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Luciargentis gen. nov., a New Genus Revealed by Morphological and Phylogenetic Evidence in the Family Lecithoceridae

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Simple Summary: The family Lecithoceridae is one of the most species-rich groups within the order Lepidoptera, yet it remains relatively underexplored. Currently, it comprises more than 1430 species across four subfamilies. Taxonomic studies of this family have primarily relied on morphological data, with molecular data been limited, which has hindered the development of its taxonomy. In this study, we try to establish a new genus based on the specimens from Tibet, China and examine its placement within the subfamily Crocanthinae, integrating both morphological and molecular evidence. Furthermore, the new genus provides additional insights that contribute to the ongoing discussion regarding the relationship between the subfamilies Torodorinae and Crocanthinae.

Abstract: In this study, we describe a new genus, *Luciargentis* Yu & Wang, gen. nov. based on the new species, *Luciargentis obesa* Yu & Wang, sp. nov. Additionally, the genus is placed within the subfamily Crocanthinae, satisfying the criteria of Crocanthinae. We conducted a phylogenetic analysis of the family Lecithoceridae using a concatenated dataset that includes one mitochondrial marker (COI) and six nuclear markers (EF-1α, GAPDH, RpS5, CAD, wingless, and MDH), incorporating 17 exemplars from NCBI and 7 newly sequenced exemplars from this study. The yield tree topologies showed that *Luciargentis obesa* forms a strongly supported monophyletic group with *Crocanthes prasinopis*, a species of Crocanthinae. Moreover, *Luciargentis* + *Crocanthes* were found to be sister groups to Torodorinae. Images of the adults, wing venation, and genitalia of the new species are provided.

Keywords: Crocanthinae; Torodorinae; Lecithocerinae; taxonomy; molecular data

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1. Introduction

Lecithoceridae is one of the most species-rich groups with Lepidoptera, comprising more than 1430 known species [1]. It ranks as the sixth-largest family of the superfamily Gelechioidea [2]. This family is widely distributed across the Oriental, Ethiopian, Australian and Palaearctic regions. Members of Lecithoceridae can be identified by several distinct external features: antennae that are as long as or longer than the forewing, sub-rectangular or lanceolate forewings, trapezoidal hindwings, and male genitalia typically characterized by a median process of the gnathos that is usually downturned, except in the subfamily Crocanthinae. Additionally, the family still remains relatively underexplored. Park *et al*. estimated that the actual global species count might be 2–3 times higher than the currently recognized number [1]. Despites its diversity, Lecithoceridae has received very little scientific attention. This neglect is likely due to its minimal economic significance and the shortage of specialists in the field. Nevertheless, the ecological importance of Lecithoceridae cannot be overlooked. Larvae of this family have been reported to feed on non-living materials and organisms [3–6], suggesting a significant role in environmental ecosystems.

Lecithoceridae is currently divided into four subfamilies. Three were proposed by Gozmány [3]: 1) Ceuthomadarinae, characterized by the absence of a proboscis; 2) Lecithocerinae, characterized by male genitalia with a costal bar and a short, posteriorly lobed uncus; 3) Torodorinae, characterized by male genitalia lacking a costal bar but possessing a well-developed, often posteriorly thorned uncus. The fourth subfamily, Crocanthinae, was proposed by Park and is defined by male genitalia with a reduced gnathos [7].

Tibet, often called the "Roof of the World," lies on the Tibetan Plateau at an average elevation exceeding 4,500 meters. Renowned for its unique geography, ecology, and environment, Tibet has become a global hotspot for biological research. The region boasts an extraordinary diversity of plant and animal species, many of which are endemic, emphasizing its significance in biodiversity and conservation studies [8]. From 2017 to 2023, our team conducted extensive fieldwork in Tibet, collecting numerous micromoth specimens. Among these, we identified many new taxa, including the species described in this paper.

The aim of this paper is to describe a newly discovered genus, and discuss its subfamily affiliation within Lecithoceridae.

2. Materials and Methods

The examined specimens were collected using GYZ 450 W high-pressure mercury lamps (Yaming, China). Morphological terminology in the descriptions was in accordance with Gozmány [3]. The wingspan was measured from the tips of the left and right forewings of fully well spread specimens. Slides of genitalia were prepared following Li [9]. Photographs of adults were captured using an M205A stereomicroscope, and genitalia photographs were taken using a DM750 microscope with Leica Application Suite software version 4.6 (Leica, Germany). All images were processed with Photoshop CC (Adobe, USA). The type series of the new species are deposited at the Insect Collection of Nankai University (NKU), Tianjin, China (NKU), and at Liaocheng University (LCU), Liaocheng, China.

In this study, a total of 7 Lecithoceridae specimens were collected independently for molecular analysis, including 3 from *Luciargentis obesa* sp. nov., 1 from *Deltoplastis acutangulata*, 1 from *Thubana dialeukos*, 1 from *Halolaguna* sp., and 1 from *Thubana quadrilatera*. Genomic DNA was extracted from legs or partial body of dried specimens using Genomic DNA Extraction Kit (Tiangen Biotech, Beijing, China).

One mitochondrial marker (Cytochrome oxidase subunit 1 [COI]), and five nuclear markers (Carbamoyl phosphate synthetase domain protein [CAD], Elongation factor 1 alpha [EF-1α], Glyceraldhyde-3-phosphate dehydrogenase [GAPDH], Ribosomal protein S5 [RpS5], and wingless) were amplified using polymerase chain reaction (PCR). The primers used sourced from previous studies [10–13]. When the published primers failed to amplify sequences, newly designed primers were used to obtain shorter fragments of the target regions in this study (Table 1). DNA amplification and sequencing protocols primarily followed those described by Wahlberg & Wheat [13]. The purified PCR products were directly sequenced using Sanger sequencing by Qingke Biotech (Beijing, China).

To construct a more comprehensive phylogenetic tree for Lecithoceridae, a total of 5,350 bp dataset was downloaded from GenBank, which includes all available mixed COI and 6 nuclear gene sequences of 17 Lecithoceridae individuals. This dataset included 1,475 bp of COI, 850 bp of CAD, 691 bp of GAPDH, 925 bp of EF-1α, 600 bp of RpS5, 400 bp of wingless, and 407 bp of MDH.

The sequences were manually edited in BioEdit v.7.2.5 [14] and examined using MEGA X software [15]. Each gene (COI, CAD, GAPDH, EF-1α, RpS5, wingless and MDH) was aligned independently, followed concatenated into a dataset with a length of 5 350 bp using software PhyloSuite v1.2.2 [16]. We performed the phylogenetic reconstructions of Lecithoceridae species based on the concatenated dataset using Maximum likelihood (ML) in IQ-TREE [17]. The Akaike Information Criterion (AIC) was used in PartitionFinder v2 [18] to select the best-fit model of sequence evolution for each locus alignmen (GTR+I+G for COI, GTR+G for CAD, GTR+I for MDH, SYM+I+G for wingless, RpS5, EF-1α and GAPDH). The bootstraps were obtained using a rapid bootstrapping algorithm with 1 000 replicates in the analysis of ML.

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Table 1. Designed primers used in this study.

Gene region	Forward primer (5′ to 3′)		Reverse primer (5′ to 3′)	
EF-1α/elongation factor-1a	**EF-1α-F**	CCYGCCAAYATCACCACTGAAG	EF-1α-R	AGAGGHGGGAACTCYTGGAAGGA
GAPDH/Glyceraldehyde-3-phosphate dehydrogenase	GAPDH-F	TCACTTGGAVGGTGGHGCCAAGAA	GAPDH-R	AGAGAGATACCAGCDGCAGCATC
CAD/carbamoyl phosphate synthetase domain protein	CAD-F	AGTTTRGACTACTGTGTAGTTAAAATA	CAD-R	TGATAAAATAACGCCATCAGGA
MDH/cytosolic malate dehydrogenase	MDH-F	TGTTGTCATGGAGCTTGCAGATT	MDH-R	CCCATATAACAACATTCTTWACATCC
RpS5/ribosomal protein S5	RpS5-F	GCAGCATGGCCGTCGATAACAT	RpS5-R	TTGATGAACCCTTGGCAGCATTAAT
wingless	wingless-F	TGCACAGTGAAAACTTGCTGGAT	wingless-R	GTTACACCTTTCCACAACGAACATG

Figure 1. The collecting site of *Luciargentis obesa* sp. nov. displayed on the Bing map.

3. Results

3.1. Molecular Analysis Results

We obtained 3105 bp sequences for our specimen, including COI 648 bp for 7 individuals, CAD 756 bp for 2 individuals, EF-1α 345 bp for 7 individuals, GAPDH 522 bp for 5 individuals, RpS5 504 bp for 5 individuals, and wingless 330 bp for 5 individuals. These gene sequences generated in this study were deposited in GenBank under Accession nos. PQ763539–PQ763545 (COI), PQ757619–PQ757625 (EF-1α), PQ757614–PQ757618 (GAPDH), PQ757626–PQ757630 (RpS5), PQ757612–PQ767513 (CAD), and PQ757631–PQ757635 (wingless).

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The Maximum Likelihood (ML) tree and Bayesian Inference (BI) tree were con-structed based on 24 exemplars representing 22 Lecithoceridae species, and the topo-logical results shows in Figure 2. According to the phylogenetic tree topology, three major clades are recognized: A, B and C. The clade A, representing Lecithocerinae group, contains ten species from six genera; The clade B, representing Torodorinae group, contains six species from four genera; The clade C, representing Crocanthinae group, contains two species including the newly described species, *Luciargentis obesa* sp. nov. The sister relationship between clade A and clade B+C was strongly supported (0.98/97%), and clade B was confirmed as the closest relative of clade C (1/100%). The branch of the new species is undoubtedly closer to the branch *Crocanthes prasinopis* (0.97/81%), and the two branches construct the clade C. Additionally, most intra-genus (e.g., *Thubana*, *Eurodachtha*, *Homaloxestis* and *Lecithocera*) and intra-species (e.g., *Luciargentis obesa* sp. nov.) relationships were strongly supported (⩾0.97/⩾ 90%). The interspecific relationships of the clade B have not been well supported, but we resolved well the taxonomic affiliation of the new species which fall closest to the Crocanthinae rather than Torodorinae branch.

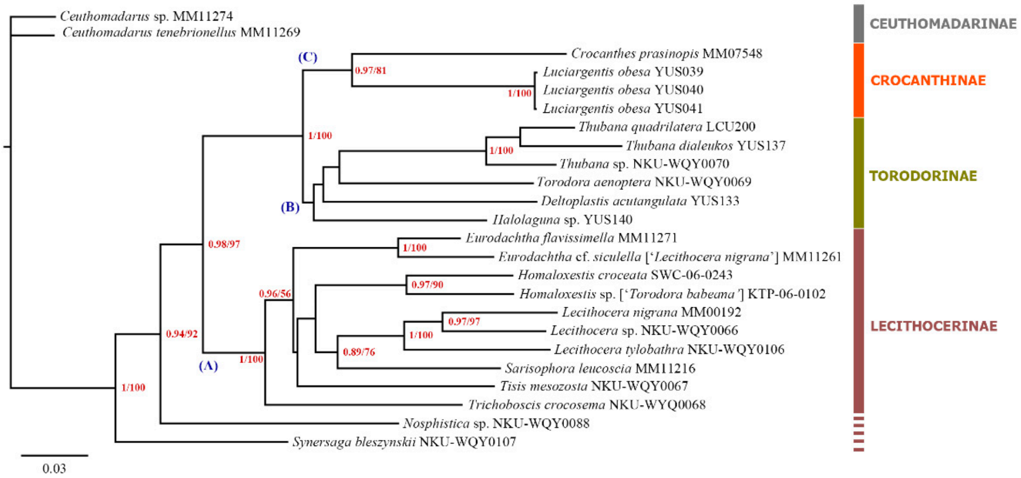

Figure 2. Phylogenetic tree of Lecithoceridae using 24 Lecithoceridae taxa based on a concatenated dataset of 5,350 bp. The first support value for each node is ABayes, and the second number indicate bootstrap support value. The branch node showed the strongly support values (PP value > 0.95 or BS value > 70%).

3.2. Morphological Results

3.2.1. *Luciargentis* Yu &Wang, Gen. Nov.

Type species: *Luciargentis obesa* Yu &Wang, sp. nov.

Gender: feminine.

Etymology: The genus name is derived from the Latin *luc*- and *argent*-, referring to the silvery marking of the forewing.

Diagnosis: *Luciargentis* gen. nov. belongs to the subfamily Crocanthinae. The new genus and another genus *Gonaepa* possessing a median process of the gnathos in the male genitalia, differs from remaining Crocanthinae genera which has a totally reduced gnathos. *Luciargentis* gen. nov. can be distinguished from *Gonaepa* Walker by the smooth antenna longer than the forewing, lanceolate forewing. Moreover, the wing venation of *Luciargentis* gen. nov. is unique.

The possible synapomorphies of the genus includes: antenna smooth, longer than the forewing; forewing lanceolate, with slivery grey marking, R_5 absent, M_1 stalked with R_{3+4}, M_2, M_3, CuA_1 and CuA_2 stalked; hindwing trapezoidal, M_2 absent; male genitalia with the reduced gnathos present of basal plate but lacking of median process.

3.2.2. *Luciargentis obesa* Yu &Wang, Sp. Nov.

Material examined: Holotype: ♂, China, Tibet, Médog, 2076 m, 29°40′N, 95°30′E, 28.vii.2018, leg. M.J. Qi, genitalia slide no. YS18209, in NKU. Paratypes: 1♂, China, Tibet, Médog, 880 m, 16.viii.2003, X.P. Wang & H.J. Xue leg., genitalia slide no. LSR12042, in NKU; 1♂, China, Tibet, Médog, 2089 m, 6.viii.2017, M.J. Qi leg., in NKU; 6♀♀, China, Tibet, Médog, 2089 m, 19.viii.2017, genitalia slide no. YS18210, in NKU; 1♀, China, Tibet, Bomi County, Tongmai Town, 2029 m, 15.viii.2018, M.J. Qi leg., genitalia slide no. YS18208, in NKU; 3♂, 3♀, China, Tibet, Médog, 1764 m, 17–18.vi.2023, S. Yu leg., genitalia slide nos. YUS039♂, YUS040♂, YUS041♀, in LCU.

Description: Wingspan 15.5–17.5 mm (Figure 3A). Head greyish black, tinged with metallic luster. Antenna about 1.5 times length of forewing, greyish black except orange yellow dorsally on scape. Labial palpus orange yellow, third palpomere as long as the second. Thorax pale orange yellow; tegula slivery grey. Forewing lanceolate; ground color orange yellow, with two large slivery grey markings: first nearly U-shaped, upper branch along costal margin from base to basal 2/5, lower branch along mesial 1/3 of fold, yellowish brown on its concavity; second horseshoe-shaped, from about distal 2/5 along costal margin through termen to distal 1/4 of dorsum, dark yellowish brown on its concavity and greyish black at the open; a greyish black band along dorsum from basal 1/4 to middle; area between the first U-shaped marking and dorsum dark yellowish brown; fringe orange yellow except dark yellowish brown around tonus; cell closed; R_1, R_2 free, R_3, R_4, M_1 stalked and arising from anterior corner of discal cell, R_5 absent, M_2, M_3, CuA_1, CuA_2 stalked and arising from posterior corner of discal cell. Hindwing trapezoidal, orange white except grey on distal 1/3 and above dorsum; fringe grey, basal line orange white; cell open; Rs and M_1 stalked, M_2 absent, M_3 and CuA_1 stalked, CuA_2 free (Figure 3B). Abdominal sternite with spiniform setae (Figure 3E).

Male genitalia (Figure 3C). Uncus listric, parallel-sided in basal half, narrowed from middle to truncate apex, setose distally on lateral sides. Gnathos with basal plate triangular. Valva wide at base, narrowed slightly to middle, widened at distal 1/3, thereafter narrowed to subacute apex, apex with a small spine; ventral margin nearly straight in basal 2/3, arched in distal 1/3; sacculus wide at base, tapered to before middle of ventral margin. Vinculum narrow, U-shaped. Juxta shield-shaped, with an imbricate process at middle on posterior margin, obtuse on anterior margin. Aedeagus about 2/3 length of valva, stout, ovate; vesica wrinkled and weakly sclerotized; cornuti absent.

Female genitalia (Figure 3D). Papillae analis short. Apophyses posteriores slightly shorter than twice length of apophyses anteriores. Antrum weakly sclerotized, large, sub-rectangular, spiculose, with a pair of digitiform lobes on posterior margin. Ductus bursae nearly as long as corpus bursae, posterior 1/3 narrowed, anterior 2/3 dilated and as wide as corpus bursae, with a weakly sclerotized, longitudinal band; ductus seminalis slender, arising from about middle of ductus bursae. Corpus bursae large elliptical; signum nearly semicircular, situated anteriorly.

Distribution (Figure 1): China (Tibet).

Etymology: The specific epithet is derived from the Latin *obesus*, referring to the stout aedeagus of the male genitalia.

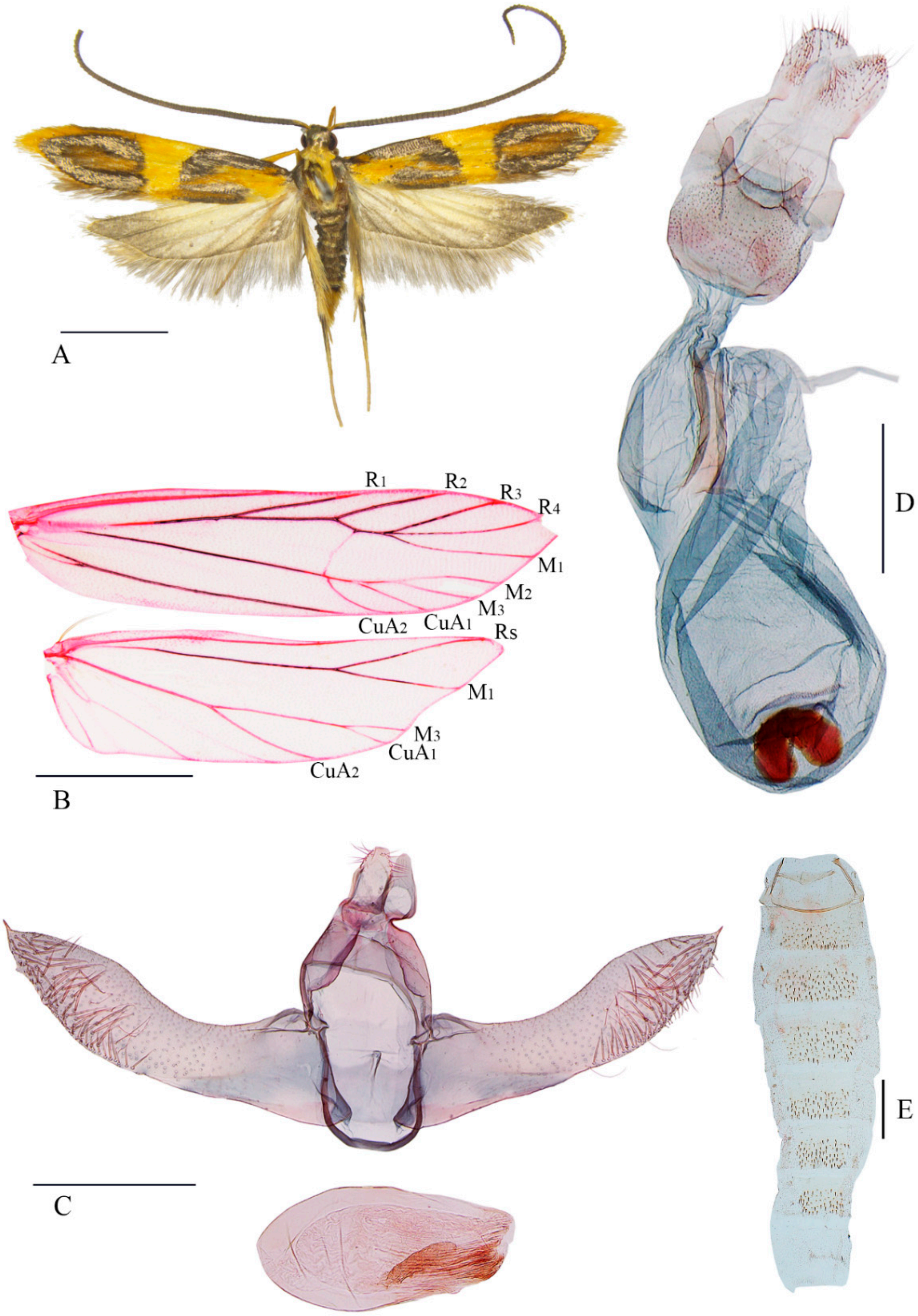

Figure 3. *Luciargentis obesa* Yu & Wang, sp. nov.: (A) adult, paratype, male; (B) wing venation, paratype, female, slide No. YS18208; (C) male genitalia, holotype, slide No. YS18209; (D) female genitalia, paratype, slide No. YS18210; (E) abdomen, paratype, slide No. YUS040. Scales: A, B = 2.0 mm; C–E = 0.5 mm.

4. Discussion

Crocanthinae currently comprises six genera, geographically restricted to the Australian, Oceanian and Oriental regions [19]. Among the known genera, *Gonaepa* Walker, 1866 stands out as distinct, possessing a reduced gnathos with a basal plate; in contrast, other genera, *Aprosoesta* Turner, 1919, *Crocanthes* Meyrick, 1886, *Lamprista* Park, 2013, *Pacificulla* Park, 2013 and *Hannara* Park, 2013 lacks a gnathos including the basal plate and the median process. Additionally, *Gonaepa* is undoubtedly a compound group, exhibiting diverse wing shapes, patterns and venation. For instance, *Gonaepa pyrochorda* Meyrick, 1910 and *G. phaeograpta* (Meyrick, 1931) has triangular forewings, whereas *G. dysthyma* Diaknoff, 1954, *G. cordata* Park, 2016, *G. nagaensis* Park, 2016, *G. ochrorhystima* Park, 2016 possess rectangular forewings. The newly described genus, *Luciargentis* gen. n. is most similar to *Gonaepa* by sharing the presence of the basal plate on the gnathos. Moreover, China has previously recorded two subfamilies, Lecithocerinae and Torodorinae. This paper is the first to report presence of the subfamily Crocanthinae in China.

Wing venation is one of the most critical morphological characters used to distinguish genera in the current Lecithocerid classification system [3,20]. We found that Crocanthinae species share a wing venational synapomorphy, independent of the genus *Gonaepa*: forewing with R_5 absent, M_3 and CuA_{1+2} connate or stalked, hindwing with M_2 absent. These wing venational characteristics support the classification of *Luciargentis* as part of the subfamily Crocanthinae.

On the other hand, the current concepts of Torodorinae and Crocanthinae, based solely on morphological characteristics, appear to overlap and failed to meet the demands of classification. According to Park et al. [7], the synapomorphy that distinguishes Crocanthinae from Torodorinae is the reduced gnathos, which is either completely absent or lacks a median process. However, some Torodorinae species also exhibits this feature, such as *Xenotodorodor stygioxanthus* Sterling, Lees & Grundy, 2023. Yu et al. [21] also noted that twelve species of *Torodora* (the type genus of Torodorinae) has a reduced gnathos with the median process absent. Additionally, as noted by Sterling et al. [22], further work is needed to confirm whether Torodorinae is a monophyletic group without including all or part of Crocanthinae. The phylogenetic tree in this study also demonstrates that the subfamilies Torodorinae and Crocanthinae are closest in the topology (1/100%). Furthermore, we find the placement of *Luciargentis* within the subfamily Crocanthinae convincing, as evidenced by the high clade node value of *Luciargentis obesa*+*Crocanthes prasinopis* (0.97/81%), which also satisfies the current research results and concepts of the subfamilies.

Author Contributions: Conceptualization, S.Y.; methodology, S.Y. and H.L.; software, S.Y. and H.L.; investigation, S.Y.; resources, S.Y. and S.W.; writing—original draft preparation, S.Y.; writing—review and editing, S.W.; funding acquisition, S.Y. All authors have read and agreed to the published version of the manuscript.

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