A new species of *Caeruleuptychia* Forster, 1964 from the Amazon basin (Lepidoptera: Nymphalidae: Satyrinae: Satyrini)

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Abstract: Here, we describe and name a new nymphalid butterfly species in the subtribe Euptychiina. *Caeruleuptychia thaliana* Nakahara & Piovesan, **n. sp.** is proposed by incorporating three independent sources of evidence: adult external morphology, DNA sequence data, and early stage biology. *Caeruleuptychia thaliana* **n. sp.** is known from two sites in the Amazon basin, in the state of Mato Grosso, Brazil, and another site situated in Madre de Dios department, Peru. A single egg of *C. thaliana* **n. sp.** was obtained while conducting field work at the latter locality, and subsequently observations were made of the larva passing through four larval stages until reaching the adult stage. The natural host plant for *C. thaliana* **n. sp.** was identified as a species of grass, *Lasiacis ligulata* Hitchcock & Chase (Poaceae: Panicoideae: Paniceae).

Key words: Brazil, *Caeruleuptychia thaliana* **n. sp.**, Euptychiina, host plant, Peru, Poaceae, taxonomy.

Resumen: Aquí, describimos y nombramos una nueva especie de mariposa ninfálida de la subtribu Euptychiina. *Caeruleuptychia thaliana* Nakahara & Piovesan, **n. sp.** es propuesta con base en tres fuentes independientes de evidencia: morfología externa del adulto, datos de secuencia de ADN e información de la biología de los estados inmaduros. *Caeruleuptychia thaliana* **n. sp.** se conoce de dos sitios en la cuenca del Amazonas, la localidad tipo se encuentra en el estado de Mato Grosso, Brasil, y el otro sitio está ubicado en el departamento de Madre de Dios, Perú. Un solo huevo de *C. thaliana* **n. sp.** se obtuvo durante el trabajo de campo en esta última localidad, y posteriormente se observó el desarrollo larval de cuatro estadios hasta llegar al estadio adulto. La planta hospedera natural de *C. thaliana* **n. sp.** se identificó como una especie de hierba, *Lasiacis ligulata* Hitchcock & Chase (Poaceae: Panicoideae: Paniceae).

Palabras clave: Brasil, *Caeruleuptychia thaliana* **n. sp.**, Euptychiina, planta hospedera, Perú, Poaceae, taxonomía.

Resumo: Aqui, descrevemos e nomeamos uma nova espécie de ninfalídeo na subtribo Euptychiina. *Caeruleuptychia thaliana* Nakahara & Piovesan, **n. sp.** é proposta, incorporando três fontes independentes de evidência: morfologia externa do adulto, sequências de DNA e biologia dos estágios imaturos. *Caeruleuptychia thaliana* **n. sp.** é conhecida de dois locais da bacia Amazônica, no estado de Mato Grosso, Brasil, e o outro local está situado no departamento de Madre de Dios, Peru. Um único ovo de *C. thaliana* **n. sp.** foi obtido durante o trabalho de campo nesta última localidade, e posteriormente foram feitas observações da larva passando por quatro ínstares larvais até atingir o estágio adulto. A planta hospedeira natural de *C. thaliana* **n. sp.** foi identificada como uma espécie de gramínea, *Lasiacis ligulata* Hitchcock & Chase (Poaceae: Panicoideae: Paniceae).

Palavras chave: Brasil, *Caeruleuptychia thaliana* **n. sp.**, Euptychiina, planta hospedeira, Peru, Poaceae, taxonomia

INTRODUCTION

It's just a name, but it's still a name. Taxonomists help fulfill our irresistible desire to produce order from the immensely chaotic diversity of life surrounding us through (imaginative) invention of new scientific names for nomenclatural purposes. These arbitrary combination of letters may seem as if they are meaningless symbols, but each one of them has its own story, receiving nonscientific influences, as well as invariably reflecting a taxonomist's state of mind and emotional stakes. This subjective aspect of taxonomy has perhaps contributed to its reputation as a frivolous branch of science. Ironically, on the contrary, naming new taxa can be an enriching scientific practice for the same reason, and these names will persist, as long as we care and communicate about the natural world. Taxonomy, indeed, is a worthwhile scientific endeavor which we greatly benefit from hereunder.

Although diverse and common in the Neotropics, the nymphalid butterfly subtribe Euptychiina received little attention from Lepidoptera researchers until recently (see https://www.floridamuseum.ufl.edu/neotropica/research/euptychiina/ for recent advancements on euptychiine systematics), perhaps partly due to their drab and unassuming adult appearance. Consequently, euptychiine classification remained chaotic for decades, with an overwhelmingly high proportion of paraphyletic and polyphyletic genera revealed through phylogenetic studies (e.g., Murray & Prowell, 2005; Peña *et al*., 2010; Matos-Maraví *et al*., 2013; Espeland *et al*., 2019). Additionally, a high number of unresolved species-level taxonomic issues exist because morphological homogeneity makes it difficult to find diagnostic characters. This cryptic nature of euptychiine species is further apparent in recent studies incorporating molecular data to uncover the subtribe's hidden diversity (e.g., Cong & Grishin, 2014; Barbosa *et al*., 2015; Nakahara *et al*., 2018b). Commonly, documentation of new euptychiine species is often based solely on the adult stage without incorporating any information on their early stage biology; as a result, approximately 80% of the species in the subtribe lack relevant life history information (Corahua-Espinoza *et al*., 2022a). However, these gaps in knowledge regarding euptychiine immature biology have steadily been filled in over the past year by a series of studies conducted at the heart of euptychiine diversity, in southeastern Peru (Corahua-Espinoza *et al*., 2022a, b, in press, in prep.), building upon earlier pioneering efforts aimed at revealing euptychiine life history (e.g., Müller, 1878, 1886; Biezanko *et al*., 1974; DeVries, 1986, 1987).

The euptychiine genus *Caeruleuptychia* Forster, 1964 was established by Walter Forster to circumscribe a group of species marked unusually with iridescent blue scales on their wings (Forster, 1964). Forster (1964) recognized three species groups within *Caeruleuptychia*: species without an androconial patch on the male dorsal wings: *C. caerulea* (Butler, 1869), *C. coelestis* (Butler, 1867), *C. divina* (Weymer, 1911), *C. coelica* (Hewitson, 1869), *C. lobelia* (Butler, 1870), *C. urania* (Butler, 1867), and *C. ziza* (Butler, 1869); species with an androconial patch close to the inner margin of the dorsal hindwing: *C. glauca* (Weymer, 1911), *C. cyanites* (Butler, 1871), *C. pilata* (Butler, 1867), *C. tenera* (Weymer, 1911), *C. penicillata* (Godman, 1905), and *C. scopulata* (Godman, 1905); and species with a circular, black androconial patch at the dorsal hindwing tornus: *C. helios* (Weymer, 1911), *C. aegrota* (Butler, 1867), and *C. aetherialis* (Butler, 1877). Simultaneously, Forster (1964) erected *Weymerana* Forster, 1964 to accommodate a single species, *Euptychia viridicans* Weymer, 1911, which is currently considered as a junior subjective synonym of *Euptychia umbrosa* Butler, 1870 (Lamas, 2004). Owing to recent contributions towards *Caeruleuptychia* taxonomy (Brévignon & Benmesbah, 2012; Nakahara *et al*., 2018b; Ríos-Málaver 2019), coupled with an ongoing molecular phylogenetic study, our understanding of *Caeruleuptychia* diversity and systematics are reaching some degree of stability. An emerging consensus is that *Caeruleuptychia* itself is monophyletic, which can be divided into three somewhat morphologically compact clades: 1) a group including species with males displaying an androconial patch on the dorsal hindwing ("*aegrota* clade"); 2) a group including mainly species with lilac-blue wings ("*caerulea* clade"); 3) a group including mainly species with brown wings, with males accompanied by secondary sexual traits ("*umbrosa* clade"). Greater understanding of *Caeruleuptychia* species diversity will undoubtedly require descriptions of a number of undescribed species concentrated mainly in the "*umbrosa* clade", and an ongoing morphological and molecular study suggests the species-richness of the genus will exceed 50 species. Members of *Caeruleuptychia* are found almost exclusively east of the Andes, including some species known from the cloud forests of the Andes and two records known from Central America (Dyar, 1914; unpublished data). In particular, the vast majority of *Caeruleuptychia* species are strictly Amazonian, with the peak of diversity found in the southwestern Amazon basin, including some taxa known only from this region. Adults of *Caeruleuptychia* species are often found in close association with bamboo stands, with males of some species exhibiting perching behavior (Nakahara *et al*., 2018b; see below). On the other hand, our understanding of immature stages and host plant records for many *Caeruleuptychia* taxa remain in infancy, with information on their natural history available for a mere four species to date (Murray, 2001; Beccaloni *et al*., 2008; Nakahara *et al*., 2018b; Corahua-Espinoza *et al*., in prep.).

Given this background, the objective of this study is to document an undescribed Amazonian species of *Caeruleuptychia* with its immature stages and natural host plant, in order to improve our understanding of *Caeruleuptychia* species diversity as well as euptychiine early stage biology. We here incorporate three independent sources of evidence to support our taxonomic hypothesis of species designation: adult external morphology, DNA sequence data, and life history. The present study also aims to recognize a seemingly endless effort and enthusiasm devoted towards discovering novel butterfly life history information by dedicating the species-group name of this new taxon to Thalia Corahua-Espinoza. Introducing this patronym will remind us in perpetuity of her contributions towards understanding the immature biology of Neotropical butterflies, including over a dozen euptychiine species, based on her studies in the Peruvian Amazon (Ccahuana *et al*., 2022; Corahua-Espinoza *et al*., 2022a, b, in press, in prep.; Duerr *et al*., in press; Nakahara *et al*., 2022; Tejeira *et al*., 2021).

MATERIALS AND METHODS

Specimens and sequences relevant to this study are based on data compiled for taxonomic revision of the genus, including study of >1,000 specimens from >20 public/private collections (see Nakahara *et al*. (2022) as an example of the repositories examined for these materials).

Acronyms and terminology. The following collection acronyms are used throughout the text: **ASA:** Alliance for a

Sustainable Amazon collection, Puerto Maldonado, Peru; **DZUP:** Coleção Entomológica Padre Jesus Santiago Moure, Departamento de Zoologia, Setor de Ciências Biológicas, Universidade Federal do Paraná, Curitiba, Brazil; **MCZ:** Museum of Comparative Zoology, Harvard University, Cambridge, USA; **STD:** Senckenberg Museum für Tierkunde, Dresden, Germany; **NHMUK:** Natural History Museum, London, UK. The terminology associated with wings and genitalia follows Nakahara *et al.* (2018a, b). We follow Hinton (1946), Murray (2001) and Corahua-Espinoza *et al.* (2022a) for terminology related to immature stages.

Morphological work. We studied adult external morphology using a Zeiss Stemi SV6 stereomicroscope at the DZUP, and a Zeiss SteREO Discovery V.20 stereomicroscope at Laboratory of Ecology and Systematic of Butterflies, Biology Department, State University of Campinas (Brazil). The genitalia were examined by separating the abdomen from the body, soaking in hot (55-60°C) 10% potassium hydroxide solution (KOH) for approximately two minutes, and rinsing in water before examination. Information on dissected individuals with associated DNA data are provided in Table 1. Subsequently, the genitalia were photographed using an optical stereomicroscope adapted with focus stacking (Leica Application Suite Version 4.12.0 [Build 86]), and images of the holotype (deposited at the DZUP) were recorded with a Sony DSC-HX100V digital camera. The head capsules were examined and photographed using Leica DFC450 attached to a Leica M205 C stereomicroscope and stacked using Leica Application Suite X (LAS X v.5.02) at the MCZ.

Molecular work. The mitochondrial gene *cytochrome oxidase I* (COI) barcoding region (*sensu* Hebert *et al.,* 2003) was sequenced for relevant individuals of *Caeruleuptychia* taxa to inform our taxonomic hypothesis. Genomic DNA extraction, PCR, primer design, and Sanger sequencing procedures for molecular samples used in the present study largely follow Corahua-Espinoza *et al.* (2022b) and Nakahara *et al.* (2020). GenBank accession numbers for *Caeruleuptychia* sequences repeatedly discussed herein are listed in Table 1. These sequences were incorporated into the matrix based on 633 base pairs, consisting in total of 63 individuals of selected *Caeruleuptychia* sequences, in addition to 14 outgroup taxa. We edited raw sequences using various versions of Geneious (Biomatters Ltd.; Kearse *et al*., 2012) and calculated patristic distance by reconstructing a Neighbour-Joining tree using the Jukes-Cantor model with 500 bootstrap replicates. To graphically illustrate and test our taxonomic hypothesis, we performed phylogenetic analysis based on the above dataset with maximum likelihood (ML) as an optimality criterion. Sequences were aligned using MUSCLE 3.8 (Edgar, 2004). We used IQ-TREE v.2.1.3 (Minh *et al.*, 2020) and ModelFinder by employing Akaike Information Criterion (AIC) to select the nucleotide substitution model TIM2+F+I+G4 (Kalyaanamoorthy *et al.*, 2017), and performed 10 independent analyses under this model. The run which produced the highest log-likelihood (LnL) was chosen and we rooted the tree manually with *Cisandina lea* (Cramer, 1777). Confidence in the phylogenetic hypothesis was assessed through 1,000 replicates of ultrafast bootstrap (UFBoot; Hoang *et al.*, 2018) with optimization by nearest-neighbor interchange, 1,000 replicates of the SH-like approximate Likelihood Ratio Test (SH-aLRT; Guindon *et al*., 2010), and approximate Bayes branch test (aBayes; Anisimova *et al*., 2011). IQ-TREE analysis was performed using supercomputer and cluster resources provided by the University of New Mexico Center for Advanced Research Computing (New Mexico, USA).

Rearing. The life cycle and natural host plant of *C. thaliana* **n. sp.** were documented at Finca Las Piedras (FLP), a research station situated approximately 50 km north of Puerto Maldonado (Madre de Dios department, Peru; -12.22789, -69.11119; elevation, approximately 240 m). Materials and methods related to the study of life history of *C. thaliana* **n. sp.** are largely in accordance with those described in Corahua-Espinoza *et al*. (2022a). A single egg was obtained from *Lasiacis ligulata* Hitchcock & Chase within the FLP property on 10 May 2021, subsequently vouchered as 2021-FLP-IMM-0371, and it developed by feeding on *L. ligulata* in captivity throughout all larval stages (see below for duration and molt dates).

SPECIES DESCRIPTION

Caeruleuptychia thaliana Nakahara & Piovesan, **new species**
ZooBank registered: urn:lsid:zoobank.org:act:83D21E6B-85DB-4E5F-9CAE-5273D15DEFBB
(Figs. 1-5)

Systematic placement. The genus *Caeruleuptychia* is recovered as a member of the so-called "*Splendeuptychia* clade" (*sensu* Murray & Prowell, 2005) based on hybrid enrichment data (Espeland *et al.*, 2019). In the present study, *C. thaliana* **n. sp.** is strongly supported as a sister to *C. umbrosa*

Table 1. GenBank vouchers of sequences for *C. thaliana* **n. sp.** and *C. umbrosa* used in the present study (names in bold denote dissected specimens).

Species	sex	DNA Voucher code	GenBank Acc. No.	Country	State/Prov./Dept.	Specific locality
Caeruleuptychia umbrosa	female	MGCL-LOAN-513	OP207987	Brazil	Bahía	Reserva Biológica de Una
Caeruleuptychia umbrosa	male	LEP-08903	OP207988	Ecuador	Pastaza	Kapawi village
Caeruleuptychia umbrosa	male	NVG-2639	OP207989	Bolivia	Beni	5 km N Rurrenambaque
Caeruleuptychia umbrosa	male	LEP-10074	MF192698	Ecuador	Morona-Santiago	Chupianza Grande
Caeruleuptychia umbrosa	female	YPH-0586	KU340888	Brazil	Minas Gerais	PE do Rio Doce, Marliéria
Caeruleuptychia umbrosa	unknown	LEPAR448	MF546867	Argentina	Misiones	Parque Nacional Iguazu
Caeruleuptychia umbrosa	male	CP01-09	GU205824	Peru	Madre de Dios	Z.R. Tambopata - Candamo
Caeruleuptychia umbrosa	unknown	DNA00-016	AY508523	Ecuador	Napo	Jatun Sacha
Caeruleuptychia thaliana	male	BC-DZ-025	ON932574	Brazil	Mato Grosso	Barra do Bugres
Caeruleuptychia thaliana	female	2021-FLP-IMM-0371	ON931448	Peru	Madre de Dios	Finca Las Piedras

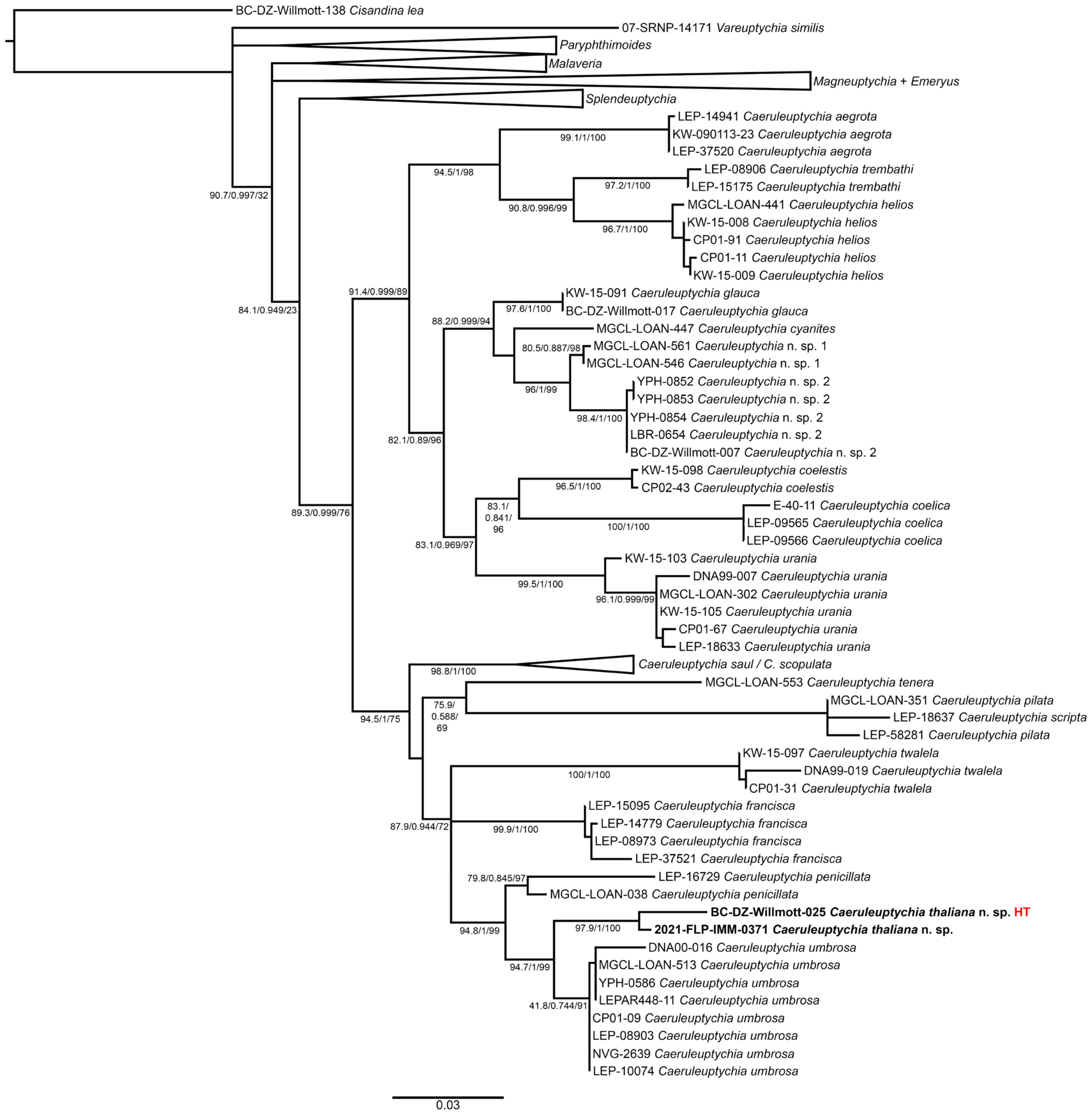

Figure 1. Maximum likelihood tree (LnL = -4894.872) showing the phylogenetic position of *C. thaliana* **n. sp.** and other *Caeruleuptychia* taxa selected for this study. Values beside branches represent UFBoot/aBayes/SH-aLRT support. HT denotes the holotype of *C. thaliana* **n. sp.**

according to the ML phylogenetic hypothesis based on COI barcode data (Fig. 1; UFBoot/aBayes/SH-aLRT = 94.7/1/99). *Caeruleuptychia penicillata* is found to be sister to this species pair (*C. thaliana* **n. sp.** + *C. umbrosa*) with high support (Fig. 1; UFBoot/aBayes/SH-aLRT = 94.8/1/99). The clade with these three taxa (*C. penicillata* + (*C. thaliana* **n. sp.** + *C. umbrosa*)) is found within the "*umbrosa* clade", with *C. twalela* and *C. francisca* (Butler, 1870) as members of the same clade.

Diagnosis. The male of *C. thaliana* **n. sp.** is readily distinguishable from *C. umbrosa* by the lack of a hair-pencil (androconial brush) on the dorsal forewing in cell Cu_2, whereas there is a hair-pencil lying near the origin of Cu_2 in this cell in *C. umbrosa* (see Fig. 2E). Nevertheless, this structure may become loose over time and it is not fully discernible in some old museum specimens. This fact, coupled with the limited number of known specimens for *C. thaliana* **n. sp.**, including one reared specimen, and its resemblance to *C. umbrosa* as well as the intraspecific variation of this latter taxon overlapping with that of the former, these following diagnostic characters should be used in combination. The male of *Caeruleuptychia thaliana* **n. sp.** is further distinguished from that of *C. umbrosa*

Figure 2. Adults of *Caeruleuptychia thaliana* **n. sp.**: A) male holotype, dorsal surface; B) male holotype, ventral surface; C) female paratype (2021-FLP-IMM-0371), dorsal surface; D) female paratype (2021-FLP-IMM-0371), ventral surface. Male specimen of *Caeruleuptychia umbrosa* (LEP-08903): E) dorsal surface, with arrow indicating the hair-pencil; F) ventral surface.

by its brown wing surface lacking an olive-grayish sheen on the dorsal and ventral surface, as well as the paler ventral surface. As a result of the ventral surface possessing an olive-grayish sheen, the ventral surface of *C. umbrosa* appears scalier due to contrasting whitish scales, especially at the distal sides of the wings. The ventral submarginal ocelli are generally larger in *C. umbrosa*. In particular, the ocellus in the ventral hindwing cells M_1 and Cu_1 may occasionally reach the intervening veins and/or the submarginal band in *C. umbrosa*. The ocellus in the ventral hindwing cell Cu_1 is also more elongated in *C. thaliana* **n. sp.** compared to the rounded corresponding ocellus of *C. umbrosa.* The submarginal bands on both the ventral forewing and hindwing appear broader in *C. umbrosa.* Furthermore, the ventral hindwing submarginal band gradually broadens in *C. thaliana* **n. sp.**, whereas this band appears rather evenly broad in *C. umbrosa*. The apical process of the valva in *C. thaliana* **n. sp.** possesses a straight dorsal margin in the lateral view, terminating in a slightly hooked, angular, and blunt point, whereas the dorsal margin of valva in *C. umbrosa* typically exhibits a concavity and the apical point is not skewed distally. The female of *C. thaliana* **n. sp.** is distinguished from that of *C. umbrosa* by the ventral forewing post-discal band fading in cell Cu_2 and failing to reach 2A, whilst this band reaches 2A in *C. umbrosa*. In accordance with the males, the ventral hindwing submarginal band of females also gradually broadens in *C. thaliana* **n. sp.**, although this character is not pronounced

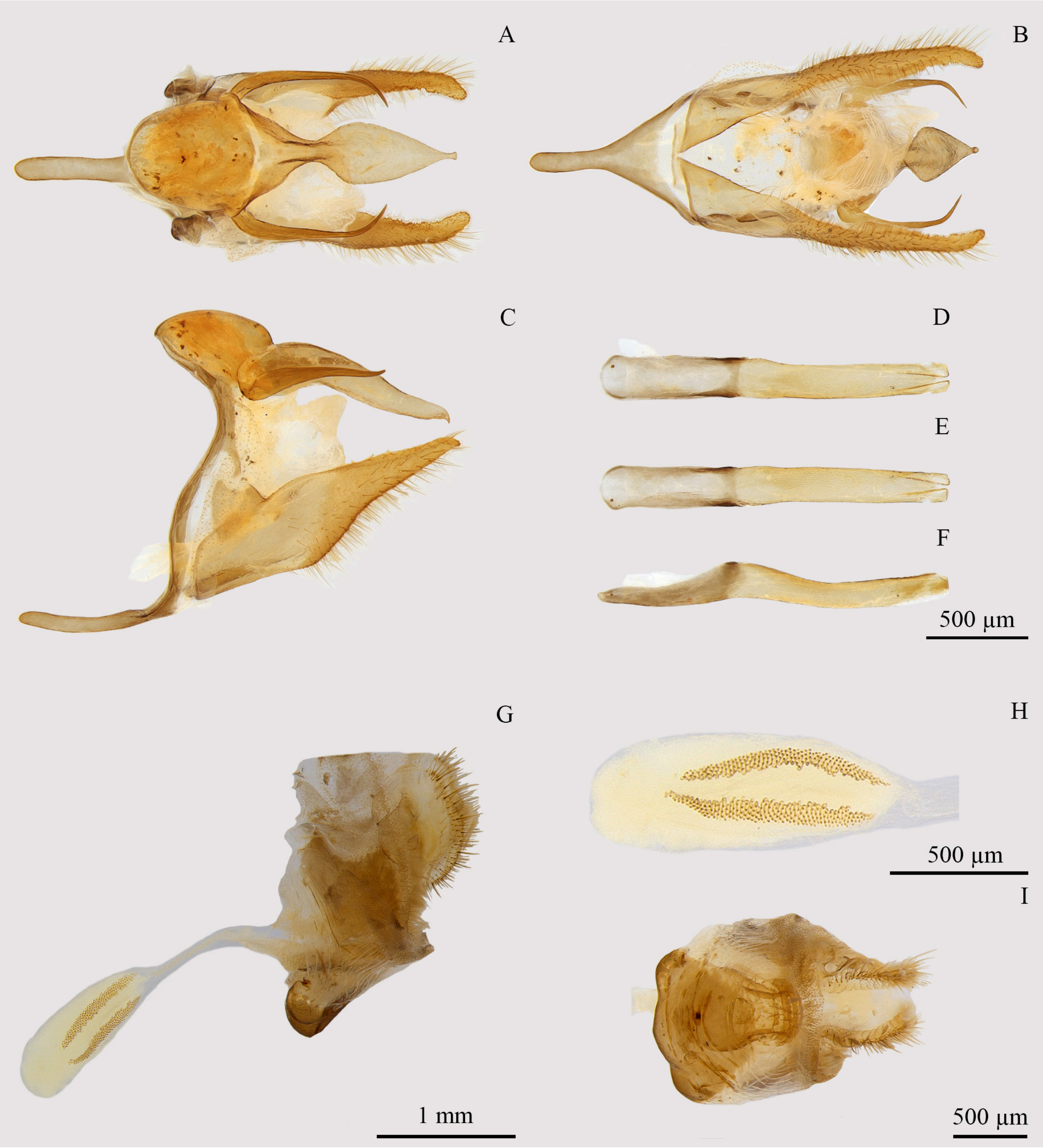

Figure 3. Genitalia of the male holotype (DZ 42. 559) and female paratype (DZ 42. 546) of *C. thaliana* **n. sp.**: A) male genitalia in dorsal view; B) male genitalia in ventral view; C) male genitalia in lateral view; D) phallus in dorsal view; E) phallus in ventral view; F) phallus in lateral view; G) female genitalia in lateral view; H) signa; I) lamella antevaginalis in ventral view.

in the reared female from Madre de Dios, Peru. Furthermore, *C. thaliana* **n. sp.** is separated from *C. umbrosa* by having more grooves along the distal side of lamella antevaginalis in ventral view, as well as having broader and longer signa. Additionally, *C. thaliana* **n. sp.** somewhat resembles species in the genus *Hermeuptychia* Forster, 1964, but *C. thaliana* **n. sp.** is readily distinguished from *Hermeuptychia* species by lacking dark scaling along the disco-cellular vein on the ventral forewing and below the origin of M_2 on the ventral hindwing, as well as lacking an indentation along the ventral margin of the valva in lateral view.

Description. MALE: Forewing length 19.7 mm (n=1; holotype).

Head: Eyes covered with dark brown hair-like setae, white scales at base; frons dark brown, with grayish and brownish scales, as well as concolourous elongated hair-like scales; first segment of labial palpi short, with dark brownish and whitish scales and concolourous long setiform scales, ventrally directed, second segment of labial palpi slightly longer than longitudinal eye depth, dorsally with dark brownish setiform scales mixed with whitish scales, laterally with whitish scales, ventrally with long dark brownish and whitish hair-like scales, longer than third segment of labial palpi, third segment of labial palpi porrect, dorsally with dark brownish and whitish scales, laterally with whitish scales and ventrally with dark brownish scales; antennae approximately two-fifths of forewing length (i.e., from wing base to R_5), shorter than discal cell length (i.e., from base to inferior disco-cellular vein), composed of 29 flagellomeres (scape and pedicel not examined), four distal flagellomeres appearing darker than others, club rather insignificant but discernible, grayish and brownish scales along antennae. **Thorax:** Dorsally and laterally with brownish scales and long hair-like scales; ventrally with light brownish hair-like scales and yellow ocher scales; prothoracic leg reduced, with grayish or brownish setiform scales; mesothoracic leg brownish, dorsally darker than ventrally (metathoracic leg not located on holotype), pair of tibial spurs, equal in length, visible at distal end of tibia, both tibia and tarsus adorned with longtitudinal rows of spines ventrally, in addition to several spines noticeable on lateral side of tibia. **Abdomen:** Eighth tergite appearing as membranous, visible as narrow band at base of eighth abdominal segment, as well as somewhat broad weakly sclerotized posterior region noticeable. **Wing venation:** Basal half of subcostal vein inflated, as well as base of cubitus; recurrent vein apparently absent in forewing discal cell; hindwing humeral vein developed. **Wing shape:** Forewing subtriangular, overall appearing rounded and broad rather than elongate, apex rounded, costal margin slightly convex, outer margin straight from M_2 to Cu_2, curved above and below these veins respectively, inner margin straight; hindwing overall slightly elongate and rounded, costal margin convex above Sc + R_1, outer margin slightly sinuate, inner margin slightly concave near tornus, anal lobe convex. **Dorsal forewing:** Ground color brown, slightly darker distally; no visible secondary sexual traits on wings; olive-greyish sheen apparently not present. **Dorsal hindwing:** Ground color brown; marginal band around Cu_1 and below; no visible secondary sexual traits on wings; olive-greyish sheen apparently not present. **Ventral forewing:** Ground color chestnut brown; brownish discal band crossing discal cell, passing area near origin of Cu_2 distally, fading in cell Cu_2; concolourous postdiscal band, broader than discal band, traversing from R_5 to 2A, anteriorly narrow and somewhat sinuate, slightly broadening posteriorly and fading in cell Cu_2; small submarginal ocellus in cell M_1, appearing as black spot with orangish-yellow ring, with two silver-ish pupils; submarginal band grayish brown, extending from apical area to 2A by gradually broadening, and jagged; concolorous marginal band traversing from apex to 2A; fringe dark ocher. **Ventral hindwing:** Ground color chestnut brown; narrow band absent at base of wing; discal band traversing from costal margin to inner margin, roughly straight and evenly broad throughout, passing area near origin of Rs basally; concolorous postdiscal band, parallel to discal band and similar in width, roughly straight but indented at origin of Cu_1; five submarginal ocelli, those in cells Rs, M_1 and Cu_2, appearing as black spot with orangish-yellow ring, ocellus in cell Rs with single large silver-ish pupil encompassing much of ocellus, ocellus in cell M_1 with single small pupil in middle, ocellus in cell Cu_2 with two small pupils and ocellus elongated vertically, ocellus in cells M_2 and M_3 appearing as creamy-yellowish smudge accompanied with barely noticeable pupil; submarginal band grayish brown, extending from cell Rs towards inner margin and apparently fused with postdiscal band at its posterior end, appearing jagged and gradually broadening; marginal band appearing slightly darker than submarginal band and slightly undulating, traversing from apex to tornus; fringe dark ocher. **Genitalia** (Figs. 3A-F): Tegumen approximately hemisphere in lateral view, dorsally convex with anterior end appearing slightly hooked in lateral view, ventral margin roughly straight; uncus approximately twice as long as tegumen in lateral view, hair-like setae not visible along uncus, base broadening in both lateral and dorsal view, dorsal margin slightly curving posteriorly in lateral view, tapering posteriorly and terminating in hooked single point in lateral view, terminating in spatula-like end in dorsal view; brachium tapering towards apex, apical point positioned above uncus in lateral view, roughly parallel to uncus with apical edge curving inwards in dorsal view; combination of ventral arms from tegumen and dorsal arms from saccus sinuate; appendices angulares present, developed and curving inwards; saccus slightly curved, shorter than uncus in length but longer than tegumen; weakly sclerotized region visible on ventral surface of anal tube; juxta present as "V-shaped" weakly sclerotized plate with acute apex; valva distally setose, valva appearing approximately parallelogram in lateral view, ventral margin convex at middle, dorsal margin of costa with concavity, apical process of valva with straight dorsal and ventral margin in lateral view, terminating in slightly hooked, angular, and blunt point; inner margin of apical process of valva serrated; phallus roughly straight, phallobase shorter than aedeagus; cornuti apparently absent.

COI barcode sequence (molecular voucher: BC-DZ-025; GenBank voucher: ON932574):

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TTTTTGGTATTTGAGCAGGAATATTGGGCACATCTCTTAGCTTAATCATTCG
AATAGAATTAGGTAACCCAGGATTTTTAATTGGAAATGACCAAATTTATAAT
ACAATTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTAATACCCA
TTATGATTGGAGGATTTGGTAATTGATTAGTTCCTTTAATATTAGGAGCTCC
TGATATAGCTTTTCCTCGTATAAATAATATAAGATTTTGGCTACTCCCCCCT
TCTTTAATTTTATTAATTTCGAGAAGTATTGTAGAAAATGGAGCTGGTACTG
GATGAACAGTTTACCCCCCCCCTTTCTCTAATATTGCTCATAGAGGCTCCTC
AGTTGATTTAGCTATTTTTTCCCTTCATTTAGCTGGAATTTCCTCAATTTTA
GGAGCTATTAATTTTATTACTACAATACTNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNTTCTTACCTGTTTTAGCAGGAGCTATCACAATACTTTTAACT
GATCGAAATTTAAACACATCTTTTTTTGATCCTGCAGGAGGAGGTGATCCTA
TTTTATACCAACATTTATTTTGATTTTTTGGTCACCCTGAAGTT
```

FEMALE: Forewing length 18.3-19.4 mm (n=2). **Similar to male except as follows:** Foretarsus divided into five segments; wing overall appearing broad and rounded, as well as paler, ventral hindwing submarginal band broader. **Abdomen and genitalia** (Figs. 3G-I): Eighth tergite fully developed; intersegmental membrane of seventh and eighth abdominal segment pleated and expandable, folded over lamella antevaginalis, with moderately sclerotized region present; lateral plate of eighth abdominal segment not fused with lamella antevaginalis; lamella antevaginalis appearing as somewhat winkled and trapezoidal sclerotized plate broadening anteriorly; ductus seminalis exiting at one-third distance from ostium bursae to corpus bursae, pair of rather broad and long signa located ventrally on corpus bursae; papilla analis elongated vertically than horizontally, with numerous setae, posterior apophysis as rounded point. **COI barcode sequence** (2021-FLP-IMM-0371; GenBank voucher: ON931448)**:** differing from holotype by 14 base pairs.

Immature stages (based on 2021-FLP-IMM-0371 throughout).

Egg (Figs. 4A, B)**:** Spherical, appearing yellowish and semi-transparent, with apparently somewhat irregular polygonal markings covering surface. Stemmata and mouth parts visible day prior to hatching. Diameter: 1.0 mm. Duration: Unknown, collected on 10 May 2021 and hatched on 11 May 2021.

First instar (Figs. 4C, D; 5A)**:** Head capsule width: 0.8 mm. Head capsule appearing black, vertex rounded and epicranial notch insignificant, with semi-rectangular scolus adorned with delated setae (scolus length 0.1 mm); five noticeable chalazae visible, M1, M2, M3 and P4, as well as one by stemma 3; four setae visible on one side of labrum; six stemmata visible, stemma 3 largest, closer to stemma 2 than 4. Body integument yellowish and semi-transparent, overall body color chartreuse due to greenish intestinal content revealed through semi-translucence; pair of white insignificant dorsal lines present, delineating reddish brown mid-dorsal region; three concolourous sub-dorsal to lateral lines present, parallel to two dorsal lines; spiracles and tracheal system noticeable along spiracles; chaetotaxy not fully discernible based on photographs but primary setae thread-like and slightly dilated at apex (described as "weakly bulbed" *sensu* Murray (2001: Fig 3.13C)), XD1 and XD2 visible on T1 and similar in length, D1, D2, SD1 and L1 apparently present from T1 to A10, D1 and D2 rather short but noticeably longer on terminal abdominal segments (length of D2 about half of D1, on A8 and A9), SV1, SV2, SV3, L2 and PP1 noticeable on A10 (but not fully discernible on A9); slightly pinkish bifid caudal filaments, appearing similar or shorter than A8 in dorsal view. Body length: 5.9 mm based on larva photographed on 17 May 2021. Duration: 8 days (11-19 May 2021).

Second instar (Figs. 4E, F; 5B)**:** Head capsule width: 0.9 mm. Head capsule appearing dark brown, epicranial notch and vertex as in previous instar, with numerous secondary setae and two developed horn-like scolus, inner margin appearing darker (darker area extends to vertex), with seta on both tips (scolus length 0.3 mm); chalazae reduced; five setae discernable on one side of labrum; six stemmata visible, arrangement similar to previous instar. Body overall appearing dark, fleshy, and granular; five creamy-whitish mid-dorsal to lateral lines present as in previous instar, appearing darker between two dorsal lines; setae thread-like and shorter; spiracles rather insignificant but noticeable on T1 and A8, tracheal system not discernable; bifid caudal filaments, appearing longer than A8 in dorsal view, inner-margin slightly pink-ish. Body length: 7.0 mm based on larva photographed on 22 May 2021. Duration: 10 days (19-29 May 2021).

Third instar (Figs. 4G, H; 5C)**:** Head capsule width: 1.5 mm; scolus length 0.5 mm. Head and body similar to immediately preceding instar except for head scolus lighter distally and labrum appearing reduced. Body length: 16.0 mm based on larva photographed on 2 June 2021. Duration: 8 days (29 May-6 June 2021).

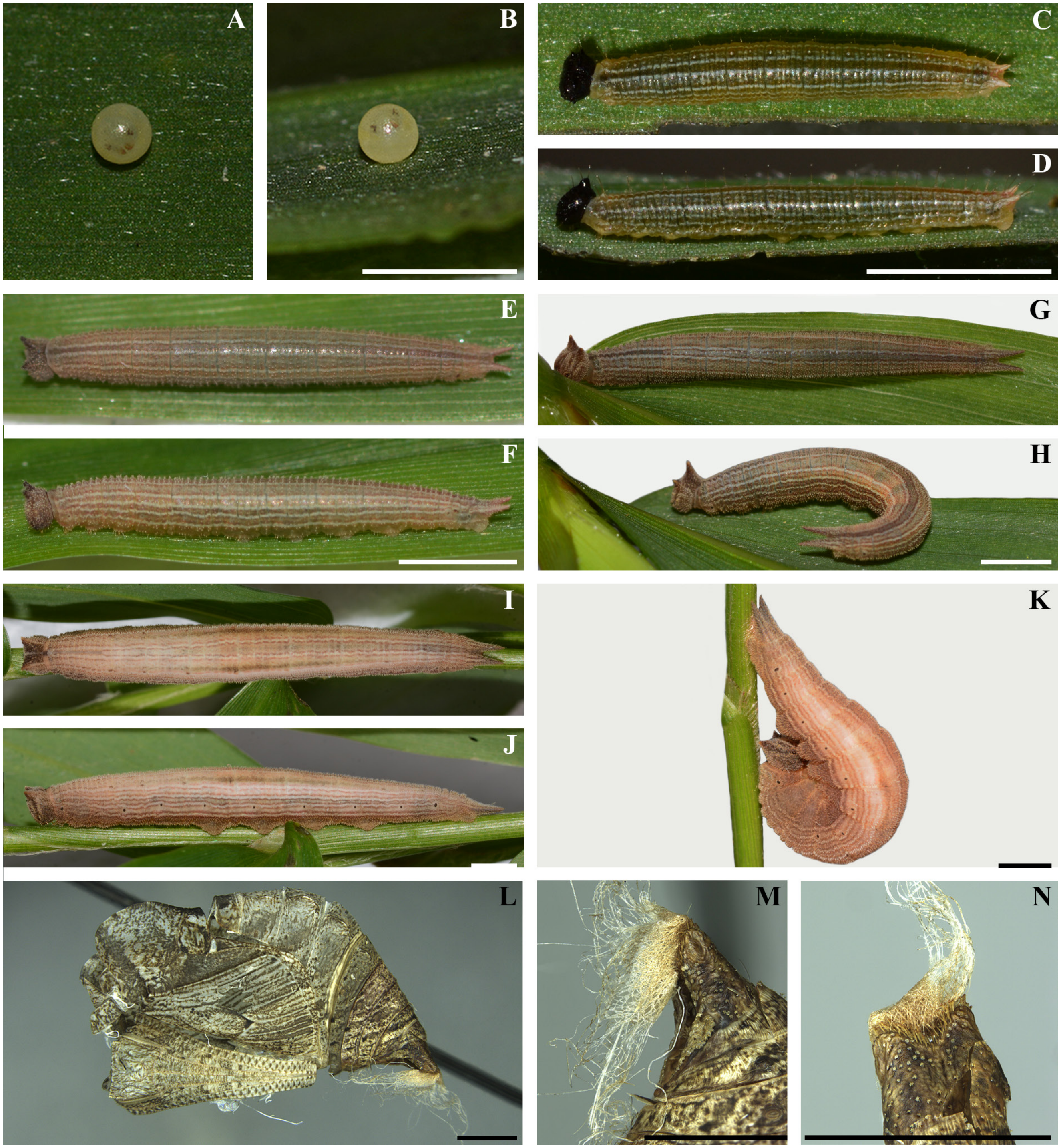

Figure 4. Immature stages of *C. thaliana* **n. sp.** based on 2021-FLP-IMM-0371: A, B) egg, with mouthparts and stemmata showing through semi-translucent; C) first larval instar in dorsal view; D) first larval instar in lateral view; E) second larval instar in dorsal view; F) second larval instar in lateral view; G, H) third larval instar in dorsal-lateral view; I) fourth (ultimate) larval instar in dorsal view; J) fourth (ultimate) larval instar in lateral view; K) prepupa; L) pupal case in lateral view; M) cremaster in lateral view; N) cremaster in dorsal view. All scale bars = 2 mm.

Fourth (ultimate) instar (Figs. 4I, J; 5D)**:** Head capsule width: 2.2 mm; scolus length 0.7 mm. Head and body similar to immediately preceding instar except base of head scolus broader, labrum appearing reduced, and body overall appearing lighter with spiracles more prominent. Body length: 26.4 mm based on larva photographed on 17 June 2021. Duration: 15 days (6-21 June 2021).

Pupa (Figs. 4L-N)**:** Pupal case as illustrated; cremaster broad, somewhat wrinkled and dark with numerous setae discernable ventrally as well as posteriorly, terminating rather broadly with concavity observed in dorsal view. Body length: not measured. Duration: 16 days (21 June-7 July 2021).

Host plant (recorded by Thalia Corahua-Espinoza). *Lasiacis ligulata* Hitchcock & Chase (Poaceae: Panicoideae: Paniceae) (Figs. 6A-C).

The natural host plant for *Caeruleuptychia thaliana* **n. sp.** was identified as a grass species in the plant family Poaceae, *Lasiacis ligulata* Hitchcock & Chase, at FLP. At FLP, this plant species is a common component of the plant community along forest edges, and it is occasionally found inside the forest,

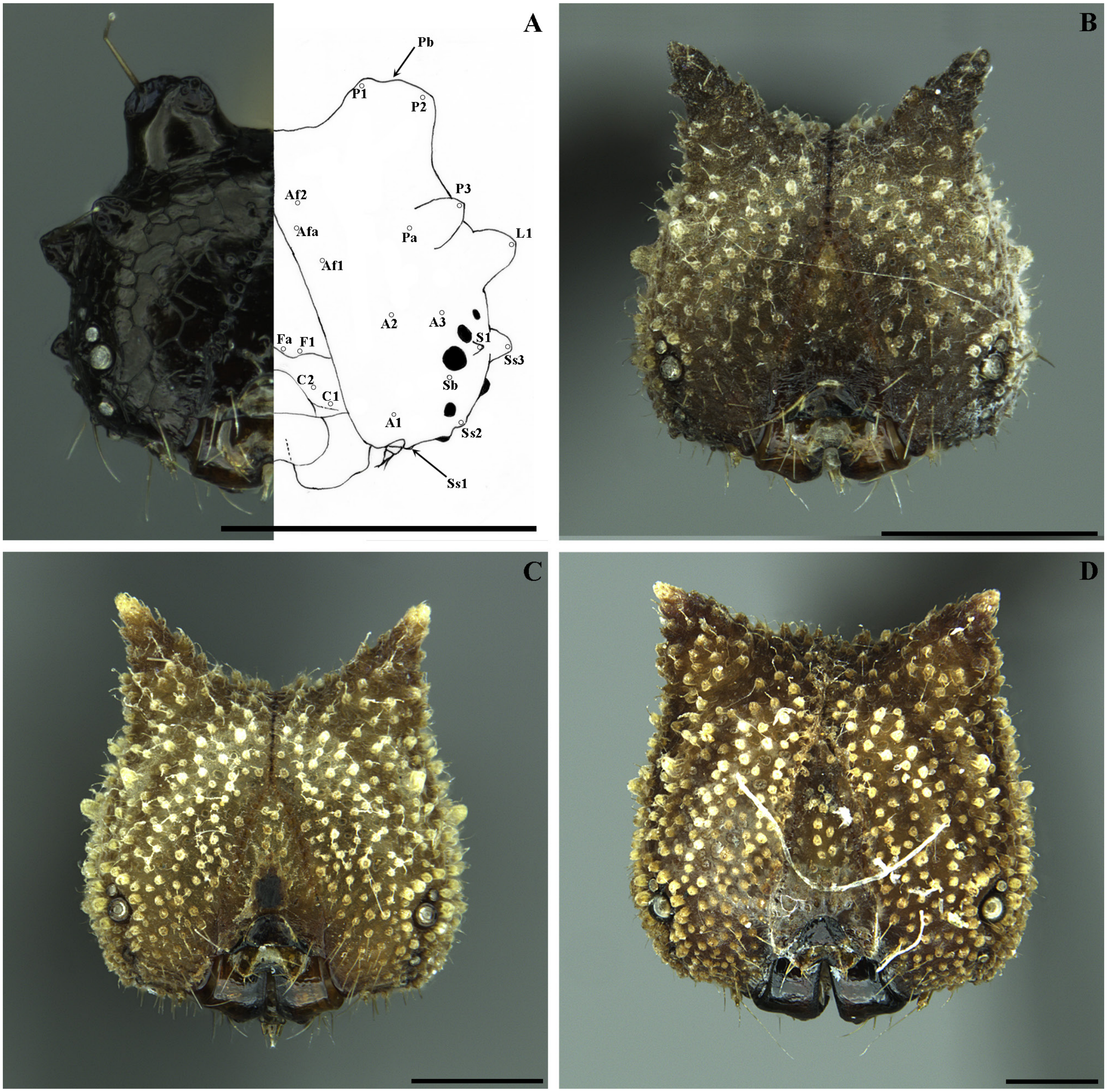

Figure 5. Head capsules of *C. thaliana* **n. sp.** based on 2021-FLP-IMM-0371: A) first instar in frontal view; B) second instar in frontal view; C) third instar in frontal view; D) fourth (ultimate) instar in frontal view. All scale bars = 0.5 mm.

especially along large forest trails. A single egg of *C. thaliana* **n. sp.** reared for the present study (2021-FLP-IMM-0371) was found at the entrance to a forest trail. At the time of sampling on 10 May 2021, the height of the plant was 2.5 m. The egg was found at a distance of 1.3 m from the ground, located on the abaxial surface, on the proximal part of the leaf blade, between the midrib and leaf margin.

Types. HOLOTYPE: male, with following labels written verbatim: //31 a 35 km NO de Barra do Bugres, Barra do Bugres, MT, 28-VI-1972 200 m, Mielke & Brown//BC-DZ-Willmott 25//DZ 42. 559//GEN. PREP. M. M. Casagrande 2021//HOLOTYPUS//HOLOTYPUS CAERULEUPTYCHIA THALIANA NAKAHARA & PIOVESAN DET. 2022// (DZUP).

PARATYPES: two females, with following labels written verbatim: //31 a 35 km NO de Barra do Bugres, Barra do Bugres, MT, 28-VI-1972 200 m, Mielke & Brown// DZ 42. 546//GEN. PREP. M. Piovesan 2022// (DZUP); //PERU: Madre de Dios Dept. Finca Las Piedras, ca. 270 m asl -12.226616º, -69.112392º approx. Reared from immature stage Adult eclosion: 07 Jul 2021 T. Corahua *leg.*// 2021-FLP-IMM-0371// (ASA).

Etymology (by Shinichi Nakahara). *Caeruleuptychia thaliana* **n. sp.** is named in recognition of Thalia Corahua-Espinoza, from Puerto Maldonado, Peru, whose study at FLP in 2021 brought numerous novel host plant records to science and significantly advanced our knowledge of Neotropical butterfly immature stages. As indicated above, her discoveries served as the basis

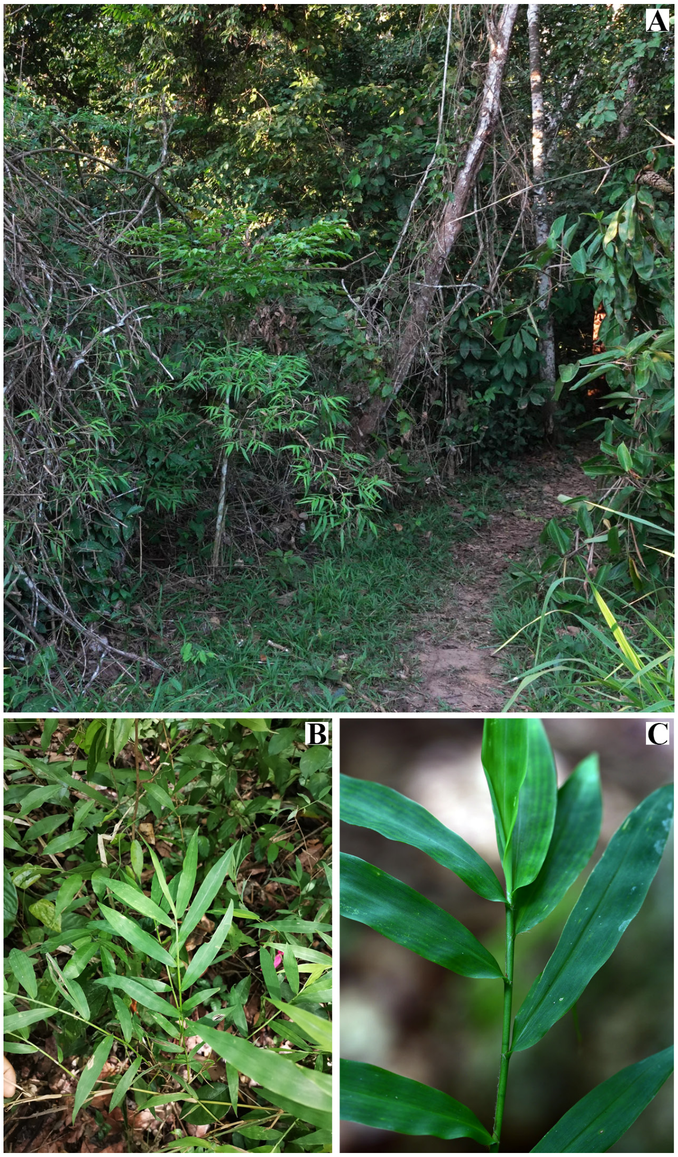

Figure 6. Habitat and host plant (*L. ligulata*) of *C. thaliana* **n. sp.**: A) Habitat at FLP where the host plant was found (photo credit: Zunilda Escalante); B) host plant *in situ*; C) close-up view of leaves and nodes.

for generating a number of life history articles (Ccahuana *et al*., 2021; Corahua-Espinoza *et al*., 2022a, b, in press, in prep.; Duerr *et al*., in press; Nakahara *et al*., 2022; Tejeira *et al*., 2021), including the present study, and these accomplishments in a given short time-frame are remarkable and unmatched. Her seemingly unlimited intrinsic motivation to revamp our understanding of Amazonian biodiversity was truly inspirational and anchored myself to Neotropical Lepidopterology by instilling me with revived interest, continuing to document butterfly diversity as a taxonomist. This patronym is also coined in appreciation for her fine company, hospitality, and tolerance throughout the course of traveling to various sites around Puerto Maldonado in June 2022. Thalia's solicitude, thoughtfulness, selflessness, and dry sense of humor coupled with her honesty, modesty, infinite patience, and (sometimes) meticulousness are all acquainted to everyone who has had the pleasure and fortune to know her in person. The specific epithet is an indeclinable Latinized noun standing in apposition with the feminine generic name.

Distribution. *Caeruleuptychia thaliana* **n. sp.** is known from two sites which are over 1,300 km apart in the Amazon basin, namely Barra do Bugres (Mato Grosso, Brazil) (type locality) and Finca Las Piedras (Madre de Dios, Peru).

DISCUSSION

The decision to place *C. thaliana* **n. sp.** in *Caeruleuptychia* is primarily influenced by the fact that the type species of the genus, *Euptychia caerulea* Butler, 1869 (i.e., junior subjective synonym of *E. urania* Butler, 1867; Ríos-Málaver (2019)), is recovered as part of a monophyletic *Caeruleuptychia* based on the ML tree (Fig. 1). However, support for the monophyly of *Caeruleuptychia* in the current study is not strong (UFBoot/aBayes/SH-aLRT = 89.3/0.999/76); therefore, we consider the fact that *C. thaliana* **n. sp.** was found as being the sister species of *C. umbrosa* to be another piece of evidence to justify this generic classification.

We here discuss two available species-group names associated with *Caeruleuptychia*, both of which have arguable applications to the concept represented by the name *C. thaliana* **n. sp.**, in order to justify our taxonomic hypothesis by excluding these possibilities. *Euptychia umbrosa* Butler, 1870 was described by Arthur G. Butler based on an unspecified number of specimen(s) collected by [Clarence] Buckley in Ecuador, owned by [William Chapman] Hewitson (Butler, 1870). Although the description predominantly reflects a typical brown euptychiine species, a certain portion of the wing description of *E. umbrosa* provided by Butler enables us to narrow down its identity: dorsal surface of the wing grayish-green (*Alae supra cinereo-virides*); ventral surface paler with white scales (*Alae subtus pallidiores albido squamosae*). The former grayish-green dorsal surface is also depicted in the illustration of its dorsal surface (on pl. XVIII [18], fig.8) accompanying the original description of *E. umbrosa*. These two features are visible in the male syntype housed in NHMUK (images available through Warren *et al.,* 2017), albeit the grayish-green sheen of the dorsal surface is apparently faded in this syntype. For an unknown reason, Forster (1964) did not classify *E. umbrosa* in any of the genera he erected in his ground-breaking work regarding euptychiine classification, and it was not until Lamas (2004) where this taxon was placed in *Caeruleuptychia*.

Euptychia viridicans Weymer, 1911 was described based on an unspecified number of specimen(s) from Peru, by Gustav Weymer (Weymer, 1911: 199, fig. 47b). The sex of the syntype was not explicitly stated in the original description, although the syntype housed at STD is a male specimen, judging from the genitalia visible at the posterior tip of the abdomen (images available through: Warren *et al.,* 2017). Subsequently, Forster (1964) established a monospecific genus *Weymerana* Forster, 1964 to accommodate *E. viridicans* and provided a somewhat ambiguous feature of the phallus/aedeagus as apparently the sole diagnostic character for *Weymerana*. Lamas (2004) considered *Euptychia viridicans* as a junior subjective synonym of *E. umbrosa* without providing rationale for this taxonomic proposal.

Despite the fact that these two authors did not depict the hair-pencil on the dorsal forewing in their description of these two taxa, the two syntypes discussed above possess all the wing pattern features mentioned above to distinguish *C. umbrosa* from *C. thaliana* **n. sp.**, except for the male syntype of *E. viridicans* apparently lacking an olive-grayish sheen on the dorsal surface (the hair-pencil on the dorsal forewing is somewhat visible in these two syntypes). This fading phenomenon of the olive-grayish sheen is also noticeable in one sequenced male of *C. umbrosa* (CP01-09; MUSM-LEP-100245), although the trace of a sheen is discernible at the base of wings in this male specimen. Nonetheless, other phenotypic features, as well those genital characters (#CP-191, MUSM), discussed as diagnostic above are clearly visible in this sequenced specimen from Madre de Dios, Peru. Thus, it seems plausible to apply the specific epithet *umbrosa* to the clade consisting of eight specimens spanning its range in the Amazon basin and beyond (see Table 1 for locality data), as well as to any individuals which can fall within the concept represented by the species-group name *umbrosa* based on these characters discussed herein. Due to the lack of genetic data from relevant types, we refrain from designating lectotypes of these two names in the current work, but it does seem reasonable to retain *E. umbrosa* as a senior subjective synonym of *E. viridicans*.

The COI barcode patristic distance between eight sequenced *C. umbrosa* and the holotype of *C. thaliana* **n. sp.** ranged from 4.1%-5.1% (mean: 4.21%), while genetic divergence among these eight *C. umbrosa* ranged from 0.1%-1.7% (mean: 0.67%). *Caeruleuptychia thaliana* **n. sp.** and *C. umbrosa* are broadly sympatric in the Amazon basin, supporting the proposed species-level status of *C. thaliana* **n. sp.** in conjunction with the presence/absence of the dorsal forewing hair-pencil. For example, 2021-FLP-IMM-0371 (*C. thaliana* **n. sp.** from FLP, Madre de Dios) and CP01-09 (*C. umbrosa* from Tambopata Research Center, Madre de Dios) originate from sites which are approximately 100 km apart and exhibited genetic distance of >3.0%. Conversely, two sequenced individuals of *C. thaliana* **n. sp.** were sampled from localities which >1,300 km apart and showed genetic divergence of <2.0%. Notwithstanding this result, one might argue that our decision to consider BC-DZ-25 conspecific with 2021-FLP-IMM-0371 can be falsified since the COI barcode sequence from the latter individual shows a somewhat high patristic distance (1.9%) from the holotype. Additionally, the patristic distance of 2021-FLP-IMM-0371 and the holotype of *C. thaliana* **n. sp.** against eight sequenced individuals of *C. umbrosa* is 3.0%-5.1% (mean: 3.74%), resulting in a rather trivial barcoding gap. Despite this situation, we observed a nonsynonymous substitution between sequences of *C. thaliana* **n. sp.** (n=2) and *C. umbrosa* (n=8): sites 148-150 are ATT in *C. thaliana* **n. sp.**, whereas GTT in *C. umbrosa*, translating to Isolucine and Valine, respectively. This amino-acid-altering substitution, which is not detected among eight sequences of *C. umbrosa*, will influence the LnL of the sequence data at this codon position 148 during the topology and branch length proposals during the maximum likelihood analysis (Felsenstein, 1981). However, when we partitioned the data into codon positions, the placement of *C. thaliana* **n. sp.** in the ML tree resulted in a paraphyletic *C. umbrosa* (data not shown). Although modeling DNA sequence data is more reasonable this way, any given gene-tree will likely illustrate some discrepancies from a species-tree (e.g., Maddison, 1997). Since *C. thaliana* **n. sp.** and *C. umbrosa* both form a clade and are recovered as sister to each other in the ML tree under a single substitution model (Fig. 1), we consider our taxonomic hypothesis is supported by showing this ML tree. *Caeruleuptychia thaliana* **n. sp.** is therefore a taxon that warrants a specific name, and application of a subspecific epithet is inappropriate.

As set forth above, our taxonomic hypothesis is supported based on adult external morphology and molecular data, as well as evidence illustrating that no available species-group names are in existence. Here, we discuss an additional potential layer of evidence which may support taxonomic status of *C. thaliana* **n. sp.** by extracting and interpreting relevant life history information presented in an unpublished portion of Murray's (2001) dissertation.

The identity of *C. scopulata*, reported to feed on species of *Guadua* Kunth (Poaceae: Bambusoideae: Bambuseae) in eastern Ecuador, in Murray's (2001) dissertation may well represent *C. umbrosa*. This assumption is supported by the fact that sequenced material from Napo province, Ecuador included in the present study (DNA00-016; see Table 1) is a molecular sample originally identified as *C. scopulata* and was generated during the course of preparing Murray (2001: Table 4.1). As discussed above, eight sequences identified as *C. umbrosa* herein, including DNA00-016, illustrated a rather low intraspecific genetic divergence and their conspecificy is graphically informed in Fig. 1. In fact, DNA00-016 was identified as *C. umbrosa* in Murray & Prowell (2005). Murray (2001: Table 4.1) indicates that DNA from this specimen was extracted from dried material. However, it is unclear whether DNA00-016 was one of the samples used to study life stages in Murray (2001), or an adult collected in the field with no associated immature stages data. If the concept of *C. scopulata* was applied uniformly to all individuals identified as this taxon studied in Murray (2001), it would be reasonable to accept that this specific epithet was misapplied to samples used to examine immature morphology and biology. Given this, the natural host plant of *C. umbrosa* recorded in Jatun Sacha (Napo, Ecuador) is an unidentified species of *Guadua* according to Murray (2001: Table 5.1). *Guadua* is a genus of Neotropical woody bamboo in the subtribe Guaduinae (Bambuseae). With over 30 species recognized, *Guadua* is the third species-rich genus of the Neotropical bamboos (i.e., Bambuseae + Olyreae) after two diverse Andean bamboo genera, *Chusquea* Kunth and *Aulonemia* Goudot (Clark & Oliveira, 2018). Unlike *Chusquea* and *Aulonemia*, *Guadua* is known for its representation in the lowlands (Clark, 1990), and among *ca*. 150 euptychiine species with some kind of associated host plant records, at least 17 species are recorded to have species of *Guadua* as a host plant (Corahua-Espinoza & Nakahara, unpublished data). It must be noted that these numbers do not include species with host plants recorded as "many grass species", "probably many grass species" and "probably *Guadua*" in Murray (2001: Table 5.1) due to ambiguity. Among these 17 euptychiine species recorded to utilize species of *Guadua*, host plant records for 10 species are represented to date only by *Guadua* species. In fact, existing evidence suggests some euptychiine species may feed exclusively on *Guadua* (e.g., *Pseudodebis valentina* (Cramer, 1779), *Posttaygetis penelea* (Cramer, 1777), *Splendeuptychia itonis* (Hewitson, 1862); Corahua-Espinoza *et al.*, in press; Murray, 2001, 2003). Based on the feeding experiments conducted by Murray (2001), *Pseudodebis valentina* and *S. itonis* consumed and pupated only by feeding on *Guadua* sp., and rejected or died shortly after consuming the following Poaceae species: *Olyra* sp., *Pariana* sp. (both Olyreae), *Orthoclada* sp. (Zeugiteae), *Lasiacis* sp. (Paniceae) (for *S. itonis* only) and *Panicum* sp. (Paniceae) (for *P. valentina* only). Murray (2003) reported a similar observation for *Posttaygetis penelea*, namely mature larvae rejecting two herbaceous bamboo species and one grass species, consuming only *Guadua* bamboo. This specialization of *P. penelea* is corroborated by recent field work at FLP, where immature stages of this taxon were found exclusively on *Guadua weberbaueri* Pilg. in nature (n=5; Zunilda Escalante, pers. comm.). Nevertheless, *C. umbrosa* is found at sites in Ecuador where *Guadua* bamboos apparently do not occur (Keith Willmott, pers. comm.), and caution must be exercised when interpreting the field experiment results of Murray (2001), thus increasing the likelihood of *C. umbrosa* utilizing non-*Guadua* plants in nature. On the other hand, Janzen & Hallwachs (2018) reported a single record of *Guadua* bamboo for *Taygetis laches* (Fabricius, 1793) in southwestern Costa Rica, whereas > 500 other records are known from various other grass species and herbaceous bamboos, including > 300 records from *Olyra latifolia*, as well as 13 records based on Cyperaceae. Thus, *Guadua* bamboo is likely not the preferred host plant for *T. laches* at Janzen & Hallwachs' (2018) study site in Costa Rica and this record may be best considered as an irregular host plant record. We see a similar case with two other *Taygetis* species according to Janzen & Hallwachs' (2018) database, where the host plant record of *Guadua* is represented as a single record along with various other Poaceae species with records for multiple individuals associated. Corahua-Espinoza *et al.* (in press) discussed that this ability to feed on various Poaceae species, as well as other plant families, might have contributed to the species diversity of *Taygetis* Hübner, [1819], although such debate is only possible through accumulation of host plant records. Unfortunately, Janzen & Hallwachs' (2018) study is based in Costa Rica, where representation of *Caeruleuptychia* is almost non-existent. *Caeruleuptychia* rivals *Taygetis* in terms of species diversity, and it would be most interesting to assess the diet breadth of the members of *Caeruleuptychia* in order to provide insights into its diversity in the Amazon basin.

Apart from *Guadua* bamboo records, to date >40 euptychiine species out of *ca*. 150 species are known to solely utilize species of woody bamboos and/or herbaceous bamboos, whilst at least 6 species are recorded to feed on other grass species as well (Corahua-Espinoza & Nakahara, unpublished data). If euptychiine species feeding on *Guadua* and other bamboo species tend to have a narrow diet breadth, that may strengthen the taxonomic hypothesis proposed herein. *Caeruleuptychia thaliana* **n. sp.** is reported to utilize a grass species, *L. ligulata* in southeastern Peru and *C. umbrosa* is reported to feed on a woody bamboo, *Guadua* sp. in eastern Ecuador, implying some degree of niche partitioning by utilizing plant species in two different subfamilies. Nevertheless, as explained above, some ambiguity regarding information presented in Murray (2001) requires clarification to develop this argument further. Our highly fragmentary knowledge regarding *Caeruleuptychia* immature stages, host plants, and their diet breadth also prevents us from continuing this debate. Apart from the two host plant records discussed and presented herein, records for a mere two species are available to us regarding *Caeruleuptychia* host plants: unidentified *Caeruleuptychia* - unidentified Poaceae in Brazil (Beccaloni *et al.*, 2008); *Caeruleuptychia urania* - study in progress (Corahua-Espinoza *et al.*, in prep.). We also add that both male and female individuals of *C. helios* Weymer, 1911 were only found in association with *Guadua weberbaueri* at FLP (pers. obs.), suggesting that *C. helios* may utilize *G. weberbaueri* in nature. *Caeruleuptychia trembathi* Willmott, Nakahara, Hall & Neild, 2017 is also found in close association with *Guadua* or *Chusquea* bamboo stands, and known females from Ecuador are always found near *Chusquea* bamboo in eastern Ecuador (see Nakahara *et al.*, 2018b). Clearly, these speculations regarding their host plants will need to be clarified by documenting immatures of these *Caeruleuptychia* species in nature. As euptychiine host plant records continue to accumulate, we see some degree of tendency and evidence towards bamboo feeding in euptychiine species to be more concentrated in the so-called "*Taygetis* clade", "*Amphidecta* clade" and "*Cyllopsis* clade". Nevertheless, there exist exceptions, such as the *Splendeuptychia* "*ashna* group" (recovered in the so-called "*Splendeuptychia* clade"), and the aforementioned sparse host plant records for *Caeruleuptychia* will not allow us to draw any conclusions as to its host plant preference and diet breadth. It hardly needs saying that a consensus regarding euptychiine natural history is only beginning to emerge.

Finally, like other species-group names published for the purposes of zoological nomenclature, *Caeruleuptychia thaliana* **n. sp.** is a name inextricably tied to the name-carrier (i.e., holotype). This will enable application of this arbitrary combination of letters to designate a corresponding concept of *C. thaliana* **n. sp.** based on the classification introduced herein. If applied to a concept, *C. thaliana* **n. sp.** becomes a taxonomic hypothesis, which can be falsified if contradicting evidence surfaces. Hence, the specific epithet may be interpreted as a mere reflection of our current understanding of this ancestor-descendant lineage to which the name-bearing type belongs. As mentioned and demonstrated herein, creation of a scientific name involves subjectivity. Additionally, application of this name is an equally subjective process, since species recognition is based on picking strands of evidence to fit a taxonomic hypothesis. These hypotheses (i.e., concepts) are subject to revisions, and consequently, scientific names can be endlessly removed, renamed, or reapplied. It is this advancement of our understanding of the natural world which causes taxonomy, the science of naming and classifying the diversity of life, to hold so much appeal.

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