argynnis Altissima ELWES, 1882: 403 (TL: Chumbi valley on the Tibetan frontier of Sikkim), pl. 25, fig. 8.

Issoria gemmata altissima: WARREN, 1956: 384.

Issoria altissima: LANG, 2012: 95, partim on record from Phari Jong, Tibet, pl. IX, fig. 10 for 1 ♂ from Phari Jong.

Material. As shown in figs. 16 and 18.

Remarks. The sequenced specimen from Phari (near the type locality) shows no genetic divergence from a sample of *I. altissima mackinnonii* (DE NICÉVILLE, 1891) in both mtDNA COI and nuDNA EF1-alpha sequences. However, another specimen of *I. altissima mackinnonii* (DE NICÉ.) from a more western locality does not cluster with them. This results in no clear genetic differentiation between the traditionally recognized *I. altissima* (Elwes) and *I. eugenia* (Eversmann) in Tibetan limit.

***Issoria altissima mackinnonii* (DE NICÉVILLE, 1891)** (figs. 17, 19, 35, 51-top, 53, 58-59, 62-64, 66, 70)

Argynnis mackinnonii DE NICÉVILLE, 1891: 346 (TL: north side of Gonas Pass, about half-way between the Pass and the Baspa Valley [now also known as Sangla Valley, a tributary of Sutlej], in previous Basahir; about 31.28-31.39 N, 78.23-78.49 E).

Issoria altissima annapurnae SMITH, 1993: 63 (TL: Annapurna, Nepal). Nomen nudum.

Material. As shown in figs. 17, 19 and 35.

Remarks. Although some individuals (figs. 17, 19 - m25) found within the range of *I. a. mackinnonii* (DE NICÉ.) resemble *I. a. altissima* (ELWES), such individuals can be distinguished from true *I. a. altissima* (ELWES) by their shorter cell streak and broader marginal markings on the hindwing underside. This subspecies deserves retention, as it occupies a vast geographic range and exhibits minimal variation.

***Issoria altissima rhea* (GRUM-GRSHIMAILO, 1891) comb. nov.** (figs. 20, 27, 34, 40, 46, 57, 61, 64, 68, 70)

Argynnis Eugenia var. *Rhea* GRUM-GRSHIMAILO, 1891: 456 (TL: In Amdo, in montibus ad lacum Kuku-Noor et in Njan Schan centrali).

Argynnis eugenia fulgens BANG-HAAS, 1927: 52 (TL: Kansu, Richthofen mont. westl. Liang-tschou).

Issoria eugenia xuanzang SAKAI, 2024: 1 (TL: Taibai Shan (Zhouzhi), Qin Ling Mts.), pl. 2, figs. 21-22. **syn. nov.**

Material. As shown in figs. 20, 27, 34, 40 and 46.

Remarks. This subspecies is distinguished in both sexes by possessing broader hindwings with a higher width-to-length ratio compared to all other subspecies. On the upper side, ♀♀ are brighter brown than those of *I. a. genia* (FRUH.) **comb. nov.**, but darker than those of *I. a. pulchella* (HUANG, 2001) **comb. nov.**, showing less distinct hindwing basal dusting.

The holotype of *Issoria eugenia xuanzang* SAKAI, 2024 shows no diagnostic differences from certain individuals collected in Gansu. Mr. YU-FEI LI (personal communication) confirmed the occurrence of this taxon in the Taibaishan Mountains, while noting that the specimens cannot be reliably distinguished from those originating from Gansu.

***Issoria altissima genia* (FRUHSTORFER, 1903) comb. nov.** (figs. 28, 33, 47, 57, 60-61, 63, 67-68, 70)

Argynnis eugenia genia (FRUHSTORFER, 1903: 124 (TL: Ta-tsien-lou).

Argynnis eugenia anargyron OBERTHÜR, 1914: 46 (TL: Ta-chien-lu).

Kuekenthaliella eugenia f. *rheaoidea* REUSS, in DRAESEKE & REUSS, 1925: 218 (TL: Szechuan).

Material. As shown in figs. 28, 33 and 47.

Remarks. The ♂♂ possess narrower hindwings than those of *I. a. rhea* (GR.-GRSH.) **comb. nov.**, while the ♀♀ exhibit darker upper sides on both wings with more extensive blackish scale dusting, particularly in the basal and subbasal areas.

***Issoria altissima pulchella* (HUANG, 2001) comb. nov.** (figs. 22, 32, 36, 42, 50, 58, 60, 62-64, 67, 70)

Kuekenthaliella eugenia pulchella HUANG, 2001: 90 (TL: Demula); TUZOV, 2003: 44, synonymy for *I. eugenia genia* (FRUHSTORFER, 1903).

Material. As shown in figs. 22, 32, 36, 42 and 50.

Remarks. The marginal silvery spots on the hindwing underside all feature triangular inner halves that are sharply pointed inward, unlike the obtusely pointed or rounded shapes found in other subspecies; this characteristic serves as a consistently reliable diagnostic feature for defining this subspecies. The hindwing underside displays uniform cinnamon-red coloration that strongly contrasts with the remaining yellow patches and silvery markings; however, this trait frequently occurs in transitional populations from NE Tibet and the Mila Pass area. ♀♀ exhibit bright brown ground coloration on the upper side, lacking the black dusting present in *I. a. genia* (FRUH.) **comb. nov.**, and show more clearly defined hindwing basal dusting compared to *I. a. rhea* (GR.-GRSH.) **comb. nov.**

Transitional Populations between *I. a. pulchella* (HUANG, 2001) comb. nov. and *I. a. genia* (FRUHSTORFER, 1903) comb. nov.

Material. As shown in figs. 21, 30, 37, 41 and 49.

Remarks. While most ♂♂ are morphologically indistinguishable from those of *I. a. genia* (FRUH.) **comb. nov.**, ♀♀ uniformly exhibit bright brown dorsal wing coloration resembling *I. a. pulchella* (HUANG) **comb. nov.** However, their ventral wing patterns show greater similarity to those of *I. a. genia* (FRUH.) **comb. nov.**

***Issoria altissima tsonaensis* YOSHINO, 2022** (figs. 24, 39, 43, 67)

Issoria altissima tsonaensis YOSHINO, 2022: 86 (TL: Tsona), figs. 15-16.

Material. As shown in figs. 24, 39 and 43.

Remarks. This subspecies classification remains valid under the methodological approach of excluding transitional populations from taxonomic consideration. It differs from *I. a. altissima* (ELWES) in possessing a shorter cell streak and more robust marginal silvery spots on the hindwing underside. These characteristics remain relatively stable among populations from Tsona, though a transitional population occurs at Mila Pass where some individuals approach *I. a. tsonaensis* YOSHINO while others more closely resemble *I. a. pulchella* (HUANG) or *I. a. genia* (FRUH.).

Transitional Populations between *I. a. pulchella* (HUANG, 2001) comb. nov. and *I. a. tsonaensis* YOSHINO, 2022

Argynnis eugenia rheia: EVANS, 1915: 540, pl. fig. for ♂ from Lu (Lang-xian) on the Tsang Po.

Material. As shown in figs. 23, 38 and 44.

Remarks. As illustrated in fig. 23, specimens et7, et9, and et10 are morphologically indistinguishable from *I. a. tsonaensis* YOSHINO, while specimen et13 closely resembles *I. a. pulchella* (HUANG) and specimen et12 approximates *I. a. genia* (FRUH.). Under an overly strict subspecies concept that attempts to incorporate all transitional populations, only the nominotypical subspecies would retain taxonomic validity, rendering all other subspecific names untenable.

***Issoria altissima tibetana* (HUANG, 1998) comb. nov.**

Kuekenthaliella eugenia tibetana HUANG, 1998: 250 (TL: N Tsochen); TUZOV, 2003: 44, synonymy for *I. eugenia genia* (FRUHSTORFER, 1903).

Material. As shown in figs. 29, 48, 58 and 61.

Remarks. The most notable aspect is that this subspecies occurs in proximity to the range of *I. a. mackinnonii* (DE NICÉ.), yet exhibits wing patterns resembling *I. a. genia* (FRUH) and *I. a. pulchella* (HUANG). This distribution pattern may indicate historical derivation from northern or eastern populations. It can be distinguished from eastern subspecies by two diagnostic characters: (1) markedly brighter and more reddish dorsal ground coloration, and (2) reduced reddish patches on the ventral hindwing surface.

***Issoria gemmata* (BUTLER, 1881) (figs. 3, 10, 52, 57, 59, 60, 63-65, 69)**

Argynnia gemmata BUTLER, 1881: 32 (TL: Darjiling; between Nepal and Tibet), pl. 4, figs. 1, 1a.; Elwes, 1882: 404, record from Chumbi valley on the Tibetan frontier of Sikkim, pl. XXV, figs. 6-7.

Issoria gemmata: WARREN, 1956: 384, pl. IV, fig. 34 for ♂ genitalia from Sikkim.

Material. As shown in figs. 3 and 10.

Remarks. WARREN (1956)'s illustration of the ♂ genitalia depicts an abnormal form characterized by an unusually narrow apical process of the ampulla. However, the costa of the valva in this species consistently exhibits greater height compared to related species.

***Issoria baileyi* (HUANG, 1998)**

***Issoria baileyi baileyi* (HUANG, 1998) stat. rev.** (figs. 6, 13, 60, 65, 66, 69)

Argynnis gemmata genia: EVANS, 1915: 540, pl. fig. for ♂ from the high country south of the Tsang Po.

Argynnis gemmata genia variety *fulva* nov. EVANS, 1915: 540. (Infrasubspecific & unavailable in nomenclature).

Kuekenthaliella baileyi HUANG, 1998: 234 (TL: Pai, Milin); TUZOV, 2003: 45, synonymy for *I. gemmata* (BUTLER, 1881).

Issoria gemmata baileyi: TUZOV & BOZANO, 2017: 66.

Material. As shown in figs. 6 and 13.

Remarks. The ♀ exhibits clearly defined black basal dusting on the hindwing upper side, with a distinct outer margin.

***Issoria baileyi milarepa* KOCMAN, 1999 comb. nov.** (figs. 5, 14, 57, 60, 63, 64, 66, 69)

Issoria gemmata milarepa KOCMAN, 1999: 59 (TL: Drigung Til, E Lhasa Pref.); TUZOV, 2003: 45, synonymy for *I. gemmata* (BUTLER, 1881); TUZOV & BOZANO, 2017: 66, synonymy for *I. gemmata baileyi* (HUANG, 1998).

Material. As shown in figs. 5, 14 and 57.

Remarks. ♀♀ exhibit paler dorsal surfaces on both wings, with grayer basal dusting that appears diffusely margined distally.

***Issoria baileyi rongxarensis* subsp. nov.** (figs. 4, 11, 57, 60, 63, 69)

Type data. Male holotype (fig. 4- b11): S Tibet, Dingri County, Mt. Everest area, Rongxar valley, 4400 m, 3.VIII.2017, H. HUANG leg. Paratype: 2 ♂♂ (CHH), same data as holotype.

Etymology. This new subspecies is named after its type locality.

Diagnosis. The new subspecies is diagnostically distinct from all other subspecies by possessing the markedly longer marginal silvery spots on the hindwing underside that are more acutely pointed inward, resembling the condition in *I. gemmata* (BUTLER).

Remarks. Mr. ZHEN-JUN WU provided photographic documentation of a population from Nyalam County that represents this subspecies, exhibiting identical diagnostic characteristics.

***Issoria baileyi songi* subsp. nov.** (figs. 7, 12, 69)

Type data. ♂ holotype (fig. 7- b13): NE Tibet, On road from Biru to Soxian, 4000 m, 25.VI.2023, H. HUANG leg.; Paratypes: 3 ♂♂, 2 ♀♀ (CSK), S Qinghai, Yushu, Jiegu, VI-VII.2020, K. SONG leg.

Etymology. This new subspecies is named in honor of Mr. KUI SONG, Xining.

Diagnosis. The new subspecies is readily distinguished from all congeners in ♂♂ by: (1) conspicuously brighter and more saturated reddish ground coloration, and (2) significantly reduced hindwing basal dusting that typically fails to obscure the wing cell.

***Issoria wui* (HUANG, 1998) stat. nov.**

***Issoria wui wui* (HUANG, 1998) stat. nov.** (figs. 1, 8, 56, 57, 60, 63, 64, 65, 69)

Kuekenthaliella gemmata wui HUANG, 1998: 234 (TL: Nage, S of Duoxiongla, Motuo); TUZOV, 2003: 45, synonymy for *I. gemmata* (BUTLER, 1881).

Issoria gemmata wui: TUZOV & BOZANO, 2017: 66.

Material. As shown in figs. 1, 8, 56 and 57.

Remarks. No additional specimens have been collected since the original description, consequently genetic characterization of this taxon remains unavailable.

Issoria wui zhenjuni **subspec. nov.** (figs. 2, 9, 55, 57, 60, 63, 64, 69)

Type data. Male holotype (fig. 2- wz1): NW Yunnan, Gongshan County, Baihanluo, West slope of Biluoxueshan Mts., 3900 m, 23.VIII.2024, M. YE leg., ex coll. Z.-J. WU. Paratypes: 1 ♂, 1 ♀ (CWZJ), same data as holotype.

Etymology. This new subspecies is named in honor of Mr. ZHEN-JUN WU, Fuzhou.

Diagnosis. The new subspecies differs diagnostically from the nominotypical subspecies in the forewing pattern: the ante-discal spots in spaces 1b and 2 align linearly with the discocellular spot rather than with the spot in the cell.

Remarks. Mr. GIAN CRISTOFORO BOZANO documented a specimen series from Yubeng, north of Dêqin County, northwestern Yunnan (fig. 55), which we assign to this new subspecies based on congruent diagnostic characters.

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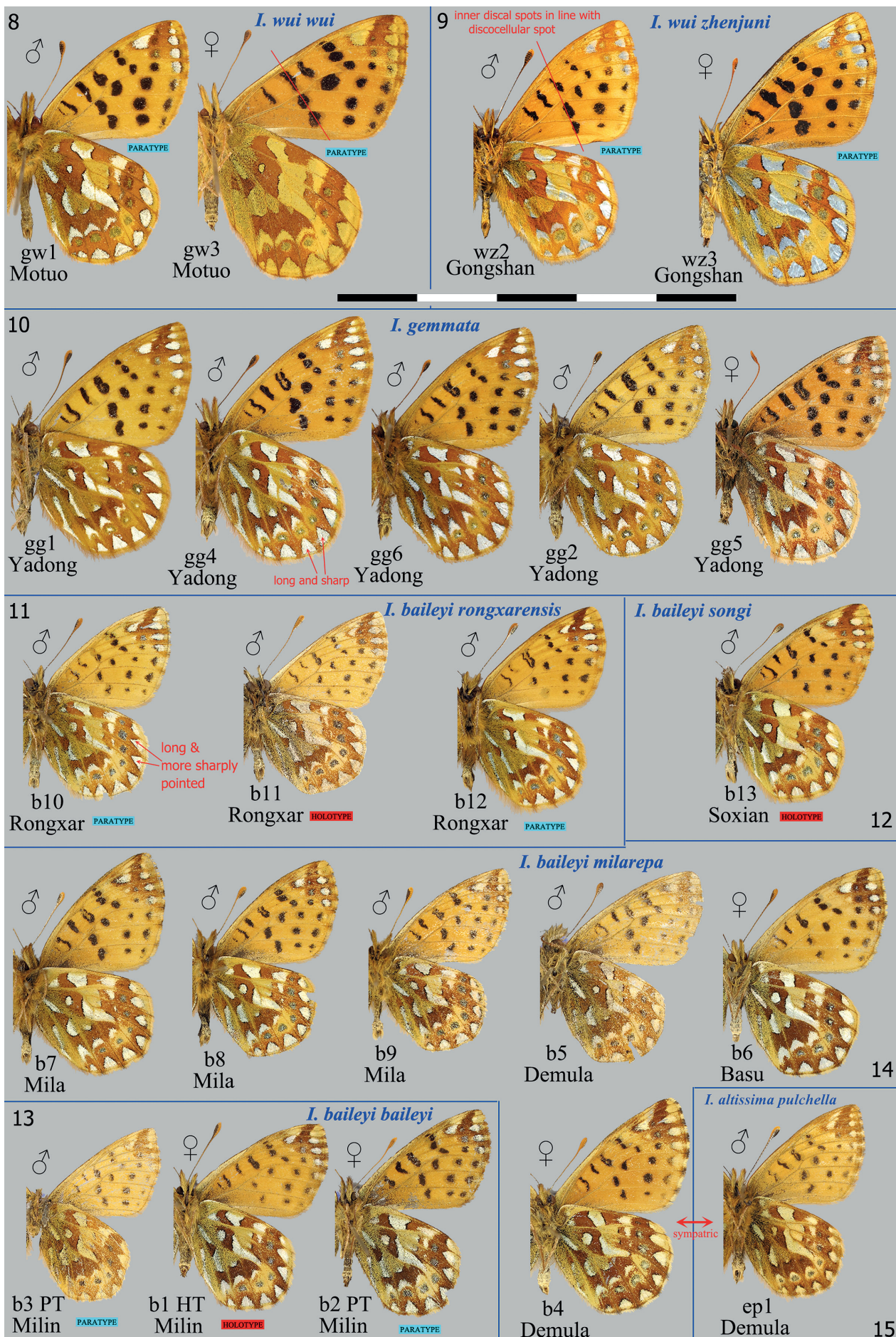
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Figs. 1-7: Habitus of *Issoria* taxa ♂♂ and ♀♀ under same scale.



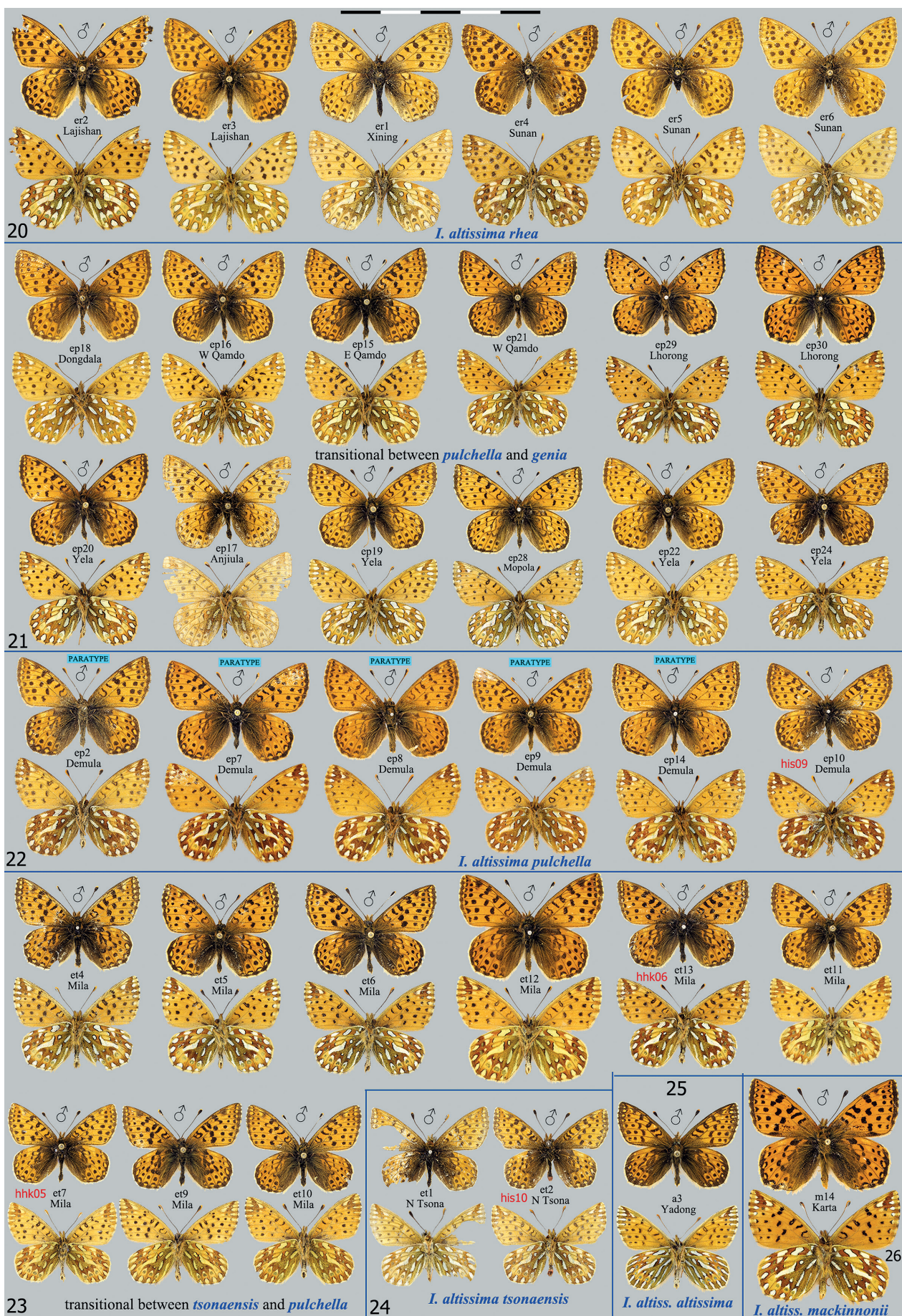
Figs. 8-15: Habitus of *Issoria* taxa ♂♂ and ♀♀ under same scale - underside.



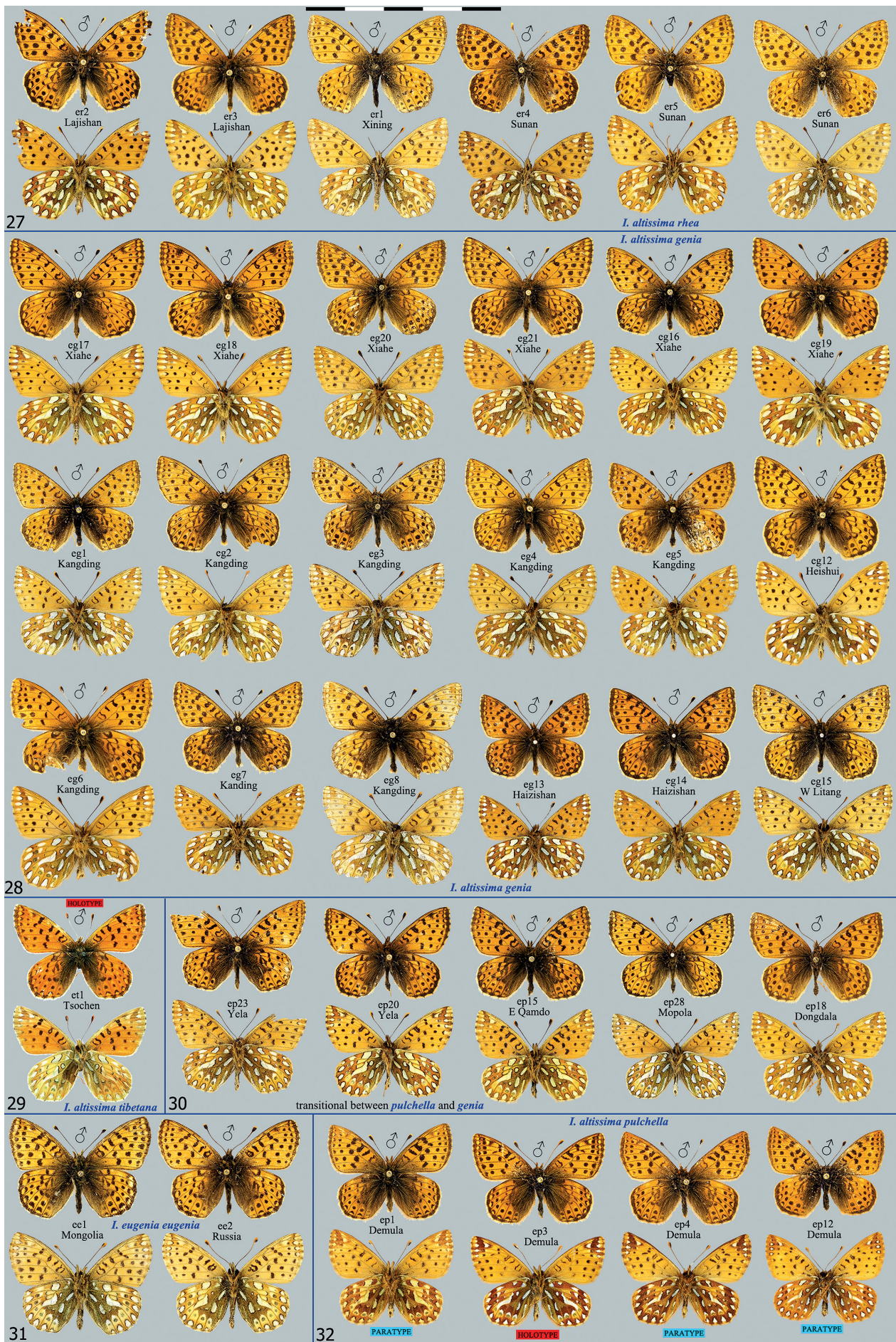
Figs. 16-17: Habitus of *Issoria* taxa ♂♂ and ♀♀ under same scale.



Figs. 18-19: Habitus of *Issoria* taxa ♂♂ and ♀♀ under same scale - underside.



Figs. 20-26: Habitus of *Issoria* taxa ♂♂ under same scale.



Figs. 27-32: Habitus of *Issoria* taxa ♂♂ under same scale.



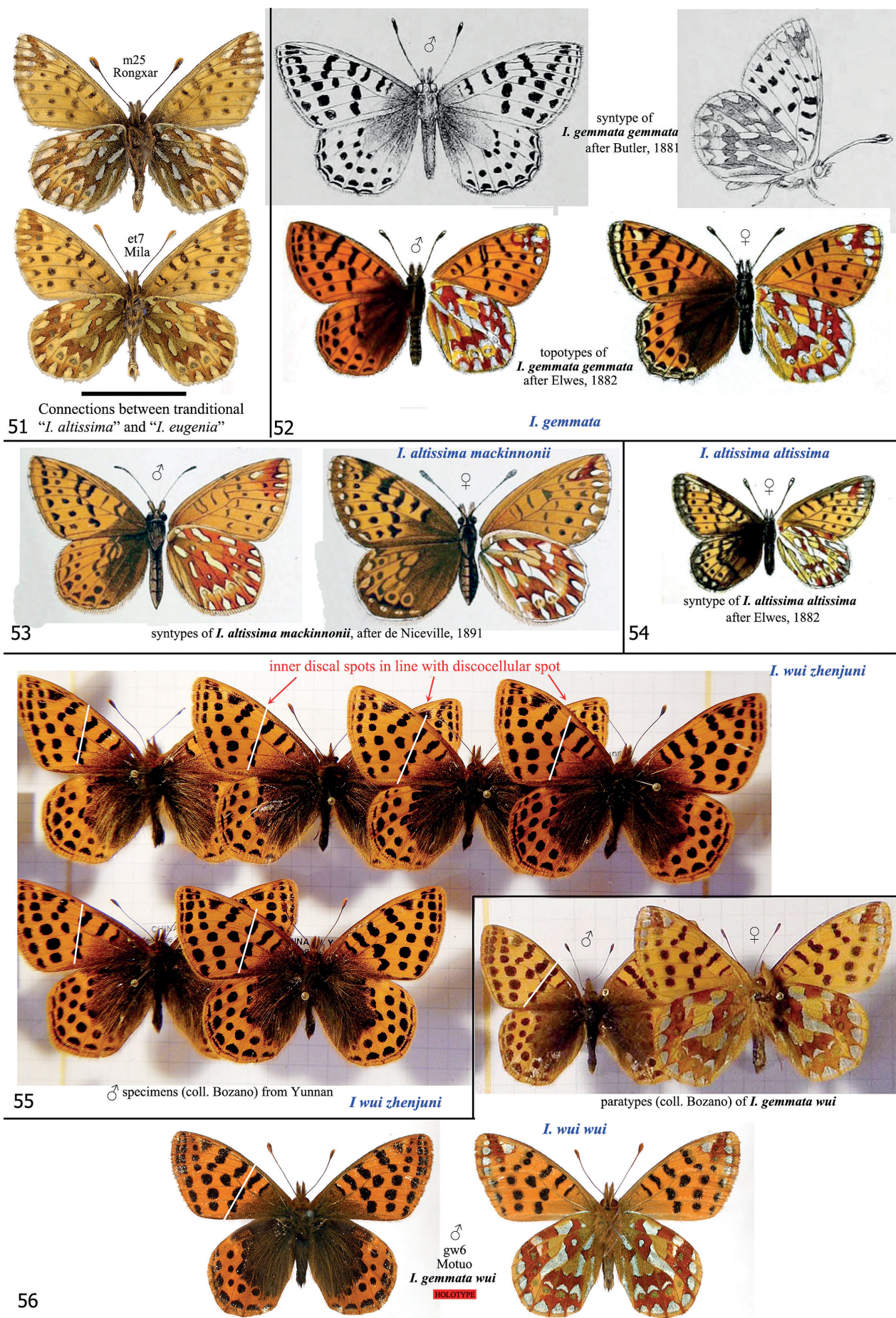
Figs. 33-39: Habitus of *Issoria* taxa ♀♀ under same scale.



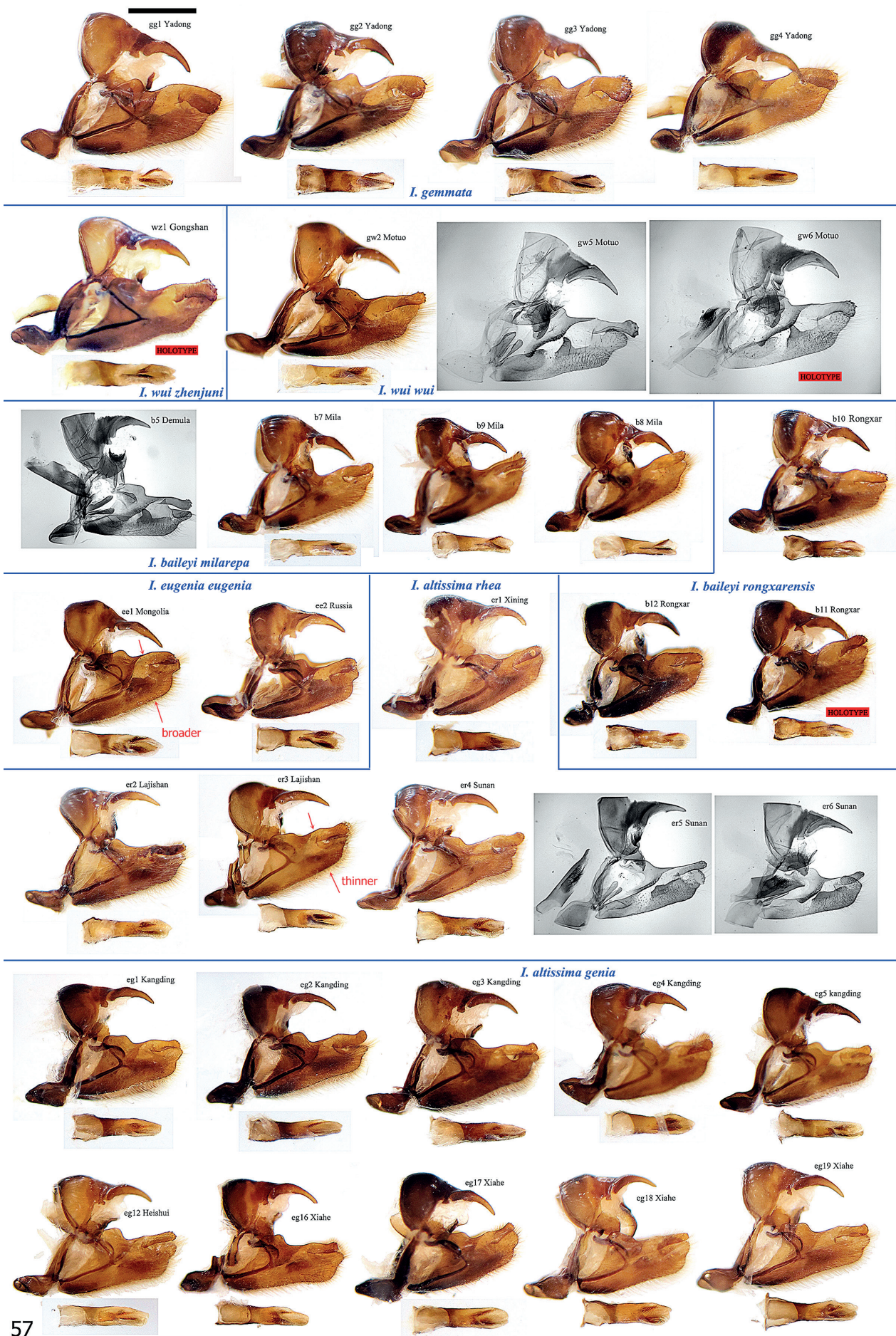
Figs. 40-44: Habitus of *Issoria* taxa ♂♂ under same scale - underside.



Figs. 45-50: Habitus of *Issoria* taxa ♂♂ under same scale - underside.



Figs. 51-56: Important specimens including special forms, type specimens figured in literature and type specimens.



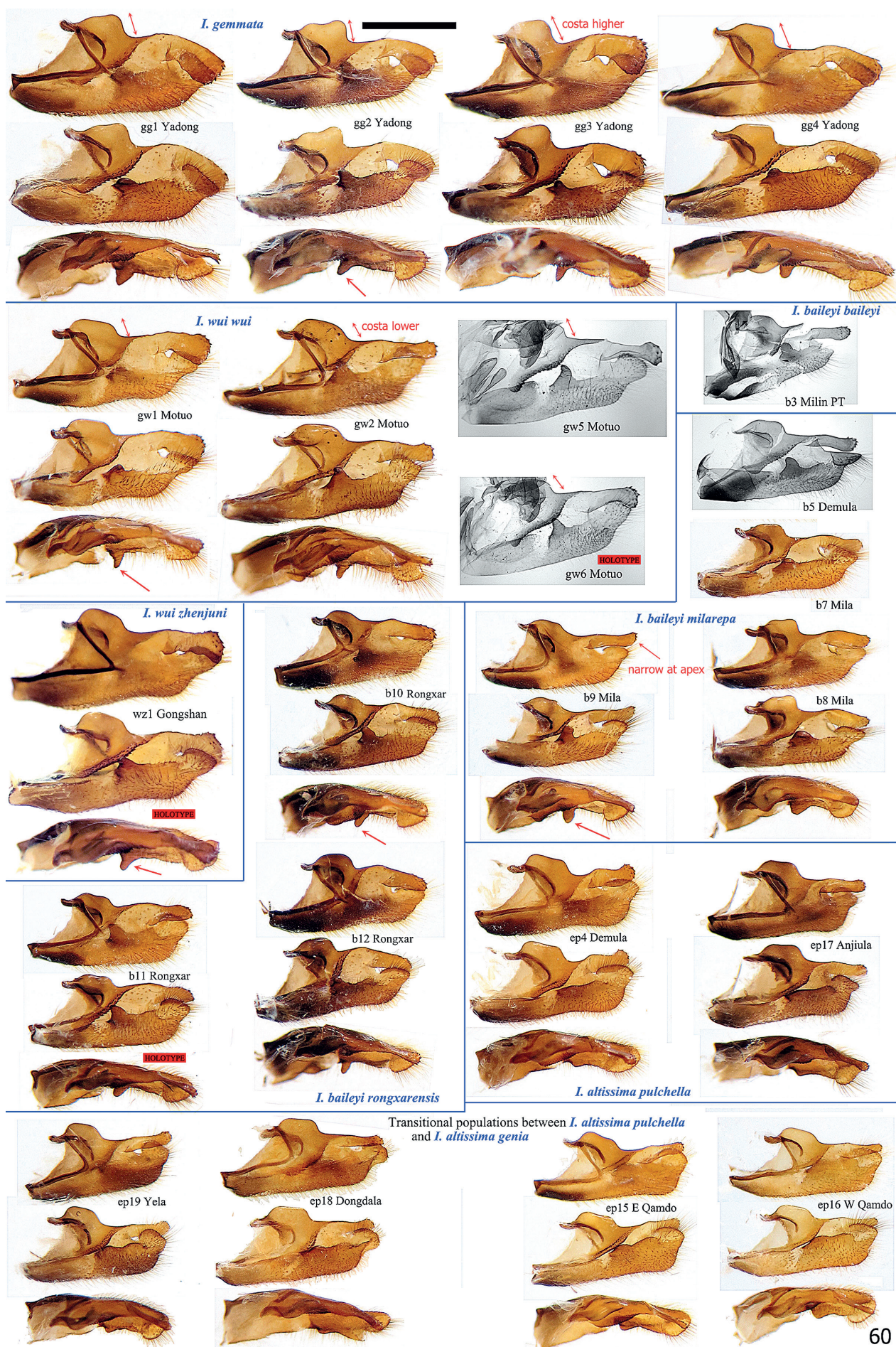
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Fig. 57: ♂ genitalia of *Issoria* taxa under same scale, consisting of whole genitalia in lateral view with aedeagus removed, and of aedeagus in dorsal view. Scale bar = 1 mm.



Fig. 58: ♂ genitalia of *Issoria* taxa under same scale, consisting of whole genitalia in lateral view with aedeagus removed, and of aedeagus in dorsal view.

Fig. 59: ♂ genitalia of *Issoria* taxa in posterior view



Figs. 60: ♂ genitalia of *Issoria* taxa under same scale, consisting of valva in outer lateral view, inner lateral view and dorsal view.

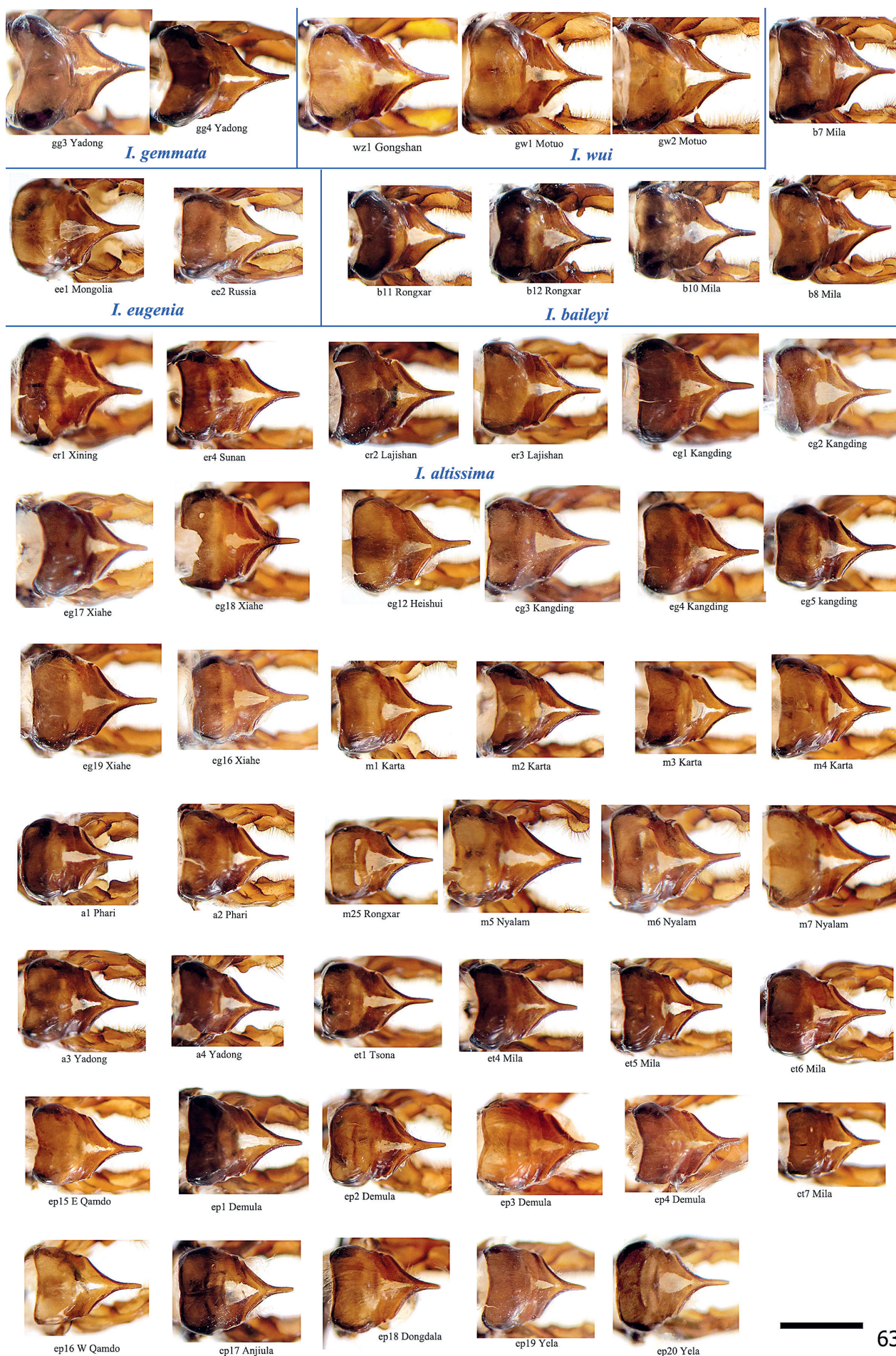


Figs. 61: ♂ genitalia of *Issoria* taxa under same scale, consisting of valva in outer lateral view, inner lateral view and dorsal view.



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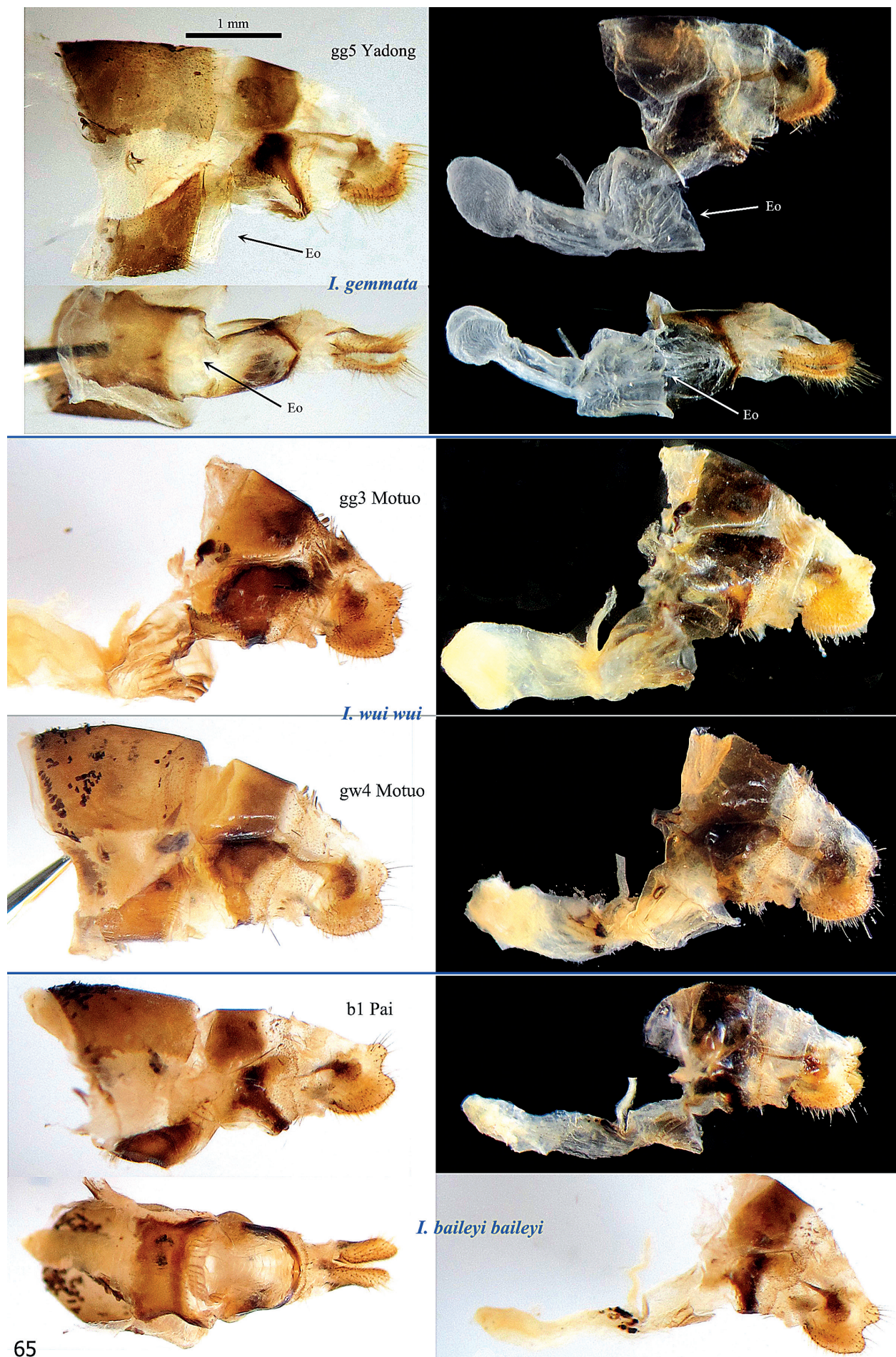
Figs. 62: ♂ genitalia of *Issoria* taxa under same scale, consisting of valva in outer lateral view, inner lateral view and dorsal view.



Figs. 63. Uncus of *Issoria* taxa in dorsal view.



Figs. 64. Aedoeagi of *Issoria* taxa in lateral, dorsal and ventral views.



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Fig. 65: ♀ genitalia of *Issoria* taxa under same scale, consisting of last segments in lateral and ventral views, and of genitalia in lateral and ventral views with lodix removed . Scale bar = 1 mm.

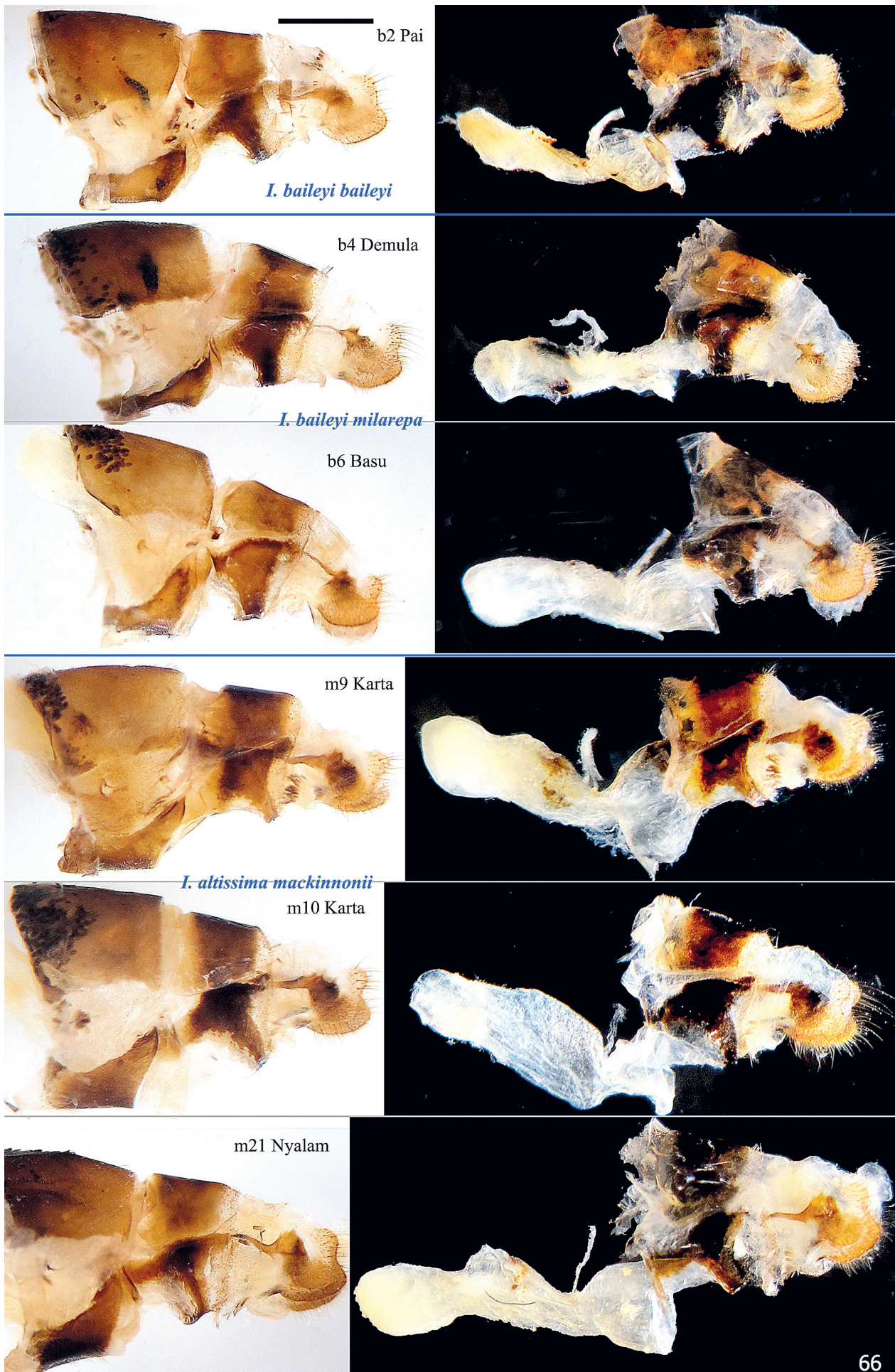


Fig. 66: ♀ genitalia of *Issoria* taxa under same scale, consisting of last segments in lateral view, and of genitalia in lateral view with lodix removed . Scale bar = 1 mm.

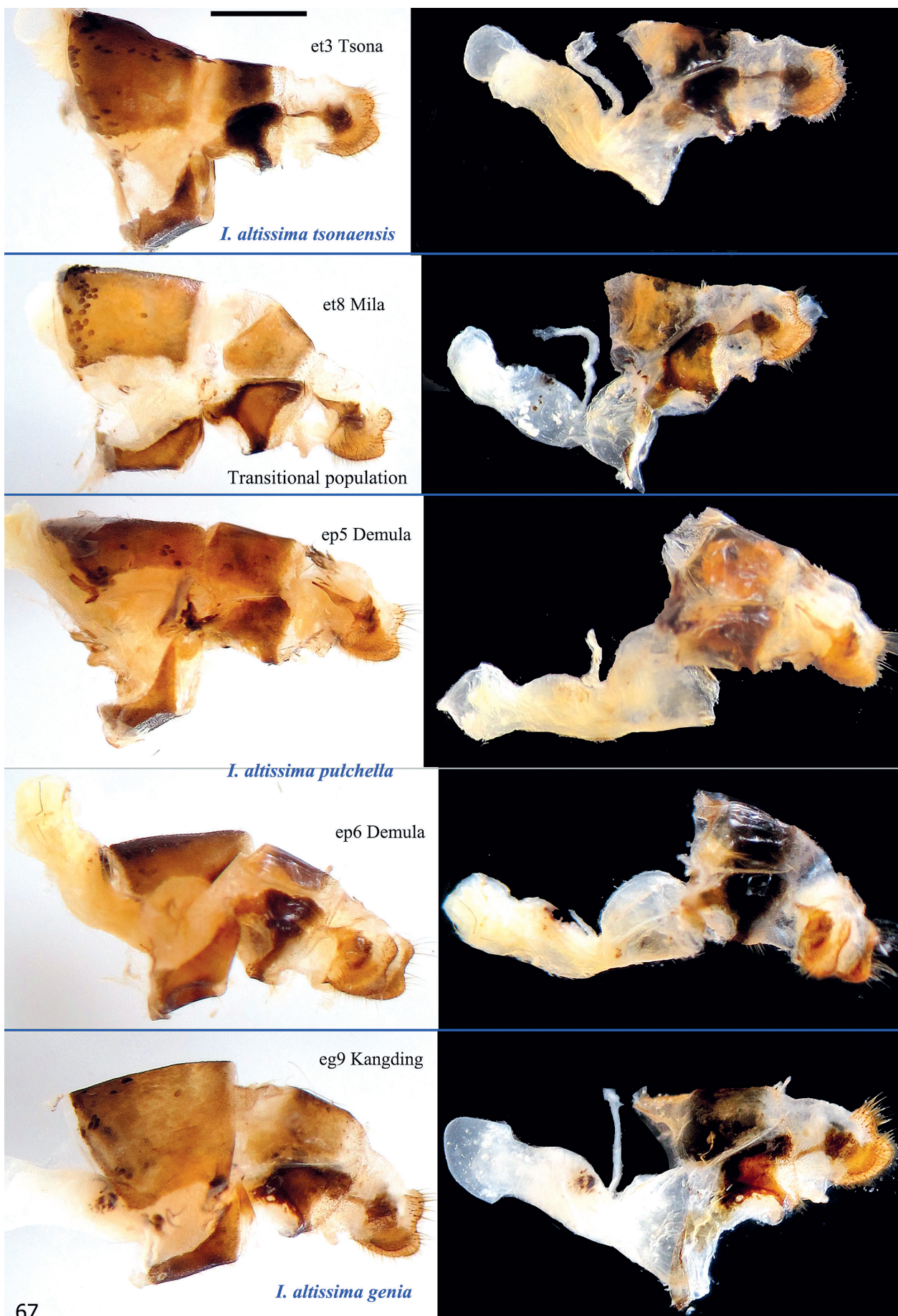


Fig. 67: ♀ genitalia of *Issoria* taxa under same scale, consisting of last segments in lateral view, and of genitalia in lateral view with lodix removed . Scale bar = 1 mm.

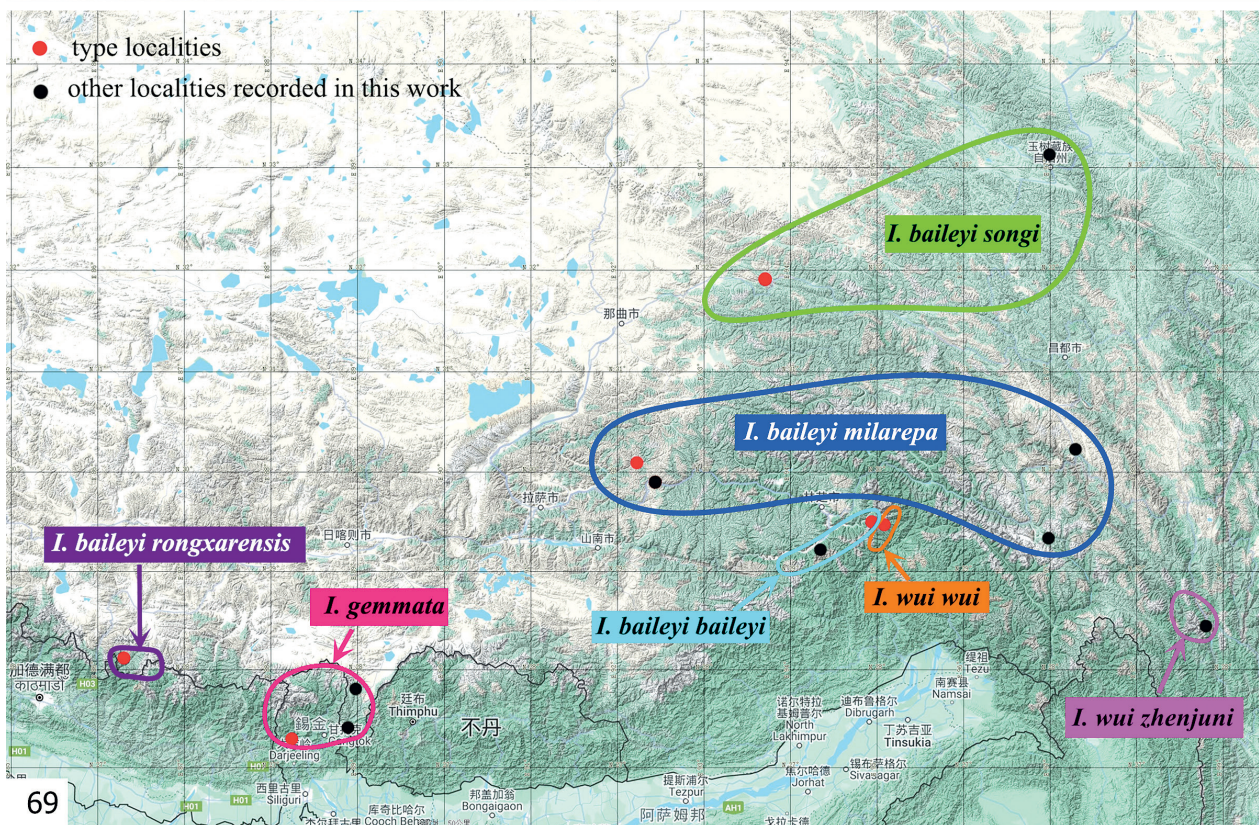
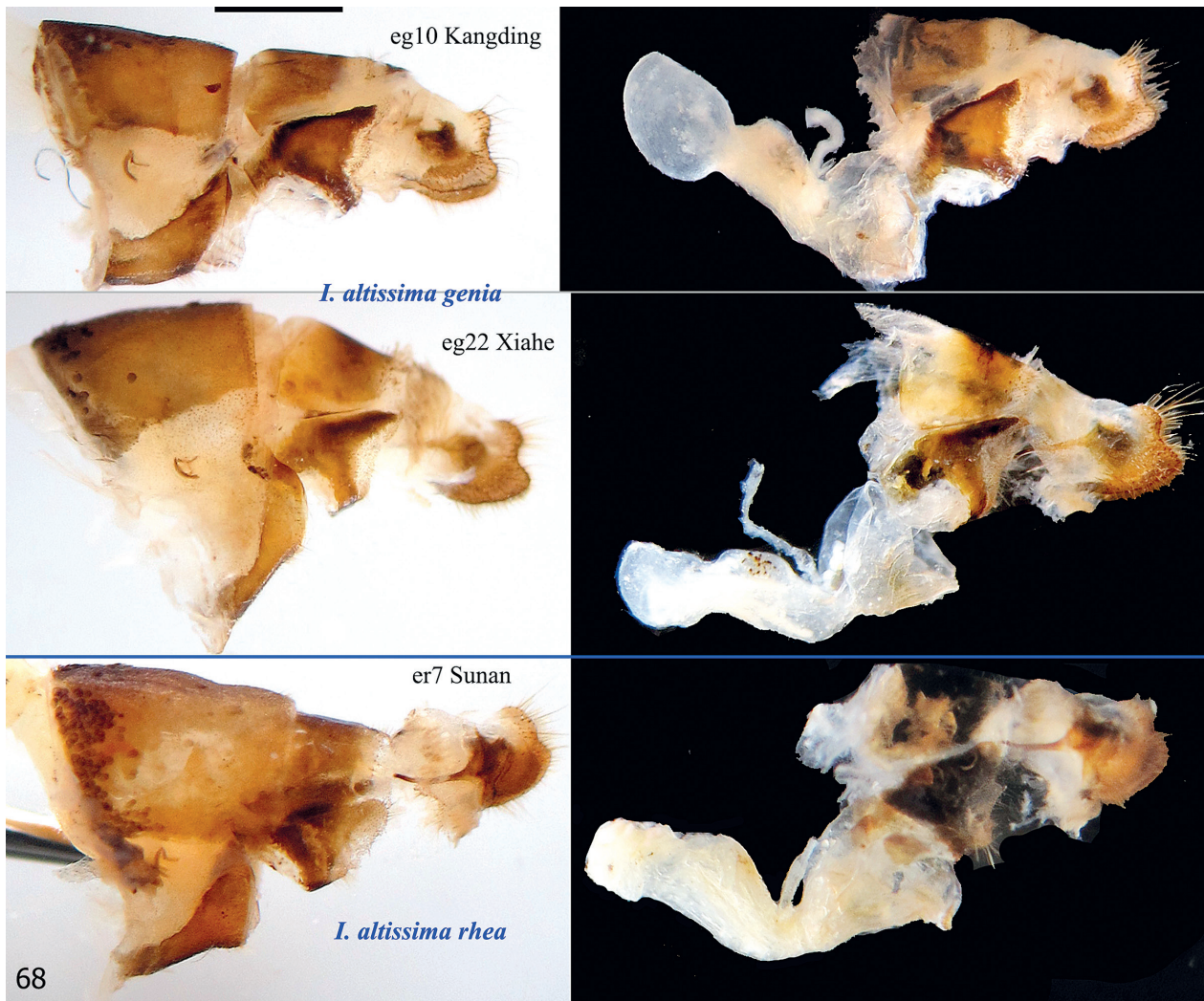
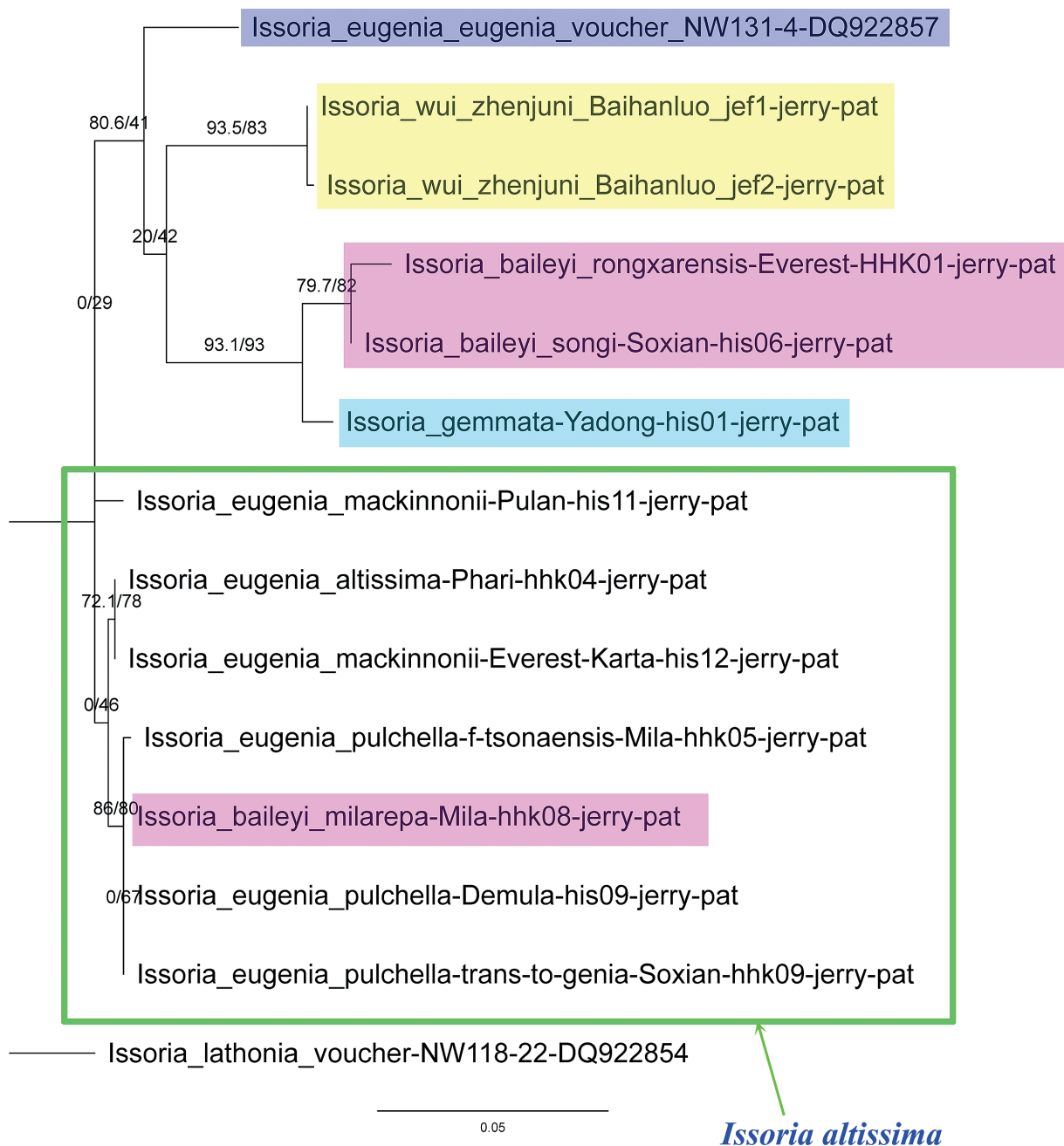


Fig. 68: ♀ genitalia of *Issoria* taxa under same scale, consisting of last segments in lateral view, and of genitalia in lateral view with lodix removed. Scale bar = 1 mm.

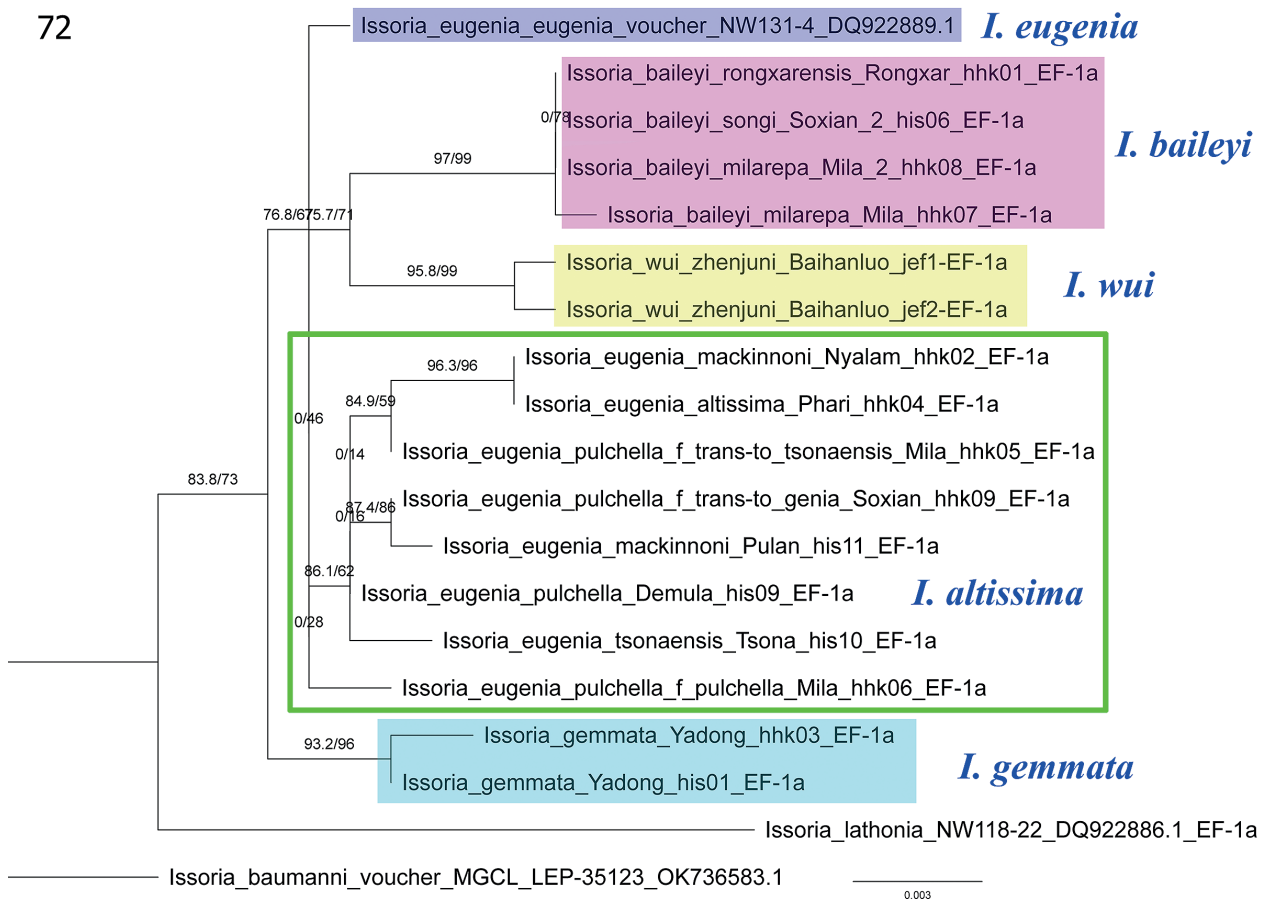
Fig. 69: Distribution of *Issoria gemmata* (BUTLER, 1881) complex.



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Fig. 71: mtDNA gene tree reconstructed by ML method using IQ-TREE based on COI fragment (761 bp).

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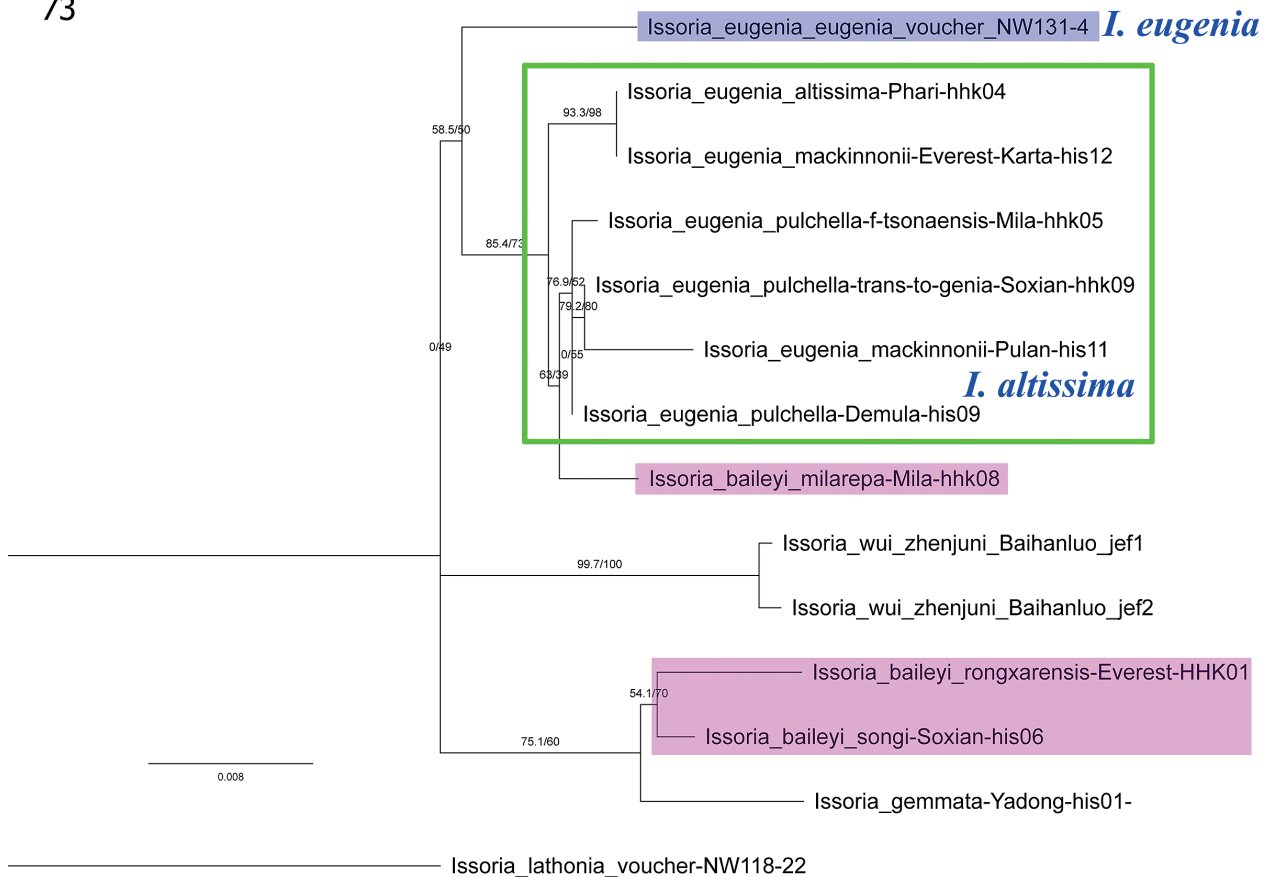


Fig. 72: nuDNA gene tree reconstructed by ML method using IQ-TREE based on two EF1-alpha fragments (1053 bp in total).
 Fig. 73: Combined gene tree reconstructed by ML method using IQ-TREE based on one COI fragment (761 bp) and two EF1-alpha fragments (1053 bp in total), with Auto substitution model.