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Descriptions of one hundred new species of HesperIIDae

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Descriptions of one hundred new species of HesperIIDae

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Abstract. A century and a half since the time of Hewitson, we are experiencing a renaissance in species discovery fueled by whole genome sequencing. A large-scale genomic analysis of HesperIIDae Latreille, 1809 (Lepidoptera), including primary type specimens, reveals a deluge of species new to science. One hundred of them (one in a new genus) are described here from the New World (type localities are given in parenthesis): *Drephalys* (*Drephalys*) *diovalis* Grishin, **new species** (Ecuador: Napo), *Euriphellus panador* Grishin, **new species** (Ecuador: Esmeraldas), *Euriphellus panamicus* Grishin, **new species** (Panama: Panama), *Cecropterus* (*Thorybes*) *viridissimus* Grishin, **new species** (Ecuador: Zamora-Chinchipe), *Cecropterus* (*Murgaria*) *dariensis* Grishin, **new species** (Panama: Darien), *Urbanus* (*Urbanus*) *mericuti* Grishin, **new species** (Ecuador: Napo), *Telegonus* (*Telegonus*) *pastus* Grishin, **new species** (Panama: Panama), *Autochton* (*Autochton*) *dora* Grishin, **new species** (Ecuador: Pastaza), *Astraptus centralis* Grishin, **new species** (Panama: Colón), *Aguna claxonica* Grishin, **new species** (Ecuador: Napo), *Aguna esmeralda* Grishin, **new species** (Ecuador: Esmeraldas), *Aguna lata* Grishin, **new species** (Guyana), *Ridens angulinea* Grishin, **new species** (Peru: Cuzco), *Pythonides lera* Grishin, **new species** (Peru: Cuzco), *Pythonides latemarginatus* Grishin, **new species** (Panama: Panama), *Gindanes variegatus* Grishin, **new species** (Brazil: Mato Grosso), *Milanion* (*Milanion*) *virga* Grishin, **new species** (Brazil: Rondônia), *Milanion* (*Milanion*) *furvus* Grishin, **new species** (Panama: Panama), *Milanion* (*Milanion*) *laricus* Grishin, **new species** (Ecuador: Napo), *Charidia ronda* Grishin, **new species** (Brazil: Rondônia), *Pseudodrephalys tinas* Grishin, **new species** (Peru: Loreto), *Pseudodrephalys argus* Grishin, **new species** (Suriname: Para), *Achlyodes calvus* Grishin, **new species** (Brazil: Santa Catarina), *Spioniades artemis* Grishin, **new species** (Panama: Panama), *Spioniades artemidoides* Grishin, **new species** (Brazil: Santa Catarina), *Myrinia orieca* Grishin, **new species** (Ecuador: Orellana), *Myrinia aragua* Grishin, **new species** (Venezuela: Aragua), *Myrinia maculosa* Grishin, **new species** (Guatemala), *Myrinia manchada* Grishin, **new species** (Guyana), *Polyctor* (*Fenops*) *lamperus* Grishin, **new species** (Panama: Darien), *Nisoniades* (*Nisoniades*) *lutum* Grishin, **new species** (Mexico: Guerrero.), *Bolla* (*Stolla*) *vena* Grishin, **new species** (Venezuela: Aragua), *Staphylus* (*Vulga*) *vula* Grishin, **new species** (Mexico: Veracruz), *Staphylus* (*Vulga*) *vulga* Grishin, **new species** (Panama: Darien), *Staphylus* (*Staphylus*) *rotundalus* Grishin, **new species** (Ecuador: Napo), *Staphylus* (*Staphylus*) *yucatanus* Grishin, **new species** (Mexico: Quintana Roo/Yucatan), *Heliopetes* (*Heliopetes*) *lana* Grishin, **new species** (Guatemala), *Canesia ella* Grishin, **new species** (Venezuela: Barinas), *Paches* (*Paches*) *loxeca* Grishin, **new species** (Ecuador: Morona-Santiago), *Clito congruens* Grishin, **new species** (Panama: Colón), *Cycloglypha corax* Grishin, **new species** (Brazil: Rio de Janeiro), *Festivia peruvia* Grishin, **new species** (Peru: Huánuco), *Decinea notata* Grishin, **new species** (Ecuador: Napo), *Pompeius fuscus* Grishin, **new species** (Brazil: Minas Gerais), *Vernia clara* Grishin, **new species** (Panama: Chiriquí), *Oligoria* (*Oligoria*) *obtena* Grishin, **new species** (Ecuador: Napo), *Thespieus mandal* Grishin, **new species** (Brazil: Rio de Janeiro), *Psoralis* (*Saniba*) *magnamacus* Grishin, **new species** (Panama: Darien), *Alychna ayonis* Grishin, **new species** (Ecuador: Napo), *Wahydra banios* Grishin, **new species** (Ecuador: Tungurahua),

Wahydra cuzcona Grishin, **new species** (Peru: Cuzco), *Cynea* (*Cynea*) *aureofimbria* Grishin, **new species** (Ecuador), *Cynea* (*Nycea*) *quada* Grishin, **new species** (Ecuador: Napo), *Cynea* (*Quinta*) *achirae* Grishin, **new species** (Mexico: Tamaulipas), *Eutus amazonicus* Grishin, **new species** (Peru: Madre de Dios), *Eutus incus* Grishin, **new species** (Peru: Cuzco), *Eutus septemaculatus* Grishin, **new species** (Brazil: Mato Grosso), *Godmia viridicapita* Grishin, **new species** (Ecuador: Napo), *Rhomba pulla* Grishin, **new species** (Peru: Cuzco), *Niconiades victoria* Grishin, **new species** (Mexico: Tamaulipas), *Lancephallus purpurus* Grishin, **new genus** and **new species** (Guyana), *Mnasicles* (*Remella*) *ecua* Grishin, **new species** (Ecuador: Pichincha), *Amblyscirtes* (*Amblyscirtes*) *aeratus* Grishin, **new species** (Mexico: Oaxaca), *Amblyscirtes* (*Mastor*) *chrysoplea* Grishin, **new species** (Mexico: Oaxaca), *Amblyscirtes* (*Mastor*) *chrysomisa* Grishin, **new species** (Mexico: Chiapas), *Amblyscirtes* (*Flor*) *meridus* Grishin, **new species** (Mexico: Veracruz), *Rectava chiriquensis* Grishin, **new species** (Panama: Chiriquí), *Cobalopsis adictys* Grishin, **new species** (Panama: Veraguas), *Cymaenes melaporphyrus* Grishin, **new species** (Mexico: San Luis Potosí), *Lerema* (*Morys*) *ecuadorica* Grishin, **new species** (Ecuador: Pichincha), *Saturnus obscurior* Grishin, **new species** (Panama: Darien), *Cantha zoirodicta* Grishin, **new species** (Peru: Madre de Dios), *Cantha meiodicta* Grishin, **new species** (Peru: Madre de Dios), *Phlebodes duplex* Grishin, **new species** (Guatemala: Cayuga), *Lychnuchus* (*Enosis*) *valle* Grishin, **new species** (Colombia: Valle), *Eutyichide ochoides* Grishin, **new species** (Peru: Cuzco), *Dion bora* Grishin, **new species** (Panama: Darien), *Dion occida* Grishin, **new species** (Peru: Madre de Dios), *Eprius* (*Eprius*) *veledinus* Grishin, **new species** (Ecuador: Pichincha), *Radiatus panamensis* Grishin, **new species** (Panama: Panama), *Pheraeus pulcher* Grishin, **new species** (Peru: Madre de Dios), *Callimormus rades* Grishin, **new species** (Panama: Panama), *Gubrus lubens* Grishin, **new species** (Ecuador: Loja), *Ludens labens* Grishin, **new species** (Panama: Darien), *Rigga isa* Grishin, **new species** (Ecuador: Napo), *Flaccilla lactea* Grishin, **new species** (Peru: Cuzco), *Falga athena* Grishin, **new species** (Panama: Darien), *Panoquina jay* Grishin, **new species** (Peru: Loreto), *Calpodes salianus* Grishin, **new species** (Peru: Madre de Dios), *Calpodes stingo* Grishin, **new species** (Ecuador: Sucumbíos), *Aides nobra* Grishin, **new species** (Panama: Colón), *Thracides pavo* Grishin, **new species** (Mexico: Tabasco), *Talides eluta* Grishin, **new species** (Peru: Cuzco), *Talides laeta* Grishin, **new species** (Peru: Cuzco), *Neoxeniades angustior* Grishin, **new species** (Brazil: Rio de Janeiro), *Damas zea* Grishin, **new species** (Guyana), *Tromba xantha* Grishin, **new species** (Mexico: Veracruz), *Perichares fura* Grishin, **new species** (Ecuador: Pichincha), *Carystoides* (*Balma*) *goliath* Grishin, **new species** (Colombia: Valle), and *Agathymus galeana* Grishin, **new species** (Mexico: Nuevo Leon). Additionally, we present evidence to support 22 taxa as species (not subspecies or synonyms) and synonymize one genus and four species. Namely, the following taxa are **species**: *Milanion pilta* Evans, 1953 (not *Milanion pilumnus* Mabilite and Boulet, 1917), *Milanion latior* Mabilite and Boulet, 1917 (not a synonym of *Milanion marcianna* Godman and Salvin, 1895), *Charidia pilea* Evans, 1953, and *Charidia pocus* Evans, 1953 (not *Charidia lucaria* (Hewitson, 1868)), *Paches* (*Paches*) *gloriosus* Röber, 1925 and *Paches* (*Paches*) *loxana* Evans, 1953 (not *Paches* (*Paches*) *loxus* (Westwood, 1852)), *Spioniades anta* Evans, 1953 (not *Spioniades abbreviata* (Mabilite, 1888)), *Decinea onasima* (Hewitson, 1877) and *Decinea formosus* (Hayward, 1940) (not *Decinea dama* (Herrich-Schäffer, 1869)), *Thespieus guerreronis* (Dyar, 1913) (not *Thespieus dalman* (Latreille, [1824])), *Cynea* (*Nycea*) *erebina* (Möschler, 1879) and *Cynea* (*Nycea*) *cleocharis* (Mabilite, 1891) (not *Cynea* (*Cynea*) *diluta* (Herrich-Schäffer, 1869)), *Amblyscirtes* (*Mastor*) *repta* Evans, 1955 (not *Amblyscirtes* (*Flor*) *florus* (Godman, 1900)), *Saturnus tiberius* (Möschler, 1883), *Saturnus conspicuus* (E. Bell, 1941), *Saturnus meton* (Mabilite, 1891), and *Saturnus obscurus* (E. Bell, 1941) (not *Saturnus reticulata* (Plötz, 1883)), *Phlebodes sifax* Evans, 1955 (not *Phlebodes campo* (E. Bell, 1947)), *Eutyichide ochus* Godman, 1900 and *Eutyichide rogersi* (Kaye, 1914) (not a subspecies and a synonym, respectively, of *Eutyichide subcordata* (Herrich-Schäffer, 1869)), *Falga mirabilis* Evans, 1955, *Falga jacta* Evans, 1955, and *Falga ombra* Evans, 1955 (not *Falga jeconia* (A. Butler, 1870)); and the following taxa are junior subjective **synonyms**: *Libra* Evans, 1955 (of *Phemiades* Hübner, [1819]), *Papilio clito* Fabricius, 1787 of *Milanion hemes hemes* (Cramer, 1777), *Pamphila hycsos* Mabilite, 1891 of *Cynea* (*Nycea*) *erebina* (Möschler, 1879), *Hesperia olympia* Plötz, 1882 of *Eutyichide subcordata* (Herrich-Schäffer, 1869), and *Hesperia ocrinus* Plötz, 1882 of *Aides aegita* (Hewitson, 1866). Furthermore, we propose **new combinations** for genus-species: *Lychnuchus* (*Enosis*) *ponka* (Evans, 1955) (not *Thoon* Godman, 1900), and species-subspecies: *Charidia pocus mayo* Evans, 1953 (not *Charidia lucaria* (Hewitson, 1868)), *Decinea onasima boliviensis* (E. Bell, 1930) (not *Decinea dama* (Herrich-Schäffer, 1869)), *Cynea* (*Nycea*) *erebina somba* Evans, 1955 (not *Pamphila hycsos* Mabilite, 1891), *Saturnus tiberius suffuscus* (Hayward, 1940) (not *Saturnus reticulata* (Plötz, 1883)), and *Falga mirabilis odol* Evans, 1955 (not *Falga jeconia* (A. Butler, 1870)). Then, *Milanion pilumnus* var. *hemestinus* Mabilite and Boulet, 1917 is a junior subjective synonym of *Milanion pilumnus pilumnus* Mabilite and Boulet, 1917, not of *Milanion leucaspis* (Mabilite, 1878). **Lectotypes** are designated for nine taxa (names in original combinations below): *Pellicia bromias* Godman and Salvin, 1894 (Mexico: Veracruz, Atoyac), *Nisoniades perforata*

Möschler, 1879 (Colombia), *Helias ascalaphus* Staudinger, 1876 (central Panama), *Pamphila hycsos* Mabilie, 1891 (Colombia), *Amblyscirtes fluonia* Godman, 1900 (Mexico: Guerrero, Xocomanatlan), *Mastor anubis* Godman, 1900 (Mexico: Guerrero, Omiltemi), *Eutychide ochus* Godman, 1900 (Mexico: Veracruz, Atoyac), *Cobalus subcordata* Herrich-Schäffer, 1869 (Southeast Brazil), and *Thracides xanthura* Godman, 1901 (Panama: Chiriquí Province, Bugaba). A **neotype** is designated for *Eudamus briccius* Plötz, 1881 (Guyana: Iwokrama Forest).

Key words. Cryptic species, biodiversity, skipper butterflies, genomics, speciation, nomenclature, taxonomy.

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Introduction

More than 150 years have passed since Hewitson's papers describing dozens of new butterfly species in a single publication (Hewitson 1867, 1868). At the time of Hewitson, wing pattern differences were nearly the only criterion for species delineation in Lepidoptera. The superficial appearance of spread specimens, as judged by an author, was described in a short paragraph preceded by a newly proposed species name. The influx of new species descriptions was fueled by increased collecting efforts in species-rich and previously unexplored tropical areas of the world. Most of the commonly encountered species differing in wing patterns were described within a few decades, suggesting to some that we have cataloged nearly all butterfly species.

The situation changed with the realization that consistent genitalic differences typically signify species-level differences even without obvious wing pattern characters. This prompted a genitalia screening approach where large series of specimens were dissected in a search for new species. In HesperIIDae, this approach proposed by Godman and Salvin (1893-1899) was used on a large scale by Evans (Evans 1937, 1949, 1951, 1952, 1953, 1955), who discovered more than 1500 species and subspecies. Genitalia screening was taken to the next level by Austin and collaborators (Austin and Mielke 1998; Austin 2000, 2008) and is being used by others (Dolibaina et al. 2014, 2017; Siewert et al. 2020). For example, revisions of *Phanus* Hübner, [1819], *Entheus* Hübner, [1819], and *Aguna* R. Williams, 1927 by Austin and colleagues nearly doubled the number of species in each genus as a result of extensive genitalic screening.

With the advent of DNA-based methods, which are particularly suited for screening due to automation in both experimental and computational pipelines, we are experiencing the next renaissance in species discovery. The COI barcoding popularized by Hebert and colleagues (Hebert et al. 2003), the most widespread approach, appears to generally fall short if unaccompanied by phenotypic inspection (Rubinoff et al. 2006) but is productive if used with caution (Lukhtanov et al. 2016). Barcoding screens yield impressive results when applied to species rich and poorly studied insect groups (Fernandez-Triana et al. 2014, 2023; Sharkey et al. 2021).

Although expensive, whole genome screens are significantly more reliable than barcode screens for this work because the genome represents its organism (i.e., genotype determines phenotype) and is ideally suited for species delimitation, identification, and discovery. We have been applying a genomic screening approach to butterflies with the focus on HesperIIDae, thus refining their higher classification (Cong et al. 2019b; Li et al. 2019; Zhang et al. 2019b, 2019c, 2022b, 2023c, 2023d) and finding new species (Zhang et al. 2022a, 2022c, 2023b). Our overall strategy is to obtain whole genome shotgun sequences using Illumina short-read sequencing from as many butterfly specimens (leg samples) from diverse localities as possible and infer phylogenetic trees from nuclear and mitochondrial genome protein-coding genes. Inspection of these trees reveals species as tight clades of specimens, as described in the "Species, subspecies, and genomics" section of Zhang et al. (2022a). Whenever possible, we identify species from the first principles, i.e., by sequencing primary type specimens and including them in phylogenetic trees. The primary types identify the clades they fall into. If type specimens were not yet sequenced or are lost, we use traditional identification methods, starting from the original description and comparing genitalia of specimens from or near type localities.

As a result, we find many clades that are not associated with available names and represent new taxa. To test whether these clades are likely to be species, we compute genetic differentiation (as F_{st}) and estimate gene exchange (as G_{min}) between taxa on proteins predicted to be located on the Z chromosome: $F_{st} > 0.20$ and $G_{min} < 0.05$ typically correspond to distinct species (Cong et al. 2019a). We also compute percent difference on the COI

barcode region, and a value $> 2\%$ (~ 13 bp) is characteristic of distinct species (Hebert et al. 2003), although some species (as delineated by genitalic differences and their biology) may exhibit smaller differences in their barcodes (Burns et al. 2008; Zhang et al. 2023b).

The degree of genetic difference between specimens of the same species is consistent: DNA differs little within species and prominently between species. Therefore, in contrast to the need for a large number of specimens to gauge phenotypic variation, a small series, even a single specimen, the holotype, is sufficient for genomic-based species delineation if genetic differentiation from its relatives is substantial. Furthermore, the genomic approach enables us not to rely on males as holotypes in placing the new species among its relatives, which was frequently necessary before because most species have been confidently identified only by male genitalia. Even a single female genetically differentiated from other species would suffice as the name bearer using the genomic approach.

After finding potential new species in genomic trees, we return to phenotypic inspection and compare wing patterns and genitalia of the proposed new species with its relatives to rationalize genomic differences phenotypically and provide phenotypic characters for species diagnosis. Such characters can usually be found, but in several instances, they should be treated with caution due to the small number of specimens sequenced. Genetic diagnoses given as DNA characters are more reliable for identifying these more cryptic species, at least before larger series of specimens are assembled and examined.

Materials and Methods

Traditionally, new species are discovered through visual comparisons of facies and genitalia, sometimes complemented with field observations about their life histories and ecology. Here, we use a genomic screen approach to species discovery: i.e., to detect new taxa or to test a hypothesis about a new species suspected from phenotypic inspection. First, we obtain whole genome shotgun sequences of many representative Hesperidae specimens of (nearly) all known species across their ranges, including phenotypically unusual specimens, using our previously established experimental protocols (Li et al. 2019; Zhang et al. 2019a). Typically, a leg of a dry pinned specimen from a collection (see the list of collections below) is used for DNA extraction. Specimens of any age are amenable to our protocol (Cong et al. 2021). Second, these genomic datasets composed of 150 bp (or less) DNA segments are subjected to computational analysis to identify and assemble (i.e., stitch together) protein-coding regions using DIAMOND (Buchfink et al. 2015) aided by a reference set of all proteins encoded in a previously assembled genome of *Cecropterus lyciades* (Geyer, 1832) (Shen et al. 2017). This procedure results in a master-slave alignment of all these regions (i.e., coding regions in each specimen are aligned to the reference), and these alignments, which are too large (about 18 million positions) for time-efficient phylogenetic analysis, are randomly subsampled for 300,000 positions (by codon) to be used in the construction of phylogenetic trees as described previously (Zhang et al. 2022b). Third, we construct phylogenetic trees using IQ-tree v1.6.12 under GTR+GAMMA model (Nguyen et al. 2015) from these randomly sampled positions in nuclear (autosomes and Z chromosome separately) and mitochondrial genomes and estimate statistical significance by codon resampling from the original complete alignment. These three trees are visualized using FigTree (Rambaut 2018) and visually compared to each other.

Inspecting the genomic-level trees, we look for high confidence clades close to the leaves that visually appear like combs (i.e., star subtrees). Such clades typically correspond to distinct species characterized by prominent genetic differentiation from other species (Zhang et al. 2022a, 2022c). Preference is given to the Z chromosome trees, which are illustrated in this work, because most of the genes important in speciation (pheromone production, wing pattern control, differences between sexes) are encoded by this chromosome, which, in addition, is more resistant to introgression (Pazhenkova and Lukhtanov 2021). Additionally, we illustrate segments of mitochondrial genome trees. Although prone to introgression, mitochondrial DNA is inherited as a single locus and frequently does not vary strongly within species but differs between species. Differences between species visually stand out in phylogenetic trees inferred from mitogenomes. The COI barcode, which is extensively used for species identification and discovery (Hebert et al. 2003), is located in the mitogenome. In many instances, only a single specimen of a species is available, and we compare its genetic distance from others with distances between specimens of the same species, using both nuclear and mitochondrial DNA.

The next step is to confidently assign available names to the clades representing species. In many instances, the assignment is supported by sequenced primary type specimens that we sequenced and included in the trees: the species represented by the clade receives the name of the type of the oldest valid name in this clade. If there are no valid names, available names in the clade serve as the basis for naming (and resurrection from synonymy). In the absence of sequenced primary types, identifications are made by the traditional phenotype-based method: comparing facies and genitalia with those of extant primary type specimens or, if types could not be found, with original descriptions while taking type localities into account. The clades or genetically differentiated branches (when only one specimen is available) that cannot be assigned available names represent potential new species and become the focus of this study. Specimens from these clades are scrutinized for their phenotypes, and genitalia are dissected to learn about morphological differences from known species.

In addition to phenotypic diagnosis, we provide diagnostic DNA characters, both in the nuclear genome and, when such characters exist, in the COI barcode. DNA characters are found in nuclear protein-coding regions using our previously developed procedure (see SI Appendix to Li et al. 2019). The logic behind the character selection was detailed in Cong et al. (2019b). The character states are provided in species diagnoses as abbreviations. For example, aly728.44.1:G672C means position 672 in exon 1 of gene 44 from scaffold 728 of the *Cecropterus lyciades* (Geyer, 1832) (formerly in *Achalarus* Scudder, 1872, thus “aly”) reference genome (Shen et al. 2017) is C, changed from G in the ancestor. When characters are given for the sister clade of the diagnosed taxon, the following notation is used: aly5294.20.2:A548A (not C), which means that position 548 in exon 2 of gene 20 on scaffold 5294 is occupied by the ancestral base pair A, which was changed to C in the sister clade (so it is not C in the diagnosed taxon). The same notation is used for COI barcode characters but without a prefix ending with ‘.’. The sequences of exons from the reference genome with the positions used as character states highlighted in green are given in the supplemental file (Zhang et al. 2023a). Providing a link to these DNA sequences from this publication ensures that the numbers given in the diagnoses can be readily associated with actual sequences. Whole genome shotgun datasets we obtained and used in this work are available from the NCBI database <<https://www.ncbi.nlm.nih.gov/>> as BioProject PRJNA1044449, and BioSample entries of the project contain the locality and other collection data of the sequenced specimens shown in the trees. Additionally, specimen data are summarized in Table S1 of the supplemental file (Zhang et al. 2023a). COI barcode sequences have been deposited in GenBank with accessions OR835792 and OR837624–OR837723. All new names have been registered with ZooBank.

Spread specimens were photographed with a Nikon 800 camera using a 105 mm Nikkor macro lens in NEF (raw) format, converted to TIF format using DxO with color-correction options adjusted to match 24 patch ColorChecker, and edited in Adobe Photoshop CS4 to standardize the background. Imperfections in specimens, such as scale damage, pinholes, and wing tear, were not digitally removed. Genitalia were prepared after DNA extraction from abdomens, which had been soaked in 10% KOH either overnight at room T (if it was convenient to take a break from work) or at 65°C for 15–60 min (depending on the size and abdomen softness after the soak) and then dissected under a binocular microscope. Genitalia were placed in glycerin and photographed using the AmScope system H800-96S-18M3 (0.7–5× zoom monocular microscope on a table stand with LED ring light and USB 18.0MP digital camera) in 3–5 focus slices, which were edited to brighten the background and merged using Adobe Photoshop CS4, and further assembled into plates. Genitalia were stored in glycerin in small vials pinned by each specimen.

The specimens were examined and sampled for sequencing from the following collections (abbreviations, which are not necessarily acronyms of the current names of these institutions, are given in parenthesis and used in Table S1 of the supplemental file (Zhang et al. 2023a)): American Museum of Natural History, New York, NY, USA (AMNH), Academy of Natural Sciences of Drexel University, Philadelphia, PA, USA (ANSP), Natural History Museum, London, UK (BMNH), California Academy of Sciences, San Francisco, CA, USA (CAS), Carnegie Museum of Natural History, Pittsburgh, PA, USA (CMNH), Colorado State University Collection, Fort Collins, CO, USA (CSUC), Cornell University Insect Collection, Ithaca, New York, USA (CUIC), Universidade Federal do Paraná, Curitiba, Paraná, Brazil (DZUP), Field Museum of Natural History, Chicago, IL, USA (FMNH), Los Angeles County Museum of Natural History, Los Angeles, CA, USA (LACM), Mississippi Entomological Museum, Starkville, MS, USA (MEM), Museum für Naturkunde, Berlin, Germany (MFNB), McGuire Center for Lepidoptera and Biodiversity, Gainesville, FL, USA (MGCL), Museo del Instituto de Zoología Agrícola

“Francisco Fernandez Yépez”, Universidad Central de Venezuela, Maracay, Venezuela (MIZA), Muséum National d’Histoire Naturelle, Paris, France (MNHP), Museum für Tierkunde, Dresden, Germany (MTD), Museo de Historia Natural, Lima, Peru (MUSM), Peabody Museum of Natural History, Yale University, New Haven, CT, USA (PMNH), Naturalis Biodiversity Center, Leiden, Netherlands (RMNH), Natural History Museum, Frankfurt, Germany (SMF), Texas A&M University Insect Collection, College Station, TX, USA (TAMU), Biodiversity Center, University of Texas at Austin, Austin, TX, USA (TMMC), National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), Burke Museum of Natural History and Culture, Seattle, WA, USA (UWBM), Zoological Institute and Museum Greifswald, Germany (ZIMG), Zentrum für Biodokumentation des Saarlandes, Schiffweiler, Germany (ZfBS), Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark (ZMUC), Zoologische Staatssammlung München, Germany (ZSMC), and research collections of Pierre Boyer, France (PBoyer), Jim P. Brock, USA (JPBrock), Ernst Brockmann, Germany (EBrockmann), Matthew J. W. Cock, UK (MJWCock), Bill Dempwolf, USA (WRDempwolf), Bernard Hermier, French Guiana (BHermier), and Kiyoshi Maruyama, Japan (KMaruyama). Type status abbreviations are HT holotype, LT lectotype, NT neotype, ST syntype, PT paratype, and PLT paralectotype.

Results and Discussion

Genomic analysis of HesperIIDae species across their ranges reveals 100 distinct unnamed phylogenetic lineages that are described below as species. These species are genotypically unique lineages separated from other similar lineages. Many of them are possibly allopatric with their closest relatives, but the transition from one species to another in genotype is abrupt, without detected intermediates. The specific rationale for each species distinction is given below in their “Definition and diagnosis.”

Species are placed in previously published identification keys (Evans 1952, 1953, 1955), and phenotypic characters are given to differentiate it from their closest relatives. A tree with the holotype included shows its position relative to other taxa. We present photographs of the dorsal and ventral sides of the holotype and, in nearly all cases, photographs of genitalia of either the holotype or a paratype. Diagnostic DNA characters in the nuclear genome and the COI barcode (if they exist) are given as abbreviations. The COI barcode sequence itself is provided for every new species. Species descriptions are accompanied by other nomenclatural acts (designation of a neotype and lectotypes) and taxonomic adjustments necessary as supporting evidence for the new species. Phylogenetic trees are shown in Fig. 1–8, specimen photographs in Fig. 9–220, 465–467 (dorsal and ventral sides are denoted by odd and even figure numbers, respectively), and genitalia images in Fig. 221–464.

In the present work, we refrain from using patronyms, partly because they may be more challenging to remember and associate with corresponding species. The new names proposed here are derived either from the names of species’ close relatives (usually making the name longer for southern counterparts, a practice that we introduce as a mnemonic), a descriptive phenotypic feature, or the type locality. We hope such names will integrate easily with the existing classification and be more straightforward to learn.

Subfamily Eudaminae Mabilie, 1877
Tribe Entheini Grishin, 2019

Drephalys (Drephalys) diovalis Grishin, new species

<https://zoobank.org/23F826FB-40E4-4664-823D-C671FF1FEDEC>

(Fig. 1 part, 9–10, 221–222)

Definition and diagnosis. Both genomic sequences and genitalia characters (valva with knobs distally and without a long process from the ampulla) place this species in the nominal subgenus *Drephalys* E. Watson, 1893. However, the yellow colors of the spots and the wing patterns show some similarity to species from the subgenus *Paradrephalys* Burns, 2000. The closest in appearance and the only known nominotypical dorsally yellow-patterned *Drephalys* with ventral hindwing pale spots instead of a band is *Drephalys opifex* Evans, 1952 (type locality in Suriname). The new species keys to it (B.6.8) in Evans (1952), although not precisely, because the hindwing

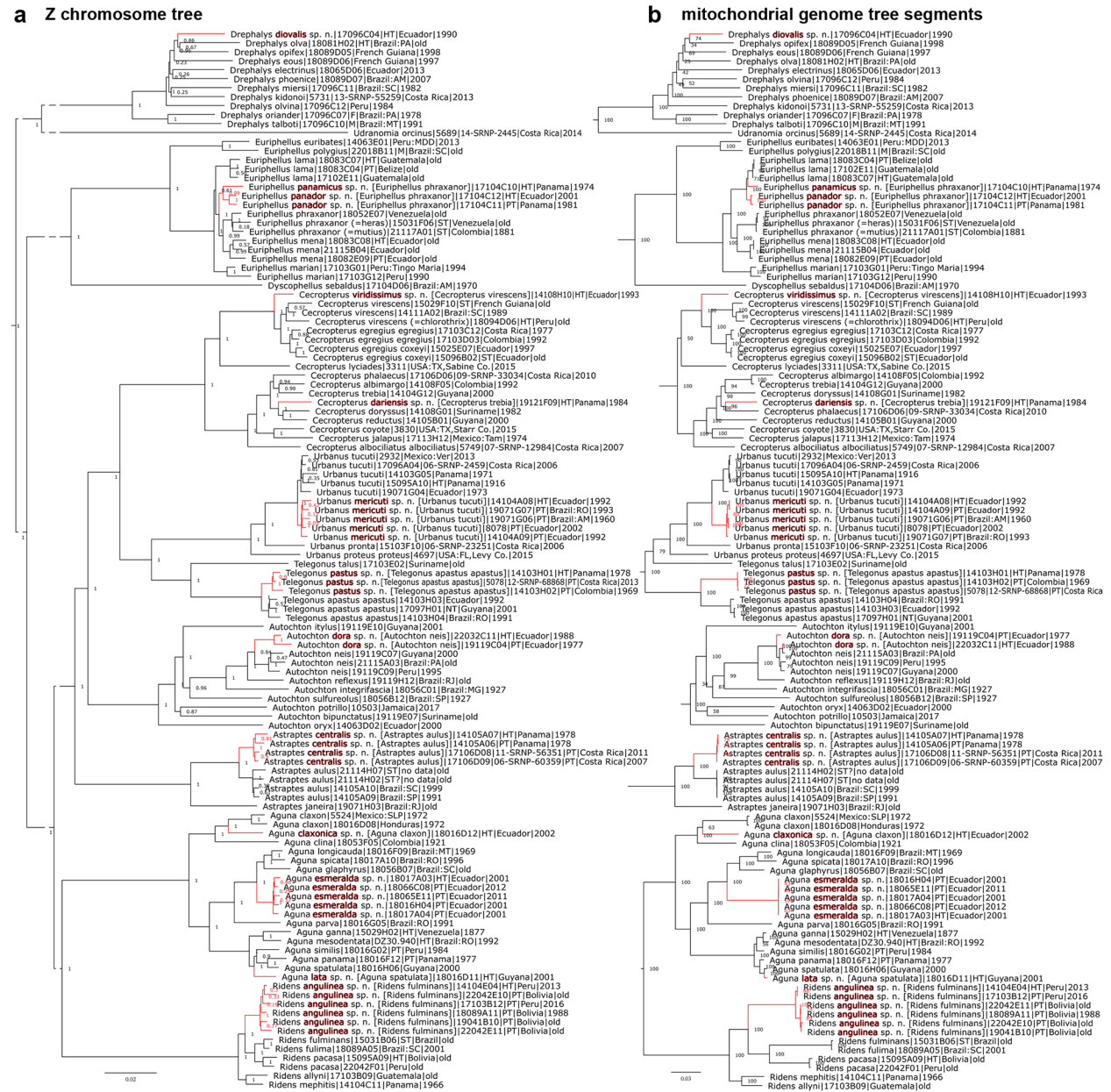


Figure 1. Phylogenetic trees of Eudaminae inferred from protein-coding regions in a) the Z chromosome; gaps in branches indicate places where vertical slices of the tree were removed to reduce its horizontal dimension (to allow an increase of the font size), i.e., branches with gaps, are longer than shown; and b) the mitochondrial genome (in segments); clades are cut from the tree and rearranged to match better the order of taxa in the Z chromosome tree and to save space. Statistical support values are shown by nodes. For each specimen, the name adopted in this work is given first, and a previously used name (or misidentification for the new species) is listed in square brackets (if different), supplemented with the DNA sample number, type status (see Materials and Methods for abbreviations), general locality, and year of collection. See Table S1 in the Supplemental file (Zhang et al. 2023a) or NCBI database entries for additional data about these specimens. Synonyms are given in parentheses preceded by “=”. The type status refers to this synonym if the synonym name is provided. The same notations are used throughout this work in other figures showing phylogenetic trees. Clades of new species proposed here are shown in red color, and their species epithets are highlighted in red. In other phylogenetic tree figures (e.g., Fig. 2), yellow highlight indicates taxonomic changes, e.g., transfer to a different genus (genus name highlighted) or change in species, subspecies, or synonym status (species epithet highlighted) and clades with taxonomic changes are shown in different colors. Green arrows point from the clade of the genus/species where a species/synonym was previously placed to the clade of its placement proposed in this work.

base in the new species is ventrally orange infused with purple instead of yellow, and palpi are whiter. More specifically, it differs from all described *Drephalys* species by a combination of honey-yellow markings on the dorsal wing surface (cell Rs-M₁ with a yellow spot), two prominent oval white spots on the purple-orange ventral hindwing, and the lack of costal fold. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly1146.54.9:A585G, aly1146.54.9:A591T, aly275211.5.3:A92G, aly2284.4.3:T87C, aly2284.4.3:T148C, aly113.11.7:C105C (not T), aly113.11.7:C138C (not T), aly2363.7.5:G102G (not A), aly525.90.3:G21G (not C), aly10226.17.2:C63C (not T), and COI barcode: T268T, T274A, T475C, T487C, C536C.

Barcode sequence of the holotype. Sample NVG-17096C04, GenBank OR837624, 658 base pairs:

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AACATTATATTTTATTTTGGGAATTTGAGCAGGAATAGTAGGAACATCTTTAAGTCTTTTAAATTCGAACTGAATTAGGAACCCAGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTTGGAGGATTTGGTAATT
GATTAGTTCCCTTTAATATAGGAGCTCCTGATATAGCTTTCCACGAATAAATAATAAGTTTTTGATTAATTCCTCCATCACTAACTCTTTTAAAT
TTCTAGAAGAATTGTAGAAAATGGAGCAGGAAGTGGATGAACAGTTTTATCCCCCTCTTTCATCAAATATTGCTCATCAAGGTTCTTCTGTAGATTTA
GCTATTTTTTCCCTTCATTTAGCTGGTATTTTCATCTATTTTAGGAGCTATTAACCTTTTACTACTACAATTTAATAATACGAATTAACAATTTATCAT
TCGATCAAATACCTTTTATTTGTATGAGCTGTAGGAATTAAGTCTTTTATTAATCTTTTACCTGTTTTAGCAGGAGCTATTACTATACTTTT
AACTGATCGAAATTTAATAACATCATTTTTTGTATCCAGCAGGAGGAGGATCCTATTTTATATCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 9–10, bears the following five rectangular labels, four white: [ECUADOR Napo | Tena-Pano Rd. 600m | 27 Sept. '90 | D. H. Ahrenholz], [*Drephalys* | dumeril | Det. ♂ | S. S. Nicolay], [DNA sample ID: | NVG-17096C04 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 00894990], and one red [HOLOTYPE ♂ | *Drephalys* | diovalis Grishin].

Type locality. Ecuador: Napo Province, Tena-Pano Road, elevation 600 m.

Etymology. The name is given for the doublet of oval spots on the ventral hindwing and is a noun in apposition.

Distribution. Currently known only from the holotype collected in Ecuador.

Tribe Phocidini Tutt, 1906

Euriphellus panador Grishin, new species

<https://zoobank.org/2CF28569-39B0-4379-9C26-25992D63BFFA>

(Fig. 1 part, 11–12, 223–224)

Definition and diagnosis. Among the clades representing named species of the *Euriphellus phraxanor* (Hewitson, 1876) group, we see a clade, sister to both *E. phraxanor* and *Euriphellus mena* (Evans, 1952) (type locality in Ecuador) that was not associated with any available name and therefore consists of new species (Fig. 1). One of these new species (see below for the second one) keys to “*Dyscophellus phraxanor phraxanor*” (D.4.2(b)) in Evans (1952) but differs from it and other relatives by a combination of flatter and narrower tegumen in lateral view, the sharper and terminally narrower basal tooth of harpe, ventral margin of harpe being only slightly shouldered (Fig. 224), but more so than that in the new species described next (Fig. 226), moderately defined hindwing discal spots, which are brown on the dorsal side, not hyaline, spot in cell M₂-M₃ offset basad from the row, comparatively (to the ventral hindwing discal yellow spots) larger forewing subapical spots, and weaker orange overscaling in the anterior part of ventral forewing (Fig. 11–12). COI barcode of this new species differs from *E. phraxanor* and *E. mena* by 4.7% (31 bp) and 4.6% (30 bp), respectively, but only 1.4% (9 bp) different from *Euriphellus lama* (Evans, 1952) (type locality in Guatemala), while being well differentiated from it in the Z chromosome (Fig. 1a). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly151.14.2:A75G, aly2090.1.4:A54G, aly127.43.4:G102A, aly127.43.4:A160G, aly443.22.1:C88A, and COI barcode: A181G, T259C, T364C, T376A, T553A.

Barcode sequence of the holotype. Sample NVG-17104C12, GenBank OR837625, 658 base pairs:

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AACTTTATATTTTATTTTGGGAATTTGAGCAGGAATGTTAGGAACCTCTTTAAGTCTTTACTAATTCGAACTGAATTAGGAACCTCCAGGATCTTTAATT
GGAAATGATCAAATTTATAATACTATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTAATGCCTATTATAATTTGGGGGATTCGGAACT
GATTAGTACCATTAATATTAGGAGCCCCAGATATAGCTTTTCCACGAATAAATAATAAGATTCTGATTAATTCCTCCCTCTTTAATATTTAAT
TTCAAGAAGAATCGTTGAAAATGGAGCAGGAACAGGATGAACAGTTTTATCCCTCTTTATCTGCTAACATTGCCATCAAGGATCATCAGTTGATTTA
GCAATTTTTCTCTTCACTTAGCTGGTATTTCTCAATTTTAGGAGCTATTAATTTTTATTACAACAATTTAATAATATACGAATTAGAACTTTATCTT
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TCGATCAAATACCATTATTTGTTTGGAGCTGTAGGAATTACAGCTTTATTATTACTTCTCTCTTTACCAGTACTAGCAGGTGCAATTACTATATTATT
AACAGACCAGAAATTTTAAATACATCTTTTTTTGATCCTTCTGGAGGAGGAGATCCTATTTTATATCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 11–12, bears the following four rectangular labels, three white: [ECUADOR: Esmeraldas | La Chaquita Exp Station | 10 Km San Lorenzo-Lita Road | 01° 13.82'S, 78° 45.95'W | 3 March 2001, 50 m | D.H. Ahrenholz leg.], [DNA sample ID: | NVG-17104C12 | c/o Nick V. Grishin], [USNMENT | {QR Code} | 00913861], and one red [HOLOTYPE ♂ | Euriphellus | panador Grishin]. **Paratype:** 1♂ NVG-17104C11, USNMENT_00913860 Panama, Darien Province, Cana (Cerro Pirre), elevation 400 m, GPS 7.9333, -77.5667, 6-Jul-1981, G. B. Small leg. [USNM].

Type locality. Ecuador: Esmeraldas Province, km 11 of San Lorenzo-Lita Road, La Chiquita Wildlife Refuge, elevation 50 m, GPS 1.23033, -78.76583.

Etymology. The name is a fusion of this species' known localities: *Pana*[ma and Ecu]a]dor. The name is a noun in apposition.

Distribution. Currently known from Ecuador and eastern Panama.

Comment. Sequencing of the *Telegonus mutius* Plötz, 1882 (type locality in Colombia) syntype we found in MFNB reveals that it is conspecific with a syntype of *Telegonus heras* Mabille, 1888 (type locality Venezuela: Porto Cabello), currently a junior subjective synonym of *Euriphellus phraxanor* (Hewitson, 1876) (type locality “New Granada”—likely referring to Colombia—and Panama: Chiriquí) (Fig. 1), thus confirming our previously hypothesized synonymy of *T. mutius* with *E. phraxanor* (Zhang et al. 2022b). We are currently undertaking a search for syntypes of *E. phraxanor* to complete this investigation.

Euriphellus panamicus Grishin, new species

<https://zoobank.org/F9D83659-187D-4AC5-8EAC-D1B5A599D972>

(Fig. 1 part, 13–14, 225–226)

Definition and diagnosis. Sister to previous species and differs from it by 1.8% (12 bp) in COI barcode. The previous species is either sympatric with this new species in Panama or comes close to it in distribution. Keys to “*Dyscophellus phraxanor phraxanor*” (D.4.2(b)) in Evans (1952) but differs from it and other relatives by a combination of more convex and wider tegumen in lateral view, terminally rounded and wider basal tooth of harpe (Fig. 226), ventral margin of harpe being even less shouldered than in *E. panador* new species (Fig. 224), well-defined hindwing discal spots, not hyaline (could be pale-centered), spot in cell M_2-M_3 nearly within the row, comparatively (to the ventral hindwing discal yellow spots) smaller forewing subapical spots, and stronger orange overscaling in the anterior part of ventral forewing (Fig. 13–14). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly671.39.2:T432C, aly887.9.1:G232A, aly102.20.9:G45T, aly272.9.2:G61A, aly272.9.2:G79A, aly2578.3.9:G222G (not T), aly2578.3.9:A230A (not G), aly2275.23.9:A72A (not G), aly4036.9.5:G321G (not A), aly27.16.1:T1497T (not C), and COI barcode: T118C, A181A, A202G, T376G, A625G.

Barcode sequence of the holotype. Sample NVG-17104C10, GenBank OR837626, 658 base pairs:

AAC TTTTATATTTTATTTTGGAAATTTGAGCAGGAATGTTAGGAACTTCTTTAAGTTTACTAATTCGAACTGAATTAGGAACTCCAGGATCTTTAATT
GGAAATGATCAAATTTATAACACTATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTAATGCCTATTATAATTGGAGGATTCGGAACT
GATTAGTGCCATTAATATTAGGAGCCCCAGATATAGCTTTCCACGAATAAACAATATAAGATTTTGATTACTTCCCCCTCTTTAATATTATTAAT
TTCAAGAAGAATCGTTGAAAATGGAGCAGGAACAGGATGAACAGTTTATCCTCCTTTATCTGCTAATATTGCTCATCAAGGATCGTCAGTTGATTTA
GCAATTTTTTCTCTTCACTTAGCTGGTATTTCTTCAATTTTAGGAGCTATTAATTTTATTACAACGATTTAATATACGAATTAGAACTTATCTT
TCGATCAAATACCATTATTTGTTTGGAGCTGTAGGAATTACAGCTTTATTATTACTTCTCTCTTTACCCTGTACTAGCAGGTGCAATTACTATATTATT
AACAGACCAGAAATTTTAAATACATCTTTTTTTGATCCTTCTGGGGGAGGAGATCCTATTTTATACCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 13–14, bears the following four rectangular labels, three white: [Cerro Jefe 2200' | Pma., Panama | April 10, 1974 | G B Small], [DNA sample ID: | NVG-17104C10 | c/o Nick V. Grishin], [USNMENT | {QR Code} | 00913859], and one red [HOLOTYPE ♂ | Euriphellus | panamicus Grishin].

Type locality. Panama: Panama Province, Cerro Jefe, elevation 2200'.

Etymology. The name is given for the type locality and is a masculine adjective.

Distribution. Currently known only from the type locality in central Panama.

Tribe Eudamini Mabille, 1877
Subtribe Eudamina Mabille, 1877

***Cecropterus (Thorybes) viridissimus* Grishin, new species**

<https://zoobank.org/855F436E-D634-4129-AB6F-FCFB51E374E0>

(Fig. 1 part, 15–16, 227–228)

Definition and diagnosis. This new species is very similar to *Cecropterus virescens* (Mabille, 1877) (type locality in French Guiana) phenotypically and keys to it (C.13.27) in Evans (1952). However, in both Z chromosome and mitochondrial genome trees, it is sister to the clade that consists of both *C. virescens* and *Cecropterus egregius* (A. Butler, 1870) (type locality unknown), which are rather different-looking species. COI barcode differs from *C. virescens* syntype by 2.7% (18 bp). Phenotypically, it differs from most *C. virescens* specimens by the white border on the hindwing underside, which harbors brown overscaling and is reduced in width from vein M_2 to the apex (Fig. 16), strongly humped in the middle dorsoposterior margin on the harpe, and wider separated uncus arms (Fig. 228). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly2668.2.9:C109T, aly2668.2.9:C123T, aly1370.7.4:A221G, aly347.8.1:A265C, aly923.7.1:A781C, aly1313.24.3:A72A (not G), aly138.12.1:A515A (not G), aly208.4.3:T84T (not C), aly5623.1.3:C1206C (not T), aly173.13.2:G59G (not A), and COI barcode: T263C, A319G, T400T, T529C, T553C.

Barcode sequence of the holotype. Sample NVG-14108H10, GenBank OR837627, 658 base pairs:

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AACTTTATATTTTATTTTGGAAATTTGAGCAGGATTAATTGGAAGCTTCATTAAGTTTACTTATTCGAACTGAATTAGGAACTCCAGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTTGGAGGATTTGGAAATTT
GATTAGTTCCCTCTTATATTAGGAGCCCTGATATAGCTTTTCCCTCGTATAAATAATATAAGATTTTGACTATTACCCCTTCATTAAGCTTTTAAAT
TTCAAGAAGTATTGTTGAAAATGGAGCGGGTACTGGATGAACTGTTTATCCTCCTTTATCTTCTAATATTGCCCATCAAGGAGCATCAGTAGATTTA
GCAATTTTTCTTTACATCTTGCAGGAATTTTCATCTATTCTTGGAGCTATTAATTTTATTACAATATTATTAATATACGAATTAATAATTTATCAT
TTGATCAAATACCATTATTTATTTGAGCTGTAGGAATTACAGCCTTATATTATTACTTTTATTACCCGTTTTAGCTGGAGCCATTACTATATTATT
AACTGATCGAAATTTAAATACTTCATTTTTTGTATCCTGAGGTGGAGGAGATCCTATTTTATATCAACATTTATTT
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Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 15–16, bears the following three rectangular labels, two white: [ECUADOR: Zamora | 56 km Loja-Zamora | 4° 2.7'S 78° 59.2'W | 4 October 1993 | S. S. Nicolay, leg.], [DNA sample ID: | NVG-14108H10 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | *Cecropterus* | *viridissimus* Grishin].

Type locality. Ecuador: Zamora-Chinchi Province, km 56 of Loja-Zamora road, elevation 976 m, GPS –4.0450, –78.9867.

Etymology. In Latin, *viridissimus* means very green or bright green. The name is given for the extensive green coloring of this species and is a masculine adjective.

Distribution. Only known from the holotype collected in Ecuador.

Comment. Curiously, in the tree constructed from autosome genes, the new species is sister to *C. virescens* in accord with phenotypic similarities, suggesting introgression and other irregularities in the evolution of its mitochondrial genome and Z chromosome.

***Cecropterus (Murgaria) dariensis* Grishin, new species**

<https://zoobank.org/269C0E17-EE28-439C-8F7C-7247A6D6CC62>

(Fig. 1 part, 17–18, 229–230)

Definition and diagnosis. Superficially somewhat resembles sympatric *Cecropterus trebia* (Möschler, 1879) but differs from it and other relatives by completely brown hindwing ventral surface (without white at the outer margin, but with whitish fringes) and 4 subapical hyaline spots on the forewing. It also resembles *Spicauda* Grishin, 2019 but differs in the hyaline spot in forewing cell M_3 -CuA₁, being dash-like and strongly offset from the cell base and discal hyaline band. Keys (imperfectly) to “*Urbanus carmelita carmelita*” (C.13. 22(b)) in Evans (1952)

but differs from this species currently known as *Cecropterus carmelita* (Herrich-Schäffer, 1869) (type locality in Brazil) by vestigial, line-like and not scalloped white outer marginal band on the hindwing underside (the fringe in mostly white from the apex to vein CuA₁); differs also from the somewhat similar *Cecropterus athesis* (Hewitson, 1867) by longer hindwing tails and hyaline spot in forewing cell CuA₂-1A+2A being better aligned with the discal band, and by the lack of a darker-brown line along the outer margin of ventral hindwing, which is replaced with a vestigial white band. In male genitalia (Fig. 229–230), most similar to *Cecropterus doryssus* (Swainson, 1831) (type locality in Brazil: Bahia) and relatives but differs from them by less angled harpe with rounder curve from ventral to posterior margin and with serrated dorsal margin that is more prominently expanded into a small distal lobe. This species is not cryptic and is unambiguously recognizable by its phenotype. The following base pairs are diagnostic in the nuclear genome: aly2750.3.3:G39A, aly515.2.2:G496T, aly1651.24.15:C120A, aly235.4.4:T51C, aly23605.18.5:G118A, aly1038.17.30:C61C (not A), aly1038.17.30:A62A (not C), aly383.7.2:T54T (not A), aly1042.3.1:A138A (not G), aly1651.24.15:C91C (not T), and COI barcode: T266C, T401C, T424A, A550G, T581C.

Barcode sequence of the holotype. Sample NVG-19121F09, GenBank OR837628, 658 base pairs:

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AACTTTATATTTTATTTTGGAAATTTGAGCAGGATTAGTTGGAACCTTCATTAAGTTTACTTATTCGAACTGAATTAGGAACTCCAGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATATAATTTGGAGGATTTGGTAATT
GATTAATCCCCCTTATATTAGGAGCCCCGATATAGCTTTCCCCCGTATAAATAAATAAGATTTTGATTACTACCTCCATCTTTAACTCTTTTAAT
TTCAGAAGAATTGTAGAAAATGGTGCAGGACTGGATGAACAGTTTACCCCCCTTTATCATCTAATATTTGCTCATCAAGGAGCATCCGTAGATTTA
GCAATTTTCTCACTACATCTTGTGGAATTTTCATCAATTTTAGGAGCTATTAATTTTATTACAACATATTATAACATACGAATTAATAATTTATCAT
TTGATCAAATACCATTATTTATTTGAGCTGTTGGAATTACAGCTTTACTATTATTACTTTTCATTCGCTGTTTTAGCTGGAGCTATTACTATACTACT
AACTGATCGAAATTTAAATACTTCTTTTTTTGACCCAGCAGGTGGGGGAGATCCTATTTTATATCAACATTTATTT
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Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 17–18, bears the following four rectangular labels, three white: [PANAMA: 1000m. | Darien, Cana | 5. Jan. 1984 | Gordon Small], [DNA sample ID: | NVG-19121F09 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01602755], and one red [HOLOTYPE ♂ | *Cecropterus* | dariensis Grishin].

Type locality. Panama: Darien Province, Cana, elevation 1000 m.

Etymology. The name reflects the type locality and is a masculine adjective.

Distribution. This species is currently known only from the holotype collected in Panama.

Urbanus (Urbanus) mericuti Grishin, new species

<https://zoobank.org/5C620BB9-A60D-42F8-B72B-8C832D79A9D4>
(Fig. 1 part, 19–20, 231–232)

Definition and diagnosis. Inspection of genomic trees reveals that most South American populations identified as *Urbanus tucuti* (R. Williams, 1927) (type locality in Panama, holotype sequenced as NVG-15095A10) are strongly differentiated genetically from *U. tucuti* (Fig. 1): e.g., their COI barcodes differ by 3.5% (23 bp), and therefore represent a new species. It keys to “*Astraptus tucuti*” (C.14.5) in Evans (1952) and differs from it by comparatively shorter harpe with a straighter dorsal margin and less acute terminal angle, the wider separation between harpe and ampulla (wider notch) (Fig. 232), uncus arms being more parallel to each other and closer together, rather than terminally diverging in dorsal view (Fig. 231), and usually absent or reduced hyaline dash in M₃-CuA₁ cell (Fig. 19). Due to the cryptic nature of this species and unexplored phenotypic variation, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly53.2.40:C42T, aly1968.11.7:A106G, aly58.10.2:C13T, aly58.10.2:G45A, aly7098.1.5:C115A, and COI barcode: A43T, A79G, T178C, T479C, T601C.

Barcode sequence of the holotype. Sample NVG-14104A08, GenBank OR837629, 658 base pairs:

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AACTTTATATTTTATTTTGGAAATTTGAGCAGGATTAATTTGGTACTTCTTTAAGATTACTTATTCGAACTGAATTAGGAACTCCAGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCCCATGCATTTATTATAATTTTCTTTATAGTTATACCTATCATAATCGGAGGATTTGGTAATT
GACTTGTACCTTTAATAATAGGTGCCCCGATATAGCTTTCCCCCGTATAAATAACATAAGATTTTGATTACTACCCCTTCCTTAACTTTATTAAT
TTCAGAAGAATTGTTGAAAATGGTGCAGGACTGGATGAACAGTTTATCCCCCTTTTATCATCTAACATTGCTCATCAAGGAGCTTCTGTTGATTTA
GCAATTTTCTCTCTTCACTTGCAGGAAATTTTCATCAATTTTGGAGCTATTAATTTTATTACAACAATTTATAACATACGAATTAATAGACTAACTT
TTGATCAAATACCCTTTATTTGTATGAGCTGTAGGAATTACAGCATTATTATTATTACTTTCTTTACCTGTTTTAGCTGGAGCTATTACTATATTTAT
AACTGATCGAAATCTAAACACATCATTTTTTTGACCCCTGCTGGAGGAGGAGATCCAATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 19–20, bears the following four rectangular labels, three white: [ECUADOR: Napo Pr. | 8 km Napo-Ahuano | 1° 2.5' S 77° 43.5' W | 9 Nov. 1992, 480m. | S. S. Nicolay, leg.], [Astraptes | Det. fulgor | S.S. Nicolay], [DNA sample ID: | NVG-14104A08 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | Urbanus mericuti | Grishin]. **Paratypes:** 4♂♂ in USNM: 1♂ NVG-14104A09 the same data as the holotype, except 13-Nov-1992; Ecuador 1♂ NVG-8078 Napo, Misahualli Jungle Lodge, 450 m, GPS –1.0257, –77.6570, 6–8-Jan-2002, J. P. W. Hall and M. A. Solis leg., genitalia NVG170208-63 (Fig. 231–232); Brazil: 1♂ NVG-19071G06 Amazonas, Benjamin Constant, Nov-1960, Jorge Kesselring leg.; 1♂ NVG-19071G06 Rondonia, 62 km S Ariquemes, Fazenda Rancho Grande, 165 m, GPS –10.533, –62.800, 14-25-Nov-1993, Brian Harris leg.

Type locality. Ecuador: Napo Province, km 8 of Puerto Napo-Ahuano Road, elevation 480 m, GPS –1.0417, –77.725.

Etymology. The name denotes a more southern range of this species than *U. tucuti*: *meri*[dionalis (Latin for southern) + *tu*]cuti. The name is a noun in apposition.

Distribution. Currently known from the upper Amazonian region in Ecuador and Brazil.

Neotype designation for *Eudamus briccus* Plötz, 1881

Eudamus briccus Plötz, 1881 was described from an unstated number of specimens from South America (Plötz 1881). Translating and assembling relevant sections of Plötz's identification key, we get for *E. briccus*: “Body and wing bases are mostly overscaled with shiny green or blue above, forewings with wide and complete, pale, oblique hyaline median band broken into spots starting from cell 1 (i.e., CuA₂-1A+2A) and reaching the costal margin, the spot in cell 3 (i.e., M₃-CuA₁) is integrated into the band; no hyaline spots by the apex, hindwings without a white transverse band. Hindwings with a smooth outer margin and uncheckered brown fringes. Underside of the hindwings is green, mixed with brown. Forewing length 31 mm. From South America.”

We were not able to locate syntypes of *E. briccus*. At least one of the syntypes was drawn by Plötz as t[afel]. 72 (Plötz 1881), which has not been found with the rest of the original Plötz drawings. This drawing is not among Godman's copies, now in BMNH (Godman 1907). However, we found a drawing labeled “briccus Pl. t. 72” (Fig. 467) in ZSMC, pinned in a drawer together with specimens, and styled similarly to Godman's copies of drawings. We hypothesize that this is either another copy by a different artist or the original, giving a visual of *E. briccus*. Currently, *E. briccus* is treated as a junior subjective synonym of *Telegonus* (*Telegonus*) *apastus* (Cramer, 1777) (type locality in Suriname), and the drawing confirms this treatment.

Next, we proceeded with the neotype designation because there is an exceptional need to clarify both the taxonomic identity and the type locality of *E. briccus*. In the light of the new species proposed below, it is essential to define *E. briccus* objectively. Hereby, N.V.G. designates a specimen in USNM, DNA sample NVG-18115F05, USNM ENT 00179346, illustrated in Fig. 465–466, with the label data given below as the **neotype** of *Eudamus briccus* Plötz, 1881. This neotype reaffirms the current treatment of *E. briccus* as a junior subjective synonym of *Telegonus* (*Telegonus*) *apastus* (Cramer, 1777) (type locality in Suriname).

The neotype satisfies all requirements set forth by the ICZN Article 75.3, namely: **75.3.1.** It is designated to clarify the taxonomic identity of *E. briccus*, which is necessary because additional species are present among its close relatives and to define the type locality that was only generally stated in the original description as South America; **75.3.2.** The characters to differentiate this taxon from others were given in the original description (Plötz 1881), and given above, we summarize them as follows: body and wing bases shiny-green, otherwise brown-black, forewing with a single broad transverse band of hyaline spots from mid-costa to near tornus, the spot in cell M₃-CuA₁ is within the band; ventral hindwing green intermixed with brown; forewing length around 31 mm; **75.3.3.** The neotype specimen is a male bearing three labels: [GUYANA: Iwokrama | Rainforest Res Middle | Essequibo R/Turtle Mt | 200-950' 20-26.III.2001 | 04°43.90'N 58°43.08'W | Leg. S. Fratello et al], [DNA sample ID: | NVG-17097H01 | c/o Nick V. Grishin], [{QR Code} | USNM ENT 00179346], the neotype has a small piece of wing missing along the margin of right hindwing; **75.3.4.** We carefully searched for syntypes of *E. briccus* in the MFNB, ZSMC, and ZIMG. We failed to find syntypes among HesperIIDae holdings in these collections and, therefore, believe that they were lost; **75.3.5.** The neotype closely agrees with the original description of

E. briccus in all characters, as evidenced by comparing the neotype illustrated in Fig. 465–466 with the characters for this taxon given in the original description (Plötz 1881) complemented with the drawing (Fig. 467) and listed above (75.3.2.); 75.3.6. The neotype is from Guyana: Iwokrama Forest, Essequibo River, Turtle Mountain, GPS 4.7317, –58.7180, which becomes the type locality of *E. briccus*, consistently with the original type locality given as “South America”; 75.3.7. The neotype is in the National Museum of Natural History, Washington, DC, USA (USNM). The COI barcode sequence of *E. briccus* neotype, sample NVG-17097H01, GenBank OR835792, 658 base pairs, is:

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AACTTTATATTTTATTTTTGGAATTTGAGCAGGATTAATTGGAACCTTCCTTAAGATTACTTATTCGAACTGAATTAGGAACCCAGGATCTTTAATT
GGAGATGATCAAATTTATAATAACAATTGTTACAGCTCATGCATTTATCATAAATTTTTTTCATAGTTATACCTATTATAAATTGGAGGATTTGGAATTT
GATTAGTACCACATAATAATAGGAGCCCCAGATATAGCATTCCCCCGTATAAATAATATAAGATTCTGATTATTACCTCCATCTTTAACATTATTAAT
TTCAAGAAGAATTGTTGAAAATGGTGCAGGATGAACAGTTTACCCCCCTTTCATCTAATATCGCTCATCAAGGAGCATCTGTTGACTTA
GCAATTTTCTCCCTTCATCTTGCTGGTATTTCTTCAATTCTTGGAGCAATTAATTTTATTACAACAATTTAATATACGAATTAACAATTTATCTT
TTGATCAAATACCTCTATTCGTTGAGCAGTAGGAATTACAGCATTATTATTACTTTCTTTACCTGTTTTAGCTGGAGCTATTACCATATTATT
AACTGATCGAAATTTAAATACTTCTTTCTTTGATCCTGCTGGTGGGAGATCCCATTTTATATCAACATTTATTT
```

Telegonus (Telegonus) pastus Grishin, new species

<https://zoobank.org/24FB11E2-E34F-4B88-B36E-B2D2CB62BBE5>

(Fig. 1 part, 21–22, 233–234)

Definition and diagnosis. Phylogenetic trees reveal prominent genetic differentiation of northern populations identified as *Telegonus apastus* (Cramer, 1777) (type locality in Suriname) (Fig. 1): e.g., their COI barcodes differ by 5.9% (39 bp), and therefore they represent a new species. The new species keys to “*Astraptes apastus*” (C.14.13) in Evans (1952) and differs from it by shorter harpe (shorter than valva) with its distal angle less acute, more robust bulge on costa-ampulla (Fig. 234) and a hyaline spot in forewing cell CuA₂-1A+2A typically more angular and extended into a “beak” towards tornus (Fig. 21 vs. 465), usually with less prominent white overscaling around this spot on ventral side (Fig. 22 vs. 466). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1038.17.34:G379A, aly125.11.2:G46A, aly499.47.2:C118A, aly1603.18.3:T185C, aly6286.2.7:T42C, and COI barcode: 49A, T91C, T226C, T382C, T571C.

Barcode sequence of the holotype. Sample NVG-14103H01, GenBank OR837630, 658 base pairs:

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AACTTTATATTTTATTTTTGGAATTTGAGCAGGATTAATTGGAACCTTCATTAAGATTACTTATTCGAACTGAATTAGGAACCCAGGATCCCTTAATT
GGAGATGATCAAATTTATAATAACAATTGTTACAGCTCATGCATTTATCATAAATTTTTTATAGTTATACCTATTATAAATTGGAGGATTTGGAATTT
GATTAGTACCACATAATAATAGGAGCCCCAGACATAGCATTCCCCCGTATAAATAATATAAGATTTTGATTATTACCCCATCTCTAACATTATTAAT
TTCAAGAAGAATTGTTGAAAATGGTGCAGGAACAGGATGAACAGTTTACCCCCCTTTCATCTAATATTGCCATCAAGGAGCATCAGTCGACTTA
GCAATTTTCTCCCTTCATCTTGCCGGTATTTCTTCAATTCTTGGGGCAATCAATTTTATTACAACAATTTAATATACGAATCAATAATTTATCAT
TTGATCAAATACCTTTATTTGTTGAGCAGTAGGAATTACAGCATTATTACTATTACTTTCTTTACCTGTTTTAGCTGGAGCTATCACTATATTATT
AACTGATCGAAATTTAAATACTTCTTTCTTTGACCCCTGCGGGAGGGGGTGACCCAATTCCTTTACCAACACTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 21–22, bears the following three rectangular labels, two white: [PANAMÁ: Panamá Prov. | Distrito de El Llano | Cordillera de San Blas | North of El Llano ca. 330 m. | VI. 1978 | Gordon B. Small: Coll.], [DNA sample ID: | NVG-14103H01 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | *Telegonus (Telegonus) | pastus* Grishin]. **Paratypes:** 2♂ in USNM: NVG-5078, 12-SRNP-68868 Costa Rica: Area de Conservación Guanacaste, Alajuela Prov., Sector Rincon Rain Forest, Palomo, el. 96 m, GPS 10.96187, –85.28045, eclosed 09-Jan-2013; and NVG-14103H02 Colombia: Caldas, Victoria, el. 2400', 9-Feb-1969, S. S. Nicolay leg.

Type locality. Panama: Panama Province, Distrito de El Llano, Cordillera de San Blas, north of El Llano, elevation 330 m.

Etymology. The name removes the negating “a” from its sister species name and is a noun in apposition.

Distribution. From southeastern Mexico to western Colombia.

Autochton (Autochton) dora Grishin, new species

<https://zoobank.org/2CBF81CD-A45A-40E8-B6B9-E4E64513578D>

(Fig. 1 part, 23–24, 235–236)

Definition and diagnosis. Ecuadorian specimens identified (incorrectly) as *Autochton neis* (Geyer, 1832) (type locality in Brazil) differ prominently from it in Z chromosome genes (Fig. 1a) and, therefore, although not differing in the COI barcode (0.15%, 1 bp), represent a new species. This new species partly keys to “*Autochton neis*” (C.16.6) in Evans (1952) and has somewhat similar male genitalia but differs from *A. neis* and other species of *Autochton* in a rounder distal end of harpe (near ventral margin), harpe with terminally smaller, rounded dorsal projection (Fig. 235–236), two (not three) subapical forewing spots, less irregular forewing hyaline discal band with spots more aligned with each other, and the spot in M_3 - CuA_1 cell being minute, dot-like (Fig. 23–24). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly159.20.1:G156A, aly159.20.1:C183A, aly214.14.1:G229T, aly525.55.2:G403T, aly275215.9.3:A42C, however COI barcodes do not differentiate this species from *A. neis*.

Barcode sequence of the holotype. Sample NVG-22032C11, GenBank OR837631, 658 base pairs:

```
AACTTTATATTTTATTTTGGAAATCTGAGCAGGATTAGTAGGACTTCTTTAAGATTACTAATTCGAACTGAACTAGGAACACCTGGATCATTAAAT
GGAGATGATCAAATTTATAATACTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATGGAGGATTTGGAACT
GACTAGTACCCCTTATACTAGGAGCTCCAGATATAGCCTTCCCACGAATAAATAATAAGATTCTGACTATTACCTCCATCAATAACTCTTTTAAAT
TTCAAGTAGTATTGTAGAAAATGGAGCAGGAAGCTGGATGAACTGTTTATCCTCCCTTTCTTCTAATATTGCTCATCAAGGAGCTTCAGTAGATTTA
GCAATTTTTCTCTTCATTTAGCAGGAATTTCTCAATTTTAGGAGCTATTAATTTTATTACAATATTATAATACGAATTAATAATATATCTT
TTGATCAAATACCTTTATTTGTATGAGCTGTAGGAATTACAGCTCTTCTTTTACTTTCTTTACCAGTTCTAGCTGGAGCTATTACTATATTTATT
AACAGATCGAAATTTAAATACTTCATTTCTTTGACCCAGCTGGGGGAGGAGATCCTATTTTATATCAACATTTTATT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 23–24, bears the following three rectangular labels, two white: [ECUADOR Pastaza | Puyo-Napo Rd. | Km 25 - 1200m | 11 Nov. '88 | S.S. Nicolay], [DNA sample ID: | NVG-22032C11 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | *Autochton* (*Autochton*) | dora Grishin]. **Paratype:** 1 ♀ NVG-19119C04, USNMMENT_01602625 the same data as the holotype but collected on 10-Sep-1977.

Type locality. Ecuador: Pastaza Province, km 25 of Puyo-Napo road, elevation 1200 m.

Etymology. The name is for its distribution in [Ecu]dor + a and is a noun in apposition.

Distribution. Known only from the type locality in Ecuador.

Astraptus centralis Grishin, new species

<https://zoobank.org/556FE76C-4D98-46DD-802A-D57449CFD0AD>

(Fig. 1 part, 25–26, 237–238)

Definition and diagnosis. Phylogenetic trees reveal that Central American specimens identified as *Astraptus aulus* (Plötz, 1881) (type locality in Brazil, a syntype sequenced as NVG-21114H07) show prominent genetic differentiation from it (Fig. 1): e.g., their COI barcodes differ by 5% (33 bp), and therefore represent a new species. This new species keys to “*Astraptus fulviluna*” (C.14.14) in Evans (1952), which is currently a junior subjective synonym of *A. aulus* and differs from it by a straighter dorsoposterior margin of harpe (Fig. 238), less extensive green area on the dorsal forewing (Fig. 25) and not pupillated pale spot by inner margin on the ventral hindwing (Fig. 26). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1341.9.2:G264C, aly1019.14.10:G1446A, aly1497.4.1:T63C, aly887.6.4:C66G, aly594.10.7:G171A, and COI barcode: T35T, T169C, A217G, T292C, T508C.

Barcode sequence of the holotype. Sample NVG-14105A07, GenBank OR837632, 658 base pairs:

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AACTCTATATTTTATTTTGGAAATTTGAGCAGGATTAGTTGGAACCTTCTTTAAGTCTTCTTATTTCGAACTGAATTAGGAACACCAGGATCCTTTAAAT
GGAGATGATCAAATTTATAATACTATTGTTACAGCTCATGCAATTTATTATAATTTTTTTTATAGTTATACCCATTATAATGGAGGATTTGGTAAT
GACTAGTACCATTAATATTAGGGGCCCTTGATATAGCTTTCCCTCGAATAAATAACATAAGATTCTGATTATTACCCCTCTTTAACTCTCTTAAAT
CTCAAGAAGTATCGTAGAAAATGGTGCCTGGTACTGGTTGAACTGTCTATCCCCACTTTTATCTAATATTGCCCACCAAGGAACCTCTGTGATTTA
GCAATTTTCTCCCTTCATCTTGCTGGAATTTCCCTCCATTTTAGGAGCTATTAATTTTATTACAATATTATAATATACGAATCAATAATTTATCAT
TTGATCAAATACCATTTATCTGAGCAGTAGGAATTACTGCATTTATTATTACTTTCTTTACCCGTAAGTACTAGCAGGAGCTATTACTATATTACT
AACTGATCGAAATTTAAATACTTCATTTTCTTTGATCCTGCAGGTGGTGGGATCCAATTTTATATCAACATTTTATT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 25–26, bears the following three rectangular labels, two white: [PANAMÁ: Canal Zone | Gamboa | X.18.78 | Gordon B. Small], [DNA sample ID: | NVG-14105A07 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | *Astraptus* | *centralis* Grishin]. **Paratypes:** 2♂♂ and 1♀ in USNM:

1♂ NVG-14105A06 the type locality, with the same data, additionally “Pipeline Road, NW of Gamboa 9° 07'N, 79° 41'W”; and Costa Rica, Area de Conservación Guanacaste, Guanacaste Prov., Sector Mundo Nuevo, Estacion La Perla, 325 m, GPS 10.76737, -85.43313: 1♂ NVG-17106D09 06-SRNP-60359 eclosed on 10-Jan-2007 and 1♀ NVG-17106D08 11-SRNP-56351 eclosed on 29-Aug-2011.

Type locality. Panama: Colón Province, Gamboa.

Etymology. The name is for the range of this species in Central America and is a masculine adjective.

Distribution. Costa Rica and Panama.

Subtribe Loboclina Grishin, 2019

Aguna claxonica Grishin, new species

<https://zoobank.org/D5952070-7C94-498A-9066-62A9F3F52544>

(Fig. 1 part, 27–28, 239–240)

Definition and diagnosis. A specimen from Ecuador identified as *Aguna claxon* Evans, 1952 (type locality in Mexico: Veracruz) is genetically differentiated from it (COI barcode difference 4.9%, 32 bp) and represents a new species. This new species keys to *Aguna claxon* (C.5.3) in Evans (1952) and differs from it by harpe less extended dorsal, thus forming a wider gap from a longer and terminally narrower process of ampulla, harpe with a more convex dorsal margin forming into distal tooth (Fig. 240), and usually wider hyaline spot in forewing cell M_3 -CuA₁ (Fig. 27). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1651.2.6:A45G, aly168.15.2:A94G, aly491.2.1:A394C, aly876.6.1:A81G, aly103.35.5:C187T, aly1405.20.9:A489A (not G), aly1405.20.9:C507C (not T), aly527.6.11:G81G (not T), aly4265.5.1:G63G (not A), aly2130.10.1:T75T (not C), and COI barcode: A22G, A316T, 361C, T385T, A550G.

Barcode sequence of the holotype. Sample NVG-18016D12, GenBank OR837633, 658 base pairs:

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AACTTTTATATTTTATTTTGGGATTTGAGCTGGTTAGTTGGTACTTCTTTAAGATTACTTATTCGAACTGAATTAGGAACCCCTGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAAATGGAGGATTTGGAAATT
GACTAGTACCCCTTATACTAGGAGCCCCAGATATAGCATTTCCCTCGAATAAATAAATAAGATTTTGATTATTACCCCATCTTTAACTCTTTTAAT
TTCTAGAAGTATTGTAGAAAATGGTGCAGGTACTGGATGAACTGTCTATCCCCCTCTTTCATCTAATATCGCCCCACCAAGGAGCTTCTGTAGATTTA
GCAATTTTCTCATTACATTTAGCAGGAATTTCTTCTATTCTTGGAGCTATTAATTTTATTACAACAATTTAATATACGAATTAATAATTTATCAT
TTGATCAAATATCATTATTTATTTGAGCTGTAGGAATTACAGCTTTATATTATTACTTTCATTGCCTGTTTTAGCAGGAGCTATTACTATATTATT
AACTGATCGTAATTTAATACATCATTTTTTGGACCCTGCAGGAGGGGGTGATCCTATTCTATACCAACATTTATTT
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Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 27–28, bears the following four rectangular labels, three white: [ECUADOR: Napo, | Misahuallí Jungle Lodge | 1° 01.54' S, 77° 39.42' W | 450 m, 6, 8 Jan 2002 | J.P.W. Hall & M.A. Solis], [DNA sample ID: | NVG-18016D12 | c/o Nick V. Grishin], [USNMNT | {QR Code} | 01450788], and one red [HOLOTYPE ♂ | *Aguna claxonica* | Grishin].

Type locality. Ecuador: Napo Province, Puerto Misahuallí, Misahuallí Amazon Lodge, elevation 450 m, GPS -1.0257, -77.6570.

Etymology. The name is formed by adding the suffix *-ica* to its sister species name, making the name longer for this more southern species. The name is a noun in apposition.

Distribution. Currently known only from the holotype collected in Ecuador.

Aguna esmeralda Grishin, new species

<https://zoobank.org/81C0476E-A9A8-4A6E-8EE9-F25C3C13130F>

(Fig. 1 part, 29–30, 241–242)

Definition and diagnosis. A species related to *Aguna glaphyrus* (Mabille, 1888) (type locality in Brazil: Santa Catarina), *Aguna longicauda* Austin and O. Mielke, 1998 (type locality in Brazil: Rondônia), and *Aguna spicata* Austin and O. Mielke, 1998 (type locality in Brazil: Rondônia) (Fig. 1), but genetically differs from them more than they are from each other, e.g., COI barcode difference from *A. glaphyrus* is 5% (33 bp). Phenotypically can be identified by the contrasting tint of upperside green overscaling: yellower on the forewing and bluer on the

hindwing (Fig. 29), short and stubby tails, nearly oval valva (when taken together with harpe), longer than in *A. glaphyrus* and *A. spicata* (among others), and separated from harpe only with a small notch, harpe rounded distad rather than narrowing, sacculus expanded distad. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly671.26.9:C88T, aly671.16.4:T181A, aly1468.8.8:A146G, aly1468.8.8:T156C, aly1340.1.1:C1566T, and COI barcode: A148G, A181T, TC208, T430G, T523C.

Barcode sequence of the holotype. Sample NVG-18017A03, GenBank OR837634, 658 base pairs:

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AACTTTATATTTTATTTTGGAAATTTGAGCAGGATTAATTGGAACCTCATTAAAGATTACTTATTCGAACTGAATTAGGAACCCCGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTTACAGCTCATGCTTTTATTATGATTTTTTTTATAGTAATAACCTATTATAAATGGTGGATTTGGAAATT
GACTTGTACCTCTCATACTAGGAGCCCCGTGATATAGCATTCCCCCGAATAAATAAATAAGATTTTGACTTTTACCCCTCCTTAACCTTTTAAAT
CTCTAGAAGCATTGTAGAAAATGGTGCAGGCACAGGATGAACAGTTTATCCCCCTCTTTCATCTAATATGACATCAGGGAGCTCCGTAGATTTA
GCAATTTTTCTTTACATTTAGCAGGAATTTCCCTCTATTCTGGGAGCTATTAATTTTATTACTACAATTTAATATACGAATTAATAATTTATCTT
TCGATCAAATATCTTTATTCATTTGAGCAGTTGGTATCACTGCATTATTACTATTACTTTCTTTACCTGTTTTAGCAGGAGCTATTACAATATTATT
AACAGATCGAACTTAAACACTTCATTCTTTGATCCTGCAGGAGGAGTGATCCTATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 29–30, bears the following four rectangular labels, three white: [ECUADOR: Esmeraldas: | Río Chuchuví, km. 12.5 Lita- | San Lorenzo rd. 800-900m | 0° 53.01' N 78° 30.90' W | I.2001 I.Aldas leg.], [DNA sample ID: | NVG-18017A03 | c/o Nick V. Grishin], [USNMENT | {QR Code} | 01450831], and one red [HOLOTYPE ♂ | Aguna esmeralda | Grishin]. **Paratypes:** 4♂♂ from Ecuador: Esmeraldas Province: 2♂♂ from the type locality: NVG-18017A04 USNMENT_01450832 the same data as the holotype, but collected in Mar-2001 [USNM]; and NVG-18066C08 Oct-2012, ex coll. M. Büche [EBrockmann]; 1♂ NVG-18016H04, USNMENT_01450823 Km 18.5 San Mateo-Pto. Libre Road, Zapatta Hilltop, 500 m, GPS 0.884500, -79.540333, 6-Mar-2001, D. H. Ahrenholz leg. [USNM]; 1♂ NVG-18065E11 Durango, 500-800 m, Mar-Jun-2011, ex coll. M. Büche [EBrockmann].

Type locality. Ecuador: Esmeraldas Province, Río Chuchuví, km. 12.5 Lita-San Lorenzo Road, elevation 800–900 m, GPS 0.883500, -78.515000.

Etymology. The name is formed from the Esmeraldas Province, the type locality of this species. The name is a noun in apposition, originating from a Greek word meaning emerald, which also nicely reflects the emerald-green color on the dorsal hindwing of this species.

Distribution. Currently known from northwestern Ecuador.

Aguna lata Grishin, new species

<https://zoobank.org/1D86CDBD-1D55-4A24-9705-84847DF9E86B>

(Fig. 1 part, 31–32, 243–245)

Definition and diagnosis. Inspection of genomic trees reveals that a specimen identified as *Aguna spatulata* Austin and O. Mielke, 1998 (type locality in Brazil: Rondônia) is sister to the clade consisting of *A. spatulata*, *Aguna panama* Austin and O. Mielke, 1998 (type locality in Panama), and *Aguna similis* Austin and O. Mielke, 1998 (type locality in Brazil: Rondônia) and therefore is a distinct species. The new species differs from its closest relatives by a more angular distal margin of lamella antevaginalis, with slightly concave lobes on the sides of the notch (Fig. 243); these lobes appear truncate rather than rounded as in other species (Austin and Mielke 1998). Due to the cryptic nature of this species and unknown males, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly37338.40.1:A567G, aly1651.2.15:T844C, aly1651.2.15:T1098C, aly1146.14.5:T39A, aly318.14.14:T432C, aly806.11.5:G1380G (not A), aly383.14.5:C90C (not T), aly114.6.2:T960T (not C), aly770.33.9:A75A (not G), aly725.4.3:A123A (not G), but the COI barcode does not distinguish this species from *A. spatulata*.

Barcode sequence of the holotype. Sample NVG-18016D11, GenBank OR837635, 658 base pairs:

```
AACTTTATATTTTATTTTGGTATTTGAGCAGGATTAGTAGGAACTCTTTAAGATTATTAATTCGAACTGAATTAGGAACACCAGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATAACCTATTATAAATGGAGGATTTGGAAATT
GACTAGTACCCCTTATACTAGGAGCTCCTGATATAGCATTCCCCCGAATAAATAAATAAGATTTTGACTTTTACCCCTTCTTTAACCTTTTAAAT
TTCTAGTAGTATCGTAGAAAATGGTGCAGGCACAGGATGAACAGTTTACCCCACTTTCATCTAATATGCCCATCAAGGAGCTTCAGTTGATTTA
```

GCAATTTTCTCCTTACACTTAGCAGGAATTTCTTCTATTCTTGGAGCTATTAATTTTATCACCACAATTATTAACATACGAATTAATAATATATCAT
TTGATCAAATATCATTATTTATTTGAGCTGTTGGAATTACAGCTTTATATTACTACTATCTTTACCAGTTTTAGCAGGAGCTATTACAAATTTATT
AACAGATCGAAATTTAAATACATCATTTTTTGTATCCTGCTGGAGGGGAGATCCTATTCTTTACCAACATTTATTC

Type material. Holotype: ♀ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 31–32, bears the following four rectangular labels, three white: [GUYANA: Trop F Res | Middle Demerara R | 200–400' | 31.I-12.II.2001 | 5°9.32'N 58°41.98'W | Leg. S.Fratello et al], [DNA sample ID: | NVG-18016D11 | c/o Nick V. Grishin], [{QR Code} | USNM ENT 00234359], and one red [HOLOTYPE ♀ | Aguna | lata Grishin].

Type locality. Guyana: Potaro-Siparuni Region, middle Demerara River, Tropenbos forest reserve, elevation 200–400', GPS 5.1553, –58.6997.

Etymology. The name is formed from its similar species, [spatu]lata, and is a noun in apposition.

Distribution. Known only from the holotype collected in Guyana.

Ridens angulinea Grishin, new species

<https://zoobank.org/F16FA82A-8646-4B46-A2F2-7C7A8DDECC6B>

(Fig. 1 part, 33–34, 246–247)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Peru and Bolivia identified as *Ridens fulminans* (Herrich-Schäffer, 1869) (type locality not specified) are not monophyletic with it and are instead sister to several species of *Ridens* Evans, 1952 (Fig. 1), and therefore represent a new species. COI barcodes of this new species and a syntype of *R. fulminans* differ by 6.8% (45 bp). The new species keys to *Ridens fulminans* (C.12.7) in Evans (1952) and differs from *R. fulminans* and *Ridens fulima* Evans, 1952 (type locality in Brazil: Espírito Santo) in typically having narrower forewing hyaline spots (although some specimens have broader spots as well) and less prominent, mostly vestigial, pale discal band on the ventral hindwing (Fig. 33–34). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly116.28.11:A377G, aly116.28.11:A405G, aly2284.34.16:A61C, aly2284.34.16:A90G, aly2311.2.8:G123A, and COI barcode: T34C, T70C, A100C, T145C, T263C.

Barcode sequence of the holotype. Sample NVG-14104E04, GenBank OR837636, 658 base pairs:

AACTTTATATTTTATTTTGGAAATTTGAGCTGGCTTAATTTGGAAGTTCCTTAAGATTACTTATTCGTACCGAATTAGGAATTCCTGGTTCTTTAATT
GGCGATGACCAAATTTATAATACTATTGTAACAGCACATGCCTTTATCATAATCTTTTTTATAGTAATACCAATTATAAATGGTGGATTGGAAAT
GATTAGTACCATTAATATTAGGAGCCCCGTGATATAGCATTCCCCCGAATAAATAAATAAGATTTTGACTATTACCCCATCTTACTCTTTTAAT
TTCTAGAAGAATTGTAGAAATGGTGCTGGAACAGTTGAAACAGTTTATCCCCCTCTTTCAACTAATATFGCCCATCAAGGGGATCTGTCGACTTA
GCCATTTTTTCTCTTCAATTTAGCTGGAATTTCTCAATTTTAGGAGCAATTAATTTTATTACACAATTTAATATATGCGAATTAATAATTTATCAT
TTGATCAAATACCATTATTTATTTGAGCCGTAGGAATTACAGCATTATTATTACTTTCTTTACCTGTATTGGCAGGAGCTATTACCATATTACT
TACCGATCGAAACTTAATACTTCATTTTTTGTATCCTGCAGGAGGTGGAGATCCAATTTTATATCAACACTTATTT

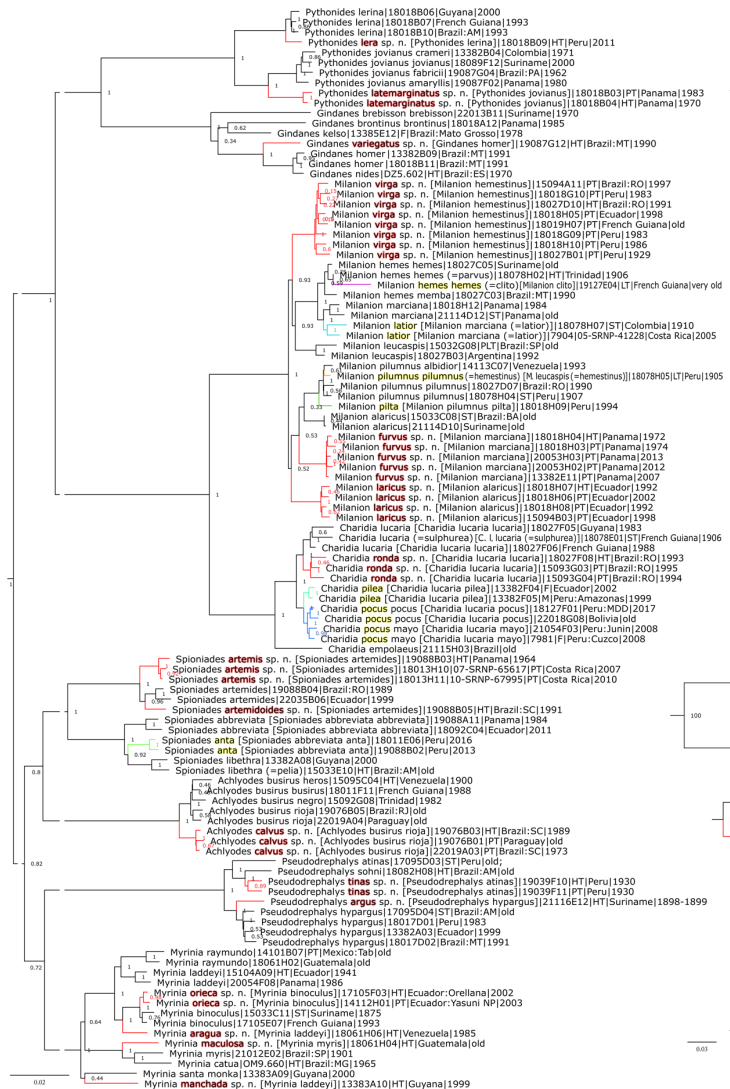
Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 33–34, bears the following three rectangular labels, two white: [PERU:Cuzco 1,194m | Bridge@1194 m | Cosnipata Road 3167 | 29.I.2013 Kinyon], [DNA sample ID: | NVG-14104E04 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | *Ridens angulinea* | Grishin]. **Paratypes:** 5♂♂: 1♂ NVG-17103B12 USNM_00913749 Peru: Cuzco, Cosnipata Valley, Quebrada Santa Isabel, 24-Oct-2016, S. Kinyon leg. [USNM]; 1♂ NVG-18089A11 Bolivia: Yungas Region, Caranavi Province, 50 km N of Coroico, 700–1200 m, Nov-1988, Carlos Tello leg. [EBrockmann]; 3♂♂ Bolivia: Rio Songo: NVG-19041B10 AMNH_IJC 00337748 750 m, coll. Fassel, genitalia slide G770 [AMNH]; and R. C. Williams, Jr. collection [ANSP]: NVG-22042E10 and NVG-22042E11 genitalia slide No. 316.

Type locality. Peru: Cuzco, Cosnipata Road, bridge at 1194 m.

Etymology. The name reflects narrower white bands and spots in many specimens of this species. It is derived from the Latin phrase “narrow lines”: *angul[stis]line[is]+a*. The name is a noun in apposition.

Distribution. Southern Peru and Bolivia.

a Z chromosome tree



b mitochondrial genome tree segments



Figure 2. Phylogenetic trees of Achlyodini inferred from protein-coding regions in **a**) the Z chromosome and **b**) the mitochondrial genome (in segments). See Fig. 1 legend for other notations.

GCTATTTTTTCCCTACACCTAGCTGGTATTTTCATCAATTTTGGAGCTATTAATTTTATTACTACAATCATTAATATACGAATTAGAAATTTATCAT
TTGATCAAATACCTTATTTGTTTGGAGCTGAGGAATTACAGCATATATATATATTATCATTACCTGTTTTAGCCGGAGCTATACCATATTATT
AACTGACCGAAATTTAAATACATCATTTTGTATCCAGCTGGTGGAGGAGATCCAATTTTATATCAACATTTATTT

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 37–38, bears the following four rectangular labels, three white: [PANAMA: Panama | Cerro Campana 2500' | 8°41'N 79°55'W | August 1970 | leg. G.B.Small], [DNA sample ID: | NVG-18018B04 | c/o Nick V. Grishin], [USNMNT | {QR Code} | 01450934, and one red [HOLO-TYPE ♂ | Pythonides | latermarginatus Grishin]. **Paratype:** 1♂ NVG-18018B03 USNMNT_01450933 Panama: Darien, Cana, 750 m, 15-Jun-1983, G. B. Small leg. [USNM].

Type locality. Panama: Panama Province, Cerro Campana, elevation 2500 ft, GPS 8.6833, –79.9167.

Etymology. The name is Latin for the broad (dark) margin and is a masculine adjective.

Distribution. Panama.

***Gindanes variegatus* Grishin, new species**

<https://zoobank.org/1855A4ED-6F31-4ED4-9416-C43CDC581D57>

(Fig. 2 part, 39–40, 252–253)

Definition and diagnosis. A specimen from Mato Grosso, Brazil, identified (incorrectly) as *Gindanes homer* (Evans, 1953) (type locality in Brazil: Mato Grosso) is genetically differentiated from it (Fig. 2): e.g., COI barcodes differ by 4.9% (32 bp). The new species keys (incompletely) to “*Pythonides homer*” (E.41.10) or “*Pythonides herennius herennius*” (E.41.7a) in Evans (1953) and differs from them and *Gindanes nides* (Mielke and Casagrande, 2002) (type locality in Brazil: Espírito Santo) by a more variegated appearance, larger forewing hyaline spots, conjoined forewing cell spots, and more extensive whitish coloration of ventral hindwing that includes its anterior part: a prominent central brown spot near costa is framed by white on both sides. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly26.1.2:C18T, aly4305.19.19:G123A, aly4305.19.19:G120T, aly264.4.18:C93T, aly253.13.3:G99A, aly276558.27.2:C121C (not A), aly276558.27.2:C144C (not T), aly1158.11.3:G702G (not A), aly1281.15.3:C82C (not G), aly6954.10.6:C1206C (not T), and COI barcode: A22G, T121T, C205C, C343G, T442C.

Barcode sequence of the holotype. Sample NVG-19087G12, GenBank OR837639, 658 base pairs:

```
AACTTTATATTTTATTTTGGGATTTGGGCAGGAATAATTGGAACATCTTTAAGCCTACTAATTGCAACTGAATTAGGTAATCCAGGATCTTTAATT
GGAGATGATCAAATTTATAACTACTATTGTTACTGCTCATGCTTTTATTATAAATTTTTTATAGTTATACCAATTATAATTGGAGATTGGAAATT
GATTAGTACCCTTAATATTAGGAGCTCCAGATATAGCTTTCCCCCGAATAAACAAATATAAGATTTTGATTATTACCTCCATCTTTATTATTATAAT
TTCAAGAAGTATTGTTGAAAATGGAGCAGGAACAGGATGAAGTGTATTCGCCCTCTTTCTGCTAATATTGCTCATCAAGGTTTCATCTGTAGATTTA
GCTATTTTTTCTTTACATTTAGCAGGATTTCCCTCAATTTTAGGAGCTATTAAGTATTTACTACAATTTAATATACGAATTAATAATCTTTTCAT
TTGATCAAATACCTTTATTTATTTGAGCAGTGGGAATTACAGCATTACTTTTATTATTATCTCTTCTGTTTTAGCAGGTTGCTATTACTATATTTAT
AACTGATCGAAATTTAAATACATCTTTTGTATCTGCGAGTGGGGTGATCCAATCTTATATCAACATTTATTT
```

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 39–40, bears the following four rectangular labels, three white: [BRASIL: Mato Grosso | Diamantino, 350–400m | Alto Rio Arinos | 14°13'S 56°12'W | 18 August 1990 | Leg. E. Furtado], [DNA sample ID: | NVG-19087G12 | c/o Nick V. Grishin], [USNMNT | {QR Code} | 01588890], and one red [HOLOTYPE ♂ | *Gindanes* | *variegatus* Grishin].

Type locality. Brazil: Mato Grosso, Diamantino, Alto Rio Arinos, elevation 350–400 m, GPS –14.217, –56.200.

Etymology. The name is given for the variegated appearance of this species. The name is a masculine perfect passive participle.

Distribution. Known only from the holotype collected in Brazil: Mato Grosso.

***Papilio clito* Fabricius, 1787 is a junior subjective synonym of *Milanion hemes hemes* (Cramer, 1777)**

Genomic sequencing of the lectotype of *Papilio clito* Fabricius, 1787 (type locality in French Guiana), currently a valid species in the genus *Milanion* Godman and Salvin, 1895 (type species *Papilio hemes* Cramer, 1777), reveals that it is conspecific with specimens we identified as *Milanion hemes hemes* (Cramer, 1777) (type locality in Suriname), including a specimen from Suriname (Fig. 2). Therefore, we propose that *Papilio clito* Fabricius, 1787 is a **new junior subjective synonym** of *Milanion hemes hemes* (Cramer, 1777).

***Milanion pilta* Evans, 1953 is a species distinct from *Milanion pilumnus* Mabille and Boulet, 1917**

Proposed by Evans (1953) as a subspecies of *Milanion pilumnus* Mabille and Boulet, 1917 (type locality in Bolivia and Peru) from Peru: Moyabamba, *M. p. pilta* is genetically differentiated from it at the level typical for distinct species: e.g., their COI barcodes differ by 6.7% (44 bp) (Fig. 2). Therefore, we propose that it is a species-level taxon *Milanion pilta* Evans, 1953, **new status**.

***Milanion latior* Mabille and Boulet, 1917 is a species distinct from *Milanion marciana* Godman and Salvin, 1895**

Sequencing of a syntype of *Milanion marciana* var. *latior* Mabille and Boulet, 1917 (type locality in Colombia), a taxon currently treated as a junior subjective synonym of *Milanion marciana* Godman and Salvin, 1895 (type

locality in Panama), reveals genetic differentiation between them (Fig. 2): e.g., COI barcodes of syntypes of these taxa differ by 3% (20 bp). Therefore, we propose to treat it as a species-level taxon *Milanion latior* Mabilles and Boulet, 1917, **new status**.

***Milanion pilumnus* var. *hemestinus* Mabilles and Boulet, 1917 is a junior subjective synonym of *Milanion pilumnus pilumnus* Mabilles and Boulet, 1917 not of *Milanion leucaspis* (Mabilles, 1878)**

Genomic sequencing of the lectotype of *Milanion pilumnus* var. *hemestinus* Mabilles and Boulet, 1917 (type locality in Peru) reveals that it is in a clade different from *Milanion leucaspis* (Mabilles, 1878) (type locality in Brazil), which is its current senior subjective synonym but is placed among specimens of *Milanion pilumnus* Mabilles and Boulet, 1917 (type locality in Bolivia and Peru). COI barcodes of the *M. p. hemestinus* lectotype and a syntype of *M. pilumnus pilumnus* differ by 0.5% (3 bp). Therefore, as proposed by the original authors, *M. p. hemestinus* is conspecific with *M. pilumnus*, and we treat these two names as synonymous.

***Milanion (Milanion) virga* Grishin, new species**

<https://zoobank.org/2C440233-C0FA-49D4-9496-A451B5F57764>

(Fig. 2 part, 41–42, 254–255)

Definition and diagnosis. As detailed above, *Papilio clito* Fabricius, 1787 and *Milanion pilumnus* var. *hemestinus* Mabilles and Boulet, 1917 are junior subjective synonyms of *Milanion hemes hemes* (Cramer, 1777) and *Milanion pilumnus* Mabilles and Boulet, 1917, respectively. As a result of this, and because no other available name applies to it, the species that Evans (1953) called “*Milanion hemestinus*” was misidentified and is new. This new species keys to (E.46.3) in Evans (1953). It differs from its relatives by a combination of the following characters: a white spot in forewing cell $CuA_2-1A+2A$, a dorsal hindwing white band about the same width as the brown marginal area, basal half of the ventral hindwing is white with a dark ray near costa from the base to costal margin (i.e., there is an elongated white spot near the base by costa); both gnathos and uncus arms are equally wide apart, tips of uncus not turned outwards; harpe broad, terminally rounded and with a spine in the middle at the dorsal margin. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly536.107.1:A81G, aly536.107.1:C93T, aly770.13.3:T153C, aly1937.10.4:C88T, aly1937.10.4:C112A, and COI barcode: T19C, T172C, A499C, A541C, T613C.

Barcode sequence of the holotype. Sample NVG-18027D10, GenBank OR837640, 658 base pairs:

```
AACTTTATATTTTATTTTTCGGAATTTGAGCAGGATTAGTAGGAACCTCTTAAAGTTTATTAATTCGAACTGAATTAGGAAATCCAGGATCTTTAATT
GGAGATGACCAAATTTATAATACTATTGTAACCTGCTCATGCATTTATTATAAATTTTTTTATAGTTATACCAATCATAAATGGTGGATTGGAAATT
GATTAGTACCATTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAACATAAGATTTTGATTATTACCCCATCTCTTATATTATTAAT
TTCAAGAAGTATTGTAGAAAATGGTGCAGGAACCTGGATGAACAGTTTATCCACCTCTTTTCAGCTAACATCGCTCATCAAGGTTTCATCAGTAGATCTA
GCAATTTTTCTTTACATTTAGCTGGAATTTCTTCAATTTTAGGAGCTATTAATTTTATTACTACTATTATTAATATACGAGTAAATAATTTATCAT
TTGATCAAATACCCTTATTTGTGTGAGCTGTAGGTATTACAGCTTTACTTTTACTCCTATCATTACCCGTATTAGCAGGTGCTATTACTATATTTAT
AACTGATCGAAATTTAAATACATCATTTTTCGACCCAGCAGGAGGAGGAGATCCAATCTTATATCAACATCTATTT
```

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 41–42, bears the following five rectangular labels, four white: [BRASIL:Rondonia | 62 km S Ariquemes | Fazenda Rancho | Grande, 165m | 10-32'S, 62-48'W | 29 Oct-10 Nov 1991 | Brian P. Harris], [Milanion | hemes | hemes], [DNA sample ID: | NVG-18027D10 | c/o Nick V. Grishin], [USNMNT | {QR Code} | 01465169], and one red [HOLOTYPE ♂ | Milanion | virga Grishin]. **Paratypes:** 5♂♂ and 2♀♀: 1♂ NVG-15094A11 the type locality, 27-Oct-1997, G. T. Austin leg. [MGCL]; 1♂ NVG-18018H05 USNMNT_01450997 Ecuador: Orellana, Yasuni Research Station, Rios Tivacuno and Tiputini, elevation 220 m, GPS -0.675000, -76.396667, 30-Oct-1998, D. H. Ahrenholz leg., genitalia NVG-22032E07 [USNM]; 1♂ NVG-18018H10 USNMNT_01465137 Peru: Madre de Dios, Tambopata Res., Rio La Torre, elevation 300 m, 6-Oct-1986, S. S. Nicolay leg., genitalia NVG-22032E02 [USNM]; 1♂ NVG-18027B01 Peru: Middle Rio Ucayali, 6-Apr-1929, H. Bassler Collection [AMNH]; 1♂ NVG-18018G09, USNMNT_01450989 Peru: 30 km SW of Pto. Maldonado, 300 m, 20-Oct-1983, S. S Nicolay leg. [USNM]; 1♀ NVG-18018G10, USNMNT_01450990 Peru: Pto. Aldonado, 290 m, 15-Oct-1983, S. S Nicolay, leg. [USNM]; 1♀ NVG-18019H07 French Guiana [AMNH].

Type locality. Brazil: Rondônia, 62 km S Ariquemes, Fazenda Rancho Grande, elevation 165m, GPS –10.533, –62.800.

Etymology. The name is given for the pale streak at the base by the costa of the ventral hindwing characteristic of this species. In Latin, *virga* means rod or streak. The name is a noun in apposition.

Distribution. Widely distributed in tropical South America: Ecuador, Peru, French Guiana, and Brazil.

Milanion (Milanion) furvus Grishin, new species

<https://zoobank.org/371AD2A6-502E-44AF-B185-91A95AC388CE>

(Fig. 2 part, 43–44, 256–257)

Definition and diagnosis. Several specimens from Panama identified as *Milanion marciana* Godman and Salvin, 1895 (type locality in Panama) are in a clade different from *M. marciana* and *Milanion latior* Mabillet and Boullet, 1917 (type locality in Colombia) and are genetically differentiated from all other species in the genus (Fig. 2). Therefore, they represent a new species. This new species does not key correctly to any species, including *M. marciana* (E.46.5), in Evans (1953) and differs from its relatives by a combination of the following characters: white spot in forewing cell $CuA_2-1A+2A$ is small, located by the vein $1A+2A$ and does not reach the middle of the cell, white patch on hindwing is broader than brown border, ventral hindwing with wide brown area by costa, cell $Sc+R_1-RS$ brown with a (usually) small white spot in the middle joined with the white central area with veins darker by the dark border. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly2027.2.5:C51T, aly971.9.9:G51T, aly2811.4.1:G248A, aly2811.4.1:C249T, aly1475.2.1:G48A, and COI barcode: T133G, T157C, T358C, T514C, A607C.

Barcode sequence of the holotype. Sample NVG-18018H04, GenBank OR837641, 658 base pairs:

```
AACTTTATATTTTATTTTGGAAATTTGAGCAGGATTAGTAGGAACCTCTTTAAGTTTATTAATTCGAACCTGAATTAGGAAACCCAGGATCTTTAATT
GGAGATGATCAAATTTATAACTATTGTAACCTGCGCATGCAATTTATTATAATTTTTTTCATGGTCATACCAATTATAATGGTGGATTTGGAAATT
GATTAGTACCTTTAATATTAGGAGCCCCAGATATAGCTTTCCCCCGAATAAATAATATAAGATTTTGATTATTACCCCATCTCTATATTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCAGGAACCTGGATGAACAGTTTACCACCTCTTTCAGCTAACATTGCCCATCAAGGCTCATCAGTAGATTTA
GCAATTTTTCTTTACATTTAGCTGGAATTTCTCAATTTTAGGAGCTATTAATTTTATTACTACTATTATAACATACGAGTAATAAATTTATCAT
TTGATCAAATACCTTTATTTGTATGAGCCGTAGGTATTACAGCTTTACTTTTTATTATTATCTTTACCTGTATTAGCAGGTGCTATTACTATATTATT
AACTGACCGAAATTTAAACACATCTTCTTTGACCCAGCAGGAGGAGATCCAATTTTATACCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 43–44, bears the following four rectangular labels, three white: [PANAMA: Panama | Farfan (C.Z.) | 8° 56'N, 79° 34'W | 6 Jan '72 | leg. S. S. Nicolay], [DNA sample ID: | NVG-18018H04 | c/o Nick V. Grishin], [USNMNT | {QR Code} | 01450996], and one red [HOLOTYPE ♂ | *Milanion furvus* Grishin]. **Paratypes:** 4♂♂ from Panama: Panama Province: 1♂ 11-BOA-13382E11 Panama City, Albroom Hotel and Area, 1–4-Aug-2007, R. H. Leuschner leg. [USNM]; 1♂ NVG-18018H03 Bayano, 23-Nov-1974, G. B. Small leg. [USNM]; 1♂ NVG-20053H02 Gamboa, Pipeline Road, 75 m, 9.127167, –79.714833, 2-Jun-2012, John R. MacDonald leg. [MEM]; 1♂ NVG-20053H03 Veracruz, ca. 50 m, GPS 8.911833, –79.565722, 2-Jul-2013, John R. MacDonald leg. [MEM].

Type locality. Panama: Panama Province, Farfan, GPS 8.933, –79.567.

Etymology. In Latin, *furvus* means dark, dusky, gloomy, or swarthy. The name, a masculine adjective, is given partly for the smaller white area and very small white spot in cell 7 on the ventral hindwing.

Distribution. Currently known only from central Panama.

Milanion (Milanion) laricus Grishin, new species

<https://zoobank.org/5BD7C016-6141-4D71-BAAB-DD8F18887811>

(Fig. 2 part, 45–46, 258–259)

Definition and diagnosis. Several specimens from Ecuador identified as *Milanion alaricus* (Plötz, 1884) (type locality in Brazil: Bahia) were not closely related to the syntype of *M. alaricus* (Fig. 2) and formed a clade distinct from all other species of the genus. Therefore, they represent a new species. This new species keys (incompletely) to *M. alaricus* (E.46.6) in Evans (1953) and differs from its relatives by a vestigial (or lacking) white spot in

forewing cell $CuA_2-1A+2A$, spot at the base of cell M_3-CuA_1 is larger, more triangular than rounded (as in *M. alaricus*) with its distal part protruding distad of the spot in the cell CuA_1-CuA_2 , ventral hindwing area by costa in basal two-thirds is not white, but is pale-brown, not the same dark color as the brown marginal wide border. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly1313.22.1:G201A, aly923.23.1:T1497C, aly15192.3.7:G100A, aly1405.11.14:C72T, aly2095.5.1:C135T, and COI barcode: T133A, T301C, A577G, A592G, A628T.

Barcode sequence of the holotype. Sample NVG-18018H07, GenBank OR837642, 658 base pairs:

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AACTTTATATTTTATTTTGGAAATTTGAGCAGGATTAGTAGGAACCTCTTTAAGTTTATTAATTCGAACCTGAATTAGGAAACCCAGGATCTTTAATT
GGAGATGATCAAATTTATAACTATTGTAACCTGCACATGCATTTATTATAAATTTTTTATAGTTATACCTATTATAAATGGTGGATTTGGAAATT
GATTAGTACCATTAATATTAGGAGCCCCAGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCATCTCTATATTATTAAT
TTCAAGAAGCATTGTGGAAAATGGTGCAGGAACCTGGATGAACAGTTTATCCCCCCTTTTCAGCCAATATTGCCCAACCAAGGTTTCATCAGTAGATTTA
GCAATCTTTTCTTTACATTTAGCTGGAATTTCTTCAATTCTAGGAGCTATTAATTTTATCACCCTATTATTAACATACGAGTAAATAACTTATCAT
TTGATCAAATACCATTATTTGTATGAGCAGTAGGAATTACTGCACTACTTTTATTGTTATCTTTTACCTGTATTAGCGGGTGCTATTACTATGTTATT
AACTGATCGGAATTTAAATACATCATTTTTTTGACCCAGCAGGAGGTGGAGATCCAATTTTATATCAACATCTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 45–46, bears the following four rectangular labels, three white: [ECUADOR: Napo Pr. | Jatun Sacha Biol St. | 1° 4.0'S 77° 37.0'W | 13 Nov. 1992. 450m. | S. S. Nicolay, leg.], [DNA sample ID: | NVG-18018H07 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01450999], and one red [HOLOTYPE ♂ | Milanion | laricus Grishin]. **Paratypes:** 3♂♂ from Ecuador: 1♂ NVG-18018H08, USNMMENT_01465135 the same data as the holotype but collected on 7-Nov-1992; 1♂ NVG-15094B03, Napo, Yasuni Research Station, Rios Tivacuno and Tiputini, 250 m, GPS –0.633, –76.600, 22-Oct-1998, J. D. Turner leg. [MGCL]; 1♂ NVG-18018H06, USNMMENT_01450998 Sucumbios, Cerro Lumbaqui Norte, 800-950 m, GPS 0.028333, –77.320333, 18-22-Aug-2002, J. P. W. Hall and M. A. Solis leg. [USNM].

Type locality. Ecuador: Napo Province, Jatun Sacha Biological Reserve, elevation 450 m, GPS –1.0667, –77.6167.

Etymology. The name *alaricus* is derived from Alariks (king of all) with the prefix “alla-” (all, everybody, entire) suggests a kingly, royal, or noble identity. *Laricus* (i.e., not *alaricus*) is a noun in apposition and a shorter name for this more northern species.

Distribution. Known only from northeastern Ecuador.

Charidia pilea Evans, 1953, and *Charidia pocus* Evans, 1953 (with *Charidia lucaria mayo* Evans, 1953 as its subspecies) are species distinct from *Charidia lucaria* (Hewitson, 1868)

Genomic sequencing of taxa currently treated as subspecies of *Charidia lucaria* (Hewitson, 1868) (type locality in French Guiana) reveals prominent genetic differentiation between some of them (Fig. 2): e.g., COI barcodes of *C. lucaria lucaria* differ from *Charidia lucaria pilea* Evans, 1953 (type locality in Colombia) and *Charidia lucaria pocus* Evans, 1953 (type locality in Peru) by 2.3% (15 bp) and 2.3% (15 bp), respectively. However, despite an obvious phenotypic difference in males having ventral hindwing largely white, *Charidia lucaria mayo* Evans, 1953 is not strongly differentiated genetically from *C. l. pocus*. However, we find an irregularity in the mitochondrial genome: *C. l. pocus* is not distinguishable from *C. l. pilea*, probably due to introgression from it, but *C. l. mayo* might have kept its original mitochondrial DNA differing by 1.2% (8 bp) in the COI barcode. Due to genetic and phenotypic differences, we propose a **new status** of a species for *Charidia pilea* Evans, 1953 and *Charidia pocus* Evans, 1953, and a **new combination** *Charidia pocus mayo* Evans, 1953 (type locality in Peru). Moreover, we found another species-level taxon in this complex that is described next.

Charidia ronda Grishin, new species

<https://zoobank.org/B46214EB-61ED-4174-8AAA-AF92820DF9BF>

(Fig. 2 part, 47–48, 260–261)

Definition and diagnosis. Sister to *Charidia lucaria* (Hewitson, 1868) (type locality in French Guiana) and keys to it (E.48.1(b)) in Evans (1953) but is genetically differentiated from it in nuclear genome at the level more typical for species-level taxa (Fig. 2), with the COI barcode distance of 1.5% (10 bp). Differs from its relatives by the following combination of characters: males with more extensive orange-yellow scaling on ventral side, e.g., forewing

tornal spots larger, hindwing overscaling more prominent towards tornus (Fig. 48) (yellow overscaling is equally extensive at the end of the discal cell and the hindwing base in more boldly patterned *C. lucaria* specimens), and costa-ampulla strongly humped (Fig 261); females with wide yellowish area on ventral hindwing with broadly brown costal margin and somewhat paler than the brown ground color subapical band on ventral forewing. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly283.5.1:T359C, aly283.5.1:G429A, aly502.6.3:C325T, aly1937.18.2:C52A, aly2202.3.1:A55T, and COI barcode: A73G, T421C, T460C, C529A, A550G.

Barcode sequence of the holotype. Sample NVG-18027F08, GenBank OR837643, 658 base pairs:

```
AACTTTATATTTTATTTTGGAAATTTGAGCAGGAATAGTAGGAACTTCTTTAAGTTTATTAATTCGAACTGAGCTAGGAAATCCAGGATCTTTAATT
GGAAATGATCAAATTTATAAATACTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTTGGAGGATTTGGAAAT
GACTAGTACCCCTTATACTAGGAAGTCCAGATATAGCTTTCCCACGAATAAATAAATAAGATTTTGATTATTACCCCATCTCTTATATATTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCAGGAAGTGGATGAACAGTTTTATCCCCCTCTTTCTGCTAATATTGCTCATCAAGGTTTCTGTAGACTTA
GCAATTTTTCATTACATTTAGCTGGAATTTCCCTCAATTTTAGGAGCTATTAATTTTATTACCCTATATCAATATACGAGTAAATAATCTATCAT
TTGATCAAATACCATTTTGTATGAGCTGTAGGAATTACAGCATTACTTTTATTACTATCATTCGCTGTATTAGCAGGAGCTATTACTATATTTATT
AACTGATCGAAATTTAAATACATCTTTTGTATCCTGCTGGAGGAGGAGATCCAATTTTATATCAACATTTTATT
```

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 47–48, bears the following five rectangular labels, four white: [BRASIL: Rondonia | 6km S Cacauplandia | Rio Pardo | 21 November 1993 | Brian Harris], [Charidia | lucaria], [DNA sample ID: | NVG-18027F08 | c/o Nick V. Grishin], [USNMENT | {QR Code} | 01465190], and one red [HOLOTYPE ♂ | Charidia | ronda Grishin]. **Paratypes:** 1♂ and 1♀ from Brazil: Rondonia [MGCL]: 1♂ NVG-15093G03 Cacauplandia, Fazenda Rancho Grande, 12-Nov-1995, D. and J. Lindsley leg.; 1♀ NVG-15093G04 5 km S of Cacauplandia, linea C-10 at Rio Pardo off B-65, 7-Jul-1994, O. Gomes leg.

Type locality. Brazil: Rondônia, 6 km S of Cacauplandia, Rio Pardo.

Etymology. The name is given for the type locality in *Rond[oni]a* and is a noun in apposition.

Distribution. Currently known only from the area around the type locality in Rondônia, Brazil.

Pseudodrephalys tinas Grishin, new species

<https://zoobank.org/37160735-2E27-4AE4-9B65-DBD0DD58B076>

(Fig. 2 part, 49–52, 262–263)

Definition and diagnosis. Genomic sequencing reveals that two specimens from Iquitos, Peru, identified as *Pseudodrephalys atinas* (Mabille, 1888) (type locality in Peru) are sister to *Pseudodrephalys sohni* Burns, 1999 (type locality in Brazil: Amazonas) with *P. atinas* being a more distant species (Fig. 2): COI barcodes differ by 4.7% (31 bp) from *P. atinas* syntype and 1.8% (12 bp) from *P. sohni* holotype. Due to genetic differentiation, the two Peruvian specimens represent a new species, which is distinguished from its relatives by a narrower valva with a larger cleft between the harpe and ampulla than in *P. sohni* and a much narrower harpe with a smaller cleft separating it from ampulla compared with *P. atinas*. In facies, males differ from *P. sohni* by the ventral hindwing white band being narrower and interrupted in the middle of the cell CuA₂-1A+2A, thus leaving an isolated spot near the anal fold; from *P. atinas* by this band reaching Sc+R₁ (instead of ending at Rs); and from both *P. sohni* and *P. atinas* by the postdiscal pale lavender line on ventral hindwing being vestigial. Females differ from *P. atinas* by a strongly concave border of the basal yellow-orange basal area of ventral hindwing and from *P. sohni* by not being similar to males in wing pattern (e.g., having a round ventral hindwing white spot instead of a band). Due to the somewhat cryptic nature of this species and unexplored phenotypic variation, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly671.6.3:T102C, aly6954.5.63:C66T, aly207.8.7:A150G, aly4456.10.1:A194G, aly1709.2.6:C87G, and COI barcode: A28G, A100T, T361C, T535C, 616C.

Barcode sequence of the holotype. Sample NVG-19039F10, GenBank OR837644, 658 base pairs:

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AACTTTTACTTTTATTTTGGAAATTTGGGCAGGAATAGTAGGTAAGTTTCTTTAAGATTATTAATTCGTAAGTATTAGGAAATCCAGGATCTTTAATT
GGTGATGATCAAATTTATAAATACTATTGTTACTGCTCATGCATTTATTATAATTTTTTTTATAGTTATGCCAATTATAATTTGGAGGATTTGGAAAT
GATTAGTACCTCTGTAGACTAGGAGCTCCTGATATAGCATTTCCCACGAATAAATAAATAAGATTTTGACTACTTCCCCCTCTTTATTGTTATTAAT
TTCAAGAAGTATTGTAGAAAATGGTGCCTGGAAGTGGATGAACGTATATCCTCCTCTTTCTTCAATATCGCCCATCAAGGAGCATCAGTAGATTTA
GCAATTTTTCATTACATTTAGCAGGAATTTCACTATTTTAGGAGCTATTAATTTTATTACAACAATTTAATATATACGAATTAATAATCTTTCTTC
```

TTGATCAATTACCTTATTCGTATGAGCTGTTGGTATCACAGCTTTACTCTTATTACTCTCTTTACCAGTATTAGCTGGAGCTATTACTATACTATT
AACTGATCGAAATTTAAATACATCTTTTTTTTGACCCTGCGGGAGGAGGATCCAATCTTATATCAACATTTATTT

Type material. Holotype: ♂ currently deposited in the American Museum of Natural History, New York, NY, USA (AMNH), illustrated in Fig. 49–50, bears the following six rectangular labels, five white: [Iquitos, Peru | XII-15 1930], [G646], [DNA sample ID: | NVG-19039F10 | c/o Nick V. Grishin], [Leg removed on | 20-Feb-2019 by | N. V Grishin for | DNA extraction], [{QR Code} | AMNH_IZC 00337700] and one red [HOLOTYPE ♂ | *Pseudodrephalys* | tinas Grishin]. **Paratype:** 1♀: NVG-19039F11, AMNH_IZC 00337701, the same data as the holotype (Fig. 51–52).

Type locality. Peru: Loreto Region, Iquitos.

Etymology. The name is formed by removing the negating prefix “a” from *atinas*. In Latin, *tinus* means small or tiny. This species has a smaller ampulla. The name is a noun in apposition.

Distribution. Currently known only from Northern Peru.

Pseudodrephalys argus Grishin, new species

<https://zoobank.org/D90B1BBA-F8B9-4EC3-8188-EC8E8667C4C1>

(Fig. 2 part, 53–54)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Suriname identified as *Pseudodrephalys hypargus* (Mabille, 1891) (type locality in Brazil: Amazonas) is genetically differentiated from a series of *P. hypargus* that included a syntype (Fig. 2), e.g., their COI barcodes differ by 2.1% (14 bp), and therefore represents a new species. This new species keys to “*Drephalys hypargus*” (B.6.13) in Evans (1952) and differs from it by being generally paler, has a paler streak along dorsal hindwing vein 1A+2A, ventral dark hindwing border is rounder and without a tooth-like contour in cell CuA₂-1A+2A. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly4105.1.1:T783C, aly54.9.3:C21A, aly2178.10.1:A52G, aly345.5.4:G72C, aly2284.13.13:G63C, aly423.15.5:A24A (not T), aly499.4.2:C81C (not T), aly15220.6.2:C129C (not A), aly151.8.3:A126A (not G), aly925.30.8:C24C (not T), and COI barcode: T97C, T220T, T277A, 322G, G622A.

Barcode sequence of the holotype. Sample NVG-21116E12, GenBank OR837645, 658 base pairs:

AACTTTATATTTTATTTTGGAAATTTGAGCAGGAATAGTAGGAACTTCTTTAAGATTATTAATTCGTACTGAATTAGGTAATCCAGGATCTTTAATC
GGAGATGATCAAATTTATAACTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTATAATTTGGAGGATTTGGAAAT
GATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCATTTCCACGAATAAATAATAAGATTTTGACTTCTTCCCTCCTCATTATTATTATTAAT
TTCAAGAAGTATTGTAGAAAATGGTGTCTGGGACAGGATGAACTGTTTACCCTCCTCTTTCTTCTAATATTGCTCATCAAGGAGCATCTGTAGATTTA
GCAATTTTTTTCATTACATTTAGCAGGAATTTTCATCTATTTTAGGAGCCATTAATTTTATTACAACAATTTAATATACGAATTAATAATCTTTCTT
TTGATCAATTACCTTTTGTATGAGCTGTTGGAATTACAGCTTTACTTTTATTACTTTCTTTACCAGTATTAGCTGGAGCTATTACCATATTATT
AACTGATCGAAATTTAAATACATCTTTTTTTTGACCCTGAGGAGGAGATCCAATTTTATATCAACACTTTATTT

Type material. Holotype: ♀ deposited in the Museum für Naturkunde, Berlin, Germany (MFNB), illustrated in Fig. 53–54, bears the following five rectangular labels, four white: [Bersaba | Surinam | 1898—9 Michls.], [Coll. | Staudinger], [] (empty label), [DNA sample ID: | NVG-21116E12 | c/o Nick V. Grishin], and one red [HOLOTYPE ♀ | *Pseudodrephalys* | *argus* Grishin].

Type locality. Suriname: Para District, Bersaba.

Etymology. The name is formed by removing *hyp* from *hypargus*. In Greek, the prefix *hyp*[o] means low, under, beneath, down, or less than normal. We removed the prefix, making this species higher. In Greek, *argos* means bright or white. The holotype is indeed brighter and whiter than *hypargus*. However, it is not clear whether this trait is general for the species or an individual variation. The name is a noun in apposition.

Distribution. Currently known only from the holotype collected in Suriname.

Achlyodes calvus Grishin, new species

<https://zoobank.org/D5824D70-DF3A-42A2-9730-6B719506E741>

(Fig. 2 part, 55–56, 266–267)

Definition and diagnosis. Phylogenetic analysis reveals that several specimens from Southern Brazil and Paraguay identified as *Achlyodes busirus rioja* Evans, 1953 (type locality in Brazil: Rio de Janeiro) are genetically

differentiated from all valid subspecies of *Achlyodes busirus* (Cramer, 1779) (type locality in Suriname), including sympatric *A. b. rioja* (Fig. 2): e.g., their COI barcodes differ by 3% (20 bp), and therefore represent a new species. This new species keys to *A. b. rioja* (F.2.1(c)) in Evans (1953) and differs from it by the absence of androconia patches (“brands” in Evans) at the base of the forewing beneath and at the humeral lobe on hindwing above (the two patches are contacting each other in spread specimens). Evans (1953) mentioned this character as a variation in *A. b. rioja*, but genomic analysis reveals that their absence corresponds to a distinct sympatric genetically differentiated species. Moreover, male genitalia are diagnostic (Fig. 266–267) and differ from sympatric *A. b. rioja* (Fig. 264–265) in the larger process of ampulla and more strongly upturned harpe with truncate, instead of rounded, distal end. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly1260.10.2:A69T, aly151.22.21:G41A, aly1349.5.5:G30T, aly2844.10.4:C132T, aly84.50.2:A45G, and COI barcode: 49A, A169G, T250C, T346C, T472C.

Barcode sequence of the holotype. Sample NVG-19076B03, GenBank OR837646, 658 base pairs:

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AACTTTATATTTTATTTTGGAAATTTGAGCCGGAATAATTGGAACCTCACTAAGTATATTAATTCGAACTGAACTAGGAAATCCAGGATCATTAAAT
GGAGATGATCAAATTTATAACTATTGTAACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCAATTATAATTTGGAGGATTTGGAAAT
GATTAGTACCCCTTATATTAGGAGCCCTGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGATTATTACCCCTCTTTAATATTATTAAT
TTCAAGAAGAATTGTTGAAAATGGAGCTGGAACAGGATGAACAGTTTATCCCCCTTTTCATCTAATATTGCTCACCAGGATCATCTGTAGATTA
GCTATTTTTCCTACATTTAGCAGGAATTTTCATCAATTTTAGGAGCTATTAATTTTATTACAACAATTTAATATACGAATCATAAATCTTTCTT
TTGATCAAATACCTCTTTTGTATGAGCTGTAGGAATTACAGCTTTACTTTTATTACTTTCCTTACCAGTACTAGCTGGAGCTATTACTATACTTTT
AACTGATCGAAATTTAAATACATCATTTTTTGTATCCTGCAGGAGGAGGAGATCCAATTTTATATCAACATTTATTT
```

Type material. **Holotype:** ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 55–56, bears the following four rectangular labels, three white: [BRAZIL:Sta Catarina | Sao Bento do Sul | 26°17' S 49°25'W | 21.II.1989 | 850m, leg. Rank], [DNA sample ID: | NVG-19076B03 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01588644], and one red [HOLOTYPE ♂ | Achlyodes | calvus Grishin]. **Paratypes:** 2♂♂: NVG-22019A03 from near the type locality, Rio Vermelho, elevation 600–850 m, 24-Feb-1973, Rank leg. [ZSMC] and NVG-19076B01, USNMMENT_01588642 Paraguay [USNM].

Type locality. Brazil: Santa Catarina, São Bento do Sul, elevation 850 m, GPS –26.283333, –49.416667.

Etymology. In Latin, *calvus* means hairless, bold, naked, or bare. It is given to this species for the lack of hair tufts. The name is an adjective.

Distribution. Southern Brazil and Paraguay.

Spioniades artemis Grishin, new species

<https://zoobank.org/994E86A1-7BEF-42D2-807F-8DC7623058E6>

(Fig. 2 part, 57–58, 268–270)

Definition and diagnosis. Phylogenetic analysis reveals that Central American specimens identified as *Spioniades artemides* (Stoll, 1782) (type locality in Suriname) are genetically differentiated from it (Fig. 2): e.g., their COI barcodes differ by 5.5% (36 bp), and therefore represent a new species. This new species keys to *S. artemides* (E.14.2) in Evans (1953) and differs from it and another new species described below by a combination of the following characters: a more regular, straight, and diffuse border between discal brown and postdiscal white area on the hindwing, lack of pale diffuse spot(s) towards inner margin and tornus of the ventral forewing, nearly evenly convex (not angled at vein Cu_{A1}) forewing outer margin (Fig. 57–58), more robust uncus in lateral view, narrower in dorsal view, deeper divided harpe with more concave distal margin in lateral view and protruding less inward in dorsal view, more concave in the middle, wavy costa with a narrower knob-like process that protrudes deeper inward (Fig. 268–270). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly378.30.2:A75G, aly1838.60.2:A36G, aly1838.60.2:A126G, aly294.15.14:C81T, aly274.33.1:G1047A, and COI barcode: T50C, T127A, T529C, A541G, T547C.

Barcode sequence of the holotype. Sample NVG-19088B03, GenBank OR837647, 658 base pairs:

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AACTTTATATTTTATTTTGGAAATTTGAGCAGGAATAGTAGGAACCTCTCAAGTTTATTAAATTCGAACTGAATTAGGAAATCCTGGAGCTCTTATT
GGAGATGATCAAATTTATAACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTTGGAGGATTTGGAAAT
```

GATTAGTTCCATTAATGCTAGGAGCCCCCTGATATAGCATTCCCTCGAATAAATAATATAAGATTCTGATTATTACCTCCATCTTTAATATTACTAAT
 TTCTAGAAGAATCGTTGAAAATGGAGCAGGTACTGGATGAACAGTTTTACCCCTCTTTTCAGCTAATATCGCACACCAAGGATCTTCAGTTGATT
 GCAATTTTTCTTTACATCTTGTGGAATTTCTCTATTTTAGGAGCTATTAATTTTATTTCTACAATTTAATATACGAATTAGAAATCTTTCAT
 TTGATCAAAATACCATTATTTGTTTGGAGCTGTAGGAATTACTGCCTTACTTTTATTTGTTATCTTTACCAGTATTAGCAGGTGCTATTACTATACCTTT
 AACTGATCGAAATCTTAATACATCATTTTTTGTATCCTGCTGGAGGAGGAGATCCAATTTTATATCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 57–58, bears the following four rectangular labels, three white: [Madden For. | Panama C.Z. | IV-4-64], [DNA sample ID: | NVG-19088B03 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01588916], and one red [HOLOTYPE ♂ | Spioniades | artemis Grishin]. **Paratypes:** 1♂ and 1♀: Costa Rica: Area de Conservación Guanacaste, Alajuela Prov.: 1♂ NVG-18013H11, 10-SRNP-67995 Sector Rincon Rain Forest, Palomo, 96 m, 10.96187, -85.28045, eclosed on 04-Nov-2010; and 1♀ NVG-18013H10, 07-SRNP-65617 Brasilia, Piedrona, 340 m, 11.01618, -85.35902, eclosed on 13-Oct-2007.

Type locality. Panama: Panama Province, Madden Road Forest Preserve.

Etymology. The name formed from its sister species, *artemides*, made shorter for this more northern species. The name is a noun in apposition.

Distribution. Costa Rica and Panama.

Spioniades artemidoides Grishin, new species

<https://zoobank.org/85986CDE-04A2-42E3-BD64-178DD5DB5583>

(Fig. 2 part, 59–60, 271–273)

Definition and diagnosis. Phylogenetic analysis reveals that a specimen from Southern Brazil identified as *Spioniades artemides* (Stoll, 1782) (type locality in Suriname) is genetically differentiated from it (Fig. 2): e.g., their COI barcodes differ by 5.0% (33 bp), and therefore represent a new species. This new species keys to *S. artemides* (E.14.2) in Evans (1953) and differs from it and *S. artemis* **new species** by the following combination of characters: the irregular, wavy, and sharp border between discal brown and postdiscal white area on the hindwing, frequent expression of pale diffuse spot(s) towards inner margin and tornus of the ventral forewing (Fig. 59–60), less robust uncus in lateral view, broader in dorsal view, shallowly divided harpe with slightly concave distal margin in lateral view and protruding deeper inward in dorsal view, nearly straight with a broader knob-like process that protrudes less inward (Fig. 271–273). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly251.4.1:G89A, aly6370.13.3:C61T, aly15220.10.2:C66T, aly2012.51.1:T768G, aly336.2.3:A52T, aly4333.9.1:C60C (not T), aly1113.5.5:T45T (not A), aly1456.5.1:T1015T (not A), aly1456.5.1:T1044T (not C), aly1139.42.1:C66C (not T), and COI barcode: T70C, T91A, T178C, T202C, T226C, A379G.

Barcode sequence of the holotype. Sample NVG-19088B05, GenBank OR837648, 658 base pairs:

AACTTTATATTTTATTTTGGAAATTTGAGCAGGAATAGTAGGAACTTCCTTAAGTTTACTAATTCGAACCGAATTAGGAAATCCTGGAGCACTTATT
 GGAGATGATCAAATTTATAATACTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTATAATCGGAGGATTTGGAAAT
 GATTAATCCCATTAATGCTAGGGGCCCTGACATAGCATTCCCTCGAATAAATAATATAAGATTTTGATTATTACCCCATCTTTAATACTTTTGAT
 TTCTAGTAGTATTGTTGAAAATGGGGCAGGTACTGGTTGAACAGTTTTATCCCTCTTTTCAGCTAATATTGCACATCAAGGATCTTCGGTTGATT
 GCAATTTTTCTTTACATCTTGTGGAATTTCTCTATTTTAGGAGCTATTAATTTTATTTCTACAATTTAATATACGAATTAGAAATCTTTCAT
 TTGATCAAAATACCATTATTTGTTTGGAGCTGTGGAATTACTGCTTTACTTTTATTTATCTTTACCAGTATTAGCTGGTGTCTATTACTATACCTTT
 AACTGACCGAAATCTTAATACATCATTTTTTGTATCCTGCTGGAGGGGAGATCCAATTTTATATCAACATTTATTT

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 59–60, bears the following four rectangular labels, three white: [Brasil:Santa Catarina | Joinville: 10–200 m | 16 Feb. 1991 | Leg. H. Miers], [DNA sample ID: | NVG-19088B05 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01588918], and one red [HOLOTYPE ♂ | Spioniades | artemidoides Grishin].

Type locality. Brazil: Santa Catarina, Joinville.

Etymology. The name is formed from its sister species name and is a noun in apposition. From north to south, short to long, we get *artemis*, *artemides*, and *artemidoides*.

Distribution. Currently known only from Southern Brazil.

Spioniades anta Evans, 1953 is a species distinct from *Spioniades abbreviata* (Mabille, 1888)

Genomic sequencing of *Spioniades abbreviata anta* Evans, 1953 (type locality in Bolivia) reveals that it is not monophyletic with *Spioniades abbreviata* (Mabille, 1888) (type locality Panama: Chiriquí) in the Z chromosome tree (Fig. 2a) and the two taxa are strongly differentiated genetically, e.g., their COI barcodes differ by 5.6% (37 bp). In addition, their male genitalia and wing shapes differ (Evans 1953). Therefore, we propose that *Spioniades anta* Evans, 1953, **new status**, is a species-level taxon.

Myrinia orieca Grishin, new species

<https://zoobank.org/E284FB0F-A886-47D0-B039-E684CA8EF130>

(Fig. 2 part, 61–62, 274–276)

Definition and diagnosis. Phylogenetic analysis reveals that specimens from eastern Ecuador identified as *Myrinia binoculus* (Möschler, 1877) (type locality in Suriname, syntype sequenced as NVG-15033C11) are genetically differentiated from it in both nuclear and mitochondrial genomes (Fig. 2): e.g., their COI barcodes differ by 1.8% (12 bp), and therefore represent a new species. This new species keys to *M. binoculus* (E.24.1) in Evans (1953) and differs from it by more elongated eyespot on the dorsal forewing, wider dark-brown forewing margins, better defined and more contrasting from the ground color bands (discal, postdiscal, and submarginal) on the ventral hindwing, and a smaller dark ventral hindwing tornal spot (Fig. 61–62). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: *aly*2178.55.2:C48T, *aly*2178.55.2:C63T, *aly*1084.13.12:C93T, *aly*276558.43.4:A408G, *aly*4645.9.3:T103C, and COI barcode: A43G, A79G, T97C, A166G, A184G, A586G.

Barcode sequence of the holotype. Sample NVG-17105F03, GenBank OR837649, 658 base pairs:

```
TACTTTTACTTTTATTTTTGGAATTTGAGCAGGAATAGTAGGGACATCCTTAAGTTTATTAATTCGTACTGAATTAGGGAATCCAGGATCATTAAATC
GGAGATGATCAAATTTATAACTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATGCCAATTATAATGGAGGGTTGGAAAT
GACTTGTTCATTAAATATTAGGTGCCCCAGATATAGCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCATCATTAAATATTATTAAT
TTCAAGAAGAATTGTAGAAAATGGAGCAGGAACAGGATGAACCTTTACCTCCTTTATCTGCTAATATGCTCATCAAGGATCCTCAGTAGATTTA
GCTATTTTTCTTTACATTTAGCTGGAATTTTCATCAATTTTAGGAGCTATTAATTTTATTACAACAATTATTAATATACGTATTAATAATCTTTTCAT
TCGATCAAATACCTTTATTTGTATGAGCAGTAGGAATTACAGCTTTATTATTACTATTATCTTTACCTGTATTAGCAGGAGCAATTACTATACCTTT
AACGGATCGAAATTTAAATACATCATTTTTTTGATCCTGCAGGTGGGGGAGATCCTATTTTATATCAACACTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 61–62, bears the following four rectangular printed labels, three white: [ECUADOR: Orellana, | Tiputini Biodiversity Station, | Lower Río Tiputini, | 0 37'55" S, 76 08'39" W | 200 m, 10–15 Aug 2002 | J.P.W. Hall & M.A. Solis], [DNA sample ID: | NVG-17105F03 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 00894950], and one red [HOLOTYPE ♂ | *Myrinia orieca* Grishin]. **Paratype:** 1♂ NVG-14112H01 Ecuador: Napo, Yasuní National Park, 20-Sep–4-Oct-2003, C. Bordelon and E. Knudson, the Texas Lepidoptera Survey collection [MGCL].

Type locality. Ecuador: Orellana Province, Lower Río Tiputini, Tiputini Biodiversity Station, elevation 200 m, GPS –0.6319, –76.1442.

Etymology. This species comes from the *Ori*[ente (eastern region) in]*Ec*[u]a[*dor*]. The name is a Latinized feminine adjective.

Distribution. Currently known only from the Amazonian region in eastern Ecuador.

Myrinia aragua Grishin, new species

<https://zoobank.org/055C6BE9-3405-428D-9BD1-B20AFA4C3F5D>

(Fig. 2 part, 63–64, 277–278)

Definition and diagnosis. Inspection of the Z chromosome tree reveals that a specimen from Venezuela identified as *Myrinia laddeyi* (E. Bell, 1942) (type locality in Ecuador) is not monophyletic with it and instead is sister to *Myrinia binoculus* (Möschler, 1877) (type locality in Suriname) (Fig. 2a), thus representing a new species. Curiously, the mitochondrial DNA of this new species is much closer to *M. laddeyi* than to any other species (Fig. 2b): COI barcode of the holotype of *M. laddeyi* differs from the new species by 1% (7 bp), suggesting either introgression or hybrid origin of this species. The new species keys to *Myrinia binoculus* (E.24.1) in Evans (1953), which

includes *M. laddeyi* that Evans misidentified and *Myrinia raymundo* H. Freeman, 1979 (type locality in Mexico, Tabasco) described later and differs from them by the following combination of characters: paler, especially on dorsal hindwing, where the marginal pale band is wider; forewing eyespot rounder, not elongated; ventral hindwing without a dark spot at tornus. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly2012.66.4:G225A, aly1222.4.1:A99G, aly890.3.2:C130T, aly887.6.1:C142T, aly1838.60.9:G111A, aly2130.12.1:C162C (not A), aly2130.12.1:A179A (not C), aly2130.12.1:C183C (not T), aly85.3.11:C106C (not T), aly4645.9.9:C156C (not T), but COI barcode is not different from *M. laddeyi*.

Barcode sequence of the holotype. Sample NVG-18061H06, GenBank OR837650, 658 base pairs:

```
TACTTTATATTTTATTTTGGAAATTTGAGCAGGAATAGTTGGAACATCTTTAAGTTTATTAATCCGTACTGAATTAGGAAATCCAGGATCGTTAATT
GGAGATGATCAAATTTATAATACTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTATAAATGGAGGATTTGGAAAT
GACTTGTCCATTAATACTAGGTGCTCCAGATATAGCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCATCATTAACTATTAAT
TTCAAGAAGAATTTGAGAAAATGGAGCAGGAACAGGGTGAACCTGTTTACCTCCTTTATCTGCTAATATTGCCCATCAAGGATCTTCTGTAGATTTA
GCTATTTTTCTTTACATTTAGCTGGAATTTTCATCAATTTTAGGAGCTATTAATTTTATTACAACAATTTAATATACGTATTAATAACCTTTTCAT
TTGATCAAATACCTTTATTTGTATGAGCAGTAGGAATTACAGCTCTATTATTATTATTATCTTTACCTGTTTTAGCAGGAGCAATTACAATACCTTTT
AAGTATCGAAATTTAAATACATCATTTTTTTGATCCTGCAGGAGGAGGAGATCCTATTCTTTTATCAACATTTATTT
```

Type material. Holotype: ♀ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 63–64, bears the following four rectangular labels, three white: [VENEZUELA-ARAGUA | Rancho Grande 1100m | 28 May '85 | S. S. Nicolay], [DNA sample ID: | NVG-18061H06 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01466907], and one red [HOLOTYPE ♀ | Myrinia | aragua Grishin].

Type locality. Venezuela: Aragua, Rancho Grande, elevation 1100 m.

Etymology. The name is given for the type locality and is a noun in apposition.

Distribution. Currently known only from the holotype collected in Aragua, Venezuela.

Myrinia maculosa Grishin, new species

<https://zoobank.org/9BB52D48-C7A3-4940-97B0-FC88016521D3>

(Fig. 2 part, 65–66, 279–281)

Definition and diagnosis. Phylogenetic analysis reveals that a specimen from Guatemala identified as *Myrinia myris* (Mabille, 1898) (type locality in Brazil: Santa Catarina) is genetically differentiated from it (Fig. 2): e.g., their COI barcodes differ by 3.2% (21 bp), and therefore represents a new species. The new species keys to *M. myris* (E.24.2) in Evans (1953) and differs from it by more contrasting wing patterns: dark bands and spots stand out on paler ground color stronger than in *M. myris*, e.g., forewing subapical dark spots. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly528.33.1:T420A, aly707.3.1:G46A, aly315.8.2:G129C, aly536.208.9:A36G, aly4645.9.3:T87A, aly728.25.1:T72T (not A), aly1475.3.2:G1077G (not A), aly600.8.1:G81G (not A), aly1720.13.9:C206C (not A), aly1350.21.3:T54T (not C), and COI barcode: A208G, A238A, T287C, A298T, T601C.

Barcode sequence of the holotype. Sample NVG-18061H04, GenBank OR837651, 658 base pairs:

```
AACTTTATATTTTATTTTTCGGAATTTGAGCAGGAATAGTTGGAACATCTTTAAGTTTATTAATTCGTACTGAATTAGGTAATCCAGGATCATTAAAT
GGAGATGATCAAATTTATAATACTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTATAAATGGTGGATTTGGTAAT
GATTAGTACCTTTGATATAGGAGCTCCAGATATAGCTTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCATCTTTAATATTACTAAT
TTCAAGTAGAATTTGAGAAAATGGAGCAGGAACAGGATGAACTGTTTATCCTCCTTTATCAGCTAATATTGCTCATCAAGGATCTTCTGTAGATTTA
GCTATTTTTCTCTACATTTAGCAGGAATTTCTCAATTTTAGGAGCTATTAATTTTATTACAACAATTTAATATACGTATTAATAACTTATCAT
TTGATCAAATACCATTTATTTGTATGAGCAGTAGGAATTACAGCTTTATATTATTATTATTATCTTTACCTGTATTAGCAGGAGGATTTACTATACCTTT
AACAGATCGAAATTTAAACACATCTTTTTTTGATCCAGCTGGAGGAGGAGATCCTATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 65–66, bears the following four rectangular labels, three white: [fromLThiel | SSebastian | Retalhuleu | Guatemala], [DNA sample ID: | NVG-18061H04 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01466905], and one red [HOLOTYPE ♂ | Myrinia | maculosa Grishin].

Type locality. Guatemala: Retalhuleu department, San Sebastián.

Etymology. In Latin, *maculosa* means spotted, speckled, dappled, mottled, or variegated. It reflects a more contrasting and spottier wing pattern compared to its closest relatives. The name is an adjective.

Distribution. Currently known only from the holotype collected in Guatemala.

***Myrinia manchada* Grishin, new species**

<https://zoobank.org/F341D06C-4741-4C54-ABCE-A7BD83C5C264>

(Fig. 2 part, 67–68, 282–284)

Definition and diagnosis. Sequencing of the holotype of *Myrinia laddeyi* (E. Bell, 1942) (type locality in Ecuador) revealed that it is a species related to *Myrinia binoculus* (Möschler, 1877) (type locality in Suriname) and not the species Evans (1953) identified as *M. laddeyi* (Fig. 2). Therefore, the species that Evans misidentified as *M. laddeyi* does not have an available name and is new. In USNM, we found a specimen that keys to E.24.4 in Evans (1953) and is distinguished from its relatives, including the true *M. laddeyi*, by larger size (forewing typically longer than 21 mm), more segments in nudum (more than 25 segments), the lack of eyespot on the ventral forewing, large dark tornal spot on the ventral hindwing, short and rounded harpe of the right valva, style of the left valva longer than harpe. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly798.33.50:A117G, aly2149.2.8:G45A, aly38.5.1:T141C, aly767.7.2:T78C, aly767.7.2:T468A, aly651.4.5:T106T (not C), aly536.173.2:C78C (not T), aly17.12.4:C112C (not T), aly17.12.4:A336A (not G), aly1022.2.1:G96G (not A), and COI barcode: T82C, 277C, T364A, T352C, T386C.

Barcode sequence of the holotype. Sample 11-BOA-13383A10, GenBank OR837652, 658 base pairs:

```
AACTTTATATTTTATTTTGGAAATTTGAGCAGGAATAGTTGGAACATCTTTAAGTTTATTAATTCGAACGAATTAGGTAACCCAGGATCATTAAAT
GGAGATGATCAAATTTATAATACTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTATAATTTGGAGGATTTGGAAAT
GACTTGTACCATTAATATTAGGAGCCCCAGATATAGCTTTCCCCCGAATAAATAAATAAGATTTTGATTATTACCCCTCCTTAATATTATTAAT
CTCCAGAAGAATTGTAGAAAATGGAGCAGGAACCTGGATGAACGTTTATCCCCCTTTATCCGCTAATATTGCACACCAAGGATCTTCAGTAGACCTA
GCTATTTTTTCTCTACATTTAGCTGGAATTTTCATCTATTTTAGGAGCTATCAATTTTATTACAACAATTTAATAATACGTATTAATAATCTTTCAT
TTGATCAAATACCATTATTCGTTTGGAGCTGTAGGAATCACAGCTTTATTATTATTATTATCTTTACCTGTATTAGCAGGTGCTATTACTATACTTCT
AACAGATCGAAATTTAAATACATCTTTTTTTTGTATCCTGCTGGAGGAGGAGATCCTATTCTTTTATCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 67–68, bears the following five rectangular labels, four white: [GUYANA: Region 8 | Potaro River nr. Tukeit | 250' – 1000' | 18-23 Mar 1999 | leg. S. Fratello], [DNA sample ID: | 11-BOA-13383A10 | c/o Nick V. Grishin], [DNA sample ID: | NVG-22034H05 | c/o Nick V. Grishin], [{QR Code} | USNM ENT 00232398], and one red [HOLOTYPE ♂ | Myrinia | manchada Grishin]. **Paratype:** 1♂: NVG-23026F10, EL83681 French Guiana, Saint-Laurent-du-Maroni, 1905, E. Le Moullet leg. [MNHP].

Type locality. Guyana: Potaro-Siparuni Region, Potaro River nr. Tukeit.

Etymology. In Spanish, *manchada* means stained, spotted, spotty, or smudgy. The name is given for the large tornal spot on the ventral hindwing and is a noun in apposition.

Distribution. The Guianas.

Tribe Carcharodini Verity, 1940

***Polyctor (Fenops) lamperus* Grishin, new species**

<https://zoobank.org/CF3D0B2D-8ED2-4D3F-AD93-03621C2AFC9B>

(Fig. 3 part, 69–70, 285–287)

Definition and diagnosis. This new species is sister to *Polyctor enops* (Godman and Salvin, 1894) (type locality in Mexico: Veracruz and Honduras) and differs from it by 2.3% (15 bp) in COI barcode and is recognizable phenotypically by paler wing ground color, larger forewing hyaline spots and mostly white ventral hindwing (marginally brown towards tornus), in particular by costa and apex, which are brown in *P. enops* and *Polyctor fera* (Weeks, 1901) (distal half of hindwing can be white). This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly85.29.3:A228G, aly214.4.1:C375T, aly3268.8.1:T900C, aly72.21.1:G933A, aly1022.3.1:G150A, aly315.8.6:G63G

(not A), aly570.6.1:G57G (not A), aly1841.5.20:T96T (not C), aly1656.40.1:C575C (not A), aly1656.40.1:A1038A (not G), and COI barcode: T50C, A100T, G353A, 445C, T529C.

Barcode sequence of the holotype. Sample NVG-19088F12, GenBank OR837653, 658 base pairs:

```
AACTTTATATTTTATTTTGGTATTTGATCAGGAATAGTAGGAACATCACTAAGTTTAAATTTATTCGATCTGAATTAGGTATACCTGGTTCATTAATT
GGTAATGATCAAATTTATAATAACAATTTGTAAGTCTGCTGCTTTTATTATAAATTTCTTCATAGTTATAACCCATTATAAATGGAGGATTCGGAAATT
GATTAGTACCCCTTATATTAGGAGCTCCTGATATAGCTTTTCCCCGAATAAATAAATAAGATTTTGATTATTACCTCCATCTTTAACTTTATTAAT
TTCAAGAAGTATTTGTTGAAAATGGTGTGGAACAGGATGAACAGTTTATCCTCCTTTATCTACTAATATGCTCATCAAGGTTCTTCTGTAGATTTA
GCAATTTTCTCTTACATTTAGCAGGTATTTCTTCAATTTTAGGTGCTATTAACCTCATTACAACATTTATTAATATACGAATTAATAATATATCTT
TTGATCAAATACCTCTTTTATTGAGCTGTTGGAATTACAGCCTTACTTTTATTATTATCTTTACCAGTTTTCAGGAGCTATTACAATATTTATT
AACTGATCGTAATTTAAATACATCTTTTGGATCCTTCAGGAGGAGGAGATCTTATCTATATCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 69–70, bears the following four rectangular labels, three white: [PANAMA: Darien | Cana 400m | 9.VII.1981 | Leg. G. B. Small | on mud], [DNA sample ID: | NVG-19088F12 | c/o Nick V. Grishin], [USNMNT | {QR Code} | 01588973], and one red [HOLOTYPE ♂ | Polycrator | lamperus Grishin].

Type locality. Panama: Darien Province, Cana, elevation 400 m.

Etymology. In Greek, λαμπερός (lamperós) means shiny bright. The name reflects the species' bright colors compared to its relatives and is a noun in apposition.

Distribution. Currently known only from the holotype collected in eastern Panama.

Lectotype designation for *Pellicia bromias* Godman and Salvin, 1894

Pellicia bromias Godman and Salvin, 1894 (type locality in Mexico, Guatemala, Costa Rica, Panama), currently in the genus *Nisoniades* Hübner, [1819] (type species *Papilio bromius* Stoll, 1787, which is a junior subjective synonym of *Nisoniades mimas* (Cramer, 1775)) was treated as a valid species, sister to *Nisoniades rubescens* (Möschler, 1877) (type locality in Suriname) by Zhang et al. (2020). To define *Nisoniades bromias* objectively due to likely polytypic type series, N.V.G. hereby designates a male syntype in the Natural History Museum, London, UK that according to its label was illustrated by Godman and Salvin (1893-1899) and bears the following seven rectangular (except the first one, which is round and with a red circle on the upper side) white labels: (Type) and on the other side (H | 707), [Atoyac, | Vera Cruz. | May. H.H.S.], [♂], [Sp. figured.], [B.C.A.Lep.Rhop. | Pellicia | bromias, | Mab.], [Godman-Salvin | Coll. 1912.—23.], and [{QR Code} | BMNH(E) 1669504], as the **lectotype** of *Pellicia bromias* Godman and Salvin, 1894. The type locality of *Nisoniades bromias* becomes Mexico: Veracruz, Atoyac.

Nisoniades (Nisoniades) lutum Grishin, new species

<https://zoobank.org/8CA203F6-1E1A-4B01-9D9E-FC3A9F5F0AA4>

(Fig. 3 part, 71–72, 288–290)

Definition and diagnosis. Genomic trees reveal that specimens from western Mexico identified as *Nisoniades bromias* Godman and Salvin, 1894 (type locality in Mexico: Veracruz) form a distinct clade that is not even monophyletic with *N. bromias* in the mitochondrial genome tree (albeit with weaker statistical support of 86%) (Fig. 3). Due to genetic differentiation, amplified by the genetic similarity within *N. bromias* and its lower evolutionary rate (comparatively shorter branches in Fig. 3), these western populations represent a new species. In the COI barcode, the new species differs from *N. bromias* and *Nisoniades rubescens* (Möschler, 1877) by 1.1% (7 bp) and 2.0% (13 bp), respectively. The new species keys to *N. rubescens* (E.19.5) in Evans (1953) and differs from its relatives by paler-brown wings with more contrasty and restricted dark-brown areas that form bands rather than ground color (Fig. 71–72), broader ampulla of the right valva, and less sharply curved inward ampulla of the left valva (Fig. 288–290). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly60.18.10:G18T, aly60.18.10:G78A, aly2165.8.15:G39C, aly2303.1.7:A31T, aly1222.34.1:G57A, and COI barcode: T82C, T292C, T328C, T619C, A628G.

Barcode sequence of the holotype. Sample NVG-4967, GenBank OR837654, 658 base pairs:

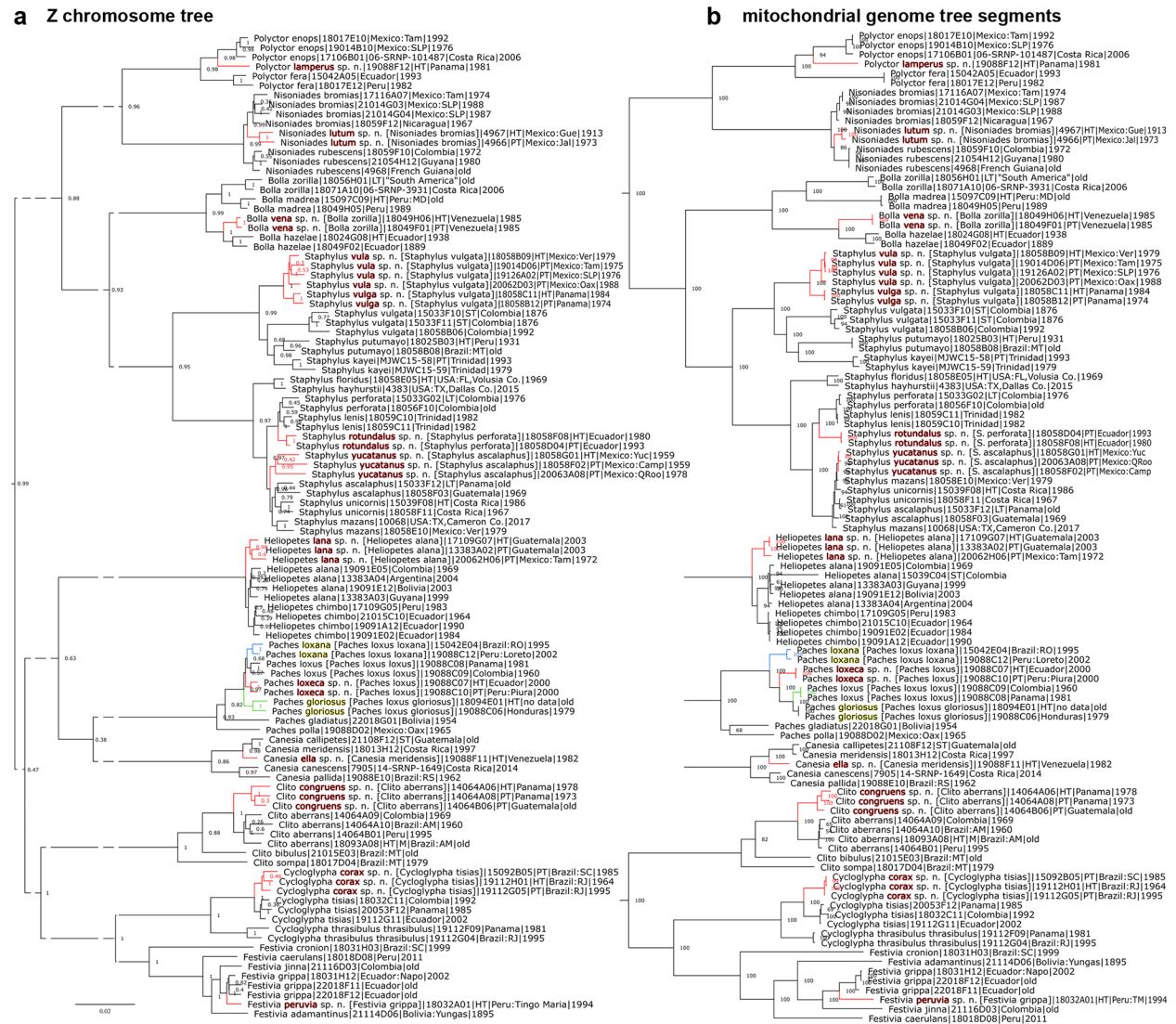


Figure 3. Phylogenetic trees of remaining Pyrginae (excluding Achlyodini) inferred from protein-coding regions in **a)** the Z chromosome and **b)** the mitochondrial genome (in segments). See Fig. 1 legend for other notations.

AACCTTTATATTTTATTTTGGTATTTGATCCGGAATAGTAGGAACATCATTAAGCTTACTAATTCGATCTGAATTAGGTAACCCAGGATTTTTAATT
 GGAGATGATCAAATTTATAACTATTGTTACAGCTCATGCCTTTATTAATTTCTTTATAGTAAATACCATTATAATTCGGAGATTCGGAATTT
 GATTAGTACCCCTTATATAGGAGCTCTGATATAGCTTTTCCCCGAATAAATAACATAAGATTTTGATTACTCTCCTCTCTACTTACTTATTAAT
 CTCAGTAGTATTTGAGAAAATGGAGCTGGAACAGGCTGAACGTGTATCCACCTTTATCATCTAATATTGCTCACCAAGGCTCATCTGTGATTTA
 GCATTTTTTCATTACATTTAGCTGGAAATTCATCTATTTAGGTCATTAATTTTACTACTATTAATCAATACGAATTAATAATTTATCAC
 TTGATCAAATACCTTTATTTGTTGAGCCGTAGGAATTACAGATTAATTTATTTATTTACTTACCAGTTTTAGCTGGAGCTATCACAAATATTT
 AACTGATCGAAATTTAAATACATCTTTTTTTGATCCCGCAGGAGGGGGAGATCCAATTTTATATCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 71–72, bears the following seven rectangular labels, six white: [Sierra de | GuerreroMex], [Jan. '13], [RMuller | Collector], [3682], [DNA sample ID: | NVG-4967 | c/o Nick V. Grishin], [genitalia: | NVG151101-18 | Nick V. Grishin], and one red [HOLOTYPE ♂ | Nisoniades | lutum Grishin]. **Paratype:** 1♂: NVG-4966 Mexico: Jalisco, Mismaloya area, Puerto Vallarta, 15-31-Oct-1973, P. M. Aubry leg., genitalia NVG151101-17 [USNM].

Type locality. Mexico: Guerrero.

Etymology. In Greek, βρωμιάς (bromias) means dirt or dirty, and *lutum* is dirt in Latin, used here as the name for the sister species of *N. bromias*. The name is a noun in apposition.

Distribution. Western Mexico, currently confirmed from Jalisco and Guerrero.

***Bolla (Stolla) vena* Grishin, new species**

<https://zoobank.org/F6F25879-BE84-46BB-9450-0F9A35F55461>

(Fig. 3 part, 73–74, 291–292)

Definition and diagnosis. In addition to the three species in the *Bolla zorilla* (Plötz, 1886) (type locality in Panama) complex, genomic trees reveal a fourth (and new) species from Venezuela (Fig. 3): it differs from its sister *Bolla hazelae* (Hayward, 1940) (type locality Ecuador: Mapoto) by 4.0% (26 bp). This new species keys to *B. zorilla* (E.31.21) in Evans (1953) and differs from its relatives by the following combination of characters: hindwing with a more scalloped outer margin, convex in the middle and noticeably concave towards tornus, a hyaline subapical spot in cell R_5-M_1 is smaller than the spot in cell R_3-R_4 (spots subequal in other species) (Fig. 73–74), ampulla with a thin style directed dorsad, harpe broader in lateral view, less extended distad, with a more prominent expansion directed dorsad, dorsal margin between the dorsal-most points of harpe and costa deeper concave (with a style in the middle) (Fig. 291–292). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1281.15.8:C123T, aly813.2.4:G44C, aly727.20.3:C69T, aly1329.6.5:G105A, aly1329.6.5:G108T, and COI barcode: A202T, C235T, T334G, T535C, A622G.

Barcode sequence of the holotype. Sample NVG-18049H06, GenBank OR837655, 658 base pairs:

```
AACTTTATATTTTATTTTGGTATTTGATCTGGTATAGTAGGAACCTTCTTAAAGAATACTTATTCGTTTCAGAATTAGGAACCCCTGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAAACAGCTCATGCTTTCATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTGGAAATT
GATTAGTTCATTAAATATTAGGAGCTCCTGATATAGCTTTTCCCTCGAATAAATAAATAAGATTTTGACTTTTACCCCTTCTTTAATACTTTTAAAT
TTCTAGAAGTGTAGTAGAAAATGGAGCAGGTACAGGATGAACGGTTTACCCCTTTCAGCTAATATGCTCATCAAGGATCATCTGTAGATTTA
GCTATTTTTCCTTCATTTAGCAGGTATTTCTTCAATTTAGGGCAATTAATTTTATCACAACCTATTATTAATATACGAATTAACAACCTATCAT
TTGATCAAATACCTTTATTTGTATGAGCAGTTGGTATCACCCTTTACTCTTATTATTATCTTTACCTGTATTAGCAGGAGCTATTACAATACTTCT
AACAGATCGAAATTTAAATACTTCATTTCTTGACCCTCGGGAGGAGGATCCTATTTTATATCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 73–74, bears the following six rectangular labels, five white: [VENEZUELA-ARAGUA | Rancho Grande 1100m | 18 May '85 | S. S. Nicolay], [*Bolla* ♂ | *zorilla* | Det. | S.S. Nicolay], [*Bolla* | *zorilla* ♂ | (Ploetz) | det. H. A. Freeman], [DNA sample ID: | NVG-18049H06 | c/o Nick V. Grishin], [USNMNT | {QR Code} | 01466668], and one red [HOLOTYPE ♂ | *Bolla vena* | Grishin]. **Paratype:** 1♀ NVG-18049F01, USNMNT_01466639 the same data as the holotype, but collected on 7-Jun-1985.

Type locality. Venezuela: Aragua, Rancho Grande, elevation 1100 m.

Etymology. The name is given for *Ven*[ezuel]*a* and is a noun in apposition.

Distribution. Venezuela.

***Staphylus (Vulga) vula* Grishin, new species**

<https://zoobank.org/1E5D2A3B-D751-4144-A814-9F916BD25F36>

(Fig. 3 part, 75–76, 293–294)

Definition and diagnosis. Phylogenetic analysis that included syntypes of *Staphylus vulgata* (Möschler, 1879) (type locality in Colombia) reveals that Mexican specimens identified as this species are strongly differentiated genetically from and are not even monophyletic with it (Fig. 3), e.g., their COI barcodes differ by 5.9% (39 bp), and therefore represent a new species. This new species keys to *S. vulgata* (E.32.6(a)) in Evans (1953) and differs from its relatives by the following combination of characters: costa of valva less convex, valva narrower in lateral view, expansion of ampulla directed distad and reaches about the middle of harpe, its terminal spines shorter, harpe semi-triangular, distally rounded, with slightly concave dorsoposterior margin (Fig. 293–294). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1146.51.1:T1173C, aly536.133.3:T30C, aly1244.6.1:C819T, aly2811.1.8:T52C, aly2811.1.8:C53A, and COI barcode: T50C, T118C, T205C, T463C, T479C.

Barcode sequence of the holotype. Sample NVG-18058B09, GenBank OR837656, 658 base pairs:

AACTTTATATTTTATTTTGGTATTTGAGCAGGAATAGTAGGAACTTCTTAAGTATTCTTATTCGATCAGAATTAGGAACCCCTGGATCTTTAATT
 GGAGATGATCAAATTTATAACACTATTGTAACCTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATGGAGGATTTGGAAATT
 GACTTGTACCCCTTATATTAGGAGCTCCTGATATAGCTTTTCCCTCGAATAAATAATATAAGTTTTTTGATTATTACCCCATCTTAATACTTCTAAT
 TTCAAGTAGCATTGTAGAAAATGGAGCAGGAAGTGGATGAACCTGTATATCCCCCACTTTCAGCCAATATTGCCATCAAGGTTTCATCTGTAGATTTA
 GCTATTTTTTCCCTTCATTTAGCTGGAATTTCTCCATTTTAGGAGCAATTAACCTTCATCACAACCTATTATTAACATACGAATTAATAATCTATCAT
 TTGATCAAATACCTTTATTTGTATGAGCTGTAGGAATCACAGCATTACTTTTACTCCTATCTTTACCAGTATTAGCTGGAGCTATTACTATACTTTT
 AACTGATCGAAATCTTAATACATCATTTTTTGGATCCCGCTGGAGGAGGTGATCCTATTTTATATCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 75–76, bears the following five rectangular labels, four white: [7 mi N Santa | Comapan, Ver., | Mex. V-22-1979 | J.R.Powers, Collr.], [Staphylus | vulgata ♂ | (Moeschler) | det. H. A. Freeman], [DNA sample ID: | NVG-18058B09 | c/o Nick V. Grishin], [USNMENT | {QR Code} | 01466683], and one red [HOLOTYPE ♂ | Staphylus | vula Grishin]. **Paratypes:** 7♂♂ from Mexico, Roy O. Kendall and C. A. Kendall leg., at TAMU, unless stated otherwise: 1♂ NVG-20062D03 Oaxaca, Pluma Hidalgo, 18-Apr-1988, J. Kemner leg., genitalia [TMMC]; 1♂ NVG-19014D06 Tamaulipas, Ciudad Mante, Los Arcos Ct., larval foodplant *Achyranthes aspera* L., 11-Jan-1975; 2♂♂ Tamaulipas, Rancho Pico de Oro, vic. Of Los Kikos: NVG-19126A03 21-Dec-1972 and 19126A05 6-Feb-1974; 1♂ NVG-19126A04 Tamaulipas, El Nacimiento, Rio Mante, 23-Jan-1974; 2♂♂ San Luis Potosi, El Naranjo: NVG-19014D03 1-Mar-1976 and NVG-19126A02 13-Feb-1976.

Type locality. Mexico: Veracruz, 7 mi north of Santa Comapan.

Etymology. The name is formed from the species epithet of *S. vulgata* (in Latin, *vulgate* means common). By significantly shortening the name, it refers to this most northern species of the *S. vulgata* complex. The name is a noun in apposition.

Distribution. Widely distributed in Mexico: recorded from Tamaulipas, San Luis Potosi, Veracruz and Oaxaca.

Comment. Reared on *Achyranthes aspera* L. by Roy O. Kendall and C. A. Kendall.

***Staphylus (Vulga) vulga* Grishin, new species**

<https://zoobank.org/1ECE61F4-A057-4903-8706-D6CD468A8B87>

(Fig. 3 part, 77–78, 295–297)

Definition and diagnosis. Phylogenetic analysis that included syntypes of *Staphylus vulgata* (Möschler, 1879) (type locality in Colombia) reveals that Panamanian specimens identified as this species are strongly differentiated genetically from and are not even monophyletic with it (Fig. 3), e.g., their COI barcodes differ by 5.9% (39 bp). These specimens are sister to *Staphylus vula* **new species** but differ genetically from it (e.g., COI barcodes differ by 1.5%, 10 bp), and, therefore, represent a new species. This new species keys to *S. vulgata* (E.32.6(a)) in Evans (1953) and differs from its relatives by the following combination of characters: costa of valva strongly convex, nearly angled at the dorsal-most point, valva broader in lateral view, expansion of ampulla directed distad and slightly ventrad towards its end, and reaches about the middle of harpe, its terminal spines longer, harpe semi-triangular, distally rounded, with concave near its base dorsoposterior margin (Fig. 295–297). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly361.16.7:C229T, aly887.42.4:A63G, aly116.34.5:G392A, aly727.17.5:G94T, aly728.49.1:T1077C, and COI barcode: A40G, T50T, 85A, A202A, 400T.

Barcode sequence of the holotype. Sample NVG-18058C11, GenBank OR837657, 658 base pairs:

AACTTTATATTTTATTTTGGTATTTGAGCAGGAATAGTGGAACTTCTTTAAGTATTCTTATTCGATCAGAATTAGGAACCCAGGATCTTTAATT
 GGAGATGATCAAATTTATAAATACTATTGTAACCTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATGGAGGATTTGGAAATT
 GACTTGTACCTCTTATATTAGGAGCTCCTGATATAGCTTTTCCCTCGAATAAATAATATAAGTTTTTTGATTATTACCCCATCTTAATACTTTTAAAT
 TTCAAGTAGCATTGTAGAAAATGGAGCAGGAAGTGGATGAACCTGTATATCCCCCACTTTCAGCCAATATTGCCATCAAGGTTTCATCTGTAGATTTA
 GCTATTTTTTCCCTTCATTTAGCTGGAATTTCTCCATTTTAGGAGCAATTAACCTTCATCACAACCTATTATTAATACGAATTAATAATTTATCAT
 TTGATCAAATACCTTTATTTGTATGAGCTGTAGGAATCACAGCATTACTTTTACTCCTATCTTTACCAGTATTAGCTGGAGCTATTACTATACTTTT
 AACTGATCGAAATCTTAATACATCATTTTTTGGATCCCGCTGGAGGAGGTGATCCTATTTTATATCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 77–78, bears the following five rectangular labels, four white:

[PANAMA:500m. | Darien, Cana | 3 Jan. 1984 | Gordon Small], [*Staphylus* ♂ | *caribbea* (Williams | and Bell) | det. H. A. Freeman], [DNA sample ID: | NVG-18058C11 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01466697], and one red [HOLOTYPE ♂ | *Staphylus* | *vulga* Grishin]. **Paratype:** 1♂ NVG-18058B12, USNMMENT_01466686 Panama: Panama, Bayano, “8°[likely 9°]03’N 78°40’W”, 26-Oct-1974, G. B. Small leg., genitalia vial H-2198 by H. A. Freeman.

Type locality. Panama: Darien Province, Cana, elevation 500 m.

Etymology. The name is formed from the species epithet of *S. vulgata* (in Latin, *vulgate* means common). By slightly shortening the name, it refers to this species in the middle of the range of the *S. vulgata* complex. The name is a noun in apposition.

Distribution. Recorded from eastern Panama.

Lectotype designation for *Nisoniades perforata* Möschler, 1879

Genomic sequencing of *Nisoniades perforata* Möschler, 1879 (type locality in Colombia and Panama) syntypes reveals that the type series is polytypic. To define this species objectively, N.V.G. hereby designates a male syntype in the Museum für Naturkunde, Berlin, Germany, that bears the following ten rectangular labels (the first three are red, green, and purple, respectively; others are white): [Lectotypus], [Columbia | *Stdr.* 76.], [Origin], [Type. | *Verhdlg. zool. | bot. Gesellschaft. | 1878. p. 223. | no⁼ 32.], [Coll. Möschl.], [Hayhursti | *Edw. Perforata Msch.*], [Hayhursti | *Edw.*], [GEN.PEP. | MIELKE | 1996], [{OR Code} <http://coll.mfn-berlin.de/u/80a649>], [DNA sample ID: | NVG-15033G02 | c/o Nick V. Grishin], as the **lectotype** of *Nisoniades perforata* Möschler, 1879, currently in the genus *Staphylus* Godman and Salvin, 1896. The type locality of *Staphylus perforata* becomes Colombia.*

Staphylus (Staphylus) rotundalus Grishin, new species

<https://zoobank.org/0568D95D-9F75-4538-823C-07E64A7D7CD0>

(Fig. 3 part, 79–80, 298–299)

Definition and diagnosis. Phylogenetic analysis reveals that specimens from Ecuador identified as *Staphylus perforata* (Möschler, 1879) (type locality in Colombia, lectotype sequenced as NVG-15033G02) are not monophyletic with it and instead are sister to both *S. perforata* and *Staphylus lenis* Steinhauser, 1989 (type locality in Trinidad) and genetically differentiated from them (Fig. 3), e.g., their COI barcodes differ by 1% (7 bp). Provided low mitochondrial DNA differentiation in these species (COI barcodes of *S. perforata* and *S. lenis* differ by only 1 base pair), the Ecuadorian specimens represent a new species. This new species keys to “*Staphylus ascaphalus*” [sic!] (E.32.20(d)) in Evans (1953) and differs from its relatives by the following combination of characters: rounder wings, most visible as more convex forewing outer margin, prominent forewing hyaline spots, especially the one in cell CuA₁-CuA₂, valva elongated with broad dorsally directed expansion between valva and harpe, rounded along its dorsal margin and armed with two large socketed bristles at the distal margin, and one medium bristle at its base, plus many smaller spines on harpe (Fig. 298–299). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1916.7.3:A81T, aly2928.14.8:T107C, aly103.40.5:C95A, aly9349.5.1:A206C, aly1249.14.3:C204A, and COI barcode: A34G, A217G, T298A, A511A, T601C.

Barcode sequence of the holotype. Sample NVG-18058F08, GenBank OR837658, 658 base pairs:

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AACTTTATATTTTATTTTGGTATTTGATCTGGGATAGTAGGAACCTCTTAAAGTATTTCTTATTCGTTCTGAATTAGGAACCTCTGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTATAATTGGAGGTTTTGGAAATT
GACTTGTTCCTCTTATATTAGGGGCCCCGTGATATAGCTTTCCCTCGAATAAATAAATAAAGATTTTGATTATTACCCCATCTTTAATACTTTTAAT
TTCAAGAAGAATCGTAGAAAATGGAGCAGGTACTGGATGAACAGTTTATCCCCCTTTTCAGCTAACATTGCCATCAAGGTTCTTCTGTAGATTTA
GCTATTTTCTTTACATTTAGCAGGTATTTCTCTATTTTAGGAGCAATTAATTTATTACAACATTTATCAATATACGAATTAATAATTTATCCT
TTGATCAAATACCTTTATTTGTTGAGCAGTTGGAATTACAGCATTATTATTACTTTTATCTTTACCAGTATTAGCAGGTGCTATTACTATACTTTT
AACAGATCGAAAATCTTAACACATCATTTTTTGGATCCTGCTGGTGGAGGAGATCTATTTTATATCAACATTTATTC
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 79–80, bears the following six rectangular labels, five white: [Rio Jondachi Napo | Ecuador 1000m | 8 July ’80 | S. S. Nicolay], [*Staphylus* | m. ♂ | *ascalaphus* | Det. Staud. |

S.S. Nicolay], [*Staphylus* | *perforatus* ♂ | (Moeschler) | det. H.A. Freeman], [DNA sample ID: | NVG-18058F08 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01466730], and one red [HOLOTYPE ♂ | *Staphylus* | *rotundulus* Grishin]. **Paratype:** 1♂ NVG-18058D04, USNMMENT_01466702 1 km E of Pto. Napo, 490 m, GPS –1.04, –77.7867, 10-Oct-1993, S. S. Nicolay leg. [USNM].

Type locality. Ecuador: Napo Province, Río Jondachi.

Etymology. In Latin, *rotund* means round, and *ala* means wings. The name is given to describe the rounder than usual wing shape and is a noun in apposition.

Distribution. Currently known from Ecuador.

Lectotype designation for *Helias ascalaphus* Staudinger, 1876

Helias ascalaphus Staudinger, 1876, the type species of a valid genus *Staphylus* Godman and Salvin, 1896, was described from several specimens from two localities in Panama. To define this species objectively with a single specimen, N.V.G. hereby designates a male syntype in the Museum für Naturkunde, Berlin, Germany, that bears the following eight rectangular labels (the first two are red and purple, respectively, others are white): [Lectotypus], [Origin], [Panama | Ribbe], [ascalaphus], [Ascalaphus | Stdgr.], [GEN.PEP., | MIELKE | 1996], [{OR Code} http://coll.mfn-berlin.de/u/ | 908619], [DNA sample ID: | NVG-15033F12 | c/o Nick V. Grishin], as the **lectotype** of *Helias ascalaphus* Staudinger, 1876. Because some of *H. ascalaphus* paralectotypes are labeled “Chiriqui” in a similar style as “Panama”, we suggest that the locality label “Panama” is more detailed than a country and refers to central Panama around Panama City. Therefore, the type locality of *Staphylus ascalaphus* is in central Panama.

Staphylus (Staphylus) yucatanus Grishin, new species

<https://zoobank.org/E2DA1C62-273A-4640-8B7D-FE16B5FBE315>

(Fig. 3 part, 81–82, 300–301)

Definition and diagnosis. Phylogenetic analysis reveals that specimens from the Yucatan peninsula in Mexico identified as *Staphylus ascalaphus* (Staudinger, 1876) (type locality in Panama: Panama, lectotype sequenced as NVG-15033F12) or *Staphylus lenis* Steinhauser, 1989 (type locality in Trinidad) are not monophyletic with either *S. ascalaphus* or *S. lenis* and instead form a separate clade that is sister to the clade of three species: *S. ascalaphus*, *Staphylus unicornis* Steinhauser and Austin, 1993 (type locality in Costa Rica, holotype sequenced as NVG-15039F08), and *Staphylus mazans* (Reakirt, [1867]) (type locality in Mexico: Veracruz) and is genetically differentiated from them (Fig. 3). Therefore, the Yucatecan specimens represent a new species. The four species (the new one, *S. ascalaphus*, *S. unicornis* and *S. mazans*) are closely related to each other and possess nearly identical DNA barcodes (0–5 bp difference) but are considered distinct due to differences in genitalia (Steinhauser and Austin 1993). This new species keys to “*Staphylus ascalaphus*” [sic!] (E.32.20(d)) in Evans (1953) and differs from it and other relatives by the following combination of characters: valva without prominent expansion directed dorsad between valva and harpe, but with a small (shorter than bristles), plate-like triangular, tooth-shaped lobe armed with three socketed bristles at its base, harpe more elongated than in relatives, terminally rounded, valva near the base of harpe and harpe towards dorsal margin armed on the outer surface with two to three dozen of long (length of harpe), medium-sized (~½ of long), and short (~¼ of long) socketed bristles (Fig. 300–301). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly419.1.7:G960A, aly1222.1.15:G494A, aly276558.8.2:C64T, aly1651.33.11:T222A, aly2555.6.3:G64C, and COI barcode: T67C, A160G, C238C.

Barcode sequence of the holotype. Sample NVG-18058G01, GenBank OR837659, 658 base pairs:

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AACTTTATATTTTATCTTTGGTATTTGATCTGGAATAGTAGGAACCTCTTAAAGTATTTCTATTCGCTCTGAATTAGGAACCTCTGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATGGTTATACCTATTATAATTGGAGGTTTTGGAAATT
GACTTGTTCCTCTTATATTAGGAGCCCCGTATATAGCTTTTCCCCGAATAAATAAATAAGATTTTGATTATTACCCCATCTTTAATACTTTTAAAT
TTCAAGTAGAATCGTAGAAAATGGAGCAGGTAAGTGGATGAACAGTTTATCCCCCTTTTCAGCTAACATTGCCCATCAAGGTTCTTCTGTAGATTTA
GCTATTTTCTTTACATTTAGCAGGTAATTTCTCTATTTTAGGAGCAATTAATTTTATTACAACCTATTATCAATATACGAATTAATAAATTTATCT
```

TTGATCAAATACCCTTATTTGTTTGGAGCAGTTGGAATTACAGCATTATTATTACTTTTATCTTTACCAGTATTAGCAGGTGCTATTACTATACTTTT
AACAGATCGAAATCTTAATACATCATTTTTTTGATCCTGCTGGTGGAGGAGATCCTATTTTATATCAACATTTTATTC

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 81–82, bears the following seven rectangular labels, six white: [Near Xcan, Quin- | tana Roo – Yuca- | tan border, | MEXICO | May 19-23, 1959 | T.C. Emmel], [♂ genitalia | slide/vial # | H169 | Prep. S.S. Nicolay], [Staphylus ♂ | m.ascalaphus | Det. Stgr. | S. S. Nicolay], [Staphylus | lenis ♂ | Steinhauser | det. H.A. Freeman], [DNA sample ID: | NVG-18058G01 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01466735], and one red [HOLOTYPE ♂ | Staphylus | yucatanus Grishin]. **Paratypes:** 2♂♂ from Mexico: NVG-18058F02, USNMMENT_01466724 Campeche, 40 km E of Escarcega, 3–4-May-1959, T. C. Emmel leg. [USNM]; and NVG-20063A08 Quintana Roo, Nuevo X-Can 25-Nov-1978 ECW leg., genitalia H-1271 H. A. Freeman (Fig. 300–301) [CSUC].

Type locality. Mexico: Quintana Roo–Yucatan border, near X-Can.

Etymology. The name is for the distribution in the Yucatan peninsula and is a noun in apposition.

Distribution. Currently known only from the Yucatan peninsula in Mexico.

Tribe Pyrgini Burmeister, 1878

Heliopetes (Heliopetes) lana Grishin, new species

<https://zoobank.org/2E6992E1-9CAE-4FF2-AD84-B73CB2C57F00>

(Fig. 3 part, 83–84, 302–303)

Definition and diagnosis. Phylogenetic analysis reveals that specimens from North America identified as *Heliopetes alana* (Reakirt, 1868) (type locality in Colombia, syntype sequenced as NVG-15039C04, sequence completeness insufficient to add it to the Z chromosome tree) are not monophyletic with it and instead are sister to both *H. alana* and *Heliopetes chimbo* Evans, 1953 (type locality in Ecuador), exhibiting notable genetic differentiation (Fig. 3): e.g., COI barcodes of a specimen from Guatemala and Colombia differ by 2% (14 bp). All available names in synonymy with *H. alana* have type localities in South America. Therefore, the North American populations are a new species. This new species keys to *H. alana* (G.2.12) in Evans (1953) and differs from its relatives by the following combination of characters: typically whiter (i.e., less yellow), especially on ventral hindwing (Fig. 84, but due to extensive variation hardly identifiable by facies), rounder in dorsal view anterior margin of tegumen, more extended harpe and, correspondingly, longer expansion of ampulla (Fig. 302–303). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1079.16.3:T70C, aly173.27.12:C85T, aly173.27.12:A144G, aly276665.11.2:T224G, aly276665.11.2:A302T, and COI barcode: A229G, C235T, A289A, T397C, A477G, T557C.

Barcode sequence of the holotype. Sample NVG-17109G07, GenBank OR837660, 658 base pairs:

AACTTTATATTTTATTTTGGAAATTTGAGCAGGAATAGTAGGTTACTTCTTTAAGTTTATTAATTCGAAGTGAATTAGGAAATCCAGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTTACAGCCCATGCTTTTATTATAATTTTTTTCATAGTAATAACCAATTATAATTGGAGGATTTGGAAATT
GATTAGTACCTTTAATATTAGGAGCCCCAGATATGGCATTTCCTCGTATAAATAAATAAGATTTTGACTTTTACCCCATCCCTAACATTATTAAT
TTCAAGAAGTGTAGTAGAAAATGGAGCAGGAAGTGGTTGAACAGTTTACCCCTCTCTCGGCTAATATTGCCATCAAGGATCTTCTGTTGATTTA
GCTATTTTCTCTTTACATTTAGCTGGAATTTTCATCTATTTTAGGAGCTATTAATTTTATTACAATATTTAATATACTGATTTAGAAGTATATCAT
TTGATCAAATACCCTTTATTTGTATGAGCGGTAGGAATTACTGCTTTTACTACTATTATCATTACCTGTTCTAGCAGGTGCCATTACAATATTTAT
AACAGATCGAAATTTAAATACATCATTCTTCGATCCTGCTGGAGGAGGAGATCCTATTTTATATCAACATTTTATTC

Type material. Holotype: ♂ deposited in the Los Angeles County Museum of Natural History, Los Angeles, CA, USA (LACM), illustrated in Fig. 83–84, bears the following three rectangular labels, two white: [GUATEMALA. Peten District | Finca Ixobel S of Poptun | 16° 18' 14" N: 89° 25' 20" W | 5-10 JUNE 2003: 1700 ft. | Ron Leuschner. coll.], [DNA sample ID: | NVG-17109G07 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | *Heliopetes* | *lana* Grishin]. **Paratypes:** 2♂♂: 11-BOA-13383A02 the same data as the holotype [USNM] and NVG-20062H06 Mexico: Tamaulipas, 1–4 km N of Gomez Farias, 350 m, 17-Aug-1972, C. J. Durden leg. (genitalia Fig. 302–303) [TMMC].

Type locality. Guatemala: Peten District, Finca Ixobel S of Poptún, elevation 1700 ft, GPS 16.3039, –89.4222.

Etymology. The name removes a negating “a” from the name of its more southern sister species *H. alana* and is a feminine noun in apposition.

Distribution. This species is currently known from Mexico and Guatemala but is expected from other Central American countries.

***Canesia ella* Grishin, new species**

<https://zoobank.org/A4979CC1-C793-4277-808B-45D5388EE312>

(Fig. 3 part, 85–86, 304–306)

Definition and diagnosis. Phylogenetic analysis reveals that a more brightly colored than typical for the genus specimen of *Canesia* Grishin, 2019 (type species *Leucochitonea canescens* R. Felder, 1869) is sister to both *Canesia meridensis* (Godman and Salvin, 1895) (type locality in Costa Rica) and *Canesia callipetes* (Godman and Salvin, 1895) (type locality in Mexico, Guatemala, and Colombia) and therefore is a new species. This new species keys to “*Carrhenes callipetes callipetes*” (E.51.3(a)) in Evans (1953) and differs from its relatives by being more vividly and vibrantly colored, more prominent dark spots, and the lack of whitish scales beneath: ventral side of wings is hay-yellow with well-developed brown spots and brown overscaling in the posterior half. This darker overscaling is not present in either *C. meridensis* or *C. callipetes*. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly1651.28.14:C132T, aly1651.28.14:C147T, aly747.2.1:A480C, aly747.2.1:T513C, aly671.50.9:T53C, aly412.9.2:A201A (not G), aly636.8.1:A84A (not G), aly6841.59.1:A39A (not G), aly5719.1.9:A24A (not C), aly1155.1.7:G112G (not T), and COI barcode: A40G, T82C, T85C, T439C, A508G.

Barcode sequence of the holotype. Sample NVG-19088F11, GenBank OR837661, 658 base pairs:

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AACTTTATATTTTATTTTGGAACTGAGCAGGAATAGTGGGTTACTTCCTTAAGTTTATTAATTCGAACTGAATTAGGAAACCCCGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTATAATGGAGGATTTGGAAATT
GATTAGTACCTTTAATATTAGGAGCCCCAGATATAGCTTTTCCCTCGAATAAATAAATAAGATTTTGATTATTACCACCTTCATTAACATTATTAAT
TTCTAGAAGTATTGTAGAAAACGGAGCAGGAACGATGGAACAGTTTACCCCCCTCTCTCAGCTAATATCGCTCATCAAGGATCTTCTGTTGATTTA
GCTATTTTTTCTTACATTTAGCTGGAATTTTCAATTTTAGGAGCTATCAATTTTATTACTACAATTTAATATGCGAATTAGAAATTTATCTT
TTGATCAAATACCATTTATTTGTGTGAGCAGTAGGTATTACTGCATTATTATTATTATTATCATTACCAGTATTAGCTGGAGCAATTACTATATTATT
AACTGATCGAAATTTAATACATCATTTTTTGTCTGCTGGTGGAGGAGACCTATTTTATATCAACATTTATTT
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Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 85–86, bears the following four rectangular labels, three white: [VENEZUELA:Barinas; | 27.4kmNW.Barinitas | 17 March 1982 | G.F. & J.F. Hevel], [DNA sample ID: | NVG-19088F11 | c/o Nick V. Grishin], [USNMNT | {QR Code} | 01588972], and one red [HOLOTYPE ♂ | *Canesia ella* Grishin].

Type locality. Venezuela: Barinas, 27.4 km NW of Barinitas.

Etymology. The name is for the type locality in [Venezu]el(l)a. Also, אֵלָה (ela) in Hebrew is Goddess. This probably is the most colorful and beautiful species of *Canesia*. The name is a noun in apposition.

Distribution. Currently known only from the holotype collected in Venezuela.

***Paches (Paches) gloriosus* Röber, 1925 and *Paches (Paches) loxana* Evans, 1953 are species distinct from *Paches (Paches) loxus* (Westwood, 1852)**

Genomic sequencing reveals that *Paches gloriosus* Röber, 1925 (type locality not given, holotype sequenced as NVG-18094E01) and *Paches loxus loxana* Evans, 1953 (type locality in Bolivia) currently regarded as subspecies of *Paches loxus* (Westwood, 1852) (type locality not given, possibly in Venezuela) are genetically differentiated from each other at the level characteristic of species (Fig. 3): e.g., COI barcodes of *P. loxus* and *P. l. loxana* differ by 3% (20 bp). Curiously, despite the strong genetic differentiation of *P. gloriosus* in the Z chromosome from all other taxa in this complex (Fig. 3a), it is more similar to *P. loxus* in the mitochondrial genome (Fig. 3b): COI barcode difference of 0.9% (6 bp). Due to phenotypic differences accompanied by genetic differentiation, we **reinstate** *Paches (Paches) gloriosus* Röber, 1925 as a species and propose a **new status** of species for *Paches (Paches) loxana* Evans, 1953.

***Paches (Paches) loxeca* Grishin, new species**

<https://zoobank.org/D34A1B66-34BC-4424-A3DF-73B6D72B695C>

(Fig. 3 part, 87–88, 307–309)

Definition and diagnosis. Phylogenetic analysis of the *Paches loxus* (Westwood, 1852) complex reveals a fourth (and new) species in addition to *P. loxus*, *Paches gloriosus* Röber, 1925 and *Paches loxana* Evans, 1953 that stands out in its genetic differentiation (Fig. 3): e.g., its COI barcodes differ from those of *P. loxus*, *P. gloriosus*, and *P. loxana* by 2.4% (16 bp), 2.7% (18 bp), and 2.9% (19 bp), respectively. This new species keys to *Paches loxus loxus* or “*Paches loxus loxana*” (E.43.1(b) or (c)) in Evans (1953) and differs from its relatives by the lack of median brown band (or its remnants) on dorsal hindwing in males and narrower brown hindwing margin (like *P. loxus*, and *P. gloriosus*, the band typically developed in *P. loxana*), more extensive dark discal area on forewing in males (like *P. loxana* and *P. gloriosus*, forewing mostly blue in *P. loxus*), white distal two-third of the ventral hindwing in females (like *P. loxus* and different from other species). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly536.116.5:T25C, aly2578.2.1:A51T, aly1079.4.3:C141T, aly1222.17.1:T51C, aly1489.18.2:C55T, and COI barcode: T97T, A202G, A214G, T274C, T412C, G620T.

Barcode sequence of the holotype. Sample NVG-19088C07, GenBank OR837662, 658 base pairs:

```
AACTTTATATTTTATTTTGGAAATTTGAGCAGGAATAGTAGGTACCTCATTAAGTTTATTAATTCGAACAGAACTAGGAAATCCAGGATCATTAAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTATAATGGAGGATTTGGAAATT
GATTAGTGCCACTAATATGAGGAGCCCTGATATAGCTTCCCTCGTATAAATAATATAAGATTTTGAATATTACCCCTCATTAAACCCTTTTAAAT
TTCTAGAAGTATTGTGGAAAATGGAGCTGGAACCGGATGAACAGTTTACCCCGCTTTCATCAAATATGCTCATCAAGGTTCTTCAGTTGATTTA
GCTATTTTCTCTTCACTTAGCCGGTATTTTCATCAATTTTAGGAGCTATTAATTTTATTACCACAATATTAATATACGTATTATAAATTTATCTT
TTGATCAAATACCTCTATTGTTTGGAGCAGTAGGAATTAAGTACTGATTATTAATTAATTTACCTGTTTGGAGGAGCTATTACAATATTATT
AACAGATCGAAATTTAAATACATCATTTTTTACCCTCTGGAGGTGGAGATCCAATCTTATATCAACACTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 87–88, bears the following four rectangular labels, three white: [ECUADOR: Morona-Santiago | 15 km S Gualaquiza, 800 m | 3° 27.6'S, 78° 33.1'W | 15 September 2000 | D H Ahrenholz, leg.], [DNA sample ID: | NVG-19088C07 | c/o Nick V. Grishin], [USNMNT | {QR Code} | 01588932], and one red [HOLOTYPE ♂ | *Paches (Paches) loxeca* Grishin]. **Paratype:** 1♀: NVG-19088C10 USNMNT_01588935 Peru: Piura, 3 km W Canchaque, 1300 m, -5.366667, -79.616667, 4-Jun-2000, R. Robbins and G Lamas, leg., genitalia NVG-22032F04 [USNM].

Type locality. Ecuador: Morona-Santiago, 15 km S of Gualaquiza, elevation 800 m, GPS -3.460000, -78.551667.

Etymology. The name is formed as *lox*[us from]*Ec*[u]a[dor] and is a noun in apposition.

Distribution. Southern Ecuador and northern Peru.

Tribe Erynnini Brues and Carpenter, 1932

***Clito congruens* Grishin, new species**

<https://zoobank.org/1F3053D3-130E-4382-894F-8C5A3EEE0D70>

(Fig. 3 part, 89–90, 310–311)

Definition and diagnosis. Phylogenetic analysis of specimens from Panama and Guatemala identified as *Clito aberrans* (Draudt, 1924) (type locality in Brazil: Amazonas, holotype sequenced as NVG-18093A08) reveals their genetic differentiation at the species level (Fig. 3): e.g., COI barcodes differ by 2% (13 bp). This species does not have an available name and is, therefore, new. This new species keys to “*Clito clito*” (which is *C. aberrans*) (E.52.3) in Evans (1953) and differs from its relatives by narrower lobe of ampulla that is twisted perpendicular to the plane of valva and extends inward, closely approaching the dorsal end of harpe with its distal margin; both this lobe over its entire surface and harpe distally are serrated (Fig. 310–311). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly2388.3.1:G181A, aly6940.3.8:G84C, aly1689.4.2:T51C, aly1779.17.11:A168G, aly151.30.3:A30G, and COI barcode: T49C, A79A, T85T, C235C, T284T, T653C.

Barcode sequence of the holotype. Sample NVG-14064A06, GenBank OR837663, 658 base pairs:

```
AACTTTATATTTTATTTTGGAAATTTGATCAGGAATAGTGGGAACCTCCTTAAGTATATTAATTCGAACCTGAATTAGGAAATCCTGGATCTTTAAATT
```

GGAGATGACCAAATTTATAATACTATTGTTACAGCTCATGCTTTCATTATAATTTTCTTTATAGTAATACCAATTATAATCGGAGGATTGGAAATT
GATTAGTTCCTTTAATATTAGGAGCCCCGTGATATAGCTTTCCTCGAATAAATAATATAAGATTTTGATTATTACCCCTTCTTTAATATTATTAAT
TTCAAGTAGTATTGTAGAAAATGGTGCAGGAACAGGGTGAAGTGTACCCCTTTATCTGCTAATATTGCCCATCAAGGATCTTCTGTAGATTTA
GCTATTTTCTCATTACACTTAGCTGGAATTTCTCAATTTTAGGAGCTATTAATTTTACTACTATTATAATATACGTGTTAGAAAATTTATCAT
TTGATCAAAATACCTTTATTTGTATGAGCAGTAGGTATTACTGCACTATTATTATTATTATCATTACCTGTTTTAGCTGGAGCTATTACAATACTTTT
AACAGATCGAAAATTTAAATACATCTTTTTTTGATCCAGCAGGAGGAGATCCTATTTTATATCAACATCTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 89–90, bears the following three rectangular labels, two white: [PANAMA:CANAL ZONE | Gatun | 9° 17'W 79° 57'W | 10.XII.1978 | leg. G.B.Small], [DNA sample ID: | NVG-14064A06 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | *Clito congruens* | Grishin]. **Paratypes:** 1♂ and 2♀♀ in [USNM]: 1♂ NVG-14064A08 Panama: Colon, 1000', 6-Jan-1973, G. B. Small leg.; 2♀♀ Guatemala: Cayuga, around 1900, Schaus and Barnes collection: NVG-14064B06 May, genitalia No. X-6371 J. M. Burns 2006 and NVG-14064B07 April.

Type locality. Panama: Colón Province, Gatún, GPS 9.2833, –79.9500.

Etymology. In Latin, *aberrans* means wandering, straying, or deviating. The word *congruens* means agreeing, agreeing, or consistent and is an antonym of *aberrans*. The name is a present active participle in the nominative case.

Distribution. Currently known from Guatemala and Panama.

Cycloglypha corax Grishin, new species

<https://zoobank.org/D267A571-CE78-45DD-B5D4-1C5BB65E9556>

(Fig. 3 part, 91–92, 312–314)

Definition and diagnosis. Phylogenetic analysis of specimens from Southeast and Southern Brazil identified as *Cycloglypha tisi* (Godman and Salvin, 1896) (type locality in Costa Rica, Panama, and Brazil: Amazon Valley) reveals their genetic differentiation (Fig. 3): e.g., COI barcode difference of 2% (13 bp), and suggests that they are a new species. This new species keys to *C. tisi* (F.9.2) in Evans (1953) and differs from its relatives by typically stronger outlined and less diffuse postdiscal and subapical brown spots inside yellower posterior area of ventral hindwing (Fig. 92), dorsally directed tooth on right harpe narrower, harpe distal end stronger bent dorsad, and right valva with bigger and more robust, rhomboid-shaped process on ampulla (Fig. 312–314). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly3241.4.3:T126C, aly10226.17.12:C156T, aly1872.5.1:A228G, aly1405.12.15:C54T, aly1283.1.11:A26C, and COI barcode: T187C, A211G, A217G, T235T, T394C, A550G.

Barcode sequence of the holotype. Sample NVG-19112H01, GenBank OR837664, 658 base pairs:

AACTTTATATTTTATTTTGGAAATTTGAGCAGGAATAGTAGGAAGTTCCTTTAAGTTTATTAATTCGAAGTGAATTAGGAAATCCAGGATCATTAAAT
GGAGATGATCAAATTTATAATAACAATTTGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCAATTATAATCGGAGGATTTCGGAAAT
GATTAGTACCTTTAATGTTAGGGCTCCTGATATAGCATTTCACGAATAAATAATATAAGATTTTGATTATTACCCCTTCAATTAATATTATTAAT
TTCAAGAAGAATCGTAGAAAATGGAGCAGGTACAGGTTGAACAGTTTTACCCCTCTTTCAGCTAATATTGCTCATCAAGGTTCTTCAGTAGATTTA
GCTATCTTTTCATTACATTTAGCTGGAATTTCCCAATTTCTGGAGCTATTAATTTTATTACAACAATTTAATATACGAATAAAACTTATCAT
TTGATCAAAATACCTTTATTTGTTGAGCAGTAGGTATTACAGCTTTACTTTTACTTTCTTTGCTGTATTAGCAGGAGCTATTACTATCTTTT
AACTGATCGAAAATTTAAATACATCTTTTTTTGATCCAGCTGGAGGAGGTGATCCAATTTTATATCAACATTTATTT

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 91–92, bears the following five rectangular labels, four white: [RIO de JAN | GUA, BRAZIL |13 Aug 64], [Collection of | Bryant Mather], [DNA sample ID: | NVG-19112H01 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01602089], and one red [HOLOTYPE ♂ | *Cycloglypha* | *corax* Grishin]. **Paratypes:** 2♂♂ from Brazil: NVG-19112G05, USNMMENT_01602081 Rio de Janeiro, Itatiaia National Park, 800 m, GPS –22.450, –44.617, 22-Feb-1995, A. Caldas and students leg. [USNM]; and NVG-15092B05 Santa Catarina, Fazenda Alpina, nr. Joinville, 25-Feb-1985, J. Y. Miller leg. [MGCL].

Type locality. Brazil: Rio de Janeiro, Guadalupe.

Etymology. *Tisias* and *Corax* were founders of ancient Greek rhetoric, and *Corax* was *Tisias*'s teacher. Although *Corax* and *Tisias* might have been the same person (Wikipedia contributors 2023), *C. corax* is a species distinct from but sister to *C. tisi*. The name is a noun in apposition.

Distribution. Southeast and Southern Brazil.

***Festivia peruvia* Grishin, new species**

<https://zoobank.org/15FFE992-AC82-4640-864B-5C549EB970CD>

(Fig. 3 part, 93–94, 315–317)

Definition and diagnosis. Genomic analysis reveals that a female from Tingo Maria, Peru, identified as *Festivia grippa* (Evans, 1953) (type locality in eastern Ecuador), is genetically differentiated from it (Fig. 4), e.g., COI barcode difference of 2.3% (15 bp) and because no published names apply to it, represents a new species. This new species keys to “*Sostrata grippa*” (E.42.5) in Evans (1953) and differs from its relatives by a combination of the following characters: forewing discal cell with one large upper hyaline spot (lower spot absent), the two segments of the hyaline spot in forewing cell CuA_1 - CuA_2 are connected to each other at their bases on both dorsal and ventral sides, ventral forewing blue basal overscaling broader, extends from costa to cover discal cell, cell CuA_2 -1A+2A with a pale spot at $\frac{1}{3}$ from its base, ventral hindwing with an apical blue spot and the dark brown streak in cell $Sc+R_1$ -RS is smaller and separated from vein $Sc+R_1$ by blue (Fig. 93–94). Due to the cryptic nature of this species and unexplored phenotypic variation, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly2700.10.9:G42A, aly300.20.2:G126A, aly116.12.4:G66T, aly2578.2.1:A22C, aly536.138.7:A319C, aly1260.2.1:T124T (not C), aly10226.27.3:A51A (not T), aly4523.3.2:C153C (not T), aly235.8.17:T150T (not C), aly10235.5.16:C81C (not T), and COI barcode: T139C, T287C, T319A, 514T, A526T, T619C.

Barcode sequence of the holotype. Sample NVG-18032A01, GenBank OR837665, 658 base pairs:

```
AAC TTTATATTTTATTTTGGAAATTTGAGCAGGAATAGTAGGAACCTCACTAAGAATATTAATTCGAAC TGAATTAGGAAACCCCGGATCTTTAATT
GGAGATGATCAAATTTATAACACTATTGTTACAGCTCATGCCTTTATTTATATAATTTTTTTCATAGTTATAACCAATTATAATTTGGAGGATTTGGAAAT
GATTAGTCCCACCTATACTAGGAGCCCCGTGATATAGCATTCCTCCGAAATAAATAAGATTTTGACTTTTACCCCTCTTTAATACTGCTAAT
TTCAAGAAGAATTTGTAGAAAATGGAGCAGGTACTGGATGAAC TGTTCACCCCTCTTTCTGCTAATATGCTCACCAGGCTCTTCTGTAGATTA
GCTATTTTTCATTACATTTAGCTGGAATTTCAATCTTGGAGCTATTAATTTTATTACAACAATTTAATATACGAATTAGAAATTTATCTT
TTGATCAAATACCTTTATTTGTTGAGCTGTAGGAATTACTGCATTATTATTACTTTCAC TACCAGTATTGGCTGGTGCTATTACTATACTATT
AACAGATCGAAATTTAAATACCTCTTTTGTGATCCCGCAGGAGGAGGAGATCCTATTTTATACCAACATTTATTT
```

Type material. Holotype: ♀ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 93–94, bears the following four rectangular printed labels, three white: [PERU: Huanuco | Tingo Maria, 800 m. | May–June, 1994], [DNA sample ID: | NVG-18032A01 | c/o Nick V. Grishin], [USNM ENT | {QR Code} | 01466114], and one red [HOLOTYPE ♀ | *Festivia peruvia* Grishin].

Type locality. Peru: Huánuco, Tingo Maria, elevation 800 m.

Etymology. The name derives from the country of the type locality and is a feminine adjective.

Distribution. Currently known only from the holotype collected in Peru.

Subfamily Hesperinae Latreille, 1809

Tribe Hesperini Latreille, 1809

Subtribe Hesperina Latreille, 1809

***Libra* Evans, 1955 is a junior subjective synonym of *Phemiades* Hübner, [1819]**

Genomic sequencing of representative species, including the type species of both genera, reveals that *Libra* Evans, 1955 (type species *Augiades aligula* Schaus, 1902) originates within *Phemiades* Hübner, [1819] (type species *Phemiades pseudophineus* de Jong, 1983) and is not monophyletic in the Z chromosome tree (Fig. 4). The two genera are genetically close to each other: e.g., COI barcodes of their type species differ by 7% (46 bp). Therefore, we propose that *Libra* Evans, 1955 is a junior subjective synonym of *Phemiades* Hübner, [1819].

***Decinea onasima* (Hewitson, 1877) with *Cobalus boliviensis* E. Bell, 1930 as its subspecies and *Decinea formosus* (Hayward, 1940) are species distinct from *Decinea dama* (Herrich-Schäffer, 1869)**

Genomic analysis of primary type specimens of the following four taxa: *Hesperia onasima* Hewitson, 1877 (type locality in Brazil: Rio de Janeiro, syntype sequenced as NVG-18043C12), *Cobalus boliviensis* E. Bell, 1930 (type

locality in Bolivia, holotype sequenced as NVG-18025E07), *Cobalus formosus* Hayward, 1940 (type locality in Ecuador, holotype sequenced as NVG-18025H07) and *Cobalus dama* Herrich-Schäffer, 1869 (type locality not specified, syntypes sequenced as NVG-15036H04 and NVG-18042G04), the former three of which are currently regarded as junior subjective synonyms of the latter, placed in the genus *Decinea* Evans, 1955 (type species *Hesperia decinea* Hewitson, 1876), reveals that they represent three genetically differentiated non-sister lineages (Fig. 4). COI barcodes of *D. dama* differ from either *H. onasima* or *C. formosus* by 7.9% (52 bp). However, *H. onasima* and *C. boliviensis* are more closely related to each other (Fig. 4). Therefore, we propose to **reinstate** *Decinea onasima* (Hewitson, 1877) and *Decinea formosus* (Hayward, 1940) as species-level taxa and, for the time being, pending further studies, treat *Decinea onasima boliviensis* (E. Bell, 1930), **new combination**, as a subspecies.

Decinea notata Grishin, new species

<https://zoobank.org/D0018528-567A-43E6-8476-17D4BD2DFE8E>

(Fig. 4 part, 95–96, 318–319)

Definition and diagnosis. Phylogenetic analysis of specimens from Ecuador identified as *Decinea lydora lyco* (Mabille, 1878) (type locality in Peru) reveals that they are not monophyletic, and the former specimens represent a most prominently differentiated new species without close relatives (Fig. 4). COI barcodes of the new species differ from *D. lydora lyco* and *D. dama* by 8.5% (56 bp) and 10% (66 bp), respectively. The new species keys to “*D. neroides lyco*” (currently *D. lydora lyco*) (L.11.5(b)) in Evans (1955) but differs from it by the abdomen being white beneath (not brown) and forewing with three well-defined subapical dots in a row. These dots are smaller, and some may be missing in *Decinea lydora* (Plötz, 1882) (type locality in Venezuela) subspecies and junior subjective synonyms. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly499.50.4:G45C, aly1656.33.2:A51T, aly291.13.2:G39T, aly291.13.2:G66A, aly2631.9.19:G72A, and COI barcode: T121C, T145C, T250C, T436C, T589C, T461C.

Barcode sequence of the holotype. Sample NVG-18118B04, GenBank OR837666, 658 base pairs:

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AACTTTATATTTTATTTTGGTATTTGAGCAGGAATATTAGGAACTTCCTTAAGTTTACTAATTCGTACAGAATTAGGTAGACCTGGATCTTTAATT
GGAGATGATCAAATTTATAATACCATCGTAACAGCTCATGCTTTATCATAATTTTTTCATAGTTATACCTATTATAATTGGAGGATTTGGAAATT
GATTAGTACCCTTAATATTAGGAGCTCCTGATATAGCCTTCCCTCGAATAAATAACATAAGATTTTGAATACTACCCCTTCTTTAACCTTATTAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGAACCTGGTTGAACAGTTTACCCCTTTATCATCAAATATTGCTCACCAAGGATCTTCAGTTGATTTA
GCTATTTTTCTCTTCATTTAGCTGGTATTTCTTCTATTTTAGGAGCCATTAATTTTATTACTACAATTATTAACATACGAATTAATAATCTATCAT
TTGATCAAATACCCTATTTGTTGATCAGTAGGAATTACAGCTTTATTATTATTATTATCTTTACCTGTTTTAGCTGGAGCTATTACTATACTTCT
TACTGACCGAAATTTAAATACTTCATTTTTGATCCTGCTGGTGGAGGAGACCTATTCTTTATCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 95–96, bears the following five rectangular labels, four white: [ECUADOR:Napo Prov | 9 km E Puerto Napo | 1° 03'S 77° 44'W | 600m 20 Sept 1990 | S S Nicolay], [♂ genitalia | slide/vial # | H1076 | Prep. S.S. Nicolay], [DNA sample ID: | NVG-18118B04 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01531768], and one red [HOLOTYPE ♂ | *Decinea* | *notata* Grishin]. **Paratype:** 1♂ NVG-18091E07 Ecuador: Morona-Santiago, Mendez, 800 m, GPS -2.42, -78.20, 10-Nov-2012, J.-C. Petit leg. [EBrockmann].

Type locality. Ecuador: Napo Province, 9 km E of Puerto Napo, elevation 600 m, GPS -1.05, -77.73.

Etymology. In Latin, *notatus* means marked, written, signified, noted, or distinguished. The name reflects the prominent subapical dots and a white abdomen below. It also reflects the prominent phylogenetic position separate from all others. The name is a feminine perfect passive participle in the nominative singular.

Distribution. Ecuador.

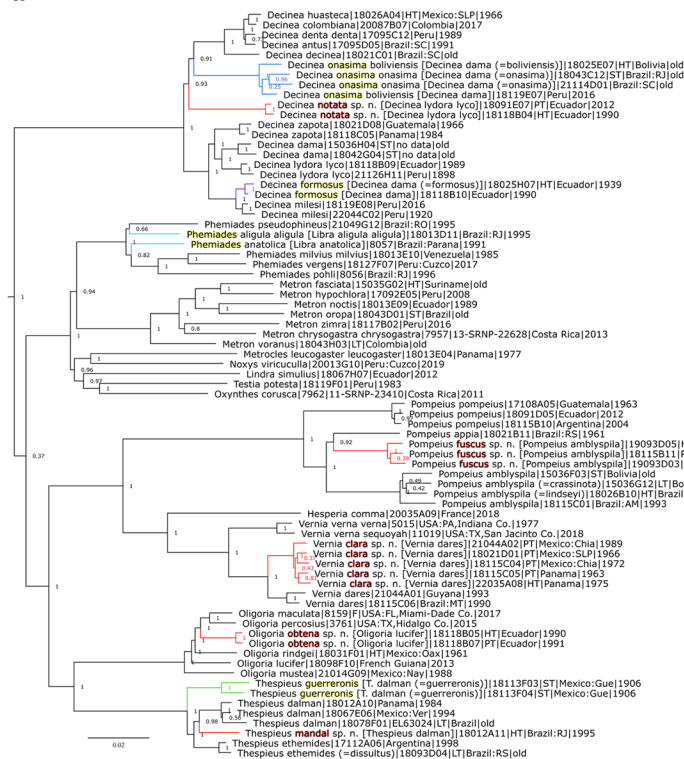
Pompeius fuscus Grishin, new species

<https://zoobank.org/A3D335E7-A11D-4361-B8C1-A9BD1924462E>

(Fig. 4 part, 97–98, 320–321)

Definition and diagnosis. Phylogenetic analysis of specimens from Brazil identified as *Pompeius amblyspila* (Mabille, 1898) (type locality in Bolivia) reveals that they are not monophyletic with and strongly differentiated genetically from it (Fig. 4): e.g., their COI barcodes differ by 4.2% (28 bp) and therefore represent a new species.

a Z chromosome tree



b mitochondrial genome tree segments



Figure 4. Phylogenetic trees of Hesperina inferred from protein-coding regions in **a**) the Z chromosome and **b**) the mitochondrial genome (in segments). See Fig. 1 legend for other notations.

Inspection of (and sequencing of two, Fig. 4) of primary type specimens of taxa placed as junior subjective synonyms of *P. amblyspila* confirms their synonymy and distinctness of the new species from Brazil. This new species keys to *P. amblyspila* (M.15.4) in Evans (1955) but differs from it and other relatives by broader wings, narrower stigma, pale spots in forewing cells CuA_1 - CuA_2 and M_3 - CuA_1 being rounder and placed farther distad from stigma, hindwing pale spots smaller and in a more even arc closer to the margin, and veins ventrally with pale overscaling towards outer margin. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly320.4.1:T75C, aly1838.7.1:T387C, aly1838.7.1:T2038C, aly1651.4.1:A404G, aly525.109.4:G81A, and COI barcode: T19C, T139C, T340C, T376A, T472C, T541C.

Barcode sequence of the holotype. Sample NVG-19093D05, GenBank OR837667, 658 base pairs:

AACTTTATATTTTATTTTCGGTATTTGAGCAGGAATATTAGGAACCTCTTAAGTTTATTAATTCGAACAGAATTAGGTAATCCTGGTCTTTAATT
GGAGATAGTCAAATTTTTAATCTATTGTTACAGCTATGCTTTATTTAATTTATTTTATAGTATTAATCAATATAATTTGGAGGATTTGGAAAT
GATTAGTACCATAATATTAGGAGCTCCAGATATGCTTTCTCGAATAAATATAAGATTTTGAATATTACCACCATCATTAACATTTAATTA
TTCAAGAAGAAATGTAGAAAATTGAGCAGGAACCTGGATGAACAGTTTACCCCTTTATCTTCTAATATGCTACCAAGGATCATCTGTGATTA
GCAATTTTCTTACATTTAGCTGGAATTTCTTCAATTTTAGGAGCTATTAATTTATTAACAACAATTTAATATAACGAATCAAAAATATATCAT
TTGATCAAATACCATTATTTGTTGATCTGTTGGAATTACAGCTTTATTTACTCTTATCTTACCTGTTTGTAGCTGGAGCTATTACTACTTCT
TACAGATCGAAATTTAATACTCTTTTTTGTATCCAGCAGGAGGAGAGATCCTATTTTATACCAACATTTATTT

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 97–98, bears the following four rectangular labels, three white: [BRAZIL:MG 1250m | Serra do Cipo | 19°16'S 43°35'W | 17 Apr 1991 | Robbins & Becker], [DNA sample ID: | NVG-19093D05 | c/o Nick V. Grishin], [USNMNT | {QR Code} | 01589476], and one red [HOLOTYPE ♂ | Pompeius | fuscus Grishin]. **Paratypes:** 2♂♂ from Brazil in USNM: NVG-18115B11 the same data as the holotype, except 18-Apr-1991 and NVG-19093D03 Mato Grosso, Diamantino, Alto Rio Arinos, 350–400 m, GPS –14.2167, –56.2000, 7-Feb-1986, E. Furtado.

Type locality. Brazil: Minas Gerais, Serra do Cipo, elevation 1250 m, GPS –19.2667, –43.5833.

Etymology. In Latin, *fuscus* means dark, muffled, dingy, brown, dusky, or tawny. Moreover, the pattern of paler yellow-brown spots and overscaling along veins in this species reminds us of the pattern observed in *Anthrenus fuscus* Olivier, 1789 (Coleoptera). The name is a masculine adjective.

Distribution. Recorded from the states of Mato Grosso and Minas Gerais in Brazil.

***Vernia clara* Grishin, new species**

<https://zoobank.org/D20A8C16-E197-4F52-806F-01921EE16C07>

(Fig. 4 part, 99–100, 322–323)

Definition and diagnosis. Genomic analysis of specimens from Mexico and Panama identified as *Vernia dares* (Plötz, 1883) (type locality not specified) reveals that they differ significantly from the South American *V. dares* (Fig. 4): e.g., COI barcodes differ by 5.8% (38 bp) and, therefore, this complex consists of at least two species. Although we were not able to locate primary type specimens, according to the original description (Plötz 1883) and the illustration in Draudt (1921–1924), which probably is a copy of an unpublished drawing by Plötz, *V. dares* is of a darker phenotype that corresponds to South American specimens. Therefore, North and Central American specimens that are characterized by more extensive yellow-orange coloration represent a new species. This new species keys to “*Pompeius dares*” (M.15.5) in Evans (1955), but differs from it by larger yellow-orange spots, more developed yellow-orange overscaling, and less contrasting dark spots on the ventral hindwing. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly2487.24.2:T675G, aly2487.24.2:T765C, aly536.138.7:T78C, aly82.18.3:T303C, aly82.18.3:G321A, and COI barcode: T5C, 31C, T46C, T193C, A283T, T536C.

Barcode sequence of the holotype. Sample NVG-22035A08, GenBank OR837668, 658 base pairs:

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AACTCTATATTTTATTTTCGGTATTTGAGCCGGTATATTAGGAACCTCTCTAAGTTTATTAATTCGAACAGAATTAGGTAATCCTGGTTCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTTACAGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCAATTATAATGGAGGGTTTGGAAACT
GATTAGTCCCATTAAATATTAGGAGCCCTGACATAGCTTTCCACGAATAAATAACATAAGATTTTGAATATTACCCCATCTTTAACTCTTTTAAAT
CTCAAGTAGAATTGTAGAAAATGGTGCAGGAACAGGTTGAACCTGTTTATCCTCCTTTATCATCAAATATTGCTCACCAGGATCTTCTGTTGATTTA
GCAATTTTTCTCTTCATTTAGCTGGAATTTTCATCTATTTTAGGAGCTATTAATTTTATTACAACAATTATTAATATACGAATTAATAACTTATCAT
TTGATCAAATACCTTTATTTGTTGATCTGTAGGAATTACAGCTTTTACTACTTTTTATCTTTACCTGTTTTAGCTGGAGCTATTACAATATTACT
TACTGATCGAAATTTAAACACTTCATTTTTGATCCTGCTGGAGGAGATCCAATTCCTTTACCAACATCTTTTC
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 99–100, bears the following three rectangular labels, two white: [Panama:Chiriquí | Santa Cruz | 10.VIII.1975 | G.B. Small], [DNA sample ID: | NVG-22035A08 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | Vernia | clara Grishin]. **Paratypes:** 2♂♂ and 3♀♀: Mexico: 1♂ NVG-22102C01, CASENT 8566973 Nayarit, 20 air mi NE of San Blas, 23-Dec-1971, C. D. MacNeill leg. [CAS]; 1♀ NVG-18021D01 San Luis Potosi, Valles, 10-Jun-1966, H. A. Freeman leg. [AMNH]; Chiapas: 1♂ NVG-18115C04, USNMMENT_01531564 35 mi W of Tuxtla Gutierrez, 16-Aug-1972, G. F. and S. Hevel leg. [USNM]; 1♀ NVG-21044A02 3 mi S of Simojovel, 3000', 22-Jun-1989, J. Kemner leg., genitalia SRS-4469 [MGCL] and Panama: 1♀ NVG-18115C05, USNMMENT_01531565 Panama, Cerro Campana, 2000', GPS 8.6833, –79.9167, 9-Mar-1963, G. B. Small leg. [USNM].

Type locality. Panama: Chiriquí Province, Santa Cruz.

Etymology. The name *clara*, which is Latin for bright and clear, is given for the brighter colors of this species. The name is an adjective.

Distribution. From Mexico to Panama.

***Oligoria (Oligoria) obtena* Grishin, new species**

<https://zoobank.org/74FCABDE-324D-4C60-A191-BD4C1E8F1B3B>

(Fig. 4 part, 101–102, 324–327)

Definition and diagnosis. Phylogenetic analysis of specimens from Ecuador identified as *Oligoria lucifer* (Hübner, [1831]) (type locality in Suriname) reveals that they are not monophyletic with it and instead are sister to both *Oligoria maculata* (W. H. Edwards, 1865) (type locality in USA: Louisiana) and *Oligoria percousius* (Godman,

1900) (type locality in Mexico, Guatemala, and Panama), being genetically differentiated from them (Fig. 4): e.g., COI barcodes of Ecuadorian specimens differ from *O. maculata* and *O. percusius* by 5.3% (35bp) and 4.6% (30 bp), respectively, and therefore they represent a new species. This new species keys to “*Decinea lucifer*” (L.11.8) in Evans (1955) but differs from its relatives by a small spot and reduced pale overscaling around it in ventral forewing cell $CuA_2-1A+2A$. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly3446.8.5:C48T, aly3446.8.5:T87C, aly127.87.2:C51T, aly127.87.2:G75A, aly903.2.14:T860C, and COI barcode: A166G, T277A, T530C, T553A, A628T.

Barcode sequence of the holotype. Sample NVG-18118B05, GenBank OR837669, 658 base pairs:

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AACTTTATATTTTATTTTGGTATTTGAGCAGGAATATTAGGAACCTCTTTAAGATTATTAATTCGTACAGAATTAGGTAATCCAGGATCATTAAAT
GGAGATGATCAAATTTATAACTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATGCCTATTATAATTGGAGGATTCGGAAATT
GATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATAAGATTTTGAATGTTACCCCCCTCATTAACATTATTAAT
TTCAAGAAGAATTGTAGAAAATGGAGCAGGAACCTGGTTGAACAGTTTATCCTCCTTTATCTTCTAATATTGCCACCAAGGATCTTCTGTTGATTTA
GCAATTTTTCCTTCATTTAGCTGGTATTTCTCTATTTTAGGAGCTATTAATTTTATTACAACAATTATTAATATACGAATTAATAATTTATCAT
TTGATCAAATACCTTTATTTGTTGATCTGTAGGTATTACTGCTCTATATTACTTTTTATCTTTACCAGTTTTAGCTGGAGCTATTACTATACTACT
TACTGATCGAAATCTTAATACCTCATTTTTTGATCCAGCAGGAGGTGGTGATCCAATTTTATACCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 101–102, bears the following five rectangular labels, four white: [ECUADOR: Napo Prov | 4 km Tena-Pano Rd | 1° 02'S, 77° 50'W | 28 Sep 1990 600 m | DH Ahrenholz leg | SS Nicolay curator], [Decinea | lucifer ♂ | Det. Hbn | S.S. Nicolay], [DNA sample ID: | NVG-18118B05 | c/o Nick V. Grishin], [USNM | {QR Code} | 01531769], and one red [HOLOTYPE ♂ | Oligoria (Oligoria) | obtena Grishin]. **Paratype:** 1♂ NVG-18118B07, USNM_01531771 Ecuador: Napo, Jatun Sacha Biological Reserve, GPS –1.0667, –77.6000, 30-Sep-1991, D. H. Ahrenholz leg., genitalia H1096 (Fig. 324–325) [USNM].

Type locality. Ecuador: Napo Province, km 4 of Tena-Pano Rd., elevation 600 m, GPS –1.033, –77.833.

Etymology. In Latin, *obtenebro* means darken, make dark, obscure, or conceal. The name is given for the reduced pale scaling near the ventral forewing tornus compared to its congeners and is a noun in apposition.

Distribution. Currently known only from the Napo Province in Ecuador.

Thespieus guerreronis (Dyar, 1913) is a species distinct from *Thespieus dalman* (Latreille, [1824])

Genomic sequencing of *Thespieus dalmani* [sic] *guerreronis* Dyar, 1913 (type locality in Mexico: Guerrero, syn-types sequenced as NVG-18113F03 and NVG-18113F04), currently a junior subjective synonym of *Thespieus dalman* (Latreille, [1824]) (type locality in Brazil, lectotype sequenced as NVG-18078F01) reveals prominent genetic differentiation between these two taxa (Fig. 4): e.g., their COI barcodes differ by 4.3% (28 bp). Therefore, we propose to treat *Thespieus guerreronis* Dyar, 1913, **new status**, as a species.

Thespieus mandal Grishin, new species

<https://zoobank.org/BA7D773F-A815-4251-B153-DC7B3CAC5B13>

(Fig. 4 part, 103–104, 328–329)

Definition and diagnosis. Phylogenetic analysis of a specimen from Rio de Janeiro, Brazil, identified as *Thespieus dalman* (Latreille, [1824]) (type locality in Brazil, lectotype sequenced as NVG-18078F01) reveals its strong genetic differentiation (Fig. 4): e.g., COI barcode difference of 3.8% (25 bp) from *T. dalman*, and therefore it represents a new species. This new species keys to *T. dalman* (O.7.4) in Evans (1955) but differs from it by a generally narrower hyaline spot in the forewing discal cell but wider spot in the hindwing cell CuA_1-CuA_2 , which is framed by a smaller and paler brown spot at the base of this cell on the ventral side, which has no brown discal dash in cell $Sc+R_1-RS$, and exhibits paler basal area in cell $1A+2A-3A$ (Fig. 103–104), harpe wider, protrudes dorsad farther than ampulla, more concave along the distal margin, saccus stronger bowed ventrad (Fig. 328–329). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly168.8.1:G313A, aly2517.1.2:T285C, aly3905.3.3:A99C, aly971.11.1:A75G, aly3268.8.1:T840C, aly10226.17.4:A204A (not C), aly320.37.1:G189G (not A), aly1656.14.1:C411C (not T), aly594.20.16:C67C (not A), aly1651.3.5:A72A (not T), and COI barcode: T50C, T133C, T340C, T352C, A379C, T640C.

Barcode sequence of the holotype. Sample NVG-18012A11, GenBank OR837670, 658 base pairs:

AAC TTTATATTTTATTTTGGTATTTGAGCAGGAATATTAGGAACTTCACTAAGATTACTAATTCGTACAGAATTAGGTAATCCAGGATCTTTAATT
 GGAGATGATCAAATTTATAATACTATTGTTACAGCCCATGCTTTATTATAAATTTTTTTATAGTTATACCTATTATAAATGGAGGATTTGGAAATT
 GATTAGTCCCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGAATAAATAATATAAGATTTTGAATATTACCTCCCTCTTTAACATTTAAT
 TTCAAGAAGAATTGTAGAAAATGGTGCAGGAACAGGTTGAACAGTATACCCCCCTTATCCTCTAATATTGCTCATCAAGGATCTTCCGTAGATTTA
 GCAATTTTCTCATTTCATTTAGCTGGAATTTCTATTTTAGGAGCTATTAATTTTATACAACAATTATAATATACGAATTAATAATTTATCAT
 TTGATCAAATACCTTTATTTGTATGATCTGTAGGTATTACAGCTTTATTATTACTTTTATCTTTACCTGTATTAGCTGGTGCTATTACCATATTATT
 AACAGATCGAAATTTAAATACTTCATTCTTTGACCCTGCAGGAGGAGATCCAATCTTATATCAACATTTATTT

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 103–104, bears the following six rectangular labels, five white: [BRAZIL, RJ, P. N. de | Itatiaia, 800m | 22°27'S, 44°37'W | 7Apr 1995 | Diversity Project UERJ], [Thespius | dalman], [no transect], [DNA sample ID: | NVG-18012A11 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01450264], and one red [HOLOTYPE ♂ | Thespius | mandal Grishin].

Type locality. Brazil: Rio de Janeiro, Itatiaia National Park, elevation 800 m, GPS –22.450, –44.617.

Etymology. The name reverses syllables in its sister species, *T. dalman*. The name is a noun in apposition.

Distribution. Southeast Brazil.

Subtribe Moncina A. Warren, 2008

***Psoralis (Saniba) magnamacus* Grishin, new species**

<https://zoobank.org/EE8B803C-DB04-4B78-9732-F18EE4B7007A>

(Fig. 5 part, 105–106, 330–333)

Definition and diagnosis. A Hesperidae specimen from Panama stood out due to its unusual appearance, with large hyaline spots on the forewing. Genomic sequencing placed it in subgenus *Saniba* Mielke and Casagrande, 2003 (type species *Hesperia sabina* Plötz, 1882) of the genus *Psoralis* Mabille, 1904 (type species *Psoralis sabaesus* Mabille, 1904, which is a junior subjective synonym of *Pamphila idee* Weeks, 1901) (Fig. 5), an affinity not immediately apparent for this recognizably new species. In the pattern of forewing, this new species resembles *Psoralis (Saniba) laska* (Evans, 1955) (type locality in Brazil: Mato Grosso) but the hyaline spots are larger, e.g., a spot occupies more than a third of the cell M_3-CuA_1 , and about a third of the cell CuA_1-CuA_2 . Only two, not three, subapical hyaline spots are present in the holotype, those in cells R_5-M_1 and R_4-R_5 . The ventral side is rusty-brown, not variegated, and much more uniformly colored than in *P. laska*: cream-colored area occupies more than a third of forewing cell $CuA_2-1A+2A$, hindwing with traces of postdiscal pale spots. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly1038.7.10:T45A, aly1038.7.10:A129G, aly322.26.7:T472G, aly1139.29.1:T21C, aly1139.29.1:T297A, aly3712.7.1:T57T (not C), aly3712.7.1:T117T (not C), aly390.23.4:T282T (not C), aly390.23.4:C397C (not T), aly1656.10.5:C136C (not T), and COI barcode: T46C, T202C, T212C, 352A, T533C, T568A.

Barcode sequence of the holotype. Sample NVG-19023H12, GenBank OR837671, 658 base pairs:

AAC TTTATATTTTATTTTGGTATTTGAGCAGGAATATTAGGAACTTCACTAAGATTACTAATTCGTACAGAATTAGGTAATCCAGGATCTTTAATT
 GGAGATGATCAAATTTATAATACTATTGTTACAGCTCATGCTTTATTATAAATTTTTTTATAGTTATACCTATTATAAATCGGAGGATTTGGAAATT
 GATTAGTCCCTTTAATACTAGGAGCTCCTGATATAGCTTTCCACGAATAAATAATATAAGATTTTGAATATTACCCCCCTTCATTAATATTATTAAAT
 TTCAAGAAGAATTGTAGAAAATGGTGCAGGAACAGGTTGAACAGTATACCCCCCTTATCATCTAATATTGCTCACCAAGGAGCTTCTGTTGATTTA
 GCAATTTTTCATTACATTTAGCAGGATTTCTTCTATTTTAGGAGCTATTAATTTTATCACTACAATTTATAATATACGAATTAGAAATTTATCAT
 TTGATCAAATACCTTTATTTGTTGATCTGTTGGTATTACAGCTTTACTACTCTTTTATCTTTACCTGTTTGTAGCAGGTGCAATTACAATACTACT
 TACAGATCGAAATCTAAATACTTCATTCTTTGATCCAGCTGGAGGAGGAGATCCTATTCTTTACCAACATTTATTT

Type material. Holotype: ♀ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 105–106, bears the following four rectangular labels, three white: [PANAMA: Darien | Cana 1200m | 22.IX.1982 | Leg. G. B. Small], [DNA sample ID: | NVG-19023H12 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532887], and one red [HOLOTYPE ♀ | *Psoralis (Saniba) magnamacus* Grishin].

Type locality. Panama: Darien Province, Cana, elevation 1200 m.

Etymology. The name is given for the big macules on the forewing. In Latin, *magnae maculae* means large spots. The name is a noun in apposition.

Distribution. This species is known only from the holotype collected in Panama.

Alychna ayonis Grishin, new species

<https://zoobank.org/050EC67D-FC69-4005-B871-A861C7D74835>

(Fig. 5 part, 107–108, 334–335)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Ecuador and Peru identified as *Alychna exclamatoris* (Mabille, 1898) (type locality in Bolivia, lectotype sequenced as NVG-18042G08) show prominent genetic differentiation from it while being its sister (Fig. 5): e.g., their COI barcodes differ by 1.5% (10 bp) and, therefore, represent a new species, more distantly related to *Alychna zenus* (E. Bell, 1942) (type locality in Ecuador) (COI barcodes differ by 3.5%, 23 bp). This new species keys to “*Psoralis exclamatoris*” (J.43.3) in Evans (1955) but differs from it by narrower stigma, narrower white spots and streaks on forewing, a semi-circle of discal pale dots on ventral hindwing (Fig. 107–108), undivided uncus, harpe strongly upcurved and protruding beyond ampulla dorsad, terminally rounded in lateral view and plate-like in dorsal view, costa-ampulla with a bump closer to ampulla, concave on both sides of the bump (Fig. 334–335). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly420.62.5:G73T, aly420.62.5:G84A, aly2041.8.2:A195C, aly2012.47.1:G1269C, aly25.10.1:G48C, and COI barcode: A85T, T163A, T169A, T205A, A553C, A631G.

Barcode sequence of the holotype. Sample NVG-22035H07, GenBank OR837672, 658 base pairs:

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AACTTTATATTTTATTTTGGTATTTGAGCAGGTATACTAGGAACTTCATTAAGTTTATTAATTCGTACAGAATTAGGAAATCCTGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATAACCAATTATAATTGGAGGATTTGGAAATT
GATTAGTTCATTAATATTAGGAGCTCCTGATATAGCTTTCCACGAATAAATAATATAAGATTTGAATATTACCCCTTCCTTAATATTATTAAT
TTCAAGAAGAATTGTTGAAAATGGTGCAGGTACTGGATGAACTGTTTATCCCCCTTCTTCTAATATCGCACACCAAGGATCATCTGTTGATTTA
GCAATTTTTTCTTTACATTTAGCTGGGATCTCTCTATTTTAGGAGCTATTAATTTTATTACTACAATTTAATATACGAATTAGAAATATATCCT
TTGATCAAATACCTTTATTTGTATGATCTGTAGGAATTACAGCTTTATTATTACTTTTATCTTTACCCGTATTAGCTGGAGCTATTACAATACTTTT
AACTGATCGAAACTTAAATACTTCTTTTTTTGATCCAGCTGGAGGGGACCCATCTTATATCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 107–108, bears the following three rectangular labels, two white: [ECUADOR Napo | Papallacta 2800m | 23 Sept. '87 | S. S. Nicolay], [DNA sample ID: | NVG-22035H07 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | *Alychna* | *ayonis* Grishin]. **Paratype:** 1♂ NVG-19021H01 the same data as the holotype but collected on 17-Sep-1987, genitalia H962 by S. S. Nicolay [USNM].

Type locality. Ecuador: Napo Province, Papallacta, elevation 2800 m.

Etymology. The name is given for the “i” on the forewing. A close relative of this species is named *exclamatoris*, probably for the exclamation mark pattern on the forewing. In the new species, the exclamation mark is thinner and resembles the letter “i” [*ay*]. The name is treated as a noun in apposition.

Distribution. Currently known only from the type locality in Napo, Ecuador.

Wahydra banios Grishin, new species

<https://zoobank.org/2BB146AF-6818-4929-AAB0-CE36EBEC299B>

(Fig. 5 part, 109–110, 336–338)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Ecuador identified as *Wahydra subhebetis* Steinhauser, 1991 (type locality in Colombia, holotype sequenced as NVG-15039G08) shows prominent genetic differentiation from it (Fig. 5): e.g., their COI barcodes differ by 2.4% (16 bp), and therefore represents a new species. This new species phenotypically is very similar to *W. subhebetis* but differs from it by an even narrower and longer harpe separated from the ampulla by a larger notch, harpe projecting dorsad and terminally narrowing to a serrated and rounded point, larger gnathos (Fig. 336–338). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1042.30.1:G732A, aly1042.30.1:G747C, aly727.26.22:G33A, aly727.26.22:A38G,

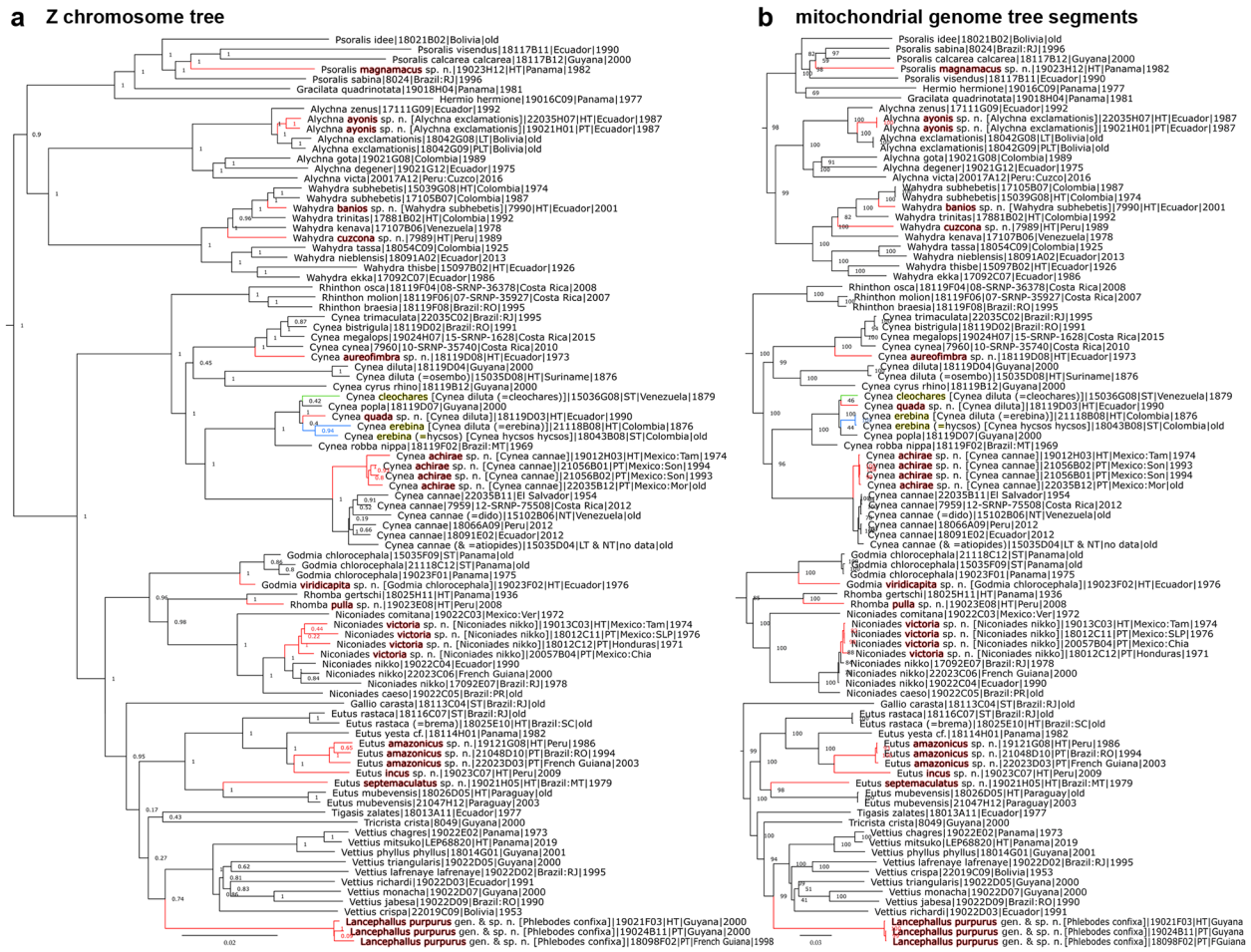


Figure 5. Phylogenetic trees of *Moncina* (part 1) inferred from protein-coding regions in **a**) the Z chromosome and **b**) the mitochondrial genome (in segments). See Fig. 1 legend for other notations.

aly208.41.1:T54C, aly822.30.12:T1050T (not A), aly822.30.12:A1055A (not G), aly536.122.6:G99G (not C), aly536.122.6:C105C (not T), aly1018.14.4:C54C (not T), and COI barcode: T5C, A100G, A166G, 337A, T460C.

Barcode sequence of the holotype. Sample NVG-7990, GenBank OR837673, 658 base pairs:

AACCTCTATATTTTATTTTGGTATTTGAGCAGGAATGTTAGGAACCTCCCTAAGTTTACTTATTCGTACAGAAATAGGTAATCCAGGATCCTTAATT
GGGATGATCAAATTTATAATACTATTGTTACAGCTCATGCTTTTATTATAATTTCTTCATAGTTATGCAATTTATAATGGAGATTCCGAAAT
GATTAGTTCCTTTAATATTAGGACACCTGATATAGCTTCCACGTAATAAATAATAGATTTTGAATATTACCTCTCCTTAATATTTAAT
TTCTAGAAGAATGTAGAAAATGGTGACAGGACTGGTTGAACAGTATATCCCCCTTTATCTAATATTCACATCAAGGATCATCTGTGATTTA
GCATTTTCTCTCATTTAGCAGGAATTTCTTCTATTAGGAGCTATTAATTTTACTACAATTTCAATATACGAATTAATAATATATCAT
TTGATCAAATACCTTTATTTGATGATCAGTAGGAATTACAGCTTACTACTACTTTTATCTTTACCAGTATTAGCTGGAGCTATTACAATCTCT
AAGTATGCAAAATTAATAACATCTTTTGTGACCTGCTGGAGGAGGATCCAATTTTATATCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 109–110, bears the following five rectangular labels, four white: [ECUADOR: Tungurahua: | Baños 3000 m. | XI.2001 I.Aldas leg.], [DNA sample ID: | NVG-7990 | c/o Nick V. Grishin], [genitalia| NVG170207-75| Nick V. Grishin], [USNMNT | {QR Code}| 01321830], and one red [HOLOTYPE ♂ | Wahydra | banios Grishin].

Type locality. Ecuador: Tungurahua Province, Baños, elevation 3000 m.

Etymology. The name is given for the type locality and is a noun in apposition.

Distribution. Currently known only from the holotype collected in Baños, Ecuador.

***Wahydra cuzcona* Grishin, new species**

<https://zoobank.org/5C35C09C-FEAE-43D3-A1FD-874FF72F0803>

(Fig. 5 part, 111–112, 339–341)

Definition and diagnosis. Phylogenetic trees reveal that a unique-looking specimen of *Wahydra* Steinhauser, 1991 (type species *Pamphila kenava* Butler, 1870) from Cuzco, Peru, belongs to the *W. kenava* group but does not show any clear affinities to a particular species, and therefore is new. This new species is genetically distant from all others; e.g., its COI barcode differs from that of *W. kenava* (type locality in Venezuela) by 7.3% (48 bp). This new species is diagnosed by a unique (for *Wahydra*) wing pattern: forewing orange spots are narrower, the cell $CuA_2-1A+2A$ is with one small elongated spot, situated along vein $1A+2A$, the spot in cell CuA_1-CuA_2 is rhomboidal and the spot in cell M_3-CuA_1 is separated from it by dark vein and shifted distad, overlapping with it by less than half of the width, the spot in cell R_5-M_1 is the smallest, slightly elongated; hindwing with a cluster of four spots in the subapical area, separated by dark veins: the spot between veins M_1 and M_3 is the largest, about a third of wing's length, other spots are less than half of this spot in length, those in cells $RS-M_1$ and M_3-CuA_1 are aligned to its distal margin (to follow the curvature of the outer wing margin) and the spot in the cell CuA_1-CuA_2 is aligned to the center of the M_1-M_3 spot, thus shifted basad from the spot in cell M_3-CuA_1 ; ventral side of wings is similar to *Wahydra thisbe* (Hayward, 1942) (type locality in Ecuador) in lacking the paler ray anterior of the dark wing section by inner margin, but the forewing yellow spots are smaller. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly3176.7.1:A170G, aly770.23.1:A79G, aly770.23.1:A93G, aly276634.3.2:C125A, aly536.138.1:T18C, aly159.13.1:A378A (not G), aly276634.3.2:C140C (not T), aly50.26.1:C33C (not G), aly587.20.1:T1440T (not A), aly499.36.22:G111G (not A), and COI barcode: T38C, T106C, T127C, T259C, T349C, A514C.

Barcode sequence of the holotype. Sample NVG-7989, GenBank OR837674, 658 base pairs:

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AAC TTTATATTTTATTTTGGAAATTTGGGCAGGAATACTAGGAACTTCTTTAAGTTTATTAATTCGTACAGAATTAGGTAATCCAGGATCTTTAATT
GGAGATGACCAAATTTATAATACTATTGTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATAACCTATTATAATTTGGAGGATTTGGAAATT
GATTAGTTCATTAAATATTAGGTGCACCTGATATAGCTTTCCACGAATAAATAATATAAGATTCTGAATATTACCTCCTTCCTTAATACTTCTAAT
TTCTAGTAGAGTCGTAGAAAATGGTGCAGGGACTGGTTGAACAGTTTACCCCCCTCCTCATCTAATATGACATCAAGGAGCATCTGCGATTTA
GCAATTTTTTCTCTTCAATTTAGCAGGAATTTCCCTCTATTTTAGGAGCTATTAATTTTACTACTACAATTTAATATACGAATAAAAATATATCAT
TTGATCAAATACCCTTATTTGTATGATCCGTAGGAATTACAGCTTTACTTTTACTTTTATCTTTACCAGTATTAGCTGGAGCTATTACAATACTTTT
AACAGATCGAAATTTAAATACATCTTTTTTTGATCCAGCAGGAGGAGAGATCCAATCCTATATCAACATTTATTT
```

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 111–112, bears the following five rectangular labels, four white: [PERU: Cusco | Qda. Morro Leguia | 13°08' 71°33' | 29 Aug 1989, 2150m | Leg. R. Robbins], [DNA sample ID: | NVG-7989 | c/o Nick V. Grishin], [genitalia| NVG170207-74 | Nick V. Grishin], [USNMMENT | {QR Code} | 01321829], and one red [HOLOTYPE ♂ | *Wahydra* | *cuzcona* Grishin].

Type locality. Peru: Cuzco Region, Cosñipata Valley, Quebrada Moro Leguia, elevation 2150 m, GPS –13.133, –71.550.

Etymology. The name is given for the type locality and is a noun in apposition.

Distribution. Currently known only from the holotype collected in the Cosñipata Valley, Peru.

***Cynea (Cynea) aureofimbria* Grishin, new species**

<https://zoobank.org/E2C5918D-5713-48C4-B171-FACD197E03B7>

(Fig. 5 part, 113–114, 342–344)

Definition and diagnosis. Phylogenetic analysis reveals that an unspotted brown specimen of *Cynea* Evans, 1955 (type species *Hesperia cynea* Hewitson, 1876) with unique orange fringes is sister to a group of species closely related to *Cynea cynea* (type locality in Venezuela) but is not genetically close to any of these species (Fig. 5): e.g., its COI barcode differs from that of *C. cynea* by 3.8% (25 bp), and therefore is a new species. This new species is recognizable by its uniformly dark brown wings on both sides, the forewing tornal area ventrally only very slightly paler than the rest of the wing due to sparse overscaling and without spots, and orange fringes on both wings (except apical areas). This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly5294.26.2:A30G, aly5294.26.2:T183A,

aly638.8.1:A318G, aly18826.6.2:A171G, aly18826.6.2:T180G, aly12063.12.6:A81A (not G), aly8211.10.1:A693A (not G), aly3277.16.1:C533C (not T), aly3277.16.1:C1022C (not T), aly37338.4.2:A48A (not C), and COI barcode: A81C, G200A, A211G, T358C, 484C, A514T.

Barcode sequence of the holotype. Sample NVG-18119D08, GenBank OR837675, 658 base pairs:

```
AACTTTATATTTTATTTTGGGAATTTGAGCAGGAATATTAGGAACTTCATTAAGATTATTAATTCGTACAGAATTAGGTACCCAGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATGGAGGATTTGGTAATT
GATTAATTCCTTTAATGTTAGGAGCCCCGTGATATAGCCTTCCCTCGAATAAATAACATAAGATTTTGAATACTTCCCCCTCATTAATATTATTAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGAACCTGGATGAACAGTTTATCCTCCTTTATCTTCTAACATGCTCACCAAGGATCCTCAGTTGATTTA
GCAATTTTTTCTCTTCATTTAGCAGGTATTTCTTCTATTTTAGGAGCTATTAATTTTTATTACAACAATCATTAATATACGAATTAATAATTTAACCT
TTGATCAAATACCTTTATTTGTTGATCTGTAGGAATTACTGCTCTTTTATTACTTTTATCTTTACCAGTATTAGCTGGAGCTATTACAATACTTTT
AACAGATCGAAATTTAAATACTTCTTTTTTTGATCCTGCTGGAGGAGGATCCTATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 113–114, bears the following six rectangular labels, five white: [Old Sto. Domingo | Rd. 1800 m ECUADOR | 7 Oct. '73 | S.S. Nicolay], [♂ genitalia | slide/vial # | H600 | Prep. S.S. Nicolay], [*Cynea* sp^s. | nr. megalops | Det. | S.S. Nicolay], [DNA sample ID: | NVG-18119D08 | c/o Nick V. Grishin], [USNMNT | {QR Code} | 01531869], and one red [HOLOTYPE ♂ | *Cynea aureofimbria* | Grishin].

Type locality. Ecuador: Pichincha/Santo Domingo de los Tsáchilas Province, Old Santo Domingo road, elevation 1800 m.

Etymology. In Latin, *aurea fimbria* means golden fringe. The name reflects the golden-orange fringe on the wings of this species and is a noun in apposition.

Distribution. Currently known only from the holotype collected in Ecuador.

Cynea (Nycea) erebina (Möschler, 1879) and *Cynea (Nycea) cleocharis* (Mabille, 1891) are species distinct from *Cynea (Cynea) diluta* (Herrich-Schäffer, 1869)

Phylogenetic analysis of *Cynea* Evans, 1955 (type species *Hesperia cynea* Hewitson, 1876) reveals that *Carystus erebina* Möschler, 1879 (type locality in Colombia, holotype sequenced as NVG-21118B08) and *Pamphila cleocharis* Mabille, 1891 (type locality Venezuela: Valera, syntype sequenced as NVG-15036G08) currently regarded as junior subjective synonyms of *Cynea (Cynea) diluta* (Herrich-Schäffer, 1869) (type locality not specified) are in a clade (and subgenus) different from a specimen from Guyana identified as *C. diluta* and the holotype of *Proteides osemba* Möschler, 1883 (type locality in Suriname), currently treated as a junior subjective synonym of *C. diluta* (Fig. 5) (Zhang et al. 2022b). The two taxa *C. erebina* and *P. cleocharis* belong to the subgenus *Nycea* Grishin, 2022 (type species *Pamphila hycsos* Mabille, 1891), differ from each other by 3.5% (23 bp) in COI barcodes and differ from other species of *Nycea* (Fig. 5). Therefore, we reinstate them as species: *Cynea (Nycea) erebina* (Möschler, 1879) and *Cynea (Nycea) cleocharis* (Mabille, 1891).

Pamphila hycsos Mabille, 1891 is a junior subjective synonym of *Cynea (Nycea) erebina* (Möschler, 1879), with lectotype designation

Genomic sequencing of the primary type specimens of *Carystus erebina* Möschler, 1879 (holotype sequenced as NVG-21118B08) and *Pamphila hycsos* Mabille, 1891 (syntype sequenced as NVG-18043B08), both from Colombia, reveals their genetic similarity (COI barcodes differ by 0.3%, 2 bp). The two type specimens are phenotypically similar and are from the same country of origin. Therefore, we propose that *Pamphila hycsos* Mabille, 1891, is a **new junior subjective synonym** of *Cynea (Nycea) erebina* (Möschler, 1879). As a result, *Cynea (Nycea) erebina somba* Evans, 1955 is a **new combination**, originally described and maintained as *Cynea hycsos somba* Evans, 1955. To stabilize these treatments, N.V.G. hereby designates a male syntype in the Museum für Naturkunde, Berlin, Germany, that bears the following nine rectangular labels (the first three are purple, blue, and red, respectively, others are white): [Origin], [Columb], [Pa. hycsos | ♂ Mab.], [Coll. Sommer], [Coll. | Staudinger], [Hycsos | Mab.], [GEN.PEP. | MIELKE | 1996], [{OR Code} http://coll.mfn-berlin.de/u/ | 44a043], [DNA sample ID: | NVG-18043B08 | c/o Nick V. Grishin], as the **lectotype** of *Pamphila hycsos* Mabille, 1891. The Sommer collection was bought by Staudinger in 1873 (before the description of *P. hycsos*), and the red label appears to be in Mabille handwriting, thus providing additional evidence that this specimen is a syntype.

***Cynea (Nycea) quada* Grishin, new species**

<https://zoobank.org/6A719582-3B76-4FD4-9C4C-FEC6DF85C27E>

(Fig. 5 part, 115–116, 345–347)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Ecuador identified as *Cynea (Cynea) diluta* (Herrich-Schäffer, 1869) (type locality not specified) or *Cynea bistrigula* (Herrich-Schäffer, 1869) (type locality not specified) is more related to *Cynea (Nycea) erebina* (Möschler, 1879), but shows prominent genetic differentiation from the latter species (Fig. 5): e.g., their COI barcodes differ by 2.6% (17 bp), and therefore the Ecuadorian specimen represents a new species. This new species keys to *C. popla* Evans, 1955 (type locality in Trinidad) (L.7.8) in Evans (1955) and differs from its relatives by narrower forewing spots, four yellowish dots on the ventral hindwing: one in the middle and three in the postdiscal area (Fig. 115–116), more concave sides of uncus in dorsal view, arms not separated but with a shallow notch between them, their distal margin relatively flat and angled on the sides, gnathos arms thinner, shorter, strongly sclerotized, sacculus distally with a couple of small teeth, harpe terminally rounded, continues into a rounded thumb-like finely serrated process directed anterodorsad, situated inner from ampulla and covered with it in outer lateral view (Fig. 345–347). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly653.3.7:G45A, aly798.8.27:G99A, aly1651.42.3:T36A, aly525.64.4:C90T, aly127.90.1:T201C, aly390.26.4:G93G (not A), aly4265.5.1:T96T (not C), aly531.44.1:C1237C (not T), aly2011.20.4:G135G (not A), aly18826.6.2:A102A (not G), and COI barcode: A100C, A253G, T268C, 325C, T500C.

Barcode sequence of the holotype. Sample NVG-18119D03, GenBank OR837676, 658 base pairs:

```
AACTTTATATTTTTATTTTTGGAATTTGAGCAGGTATATTAGGAACCTTCCTTAAGATTATTAATTCGTACAGAATTAGGTAACCCAGGATCATTAAAT
GGCGATGATCAAATTTATAACTATTGTAACAGCTCATGCCTTTATTATAATTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGTAATT
GATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCCGAATAAATAACATGAGATTTGAATACTCCCACCTTTAATACTACTAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGAACCGGTTGAACAGTTTACCCCCCTCTTTCATCTAATATTGCCCATCAAGGAAGTTTCAGTTGATTTA
GCAATTTTTTCCCTTCATTTAGCGGGAATTTCTTCTATTTTAGGGCTATCAATTTTATTACAACAATTTAATATACGAATCAATAATATATCAT
TTGATCAAATATCCCTATTATTGATCAGTAGGTATTACAGCACTTTTATTACTTTTTATCCTTACCAGTATTAGCAGGAGCTATTACTATACTTTT
AACAGATCGAAATTTAATACTTCTTTTTTTGATCCTCGAGGAGGAGATCCTATTTTATATCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 115–116, bears the following six rectangular labels, five white: [ECUADOR: Napo Prov | 4 km Tena-Pano Rd. | 1° 02'S 77° 50'W | 600m 27 Sep 1990 | S S Nicolay leg], [♂ genitalia | slide/vial # | H1068 | Prep. S.S. Nicolay], [*Cynea* ♂ | *bistrigula* | Det. H-S. | S.S. Nicolay], [DNA sample ID: | NVG-18119D03 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01531867], and one red [HOLOTYPE ♂ | *Cynea quada* | Grishin].

Type locality. Ecuador: Napo Province, km 4 of Tena-Pano Rd., elevation 600 m, GPS –1.033, –77.833.

Etymology. The name is for the four points on each ventral hindwing and four major spots on both forewings taken together and also for the type locality in Ecuador. The name is a noun in apposition.

Distribution. Currently known only from the holotype collected in Napo, Ecuador.

***Cynea (Quinta) achirae* Grishin, new species**

<https://zoobank.org/1E962C5C-976E-4C07-9D15-B8FBD3EE63FF>

(Fig. 5 part, 117–118, 348–349)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Mexico identified as *Cynea (Quinta) cannae* (Herrich-Schäffer, 1869) (type locality not specified, possibly in Venezuela, lectotype sequenced as NVG-15035D04) show prominent genetic differentiation from it in the Z chromosome (Fig. 5) (although COI barcodes differ only by 0.8%, 5 bp), and therefore represent a new species. This new species keys to “*Quinta cannae*” (L.6.1) in Evans (1955) but differs from it by usually less contrasting patterns of wings venter (Fig. 118), shorter and directed dorsad (not dorsoposteriad) process at the base of harpe, overlapping the process of ampulla for its entire width, but not projecting much dorsad of it in lateral view (Fig. 349). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1011.4.6:C72T, aly37338.16.1:C549T, aly37338.16.1:C573T, aly390.11.3:C108G, aly2612.8.8:T199C, and COI barcode: 352C, T367C, A586C.

Barcode sequence of the holotype. Sample NVG-19012H03, GenBank OR837677, 658 base pairs:

AACTTTATATTTTATTTTCGGAATTTGAGCAGGAATATTAGGAACTTCTTAAAGATTATTAATTCGTACAGAATTAGGAAATCCAGGATCTTTAATT
GGAGATGATCAAATTTATAACTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATCATAATGGAGGATTTGGTAATT
GATTAGTTCCTCTTATATTAGGAGCCCCGTATATAGCTTTCCACGAATAAATAATATAAGATTCTGAATACTCCCCCATCTTTAATATTATTAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGTACAGGCTGAACAGTATATCCCCCTCTTTCCTCTAATATGCTCACCAAGGAAGATCTGTTGACTTA
GCTATTTTTTCTCTCATTTAGCTGGAATTTTCATCTATTTTAGGAGCTATTAATTTTATTACAACAATTATCAATATACGAATTAGTAATATATCAT
TTGATCAAATACCTTTATTTGTATGATCTGTAGGTATTACAGCTCTTTTATTATTATTATCCTTACCTGTATTAGCTGGAGCAATTACTATATTATT
AACCGATCGAAATTTAAATACCTCATTTTTTGACCCTGCAGGAGGAGGTGATCCTATTTTATATCAACATTTATTT

Type material. Holotype: ♂ deposited in the Texas A&M University Insect Collection, College Station, TX, USA (TAMU), illustrated in Fig. 117–118, bears the following seven rectangular labels, six white: [MEXICO: | Tamaulipas, | Ciudad Mante | Los Arcos Ct.], [ex pupa | 7 Feb 1974 | Roy O. Kendall | & C. A. Kendall], [CHROMOSOMES: | Kendall Log- | H-201 -M | N=30¹, 31⁵], [Larva Foodplant: | CANNACEAE | *Canna indica* | Linnaeus | (foliage)], [HESPERIIDAE, | Hesperinae: | Quinta cannae | (Herr.-Schaffer, 1869) | ♂ det. R. O. Kendall | [M. & B. No. 138.2], [DNA sample ID: | NVG-19012H03 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | *Cynea achirae* | Grishin]. **Paratypes:** 3♂♂ from Mexico: 1♂ NVG-22035B12 Cuernavaca, Jun-1906, genitalia vial NVG230216-44 (Fig. 348–349) [USNM] and 2♂♂ Sonora, Alamos, J. P. Brock leg., ex larvae on *Canna indica* L.: NVG-21056B01 eclosed Sep-1994; NVG-21056B02 eclosed 8-Oct-1993.

Type locality. Mexico: Tamaulipas, Ciudad Mante, Los Arcos Ct.

Etymology. Achira is one of the common names for *Canna indica* L., a frequent larval foodplant of this species. The name is treated as a noun in apposition.

Distribution. Mexico.

***Eutus amazonicus* Grishin, new species**

<https://zoobank.org/FE50E403-652D-4E02-8EB3-6EAA7C30B600>

(Fig. 5 part, 119–120, 350–352)

Definition and diagnosis. Phylogenetic trees reveal that specimens from the Amazonian region that were challenging to place belong to the genus *Eutus* Grishin, 2022 (type species *Cobalus rastaca* Schaus, 1902) and are the closest to *Eutus yesta* (Evans, 1955) (type locality in Peru: Inambari) or its relative (Fig. 5) but are phenotypically distinct and therefore represent a new species. Identified by the following combination of characters: wings are narrower than in *E. yesta*, forewing is with a contrasting black wedge-shaped brand at the base of forewing cell CuA₁-CuA₂, hyaline spot shaped as an angle bracket distad of the brand, three round spots of decreasing size in cells M₃-CuA₁, R₅-M₁, and R₄-R₅, and a small spot at the upper side of forewing discal cell; ventral forewing is with a large (about half of wing length) cream area near tornus, ventral hindwing with more or less apparent yellowish spots and a trace of a pale ray in the cell CuA₂-1A+2A. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly1656.16.2:A48C, aly1656.16.2:A63G, aly4456.8.2:C72T, aly517.17.2:C372G, aly517.17.2:G516A, and COI barcode: A22G, T25C, T103C, T157C, T304C, A586C.

Barcode sequence of the holotype. Sample NVG-19121G08, GenBank OR837678, 658 base pairs:

AACTTTATATTTTATTTTGGGATCTGAGCAGGAATATTAGGAACTTCTTAAAGTTTATTAATTCGTACTGAATTAGGAAATCCGGGTTCTTTAATT
GGAGACGATCAAATTTATAACACTATCGTTACAGCACATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTATAATGGTGGATTTGGAAAT
GACTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCACGAATAAATAATATAAGATTTTGAATATTACCCCTTCTTTATTTTATTAAT
TTCAAGAAGAATCGTAGAAAATGGAGCAGGAACAGGATGAACAGTATACCCCTCTTTATCTTCTAACAATTGCCACCAAGGATCTCTGTTGATTA
GCAATTTTTTCTCTACATTTAGCAGGAATTTTCATCCATTTTAGGAGCTATTAATTTTATTACTACAATTTAATATACGAATTAGAAATATATCAT
TTGACCAAAATACCTTTATTTGTATGATCTGTAGGTATTACCGCTTTATFACTACTCTTTATCTTTACCTGTATTAGCTGGAGCTATTACTATACCTTT
AACCGATCGAAATTTAAATACCTCATTTCTTTGATCCTGCTGGAGGAGGAGATCCTATTTTATACCAACATTTATTT

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 119–120, bears the following six rectangular labels, five white: [PERU Madre De Dios | Rio La Torre 300m | Tambopata Res. | 5 Oct. '86 | S.S. Nicolay], [♂ genitalia | slide/vial # | H956 | Prep. S.S. Nicolay], [Thoon ♂ | Det. ponka | S.S. Nicolay], [DNA sample ID: | NVG-19121G08 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01602763], and one red [HOLOTYPE ♂ | *Eutus amazonicus* | Grishin]. **Paratypes:** 1♂ NVG-22023D03, H20815 French Guiana, Montagne Favard, GPS 4.500, -52.050, 18-Sep-2003, B. Hermier leg. [BHermier] and 1♀: NVG-21048D10 62 km S of Ariquemes, linha C-10, 5 km S of Cacaulandia, 8-Oct-1994 O. Gomes leg. [MGCL].

Type locality. Peru: Madre de Dios, Tambopata National Reserve, Rio La Torre, elevation 300 m.

Etymology. The name is for the Amazonian distribution of this species and is a noun in apposition.

Distribution. The Amazonian region: recorded from Peru, French Guiana, and Brazil.

Eutus incus Grishin, new species

<https://zoobank.org/9ACA4D61-7A97-46AC-A262-E1DBD30EC6D2>

(Fig. 5 part, 121–122, 353–354)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from the Cosñipata Valley in Peru that was superficially similar to *Eutus amazonicus* new species is genetically differentiated from it (Fig. 5): e.g., their COI barcodes differ by 6.5% (43 bp) and, therefore, represents a new species. This new species is similar to *Eutus amazonicus* new species and differs from it by having a larger brand at the base of forewing cell CuA₁-CuA₂, larger hyaline spots, smaller ventral hindwing tornal pale area, and larger (although still small, dot-like) yellowish spots on ventral hindwing. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly85.15.2:A144C, aly349.15.2:A54G, aly1468.20.2:T507C, aly18826.15.1:T129C, aly1432.18.2:A42G, aly1656.16.2:A48A (not C), aly1656.16.2:A63A (not G), aly4456.8.2:C72C (not T), aly425.14.6:C90C (not T), aly517.17.2:C372C (not G), and COI barcode: T10C, A34G, T112C, T223A, T499C.

Barcode sequence of the holotype. Sample NVG-19023C07, GenBank OR837679, 658 base pairs:

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AACTTTTACTTTTATTTTGGAAATTTGAGCAGGGATATTAGGAACTTCTTTAAGTTTATTAATTCGTACTGAATTAGGAAATCCAGGCTCTTTAATT
GGAGATGATCAAATCTATAATACTATTGTTACAGCACATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTATAAATGGAGGATTTGGAAATT
GATTAGTTCCTTTAATATTAGGGGCCCCAGACATAGCTTTCCACGAATAAATAAATAAGATTTTGAATACTACCTCCTCTTTATTTTATTAAT
CTCAAGAAGAATTGTAGAAAATGGAGCAGGTACAGGATGAACAGTTTACCCCTCTATCTTCTAATATGCCCCACCAAGGATCCTCTGTGATTTA
GCAATTTTTTCTTACATTTAGCAGGAATTTTCATCCATTTTAGGAGCTATTAATTTTATTACTACAATTTAATATACGAATTAGAAATATATCAT
TTGATCAAATACCCTTATTTGTTGATCTGTAGGTATTACTGCTTTATTATTACTTTTATCTTTGCCCCGATTAGCTGGAGCTATTACTATACTTTT
AACTGATCGAAATTTAAATACTTCATTTTTTGTATCCTGCTGGAGGAGGAGATCCTATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 121–122, bears the following four rectangular labels, three white: [PERU: Cuzco: Cosñipata Valley | Quebrada Quitacalzón 1,050m. | 13° 01' 13"S, 71° 29' 50"W | 12 August 2009 Brian Harris], [DNA sample ID: | NVG-19023C07 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532830], and one red [HOLOTYPE ♂ | *Eutus incus* | Grishin].

Type locality. Peru: Cuzco Region, Cosñipata Valley, Quebrada Quitacalzón, elevation 1050 m, GPS –13.020278, –71.497222.

Etymology. The name is for the type locality in Cuzco, the center of the Inca Empire. The name is a noun in apposition.

Distribution. Currently known only from the holotype collected in Cosñipata Valley, Peru.

Eutus septemaculatus Grishin, new species

<https://zoobank.org/3F5D4627-A738-4C6B-9DB4-687DFCA5FE1D>

(Fig. 5 part, 123–124, 355–356)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Mato Grosso Brazil with wing pattern similarities to *Eutus mubevensis* (E. Bell, 1932) (type locality in Paraguay) shows prominent genetic differentiation from it (Fig. 5): e.g., their COI barcodes differ by 9.1% (60 bp) and, therefore, represents a new species. This new species keys to “*Decinea mubevensis*” (L.11.9) in Evans (1955) but differs from it (males) by rounder hindwings, larger hyaline forewing spots, and brighter ventral forewing tornal area (Fig. 123–124), harpe more robust, not shorter than valva, and ampulla process more massive, only slightly shorter than costa (Fig. 355–356). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly18826.14.1:C60G, aly1295.8.3:A42T, aly207.9.6:T195C, aly207.9.6:A312G, aly5294.34.2:A116G, aly490.2.1:T435T (not C), aly490.2.1:A501A (not T), aly531.12.1:T103T (not A), aly1146.43.2:T93T (not C), aly2127.7.4:T726T (not C), and COI barcode: T50C, A101G, T346A, T382A, A421C.

Barcode sequence of the holotype. Sample NVG-19021H05, GenBank OR837680, 658 base pairs:

```
AACTTTATATTTTATTTTGGAAATTTGAAGAGGTATATTAGGAACTTCTCTAAGTTTATTAATTCGTACAGAATTAGGTAATCCTGGATCTTTAATT
GGAAATGACCAAATTTATAACTATATCGTAACAGCTCACGCTTTCATTATAATTTTTTTTATAGTTATACCTATTATAATTTGGTGGATTTGGAAAT
GATTAGTACCTTTAATATTAGGAGCACCTGATATAGCTTTCCACGAATAAATAAATAAGATTTTGAATATTACCCCTTCTTTAATATTATTAAT
TTCAAGAAGAATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATATCCCCACTTCTTCTAATATTGCCATCAAGGATCTTCTGTAGATTTA
GCAATTTTCTCCCTTCATTTAGCTGGTATTTCCCTCTATTTAGGAGCTATTAATTTTATTACTACAATTATAATATACGAATTAATAATATATCCT
TTGATCAAATACCATTATTTGTTTGGATCGGTAGGAATTACAGCTCTTTTATTACTTTTATCTTTACCAGTATTAGCAGGACCAATTAATATATT
AACAGATCGAAATTTAAATACTTCATTTTTGATCCTGCTGGAGGAGGAGACCTATTTTATATCAACATCTATTT
```

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 123–124, bears the following five rectangular labels, three white: [BRAZIL MT | Cuiaba/Santarem | Sinope-km 500 | 13 July 1979 | leg. S.S. Nicolay], [DNA sample ID: | NVG-19021H05 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532718], and one red [HOLOTYPE ♂ | *Eutus septemaculatus* | Grishin].

Type locality. Brazil: Mato Grosso, km 500 of Cuiabá–Santarém highway, Sinop.

Etymology. The name is for seven spots on the forewing. In Latin, *septem* means seven, and *macula* means spot. The name is a masculine perfect passive participle in the nominative singular.

Distribution. Currently known only from the holotype collected in Mato Grosso, Brazil.

Godmia viridicapita Grishin, new species

<https://zoobank.org/6255941E-1A19-4ED0-810E-A334F5C57211>

(Fig. 5 part, 125–126, 357–358)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Ecuador identified as *Godmia chlorocephala* (Godman, 1900) (type locality in Panama) shows prominent genetic differentiation from it (Fig. 5): e.g., their COI barcodes differ by 4.7% (31 bp), and therefore represents a new species. This new species keys to “*Onophas chlorocephala*” (J.51.3) in Evans (1955) but differs from it by less elongated upper part of the brand, both upper and lower segments, and even weaker developed forewing pale spots (essentially none visible in the holotype) (Fig. 125–126), uncus arms thin, bowed, terminally converging, space between them is drop-shaped in dorsal view, harpe is not separated from valva, together they form semi-rectangular shape in lateral view, gnathos with flattened, blade-like overlapping arms, harpe with a semi-circular ridge on the inner surface, saccus is the same length as uncus (Fig. 357–358). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1405.6.4:A75G, aly1405.6.4:T78C, aly15220.1.1:G864T, aly525.64.4:C108T, aly525.64.4:G162A, aly5773.2.5:T315T (not C), aly1175.3.8:G72G (not C), aly1175.3.8:G93G (not A), aly1772.7.1:G714G (not A), aly5294.37.11:G897G (not A), and COI barcode: A64G, T67C, T103C, T403C, A559T.

Barcode sequence of the holotype. Sample NVG-19023F02, GenBank OR837681, 658 base pairs:

```
AACTTTATATTTTATTTTGGTATTTGAGCAGGAATATTAGGAAACATCTCTTAGTTTATTTGATTGCTCAGAATTAGGAAATCCAGGATCTTTAATT
GGAGACGATCAAATTTATAACTATTGTAAGTCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTTGGAGGATTTGGAAAT
GATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTCCACGAATAAATAAATAAGATTTTGAATATTACCACCTTCTTTAATATTATTAAT
TTCAAGAAGAATCGTAGAAAATGGTGGCTGGAACAGTGGATGAACAGTTTATCCCCCTTTCATCTAATATTGCCATCAAGGATCATCTGTTGATCTA
GCAATTTTTTCTCCACTTAGCAGGTATTTTCATCAATCTTAGGGCTATTAATTTTATTACTACAATTATAATATACGAATTAATAATTTATCTT
TTGATCAAATACCCTTTATTTGTTTGGATCTGTAGGAATTACAGCACTATTATTACTACTATCTTTACCTGTACTTGCAGGAGCTATTACTATATTATT
AACAGATCGAAATTTAAATACTTCATTTTTGACCCTGCTGGAGGAGGAGATCCAATTTTATATCAACACTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 125–126, bears the following five rectangular labels, four white: [Cotundo NAPO | ECUADOR 800m | 3 Oct '76 | S. S. Nicolay], [*Onophas* ♂ | *chlorocephala* | Det. God. | S.S. Nicolay], [DNA sample ID: | NVG-19023F02 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532855], and one red [HOLOTYPE ♂ | *Godmia viridicapita* | Grishin].

Type locality. Ecuador: Napo Province, Cotundo, elevation 800 m.

Etymology. The name is Latin from the Greek name of its sister species, *G. chlorocephala* (i.e., green-headed). In Latin, *viridi capite* is green head. The name is a feminine adjective.

Distribution. Only known from the holotype collected in northcentral Ecuador.

***Rhomba pulla* Grishin, new species**

<https://zoobank.org/8AE2A86B-97B8-4871-B55F-994B301AA720>

(Fig. 5 part, 127–128, 359–360)

Definition and diagnosis. Phylogenetic trees reveal that a nearly unmarked HesperIIDae specimen from San Pedro Lodge in Peru is closely related to *Rhomba gertschi* (E. Bell, 1937) (type locality in Panama) while showing prominent genetic differentiation from it (Fig. 5): e.g., their COI barcodes differ by 4.3% (28 bp) and, therefore, represents a new species. This species is similar to *R. gertschi* in the shape of brands (although the brand segments are bulkier), spotting of the ventral hindwing, and morphology of genitalia, but differs from it by the lack of hyaline spots, which gives it a very different appearance. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly728.22.1:A207G, aly2163.5.1:A138C, aly2163.5.1:T169G, aly736.5.4:A39G, aly736.5.4:T87C, aly1585.9.2:G97G (not T), aly2011.4.1:A84A (not G), aly2011.4.1:T90T (not C), aly85.11.3:G162G (not A), aly3312.7.2:T120T (not A), and COI barcode: T16C, C235T, A241T, T406C, A433G, T457C.

Barcode sequence of the holotype. Sample NVG-19023E08, GenBank OR837682, 658 base pairs:

```
AACTTTATATTTTATCTTTGGTATTTGAGCAGGAATATTAGGAACCTTCTTTAAGTTTATTAATTCGTACAGAATTAGGTAATCCAGGATCATTAAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTATAATGGAGGTTTTGGAAATT
GATTAGTACCATTAATATAGGGGCCCCAGATATAGCCTTTCCACGTATAAATAATATAAGATTTTGAATATTACCACCTTCATTAATATTACTAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGAACCTGGTTGAACAGTTTATCCACCTTTATCCTCTAATATCGCTCATCAAGGATCTTCTGTAGATTTA
GCAATTTTTCCCTTCACTTAGCAGGAATTTTCACTCAATTTTAGGGGCAATTAATTTTATTACAACAATCATTAAATATACGAATTAGAAATTTATCAT
TTGATCAAATACCTTTATTTATTGATCAGTAGGTATTACAGCAGCTTTTATTACTTTTATCTTTACCTGTTCTAGCTGGTGCTATTACTATACTTTT
AACAGATCGAAATTTAAATACTTCATTTTTTGTATCCAGCTGGTGGAGGTGATCCAATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 127–128, bears the following five rectangular labels, four white: [PERU:Cuzco, 1450m. | San Pedro Lodge | Cosnipata Rd 548 | 9-XI-2008 Kinyon], [DNA sample ID: | NVG-19023E08 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532850], and one red [HOLOTYPE ♂ | *Rhomba pulla* Grishin].

Type locality. Peru: Cuzco Region, Cosñipata Road, San Pedro Lodge, elevation 1450 m.

Etymology. In Latin, *pullus* means blackish or dark colored. The name is given for this darker (thus far) nearly unspotted species of the genus and is a feminine adjective.

Distribution. Currently known only from the holotype collected in the Cosñipata Valley, Peru.

***Niconiades victoria* Grishin, new species**

<https://zoobank.org/216DED72-3642-44BA-B553-22AD2C42EFF6>

(Fig. 5 part, 129–130, 361–363)

Definition and diagnosis. Genomic analysis of specimens we identified as *Niconiades nikko* Hayward, 1948 (type locality Argentina: Misiones) reveals their partitioning into two clades genetically differentiated in the Z chromosome (Fig. 5a) but not in the mitogenome (Fig. 5b). Due to prominent genetic differentiation in the nuclear genome, the two clades represent species-level taxa, and the North American species is new. This new species keys to *N. nikko* (O.11.6) in Evans (1955) and differs from it by typically weaker defined whitish band on the ventral hindwing and more extensive greenish-yellow overscaling (Fig. 130). Due to the cryptic nature of this species and significant wing pattern variability, most reliable identification is achieved by DNA and a combination of the following nuclear genomic base pairs is diagnostic: aly366.12.1:A1164G, aly383.17.7:C1401T, aly383.17.7:G1869A, aly1651.5.1:T1086C, aly694.1.1:A441C. There are no consistent differences between the new species and *N. nikko* in COI barcodes.

Barcode sequence of the holotype. Sample NVG-19013C03, GenBank OR837683, 658 base pairs:

```
AACTTTATATTTTATTTTGGTATTTGGGCTGGAATATTAGGAACCTTCCCTCAGTTTATTAATTCGTACAGAATTAGGTAATCCAGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATGGAGGATTTGGTAATT
GATTAGTACCCTTTAATATAGGAGCACCTGATATGGCTTTCCCCCGAATAAATAATATAAGATTTTGAATATTACCCTTCTTTAATATATTAAAT
CTCAAGAAGAATTGTAGAAAATGGTGTGGAACCTGGATGAACAGTTTACCCCTCTATCCTCTAATATTGCCACCAAGGATCATCAGTTGATTTA
GCAATTTTCTCTCTCATCTAGCCGGAATTTCTCAATTTCTAGGAGCAATTAATTTTATTACTACAATCATTAAATATACGAATTAGTAATATATCAT
TTGATCAAATACCTTTATTTGTTGATCTGTAGGTATTACAGCATTATTATTACTTTTTATCTTTACCAGTTTTAGCAGGGGCTATTACTATACTTCT
TACAGATCGAAATTTAAACACTTCATTTTTTGTATCTGCGAGGAGGAGATCCAATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the Texas A&M University Insect Collection, College Station, TX, USA (TAMU), illustrated in Fig. 129–130, bears the following seven rectangular labels: six white [MEXICO: | TAMAU-LIPAS | Rancho Pico de Oro | vic. of Los Kikos], [ex larva | 26 Dec 1974 | Roy O. Kendall | and C. A. Kendall], [Larval foodplant: | GRAMINEAE | Bambusa vulgaris | Schrad. | (foliage -)], [Niconiades ♂ | nikko | Hayward | det.H.A.Freeman], [HESPERIIDAE: | Hesperiiinae: | Niconiades nikko | ♂ Hayward, 1948 | Det. R. O. Kendall | [M. & B. No. 264.3]], [DNA sample ID: | NVG-19013C03 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | Niconiades | victoria Grishin]. **Paratypes:** 2♂ and 1♀: 1♀ NVG-18012C11, USNMENT_01450288 Mexico: San Luis Potosi, Cd. Valles, 15-Oct-1976, E. C. Knudson leg., genitalia X-3289 J. M. Burns 1992 [USNM], 1♂ NVG-20057B04 Mexico: Chiapas (no other data), genitalia vial NVG231118-03 [TMMC] (Fig. 361–363), and 1♂ NVG-18012C12, USNMENT_01450289 Honduras, San Pedro Sula, 24-Dec-1971, Robert D. Lehman leg., genitalia X-3249 J. M. Burns 1992 [USNM].

Type locality. Mexico: Tamaulipas, vic. Los Kikos, Rancho Pico de Oro.

Etymology. In Greek, νίκη (nike) is the word for “victory” which sounds similar to the name *N. nikko*, the sister species. In Latin, victory is *victoria*, the word used as this species’ epithet. The name is a noun in apposition.

Distribution. From eastern Mexico to Guatemala, at least.

***Lancephallus purpurus* Grishin, new genus and new species**

<https://zoobank.org/3AD6C438-4774-4FE6-9020-54F6A4A6D92E>

<https://zoobank.org/7BACF558-7208-4EFE-AF4C-923515E25AE5>

(Fig. 5 part, 131–134, 364–365)

Definition of the new genus. Phylogenetic analysis places specimens that agree with Evans’ unpublished (curation in BMNH only) concept of males of *Phlebodes confixa* (A. Butler, 1877) (type locality in Brazil: Amazonas) as a unique lineage sister to *Vetti* Godman, 1901 (type species *Papilio phyllus* Cramer, 1777) (Fig. 5). This lineage is prominently separated in trees from *Vetti*, stronger than *Vetti* species within the genus, and therefore represents a new genus. This new genus is diagnosed by unique male genitalia, in particular, by the shape of the aedeagus with extended caudal end, slightly curved and terminating in a sharp point and valva with a spike-like projection from the ampulla and rounded harpe, uncus arms strongly divergent, gnathos arms convergent. Males have a bi-partite brand with a longer section along cubitus between the origins of veins CuA_1 and CuA_2 and a dash below it, below vein CuA_2 . In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly2178.10.1:G66A, aly2178.10.1:T109C, aly1260.24.1:G228A, aly1019.12.6:C66T, aly1019.12.6:G78A.

Type species. *Lancephallus purpurus* Grishin, **new species.**

Species included in the genus. Only the type species.

Parent taxon for the genus. Subtribe Moncina A. Warren, 2008

Definition of the new species. While we have not sequenced true *P. confixa*, females of *Lancephallus* that were associated with males by DNA sequencing (and specimens in copula in BMNH) do not resemble the only known *P. confixa* syntype, a female, in having sharply defined pale spots on the ventral hindwing, which has a strong purple sheen and slightly paler veins. Therefore, this species of *Lancephallus* is new. In wing patterns, it is uniquely different from all of its closest relatives in *Vetti*, its sister genus. The only similarly patterned species formerly associated with *Vetti* was *Phlebodes fuldai* (E. Bell, 1930) (type locality in Colombia), now transferred to its rightful genus *Phlebodes* Hübner, [1819] (type species *Papilio pertinax* Stoll, [1781]) (Zhang et al. 2022b), which *Lancephallus* resembles. However, *Lancephallus* and *Phlebodes* are not closely related to each other (Fig. 5, 6). This new species is identified by chestnut-brown wings with small and narrow (in males) yellowish forewing spots in cells CuA_1 - CuA_2 and M_3 - CuA_1 , and in some specimens, one to three subapical dots, spots are larger and paler in females who may have a spot in upper discal cell beneath; ventrally with strong purple sheen, especially on hindwing that has variously developed postdiscal pale dots and a dot in the center, veins are paler. In DNA, a combination of the following base pairs is diagnostic in the COI barcode: T38C, A184T, A208T, A334C, A532C.

Barcode sequence of the holotype. Sample NVG-19021F03, GenBank OR837684, 658 base pairs:

AACTTTATATTTTATTTTGGAACTCTGAGCAGGAATACTAGGAACTTCTTTAAGTTTATTAATTCGTTTCAGAATTAGGAAATCCAGGTTTCATTAATT
GGAGATGATCAAATTTATAACTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTATAGTTATACCTATTATAATTGGAGGTTTTGGAAAT

GATTAGTACCTCTTATATTAGGAGCCCCGTGATATAGCTTCCCTCGAATAAATAATATAAGATTCTGAATACTTCCCCCTCATAATATTATTAAT
 TTCAGAAGAATTGTAGAAAATGGTGCAGGAAGCTGGATGAACCGTTTACCCCCCTCTTCTTCTAATATTGCTCATCAAGGATCTTCAGTAGATT
 GCTATCTTTTCCCTTCATTTAGCAGGAATTTTCATCTATTCTAGGAGCTATTAATTTTATTACTACAATTATTAATATACGAATTAATAATTTATCTT
 TTGATCAAATACCTTTATTTGTATGATCAGTAGGAATTACTGCACCTTATTACTTTTATCTTTACCTGTATTAGCAGGAGCTATTACTATACCTTT
 AACAGATCGAAATTTAAATACTTCATTTTGTATCCAGCAGGAGGAGGAGATCCTATTCTATATCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 131–132, bears the following five rectangular labels, four white: [GUYANA: Cuyuni R, | Kamaria Falls 100' | 30.XI.–5.XII.2000 | 6° 24'N 58° 54.6'W | Leg. S. Fratello et al] (GPS given as “546'W”), [DNA sample ID: | NVG-19021F03 | c/o Nick V. Grishin], [{QR Code} | USNM ENT 00275117], and one red [HOLOTYPE ♂ | Lancephallus | purpurus Grishin]. **Paratypes:** 5♂♂ and 2♀♀: 1♂ Colombia/Venezuela border, Orinoco River, Maipures, Dec-1898, Cherrie leg. [BMNH]; 1♂ Venezuela, Suapure, 2-Mat-1899, Klages leg. [BMNH]; 2♂♂ NVG-18098F02, H15049 and (not sequenced) H15046 French Guiana, Bagne des Annamites, GPS 4.8333, –52.5167, H. Crampette leg., 12-Jul-1998 [BHermer], 1♂ and 1♀ in copula, Guyana 1962–3 [BMNH]; 1♀ NVG-19024B11, USNM ENT 00275122 Guyana: Acarai Mts., Sipu River, elevation 900 ft, GPS 1.4183, –58.9533, 24-Oct-12-Nov-2000, S. Fratello et al. leg. [USNM] (Fig. 133–134).

Type locality. Guyana: Cuyuni-Mazaruni Region, Cuyuni River, Kamaria Falls, approx. GPS 6.40, –58.91.

Etymology. In Latin, *lancea* means spear, lance, or pike. The name is given for the spear-shaped aedeagus (*phallus*), and the species epithet is for the extensive purple sheen on the ventral side of the wings. The name of the genus is a masculine noun in the nominative singular, and the species name is a masculine adjective.

Distribution. Venezuela, Guyana, and French Guiana.

Mnasicles (Remella) ecua Grishin, new species

<https://zoobank.org/E5849270-FF1F-4A4A-B099-B9097FABABDF>

(Fig. 6 part, 135–136, 366–367)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Ecuador identified as *Mnasicles (Remella) remus* (Fabricius, 1798) (type locality in “Caiena”) shows prominent genetic differentiation from it (Fig. 6): e.g., their COI barcodes differ by 4.6% (30 bp), and therefore represents a new species. This new species keys to “*Moeris remus*” (J.33.1) in Evans (1955) but differs from it by more developed pale area at the apex of ventral forewing (Fig. 136), not strong spots as in *Mnasicles (Remella) rita* (Evans, 1955) (type locality in Guatemala) and relatives, but more prominent than in most *M. remus*, uncus smaller, terminally knob-like, strongly humped in lateral view, tegumen short, not much longer than vinculum width, harpe shorter, with less developed tooth on the dorsal side, costa convex in the middle and slightly concave before ampulla that is separated from harpe by a narrower groove (Fig. 366–367). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly216.58.1:T366A, aly216.58.1:A492C, aly1456.2.1:T15C, aly1139.65.24:T108A, aly1139.65.24:A117C, aly2954.3.1:T525T (not A), aly2954.3.1:C800C (not T), aly127.87.1:T24T (not G), aly127.87.1:A177A (not G), aly11700.1.14:A59A (not T), and COI barcode: T5T, A37G, A100G, T316G, T463C.

Barcode sequence of the holotype. Sample NVG-19017B02, GenBank OR837685, 658 base pairs:

AACTTTATATTTTATTTTGGAAATTTGAGCAGGAATATTAGGAAGCTTCTTAAAGTTTATTAATTCGAACAGAATTAGGTAATCCAGGATCTTTAATT
 GGAGATGATCAAATTTATAACACTATTGTAACAGCTCATGCTTTTATTATAATTTTTCATAGTTATACCTATTATAATTTGGAGGATTTGGTAATT
 GATTAGTTCCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCACGAATAAATAATATAAGATTTGAATACTTCCCTCCTTTAATACTTTTAAAT
 TTCAGAAGAATCGTAGAAAATGGGGCAGGTAAGTGGTGAACAGTTTATCCTCCTTTATCTTCTAATATTGCTCATCAAGGTTTATCTGTTGATT
 GCAATTTTCTTTACATTTAGCAGGAATTTTCATCTATTATTAGGAGCTATTAATTTTATTACTACAATTATTAACATACGAGTAAGAACTTATCAT
 TTGATCAAATACCTTTATTTGTATGATCAGTAGGATTTACTGCTTTATTATTACTTTTATCTTTACCTGTATTAGCAGGAGCTATTACTATACCTTT
 AACTGATCGAAATTTAAATACTTCATTTTGTGACCTGCTGGAGGAGGAGATCCTATTTTATACCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 135–136, bears the following four rectangular labels, three white: [ECUADOR-Pich. | Napac-1000m | 12 Sept. 1976 | leg.S.S.Nicolay], [DNA sample ID: | NVG-19017B02 | c/o Nick V. Grishin], [USNM ENT | {QR Code} | 01532380], and one red [HOLOTYPE ♂ | *Mnasicles (Remella) ecua* Grishin].

Type locality. Ecuador: Pichincha Province, Río Napac, elevation 1000 m.

Etymology. The name is given for *Ecuad[or]*, the type locality of this species, and is a noun in apposition.

Distribution. Only known from the holotype collected in the Andean region of northern Ecuador.

Lectotype designation for *Amblyscirtes fluonia* Godman, 1900

Amblyscirtes fluonia Godman, 1900 was described from a series of specimens collected at different localities in Mexico: Guerrero and Jalisco. To define the type locality more precisely, N.V.G. hereby designates a male syntype in the Natural History Museum, London, UK, that, according to its label was illustrated by Godman (1899–1901) and bears the following nine rectangular (except the first two, which are round and with a red circle on the upper side) white labels: (Type) and on the other side (H | 2162), (Type | H. T.), [Xucumanatlan, | Guerrero, | 7000 ft. | July. H.H.Smith.], [♂], [Sp. figured.], [B.C.A.Lep.Rhop. | Amblyscirtes | fluonia, | Godm.], [Godman-Salvin | Coll. 1913.—2.], [{QR Code} | NHMUK 012824161], and [MOLECULAR | 0247279852], as the **lectotype** of *Amblyscirtes fluonia* Godman, 1900. This specimen was sequenced as NVG-18082H01. The type locality of *A. (Amblyscirtes) fluonia* becomes Mexico: Guerrero, Xocomanatlan, elevation 7000 ft, approximate GPS 17.550, –99.617.

Amblyscirtes (Amblyscirtes) aeratus Grishin, new species

<https://zoobank.org/02F9C1E1-2242-4E8B-9276-C8F3614C6FD2>

(Fig. 6 part, 137–140, 368–369)

Definition and diagnosis. Phylogenetic trees reveal that a number of specimens identified as *Amblyscirtes (Amblyscirtes) fluonia* Godman, 1900 (type locality in Mexico: Guerrero) show prominent genetic differentiation from it (Fig. 6): e.g., their COI barcodes differ by 5.6% (37 bp). These specimens are not even monophyletic with *A. fluonia* and therefore belong to a new species. This new species keys to *A. fluonia* (N.2.7) in Evans (1955) but differs from the true *A. fluonia* (Fig. 141–144) by the lack of pebbly variegated appearance on the ventral side of wings, in particular on the hindwing and the submarginal area of forewing. In wing pattern, it resembles *Amblyscirtes aenus* W. H. Edwards, 1878 (type locality in USA: Colorado) more than *A. fluonia*, but the spots are more diffuse and less defined, e.g., forewing apical spots are smaller and yellow, and ventral hindwing postdiscal band is composed of diffuse and interconnected blotches rather than smaller and separated spots. In DNA, and a combination of the following base pairs is diagnostic in the nuclear genome: aly522.2.4:T99A, aly522.2.4:C124T, aly587.21.2:G153A, aly587.21.2:T156C, aly669.9.1:T201A, and COI barcode: T205C, T206C, A295T, T397C, T418C, A565G.

Barcode sequence of the holotype. Sample NVG-18063E02, GenBank OR837686, 658 base pairs:

```
AACTTTATATTTTATTTTGGTATTTGAGCAGGTATATTAGGAACTTCTTTAAGTTTATTAATTCGAACAGAATTAGGTAATCCTGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTTGGAGGTTTTGGAAAT
GATTAGTCCCTTATATTAGGAGCTCCTGATATAGCTTTCCACGAATAAATAATATAAGATTTTGAATACTTCCCTTCTTTATTACTTTTAAAT
TTCTAGAAGAATTGTAGAAAATGGTGCAGGAACAGGATGAACAGTTTTATCCCCCTCTTTCTTCTAATATTGCACATCAAGGATCATCAGTTGATTTA
GCAATTTTCTCTCTTCATTTAGCAGGAATCTCTTCTATTCTAGGAGCTATTAATTTTATTACTACAATTTAATATACGAGTTAGAAAATTTAATAT
TTGATCAAATACCTTTATTTGTTTGATCAGTAGGTATTACTGCTTTATATTACTTTTTATCTTTACCAGTTCTAGCTGGGCTATTACTATACTTCT
TACAGATCGAAATTTAAATACTTCAATTTTTGATCCTGCTGGAGGAGGGGATCCAATTTTATACCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 137–138, bears the following four rectangular labels, three white: [MEXICO: OAXACA | El Vado-San Sebastian | 5500-6500 ft | c 16° 53' N 96° 53' W | 27-Jun-1992 J. Kemner], [DNA sample ID: | NVG-18063E02 | c/o Nick V. Grishin], [USNMNT | {QR Code} 01466204] and one red [HOLOTYPE ♂ | Amblyscirtes | aeratus Grishin]. **Paratypes:** Mexico: 1♂ NVG-19042F06 Colima, Jun-1918, C. C. Hoffmann leg., AMNH_IZC 00337883 [AMNH] and 1♀: NVG-19122A02 Oaxaca, La Canada, 2 mi S Domingullo, ca. 2500 ft, GPS 17.6500, –96.9167, 8,10-Aug-1991, J. Kemner leg. [USNM] (Fig. 139–140).

Type locality. Mexico: Oaxaca, El Vado–San Sebastián, elevation 5500–6500 ft, GPS 16.8833, –96.8833.

Etymology. Like *aenus*, the name *aeratus* in Latin means made or covered with brass or bronze. *Fluonia* means a flow, and the pebbly appearance is like a flow on the wings, which is not present in this species. The name is an adjective.

Distribution. At least southwestern Mexico, known from Colima and Oaxaca.

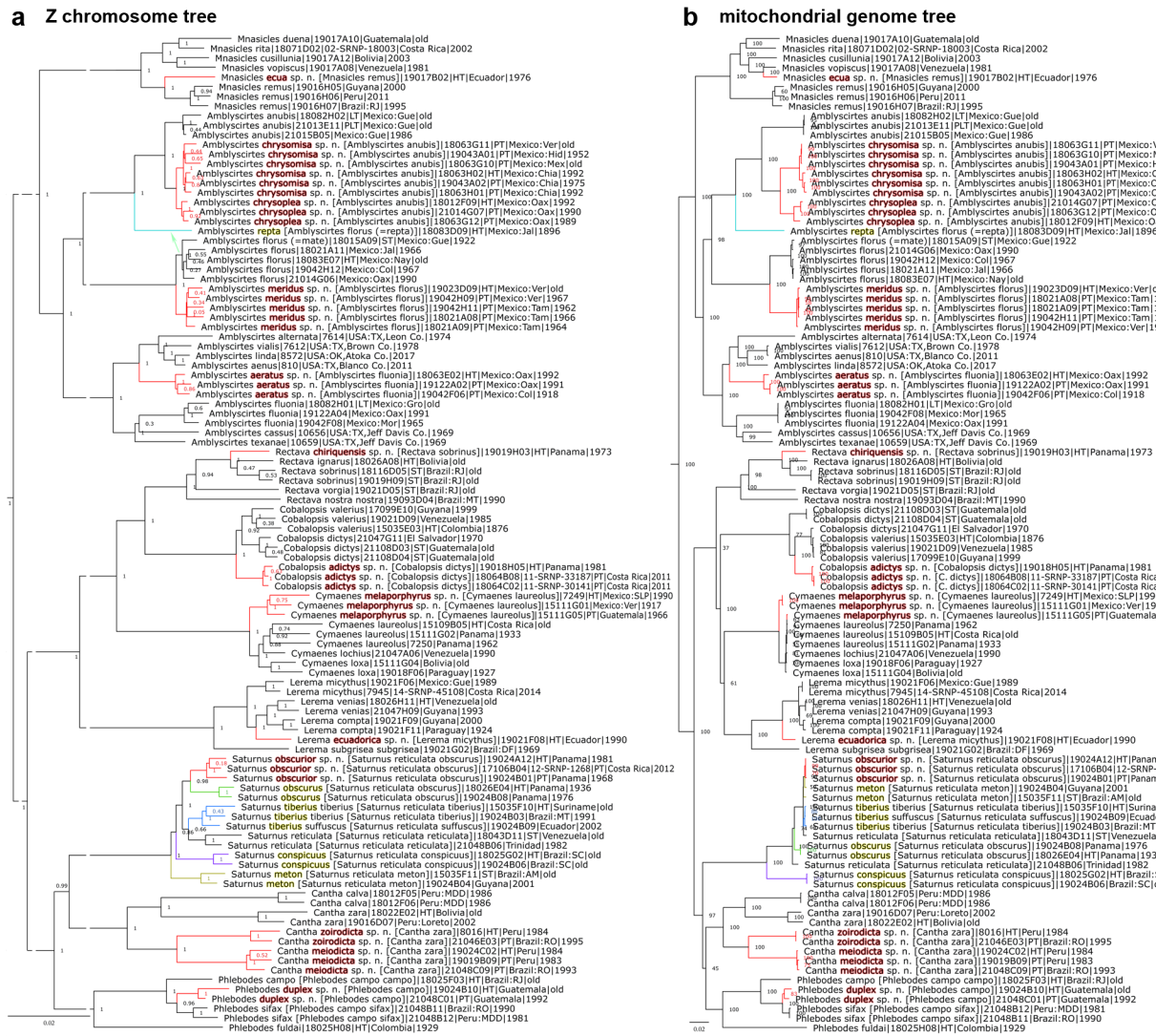


Figure 6. Phylogenetic trees of *Moncina* (part 2) inferred from protein-coding regions in a) the Z chromosome and b) the mitochondrial genome. See Fig. 1 legend for other notations.

Lectotype designation for *Mastor anubis* Godman, 1900

Mastor anubis Godman, 1900, currently in the genus *Amblyscirtes* Scudder, 1872 (type species *Hesperia vialis* W. H. Edwards, 1862) was described from a series of specimens collected at different localities in Mexico: Guerrero and Veracruz. Due to the polytypic type series and to define the type locality more precisely, N.V.G. further designates a male syntype in the Natural History Museum, London, UK, that, according to its label, was illustrated by Godman (1899–1901) and bears the following nine rectangular (except the first two, which are round and with a red circle on the upper side; white labels: (Type) and on the other side (H | 2164), (Type | H. T.), [Omilteme, | Guerrero, | 8000 ft. | July. H.H.Smith.], [♂], [Sp. figured.], [B.C.A.Lep.Rhop. | Mastor | anubis, | Godm.], [Godman-Salvin | Coll. 1914.—5.], [{QR Code} | NHMUK 012824162], and [MOLECULAR | 0247281638], as the lectotype of *Mastor anubis* Godman, 1900. This specimen was sequenced as NVG-18082H02. The type locality of *Amblyscirtes (Mastor) anubis* becomes Mexico: Guerrero, Omilteme, elevation 8000 ft. The name *Anubis* is associated with “dark” as it was an ancient Egyptian god of the dead. Fittingly, the lectotype designation makes *A. anubis* the darkest species (darkest fringes) among its close relatives.

***Amblyscirtes (Mastor) chrysoplea* Grishin, new species**

<https://zoobank.org/81EE321D-0271-4A7C-A136-ED06491AB494>

(Fig. 6 part, 145–146, 370–371)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Oaxaca, Mexico, identified as *Amblyscirtes anubis* Godman, 1900 (type locality in Mexico: Guerrero), show prominent genetic differentiation from it (Fig. 6): e.g., their COI barcodes differ by 5.8% (38 bp), and therefore represent a new species. This new species keys to *A. anubis* (N.2.21) in Evans (1955) but differs from it in having bright-orange forewing fringes, hindwing fringes typically with some orange scales, and ventral hindwing essentially unspotted (better defined, rounder ventral hindwing spots are typical for *A. anubis*). Due to the cryptic nature of this species, most reliable identification is achieved by DNA, and a combination of the following base pairs is diagnostic in the nuclear genome: aly216.64.14:G57A, aly216.64.14:A87G, aly103.15.43:C102T, aly3125.2.3:G201A, aly6398.11.1:G1269A, and COI barcode: 88T, A199G, T277C, T358C, T487C, A643G.

Barcode sequence of the holotype. Sample NVG-18012F09, GenBank OR837687, 658 base pairs:

```
AACTTTATATTTTATTTTGGTATTTGAGCAGGAATACTAGGAACTTCATTAAGATTATTAATTCGTACAGAATTAGGAAACCCCTGGTTCATTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAAATGGAGGATTTGGTAATT
GATTGGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCACGGATAAATAATATAAGATTTTGAATACTCCCCCATCCCTAATACTTTTAAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGAACAGGATGAACAGTATACCCCCCTTTATCATCTAACATTTGCCCATCAAGGTTTCATCTGTTGATTTA
GCTATTTTTTCCCTTCATTTAGCTGGAATTTCCCTCAATTTTAGGAGCAATTAATTTTATTACCACAATTTAATATACGAGTTAGAAAATATATCAT
TCGATCAAATACCCCTATTTGTTTGTATCTGTAGGTATTACTGCTTTATATTACTTTTTATCTTTTACCTGTATTAGCAGGTGCTATCACAACTACTCCT
CACTGATCGAAATTTAATACTTCTTTTTTGTATCTGCTGGAGGAGGGGATCCAATTTCTGTATCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 145–146, bears the following four rectangular labels, three white: [MEXICO: OAXACA | Putla-Tlaxiaco | 5000-7000 ft | 5-7-VIII-1992 | J. Kemner], [DNA sample ID: | NVG-18012F09 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01450312], and one red [HOLOTYPE ♂ | *Amblyscirtes (Mastor) chrysoplea* Grishin]. **Paratypes:** 2♂♂ Mexico: Oaxaca, Sierra Madre del Sur, J. Kemner leg.: NVG-18063G12, USNMMENT_01466218 El Guajolote, 7700', 14-Jun-1989, genitalia X-2924 J.M.Burns 1990 [USNM] and NVG-21014G07 Sierra Madre del Sur, La Soledad–Buena Vista, 5000', 14-Apr-1990 [CMNH].

Type locality. Mexico: Oaxaca, Putla–Tlaxiaco, elevation 5000-7000 ft.

Etymology. The name is formed from the Greek χρυσός (*chrysós*), meaning gold and πλέον (*pléon*), meaning most. The name is given for the orange fringes not only on the forewing but also partly on the hindwing, making this species the most orange-colored member of the *A. anubis* group. The name is a noun in apposition.

Distribution. Mexico: Oaxaca.

***Amblyscirtes (Mastor) chrysomisa* Grishin, new species**

<https://zoobank.org/713888C4-2DD4-4996-B0B7-05226B4462D0>

(Fig. 6 part, 147–148, 372–374)

Definition and diagnosis. Phylogenetic trees reveal that a number of specimens identified as *Amblyscirtes anubis* Godman, 1900 (type locality in Mexico: Guerrero) show prominent genetic differentiation from it and from their sister species *Amblyscirtes chrysoplea* new species (Fig. 6): e.g., their COI barcodes differ from the latter species by 4% (26 bp), and therefore represent a new species. This new species keys to *A. anubis* (N.2.21) in Evans (1955) but differs from its closest relatives in having yellow-orange forewing fringes, dark-brown hindwing fringes, and ventral hindwing essentially unspotted (better defined, rounder ventral hindwing spots are typical for *A. anubis*). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly390.21.1:C54T, aly2011.1.3:C213T, aly2487.17.5:T57A, aly2275.11.10:G75C, aly1158.9.10:C114T, and COI barcode: 88C, T103C, 268C, T349G, T386C, T553G.

Barcode sequence of the holotype. Sample NVG-18063H02, GenBank OR837688, 658 base pairs:

```
AACTTTATATTTTATTTTGGTATTTGAGCAGGAATACTAGGAACTTCATTAAGATTATTAATTCGTACAGAATTAGGAAACCCCTGGCTCATTAATT
GGAGACGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAAATGGAGGATTTGGTAATT
GATTAGTTCCTTTAATATTAGGGGCCCTGATATAGCTTTCCACGGATAAATAATATAAGATTTTGAATACTCCCCCATCTCTAATACTTTTAAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGAACAGGATGAACAGTGTACCCCCCTCTGTATCCAATATTGCCCATCAAGGATCATCTGTTGATCTA
GCTATTTTTTCCCTTCATTTAGCAGGAATTTCTCAATTTTAGGAGCAATTAATTTTATTACTACAATTTAATATACGAGTTAGAAAACATATCGT
```

TTGATCAAATACCCCTATTTGTTTGATCTGTAGGTATTACTGCTTTATTATTACTTTTATCTTTACCGGTATTAGCAGGTGCTATCACAATACTCCT
TACCGATCGAAATTTAAATACTTCATTTTTTTGATCCTGCTGGAGGAGGGGATCCAATTTTATATCAACATTTATTT

Type material. Holotype: ♀ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 147–148, bears the following four rectangular labels, three white: [MEXICO: CHIAPAS | nr. Navenchauc | c. 8000 ft 4-VII-1992 | J. Kemner & A. Vasquez], [DNA sample ID: | NVG-18063H02 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01466220], and one red [HOLOTYPE ♀ | *Amblyscirtes* (Mastor) | *chrysomisa* Grishin]. **Paratypes:** 4♂♂ and 1♀ from Mexico: 1♂ NVG-18063G10, USNMMENT_01466216 no data, Collection Wm Schaus, old, genitalia X-2556 J.M.Burns 1988 [USNM]; 1♀ NVG-18063G11, USNMMENT_01466217 Veracruz, Xalapa, old [USNM]; 1♂ NVG-19043A01, AMNH_IZC 00337914 Mexico: Hidalgo, Apulco, Apr-1952, T. Escalante leg. [AMNH]; 1♂ NVG-18063H01, USNMMENT_01466219 Chiapas, nr. Navenchauc, c. 8000 ft, 4-Jul-1992, J. Kemner and A. Vasquez [USNM]; 1♂ NVG-19043A02, AMNH_IZC 00337915 Chiapas, Ochuc, Rancho San Ramon, 7-Jul-1975, Peter Hubbell leg. [AMNH].

Type locality. Mexico: Chiapas, nr. Navenchauc, elevation about 8000 ft.

Etymology. The name is formed from the Greek χρυσός (*chrysós*), meaning gold, and μισα (*misa*), meaning half. It is given for the forewings with orange fringes and hindwings with dark fringes. The name is a noun in apposition.

Distribution. Southeastern Mexico.

Amblyscirtes (*Mastor*) *repta* Evans, 1955 is a species distinct from *Amblyscirtes* (*Flor*) *florus* (Godman, 1900)

Genomic sequencing of the holotype of *Repens repta* Evans, 1955 (type locality Mexico: Jalisco, Guadalupe) currently a junior subjective synonym of *Amblyscirtes* (*Flor*) *florus* (Godman, 1900) (type locality in Mexico: Nayarit, holotype sequenced as NVG-18083E07) reveals that these two taxa are not monophyletic and *R. repta* is sister to the clade with *Amblyscirtes* (*Mastor*) *anubis* Godman, 1900, the type species of the subgenus *Mastor* Godman, 1900 (Fig. 6). Therefore, we **reinstate** *R. repta* as a valid species and transfer it to the subgenus *Mastor*: *Amblyscirtes* (*Mastor*) *repta* Evans, 1955.

Amblyscirtes (*Flor*) *meridus* Grishin, new species

<https://zoobank.org/9BBDAAEE2-FF8A-4F93-A33D-7C95FDCC5BE6>

(Fig. 6 part, 149–150, 375–376)

Definition and diagnosis. Phylogenetic trees reveal that a number of specimens from southeastern Mexico identified as *Amblyscirtes florus* (Godman, 1900) (type locality in Mexico: Nayarit, holotype sequenced as NVG-18083E07) show prominent genetic differentiation from it (Fig. 6): e.g., their COI barcodes differ by 4.1% (27 bp), and therefore represent a new species. This new species keys to *A. florus* (N.2.20) in Evans (1955) but differs from it by uncheckered fringes, less developed ventral white overscaling, and frequently better developed blotchy postdiscal pale band on ventral hindwing. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly2195.3.17:C141T, aly252.16.2:T159C, aly1259.29.5:C66A, aly536.215.2:T210C, aly3268.16.2:A96G, and COI barcode: T118C, A166G, T193C, T304C, 373C.

Barcode sequence of the holotype. Sample NVG-19023D09, GenBank OR837689, 658 base pairs:

AACTTTATATTTTATTTTGGTATTTGAGCAGGAATATTAGGAACCTCGTTAAGATTATTAATTCGTACTGAATTAGGAAATCCTGGATCTTTAATT
GGAGATGACCAAATTTATAACACTATTGTAACAGCTCATGCCTTTATTATAATTTCTTTATAGTTATGCCTATTATAATGGAGGTTTTGGAACT
GATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTTCCCTCGAATAAATAAATAAGATTTTGAATATTACCTCCTTCATTAATATTATTAAT
TTCAAGAAGAATCGTGGAAAATGGTGCAGGTACTGGATGAACAGTTTATCCCCCTTTTCATCAAATATTGCACATCAAGGCTCATCTGTTGATTTA
GCTATTTTCCCTTCATTTAGCTGGTATTTCTCTATTTTAGGAGCTATTAATTTTATTACTACAATTATTAATATACGAATTAATAAATATATCAT
TTGATCAAATACCCCTATTTGTTTGATCAGTAGGTATTACTGCTTTATTACTACTTTTATCTTTACCTGTTTTAGCAGGAGCTATTACTATACTTCT
TACAGATCGAAATTTAAATACTTCATTTTTTTGATCCTGCTGGAGGAGGAGATCCAATTTTATATCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 149–150, bears the following seven rectangular labels, six white: [Paso San Juan | V. Cruz.], [♂], [B.C.A.Lep.Rhop. | Eutyichide | asema | Mab.], [Collection | W. Schaus],

[DNA sample ID: | NVG-19023D09 | c/o Nick V. Grishin], [USNMENT | {QR Code} | 01532841], and one red [HOLOTYPE ♂ | *Amblyscirtes* (Flor) | *meridus* Grishin]. **Paratypes:** 4♂♂ from Mexico, H. A. Freeman leg. [AMNH]: NVG-18021A08 Tamaulipas, 15 mi S of Llera de Canales, 27-Jul-1966; NVG-18021A09 Tamaulipas, Monte, 22-Jul-1964, genitalia H-137; NVG-19042H11, AMNH_IZC 00337912 Tamaulipas, Victoria, 16-Aug-1962; NVG-19042H09, AMNH_IZC 00337910 Veracruz, Catemaco, 10-Aug-1967.

Type locality. Mexico: Veracruz, Paso San Juan.

Etymology. In Latin, *meridiam* stands for midday and southeastern and signifies more eastern distribution of this species than its sister *A. florus*. The name is an adjective.

Distribution. Southeastern Mexico.

Rectava chiriquensis Grishin, new species

<https://zoobank.org/B38D4A96-FE18-495F-9423-AB1EC92348CD>

(Fig. 6 part, 151–152, 377–379)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Panama identified as *Rectava sobrinus* Schaus, 1902 (type locality Brazil: Rio de Janeiro) shows prominent genetic differentiation from it (Fig. 6): e.g., their COI barcodes differ by 3.8% (25 bp), and therefore represents a new species. This new species keys to “*Papias sobrinus*” (J.36.2) in Evans (1955) but differs from similar-looking species by more expressed pale overscaling on somewhat darker ventral wing distal areas, smaller but visible pale spots between veins in most cells on ventral hindwing (Fig. 152), harpe shorter, its ventral margin rounder and less extended in lateral view, dorsal margin with a tooth projecting dorsad and separated from ampulla, costa only slightly concave (Fig. 377–379). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly499.36.11:A168G, aly2680.6.3:A79T, aly2680.6.3:C80A, aly113.6.1:G3177C, aly357.1.11:A96G, aly7186.4.1:A787A (not T), aly173.79.3:C261C (not T), aly88.15.4:C31C (not T), aly423.11.2:G129G (not A), aly529.34.2:A18A (not G), and COI barcode: T38C, T49C, A286G, T499A, T574C.

Barcode sequence of the holotype. Sample NVG-19019H03, GenBank OR837690, 658 base pairs:

```
AACTTTATATTTTATTTTCGGAATTTGAGCCGGAATACTAGGTACATCCTTAAGTTTATTAATTCGAACAGAATTAGGTAATCCAGGATCATTAAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAAATGGAGGATTTGGTAATT
GATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTTCCACGAATAAATAAATAAGATTCTGAATACTTCCCCCTTCCTTAATATTTGTTAAT
TTCAGAAGAATTGTAGAAAATGGTGCAGGCACTGGTTGAAGTGTATATCCCCCTTTCTTCTAATATTGCACATCAAGGAGCTTCAGTCGATCTA
GCAATTTTTCTTTACATTTAGCAGGTATTTCTCAATTTTAGGAGCTATTAACCTTTATCACCACAATTATTAATATACGAATTATAAATTTATCAT
TTGATCAAATACCATTATTTGTTGATCAGTTGGAATTACAGCTTTATTATTACTTTTATCTTTTACCTGTATTAGCTGGTGCTATTACCATACTCTT
AACTGATCGAAATTTAAATACTTCTTTTTTTGATCCTGCCGAGGAGAGATCCTATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 151–152, bears the following six rectangular labels, five white: [Volcan | Chiriqui, Panama | 18 April '73 | S. S. Nicolay], [♂ genitalia | slide/vial # | H569 | Prep. S.S. Nicolay], [*Papias* ♂ | *sobrinus* | Schs | DET. BY S.S.NICOLAY], [DNA sample ID: | NVG-19019H03 | c/o Nick V. Grishin], [USNMENT | {QR Code} | 01532625], and one red [HOLOTYPE ♂ | *Rectava chiriquensis* | Grishin].

Type locality. Panama: Chiriquí Province, Volcán.

Etymology. The name is given for the type locality and is a feminine adjective.

Distribution. Currently known only from the holotype collected in Chiriquí Province, Panama. This is the only *Rectava* species known from Central America.

Cobalopsis adictys Grishin, new species

<https://zoobank.org/CBF4DB85-179A-4240-912C-8B7186AFB049>

(Fig. 6 part, 153–154, 380–381)

Definition and diagnosis. Phylogenetic trees reveal that a number of specimens identified as *Cobalopsis dictys* (Godman, 1900) (type locality in Mexico: Veracruz, Guatemala, Costa Rica, Panama, illustrated specimen from Guatemala) show prominent genetic differentiation from it (Fig. 6): e.g., their COI barcodes differ by 3.3% (22

bp), and therefore represent a new species. This new species keys to “*Papias dictys*” (J.36.6) in Evans (1955) but differs from it by comparatively darker ventral forewing and hindwing area by inner margin, vestigial or absent forewing apical spot (Fig. 153–154), smaller tooth on ventral margin of harpe, distal margin of harpe stronger projecting dorsad, and more angled connection between tegumen and uncus in lateral view (Fig. 381). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1905.5.2:A148G, aly260.3.2:A28T, aly260.3.2:T51C, aly451.31.3:C84T, aly318.41.3:G78A, and COI barcode: A100T, T112C, C343T, T445C, T536C.

Barcode sequence of the holotype. Sample NVG-19018H05, GenBank OR837691, 658 base pairs:

```
AACTTTTATACTTCATCTTTGGAATTTGAGCCGGAATATTAGGAACTTCTTTAAGATTATAAATTCGAACAGAATTAGGTAATCCCTGGATCTTTAATT
GGTGATGATCAAATCTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAAATGGAGGATTTGGAAAT
GATTAGTACCCTAATACTTTGGTGCTCCTGATATAGCTTTCCACGAATAAATAAATAAGTTTTTGAATACTACCACCTTCCCTAATATTACTAAT
TTCAAGAAGAATTGTAGAAAATGGGGCAGGTACTGGTTGAACTGTATACCCTCCTCTTTCTTCTAATATTGCACATCAAGGAGCATCTGTGATTA
GCAATTTTTTCTCTTCATTTAGCTGGTATTTCTTCTATTCTAGGAGCTATTAATTTTACTACTACAATTTAATATACGAATTAATAATTTATCTT
TTGATCAAATACCTTTATTTGTCTGATCAGTTGGAATTACAGCTTTACTACTACTATTATCTTTACCTGTACTAGCAGGAGCTATTACTACTTCT
TACTGATCGAAATTTAAATACTTCTTTTTTTGATCCTGCAGGAGGAGGAGATCCTATTTTATACCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 153–154, bears the following four rectangular labels, three white: [PANAMA:VERAGUAS | Sante Fe | 8°31'N 81°05'W | 12.IX.1981 | leg. G.B.Small], [DNA sample ID: | NVG-19018H05 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532536], and one red [HOLOTYPE ♂ | Cobalopsis | adictys Grishin]. **Paratypes:** 2♂♂ from Costa Rica: Area de Conservación Guanacaste, Guanacaste Prov., Sector Pitilla [USNM]: NVG-18064B08, 11-SRNP-33187 Sendero Nacho, 710 m, GPS 10.9845, –85.4248, eclosed 17-Nov-2011; NVG-18064C02, 11-SRNP-30141 Sendero Laguna 680 m GPS 10.9888, –85.4234, eclosed 3-Mar-2011.

Type locality. Panama: Veraguas Province, Santa Fe, GPS 8.5167, –81.0833.

Etymology. The name is derived by combining *dictys* with the negating prefix “a”. As a mnemonic, a longer name indicates it is a more southern species than *C. dictys*. The name is a noun in apposition.

Distribution. Costa Rica and Panama.

Cymaenes melaporphyrus Grishin, new species

<https://zoobank.org/48D8BE5E-3F74-4EA4-948F-F9D60BB59FFC>

(Fig. 6 part, 155–156, 382–383)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Mexico and Guatemala identified as *Cymaenes laureolus* (Schaus, 1913) (type locality in Costa Rica, holotype sequenced as NVG-15109B05) are not monophyletic with it and show prominent genetic differentiation from it in the Z chromosome (Fig. 6), although their COI barcodes differ by only 0.9% (6 bp), and therefore represent a new species. This new species keys to *Cymaenes laureolus laureolus* (J.27.6(a)) in Evans (1955) but differs from it by better developed white subapical spots on forewing and more prominent pale areas on ventral hindwing that are tinted with purplish brown rather than plain brown (Fig. 155–156), valva is broader, more square, and teeth on the harpe are more prominent (Fig. 382–383). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1249.14.4:C96T, aly1249.14.4:A147G, aly527.6.11:A63G, aly594.19.2:C72T, aly3936.3.3:C88T, and does not consistently differ from its close relatives in COI barcode.

Barcode sequence of the holotype. Sample NVG-7249, GenBank OR837692, 658 base pairs:

```
AACTTTTATATTTTATTTTGGAAATTTGAGCCGGAATATTAGGAACATCTTTAAGTTTATTATAAATTCGAACAGAATTAGGTAATCCAGGTTCTCTAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAAATGGAGGATTTGGTAATT
GATTAGTTCCTAATAATTAGGAGCTCCTGATATAGCATTTCCACGAATAAATAAATAAAGTTTTTGAATATTGCCTCCTCTTTAATACTATTAAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGAAGTGGTTGAACTGTTTATCCTCCTCTTTCTTCTAATATTGCTCACCAGGAGCTTCAGTTGATTTA
GCAATTTTTTCTCTTCATTTAGCAGGTATTTCTTCTATTCTAGGAGCTATTAATTTTATTACTACAATTTAATATACGAGTTAGAAAATTTATCAT
TTGATCAAATACCTTATTTGTTGATCAGTTGGAATTACAGCTTTATTATTACTTTTATCTTTACCTGTATTAGCAGGTTGCTATTACTACTATTTT
AACTGATCGAAATTTAAATACTTCAATTTTTTGACCCTGCTGGAGGAGGAGATCCTATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 155–156, bears the following six rectangular labels, five white:

[Mex: S.L.P. La Mera Ceiba |13 July 1990 - el. 700' | John Kemner], [*Cymaenes* ♂ | laureolus | Schaus | Det. H.A. Freeman], [DNA sample ID: | NVG-7249 | c/o Nick V. Grishin], [genitalia | NVG161005-76 | Nick V. Grishin], [USNMMENT | {QR Code} | 01321097], and one red [HOLOTYPE ♂ | *Cymaenes* | melaporphyrus Grishin].

Paratypes: 2♂♂ AMNH: NVG-15111G01 Mexico: Veracruz, Coatepec, Jun-1917; NVG-15111G05 Guatemala: Alta Verapaz, Municipio San Cristobal Verapaz, Baleu, >1350 m, 14-Jun-1966, E. C. Welling leg.

Type locality. Mexico: San Luis Potosí, La Mera Ceiba, elevation 700 ft.

Etymology. In Greek, μελανό (melano) means dark, and πορφύρα (porphyra) means purple. The name is given for the purplish sheen of the ventral hindwing in this dark-brown species and is an adjective.

Distribution. Currently known from Mexico and Guatemala.

Lerema (Morys) ecuadorica Grishin, new species

<https://zoobank.org/0047F48A-FECF-40CC-82C0-43631FD3A5CE>

(Fig. 6 part, 157–158, 384–385)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Ecuador identified as *Lerema (Morys) miccythus* (Godman, 1900) (type locality in Mexico: Guerrero and Tabasco, and Costa Rica, illustrated specimen from Tabasco) is not monophyletic with it and shows prominent genetic differentiation from it (Fig. 6): e.g., their COI barcodes differ by 2.3% (15 bp) and, therefore, represents a new species. This new species keys to “*Morys compta miccythus*” (J.40.2(a)) in Evans (1955) but differs from it and other relatives by wings unspotted on both sides (Fig. 157–158) and harpe massively expanded posteriad, somewhat ax-shaped, its dorsal tooth longer and narrower, smoothly merged with harpe without separation between them (Fig. 384–385). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly18312.9.17:A27T, aly18312.9.17:C39T, aly6841.19.2:A449G, aly4778.7.5:A84C, aly37338.27.1:G351A, aly1042.2.2:C27C (not T), aly1042.8.5:C138C (not G), aly1042.8.5:C151C (not T), aly29.8.12:C153C (not A), aly536.180.3:T69T (not C), and COI barcode: A100G, T169C, T304C, C355T, T616C.

Barcode sequence of the holotype. Sample NVG-19021F08, GenBank OR837693, 658 base pairs:

```
AACTTTATATTTTATTTTCGGAATTTGAGCAGGAATATTAGGAAGTCTTTAAGTTTATTAATTCGAACAGAATTAGGTAATCCAGGATCTTTAATT
GGGGATGACCAAATTTATAATACTATTGTTACTGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTATAAATGGAGGATTTGGTAATT
GATTAGTTCATTAATATTAGGAGCACCTGATATAGCATTTCCCTCGAATAAATAAATAAGATTTGAATACTTCCCTCCCTTAATATTATTAAT
TTCAAGAAGAATCGTAGAAAATGGAGCAGGAACAGGATGAAGTGTATTCCTCCTTTATCTTCTAATATGCTCATCAAGGAGCTTCAGTTGATTTA
GCAATTTTTTCTCTTCAATTTAGCTGGTATTTCTTCTATTTAGGTGCTATTAATTTTATTACTACAATTTAATATACAGGATAGAAATTTATCTT
TTGATCAAATACCTTTATTTGTTGATCTGTAGGAATTACTGCATTATTATTACTTTTATCATTACCTGTATTAGCAGGTGCTATTACTATACTTTT
AACTGATCGAAATTTAAATACTTCATTTTTTGACCCTGCCGGAGGAGGATCCTATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 157–158, bears the following four rectangular labels, three white: [ECUADOR, Pichincha | Prov.: Tinalandia | 2200' 18–20 Apr 1990 | coll J. W. Brown], [DNA sample ID: | NVG-19021F08 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532698], and one red [HOLOTYPE ♂ | *Lerema (Morys) | ecuadorica* Grishin].

Type locality. Ecuador: Pichincha Province, Tinalandia, elevation 2200 ft.

Etymology. The name is given for the type locality. The name is a feminine adjective.

Distribution. Currently known only from the holotype collected in Pichincha Province, Ecuador.

Saturnus tiberius (Möschler, 1883) (with *Phlebodes tiberius* form *suffuscus* Hayward, 1940 as its subspecies), *Saturnus meton* (Mabille, 1891), *Saturnus conspicuus* (E. Bell, 1941), and *Saturnus obscurus* (E. Bell, 1941) are species distinct from *Saturnus reticulata* (Plötz, 1883)

Genomic sequencing taxa currently treated as subspecies of *Saturnus reticulata* (Plötz, 1883) (type locality in Venezuela and Panama, syntype sequenced as NVG-18043D11), namely: *Apaustus tiberius* Möschler, 1883 (type locality in Suriname, holotype sequenced as NVG-15035F10), *Phamphila* [sic] *meton* Mabille, 1891 (type locality in Brazil: Amazonas, syntype sequenced as NVG-15035F11), *Phlebodes tiberius* form *suffuscus* Hayward, 1940 (type locality in Ecuador), *Phlebodes tiberius* race *obscurus* Bell, 1941 (type locality Panama: Chiriquí, holotype

sequenced as NVG-18026E04), *Phlebodes tiberius* race *conspicuus* Bell, 1941 (type locality in Brazil: Santa Catarina, holotype sequenced as NVG-18025G02) reveals that all but *P. t. suffuscus* are genetically differentiated from each other in the Z chromosome at the level characteristic of species (Fig. 6), and the latter taxon is closely related to *A. tiberius*. Curiously, the mitochondrial genome (Fig. 6b) does not follow the evolutionary path of the nuclear genome (Fig. 6a), likely due to gene exchange and introgression. Therefore, the COI barcodes of some of these taxa do not differ, while others (*Saturnus reticulata*) are not monophyletic in mitogenomes. The southernmost *P. t. conspicuus* exhibits the largest divergence in COI barcodes: 5.5% (36 bp) (likely due to more restricted gene exchange with other taxa, mitochondrial genome remained unaffected), while not being the most divergent taxon in the nuclear genome (Fig. 6a). This example illustrates that it is not always possible to rely on mitochondrial DNA in general and on COI barcodes in particular in taxonomic and phylogenetic studies. As suggested by nuclear genome analysis and supported by phenotypic differences, we **reinstate** the following taxa as species: *Saturnus tiberius* (Möschler, 1883) and *Saturnus meton* (Mabille, 1891), and propose a **new status** of species for *Saturnus conspicuus* (E. Bell, 1941), and *Saturnus obscurus* (E. Bell, 1941). We leave one taxon as a subspecies but **reinstate** its original species-subspecies **combination**: *Saturnus tiberius suffuscus* (Hayward, 1940). As a result, *S. reticulata* becomes monotypic.

***Saturnus obscurior* Grishin, new species**

<https://zoobank.org/6DBB3DEA-776E-42D3-8940-41664259C043>

(Fig. 6 part, 159–160, 386–387)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Costa Rica and Panama identified as *Saturnus obscurus* (E. Bell, 1941) (type locality in Panama, holotype sequenced as NVG-18026E04) show prominent genetic differentiation from it in the Z chromosome (Fig. 6), although their COI barcodes differ by only 1.2% (8 bp), and therefore represent a new species. This new species keys to “*Saturnus tiberius obscurus*” (L.1.4(a)) in Evans (1955) but differs from it by being darker overall, e.g., ventral hindwing in males lacks the large yellow patch and is only tinted in yellow: in the middle, along the veins and as a series of postdiscal spots; forewing yellow spots are more widely separated from each other. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly499.34.3:T132C, aly1838.37.3:A57G, aly2011.20.4:C183T, aly1113.2.10:C121T, aly1603.31.2:C163A, and COI barcode: T193T, A217A, 235T, A607C.

Barcode sequence of the holotype. Sample NVG-19024A12, GenBank OR837694, 658 base pairs:

```
AAC TTTATATTTTATTTTGGAAATTTGAGCAGGAATACTAGGAACATCTTTAAGTTTATTAATTCGAACAGAAATTAGGAAATCCAGGTTCTTTAATT
GGAGATGATCAAATTTATAACTATTGTAACAGCCCATGCAATTTATTATAAATTTTTTCATAGTAATACCAATCATAATTGGAGGTTTTGGTAATT
GATTAGTACCATTAATATTAGGAGCCCTGATATAGCTTTTCCCTCGAATAAATAACATAAGATTTTGAATACTTCCCCCTTCATTAATATTATTAAT
TTCAAGAAGAATTGTAGAAAATGGAGCTGGTACTGGTTGAACAGTTTACCCCTCTTTCTGCTAATATTGCACATCAAGGAGCATCTGTAGATTTA
GCAATTTTTTCACTTCATTTAGCAGGAATTTCTTCTATTTAGGAGCTATTAATTTTACTACTACAATTTAATATACGAATTAGAAATTTATCAT
TTGATCAAATACCCCTTATTTGTATGATCAGTTGGTATTACTGCATTACTTTTACTTTTATCCTTACCTGTTTTAGCAGGGGCTATCACTATACCTT
AACTGATCGAAATCTTAATACATCCTTTTTTGATCCAGCAGGAGGAGACCCAATCCTCTATCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 159–160, bears the following four rectangular labels, three white: [PANAMA: Darien | Cana 400m | 27.VI.1981 | Leg. G. B. Small], [DNA sample ID: | NVG-19024A12 | c/o Nick V. Grishin], [USNM | {QR Code} | 01532899], and one red [HOLOTYPE ♂ | Saturnus | obscurior Grishin]. **Paratypes:** 2♂♂ [USNM]: NVG-17106B04, 12-SRNP-1268 Costa Rica, Area de Conservación Guanacaste, Alajuela Prov., Sector San Cristobal, Sendero Huerta, 527 m, GPS 10.9305, -85.3722 eclosed 26-Apr-2012; NVG-19024B01, USNM_01532900 Panama: Panama Province, Madden Forest Preserve, 6-Feb-1968, S. S. Nicolay leg., genitalia H337 prep. S. S. Nicolay.

Type locality. Panama: Darien Province, Cana, elevation 400 m.

Etymology. In Latin, *obscurior* means darker, dimmer, duskier, or more obscure. The name is given for the darker appearance of this species due to the loss of paler coloration. The name is a comparative adjective treated as a noun in apposition.

Distribution. Costa Rica and Panama.

***Cantha zoirodicta* Grishin, new species**

<https://zoobank.org/7874E2A2-2FE3-45BD-BA94-F363C90CB2CE>

(Fig. 6 part, 161–162, 388–390)

Definition and diagnosis. Phylogenetic trees reveal that two specimens identified as *Cantha zara* (E. Bell, 1941) (type locality in Bolivia, holotype sequenced as NVG-18022E02) show prominent genetic differentiation from it (Fig. 6): e.g., their COI barcodes differ by 6.5% (43 bp), and therefore represent a new species. This new species keys to “*Cantha celeus zara*” (I.9.1(b)) in Evans (1955) but differs from it by rounder wings, browner (not reddish) ground color, and yellow framing at outer margins of both wings beneath, in addition to yellow veins. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly2178.10.1:C102T, aly363.37.1:A909G, aly363.37.1:T3771G, aly1139.50.8:T279G, aly1139.50.8:T372G, and COI barcode: 67G, T74C, A88T, T508C, A535G, A565G.

Barcode sequence of the holotype. Sample NVG-8016, GenBank OR837695, 658 base pairs:

```
AACTTTATATTTTATTTTGGAAATTTGAGCAGGAATATTAGGAACATCATTAAGTTTATTAATTCGGACAGAAGTACCTGGTCTCTTATT
GGAGATGATCAAATTTATAATACCATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTATAATTTGGTGGATTTGGAAAT
GATTAGTACCCCTAATATTAGGGGCCCTGATATAGCTTTCCACGAATAAATAATATAAGATTTTGAATATTACCCCTTCTTTAATATTATTAAT
TTCAAGAAGAATCGTAGAAAATGGTGCAGGAAGTGGATGAACTGTTTATCCTCCTCTTTCATCTAATATTGCCCATCAAGGAGCATCTGTTGATTA
GCAATTTTTCTTTACATTTAGCAGGAATTTCTTCTATTTTAGGAGCTATTAATTTTATTACTACAATTTAATATACGAATTAATAATATATCAT
TTGATCAAATACCTTTATTTGTCTGATCAGTTGGTATTACCGCATTTATTGTTACTTTTTATCTTTACCGGTATTAGCTGGGGCTATTACTACTTTT
AACGGATCGAAATTTAATACATCATTTTTTTGATCCTGCTGGAGGAGGGATCCTATTTTATACCAACATTTATTT
```

Type material. **Holotype:** ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 161–162, bears the following seven rectangular labels, six white: [PERU 300m | 30 Km S. W. | Pto. Maldonado | 8 May '84 | S. S. Nicolay], [♂ genitalia | slide/vial # | H864 | Prep. S.S. Nicolay], [*Cantha* ♂ | *celeus* | Det. zara Bell | S.S. Nicolay], [DNA sample ID: | NVG-8016 | c/o Nick V. Grishin], [genitalia | NVG170208-01 | Nick V. Grishin], [USNMMENT | {QR Code} | 01321856], and one red [HOLOTYPE ♂ | *Cantha zoirodicta* | Grishin]. **Paratype:** 1♂ NVG-21046E03 Brazil: Rondonia, 62 km S of Ariquemes, linha C-10, 5 km S of Cacauplandia, 25-Apr-1995, G. T. Austin leg., genitalia GTA-8707 [MGCL].

Type locality. Peru: Madre de Dios Region, 30 km SW of Puerto Maldonado, elevation 300 m.

Etymology. The name is a compound word of Greek ζωηρός (*zoiros*) meaning lively, vivid, or vibrant, and δικτυωτός (*diktyotos*) meaning reticulated. The name reflects the bright reticulated pattern of this species and is a noun in apposition.

Distribution. Amazonian Peru and Brazil.

***Cantha meiodicta* Grishin, new species**

<https://zoobank.org/7756C17B-E4A5-42D2-B809-ECD97BC3EA77>

(Fig. 6 part, 163–164, 391–393)

Definition and diagnosis. Phylogenetic trees reveal that several specimens identified as *Phlebodes eteocla* (Plötz, 1882) or *Phlebodes virgo* Evans, 1955 are not closely related to these species and instead are conspecific, belong to *Cantha* Evans, 1955 (type species *Cantha celeus calva* Evans, 1955), and are a distant sister to *Cantha zoirodicta* new species (Fig. 6): e.g., their COI barcodes differ by 5.9% (39 bp), and therefore represent a new species. This new species is similar to *C. zoirodicta* new species but the hindwings are more pointed at the tornus, the amount of yellow framing of margins and veins beneath is reduced, and yellow spots are smaller, especially on the dorsal hindwing, which is completely unspotted in the holotype. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly1935.7.3:G30C, aly1935.7.3:G87A, aly1497.7.1:A1020T, aly103.32.1:T650A, aly103.32.1:A681G, and COI barcode: A34T, A67T, T124C, A184G, A256T, T517C.

Barcode sequence of the holotype. Sample NVG-19024C02, GenBank OR837696, 658 base pairs:

```
AACTTTATATTTTATTTTGGAAATTTGAGCAGGTATATTAGGAACATCATTAAGTTTATTAATTCGTACTGAATTAGGAAATCCTGGATCTCTTATT
GGAGATGATCAAATTTATAATACTATCGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTATAATTTGGAGGGTTTGGGAATT
GATTAGTACCTTTAATATTAGGAGCCCTGATATAGCTTTTCCTCGAATAAATAACATAAGTTTTTGAATATTACCTCCTTCTTTAATATTATTAAT
TTCAAGAAGAATTTGTAGAAAATGGTGCAGGAAGTGGATGAACTGTTTATCCTCCTCTTCTTCTTAATATTGCTCACCAAGGTTTCATCTGTTGATCTA
```

GCAATTTTTCTTTACATTTAGCAGGTATTTCTTCTATTTTAGGAGCTATTAATTTTATTACTACAATTATTAATATACGAATTAATAATATATCAT
TCGACCAAATACCTTTATTTGTTTGATCAGTCCGAATTTACTGCTTTATATTACTTTTTATCTTTACCTGTATTAGCAGGAGCTATTACTATACTTTT
AACGGATCGAAATTTAAATACATCATTTTTTTGATCCTGCTGGAGGAGAGATCCTATTTTATATCAACATTTATTT

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 163–164, bears the following seven rectangular labels, six white: [PERU 300m | 30 Km S. W. | Pto. Maldonado | 8 May '84 | S. S. Nicolay], [♂ genitalia | slide/vial # | H880 | Prep. S.S. Nicolay], [Phlebodes | eteocla ♂ | Det. | S.S. Nicolay], [Parphorus sp. n.], [DNA sample ID: | NVG-19024C02 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532910], and one red [HOLOTYPE ♂ | *Cantha meiodicta* | Grishin]. **Paratypes:** 2♂♂ NVG-19019B09, USNMMENT_01532561 the same data as the holotype but 17-Oct-1983 and not dissected and NVG-21048C09 Brazil: Rondônia, 62 km S of Ariquemes, linha C-10, 5 km S of Cacaullandia, 10-Jul-1993, O. Gomes leg., genitalia GTA-3649 [MGCL].

Type locality. Peru: Madre de Dios Region, 30 km SW of Puerto Maldonado, elevation 300 m.

Etymology. The name is a compound word of Greek μειώ (meiό) meaning reduce, decrease, or lessen, and δικτυωτός (diktyotós) meaning reticulated. The name points to less contrasting lattice patterns compared to the previous species and is a noun in apposition.

Distribution. Amazonian Peru and Brazil.

Phlebodes sifax Evans, 1955 is a species distinct from *Phlebodes campo* (E. Bell, 1947)

Genomic sequencing of *Phlebodes campo sifax* Evans, 1955 (type locality in Brazil: Amazonas) and *Phlebodes campo campo* (E. Bell, 1947) (type locality in Brazil: Rio de Janeiro, holotype sequenced as NVG-18025F03) reveals prominent genetic differentiation between them (Fig. 6): e.g., their COI barcodes differ by 4.1% (27 bp). Therefore, we propose that the former is a species-level taxon *Phlebodes sifax* Evans, 1955, **new status**.

Phlebodes duplex Grishin, new species

<https://zoobank.org/0AEAD528-03AB-4BD0-B8C1-D78CD4EFCB98>

(Fig. 6 part, 165–166, 394–395)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Guatemala identified as *Phlebodes campo* (E. Bell, 1947) (type locality Brazil: Rio de Janeiro, holotype sequenced as NVG-18025F03) show prominent genetic differentiation from it (Fig. 6): e.g., their COI barcodes differ by 4% (26 bp), and therefore represent a new species. This new species keys to *Phlebodes campo campo* (L.2.3(b)) in Evans (1955) but differs from its relatives by having a doublet of (merged) pale spots (rather than one spot or a large cream-colored area) in the forewing cell CuA₂-1A+2A beneath and yellow framing of veins less developed than in *Phlebodes sifax*. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1139.40.3:T144A, aly2659.10.1:A136G, aly2659.10.1:C137A, aly2659.10.1:G139A, aly2659.10.1:A140G, and COI barcode: T91T, T106C, C529C, A532A, T619T.

Barcode sequence of the holotype. Sample NVG-19024B10, GenBank OR837697, 658 base pairs:

AAC TTTACTTTTATTTTCGGAATTTGAGCAGGAATATTAGGAACATCTTAAAGACTACTAATTCGTACAGAATTAGGAAATCCAGGATCTTTAATT
GGAGATGACCAAATTTATAACACTATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTATAAATGGAGGATTTGGAAATT
GATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCTCGTATAAATAATATAAGATTTTGAATACTTCCCCCTTCTTTAATATTACTAAT
CTCAAGAAGAATCGTAGAAAATGGAGCAGGAAGTGGTGAAGTGTATCCCCCTTTCTCTAATATCGCCCATCAAGGATCTTCTGTGATTTA
GCAATTTTTCTCTTCACTTAGCAGGTATTTCTTCTATTTTAGGAGCTATTAATTTTATTACTACAATTATTAATATACGAATTAGAAATTTATCAT
TCGATCAAATACCTTTATTTGTTTGATCAGTAGGTATTACAGCCTTATTATTACTTTTTATCTTTACCTGTATTAGCTGGAGCTATTACTATACTTTT
AAGTATCGAAATTTAAATACATTTTGTGATCCTGCTGGTGGAGGAGATCCAATTTCTCTATCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 165–166, bears the following six rectangular labels, five white: [Cayuga | Guat.], [Sept.], [Schaus and | Barnes | coll], [DNA sample ID: | NVG-19024B10 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532907], and one red [HOLOTYPE ♂ | *Phlebodes duplex* Grishin]. **Paratype:** 1♂ NVG-21048C01 Guatemala: Peten, Parque Nacional Tikal, 31-May-1992, N. M. Haddad leg., genitalia GTA-3240 [MGCL].

Type locality. Guatemala: Cayuga.

Etymology. In Latin, *duplex* means twofold, double, dual, both, thick, or strong. The name is given for the double (diffuse) spot in the ventral forewing cell $CuA_2-1A+2A$ and is a noun in apposition.

Distribution. Currently known only from Guatemala.

Lychnuchus (Enosis) ponka (Evans, 1955), new combination

Genomic sequencing reveals that *Thoon ponka* Evans, 1955 (type locality in Brazil: Para) is in a different clade from *Thoon* Godman, 1900 (type species *Proteides modius* Mabille, 1889), and instead originates within the subgenus *Enosis* Mabille, 1889 (type species *Enosis dognini* Mabille, 1889) of *Lychnuchus* Hübner, [1831] (type species *Lychnuchus olenus* Hübner, [1831]), which is a junior subjective synonym of *Hesperia celsus* Fabricius, 1793) (Fig. 7). Therefore, we propose a **new combination** *Lychnuchus (Enosis) ponka* (Evans, 1955).

Lychnuchus (Enosis) valle Grishin, new species

<https://zoobank.org/97BEB2D4-9C1E-42D1-82F5-A1E7102CFF7F>

(Fig. 7 part, 167–168, 396–398)

Definition and diagnosis. Phylogenetic trees reveal that two females from eastern Colombia identified as *Lychnuchus (Enosis) topo* (Nicolay, 1980) (type locality in Ecuador) show prominent genetic differentiation from it (Fig. 7): e.g., their COI barcodes differ by 5.8% (38 bp), and therefore represent a new species. This new species differs from *L. topo*, which is known only from males, by vestigial or lacking pale dot on the ventral hindwing and darker tornal area of the ventral forewing. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly320.2.13:T495C, aly1603.33.3:G145A, aly770.42.5:A69T, aly2096.2.3:G151C, aly3370.5.2:C48A, and COI barcode: T10C, T64C, T451C, A535T, T574C.

Barcode sequence of the holotype. Sample NVG-19021G09, GenBank OR837698, 658 base pairs:

```
AACTTTTACTTTTATTTTTGGAAATTTGAGCAGGAATATTAGGAACCTTCTTTAAGATTATTAATCCGTACAGAAGTACCTAGGTAATCCAGGTTCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTTACAGCCCATGCTTTTATTATAATTTCTTTATAGTTATACCTATTATAATTTGGAGGATTTGGTAATT
GATTAGTTCCTTTAATATTAGGAGCACCTGATATAGCTTTCCACGAATAAATAACATAAGATTTGAATATTACCTCCCTCTTTAATGTTATTGAC
TTCAAGAAGTATCGTAGAAAATGGTGCAGGTACAGGATGAACAGTTTATCCTCCTTTATCTTCTAATATTGCTCATCAAGGTTCTTCTGTTGACTTA
GCTATTTTTTCTTACATTTAGCAGGAATTTTCATCTATTTTAGGAGCTATTAATTTTATTACCACAATTATTAATATACGAATTAATAATATATCAT
TTGATCAAATACCTTTATTTGTTTGGATCAGTAGGTATTACAGCCCTACTTTTACTTTTATCTTTACCTGTTTTAGCTGGAGCTATTACCATACTTCT
AACTGATCGAAATTTAATACTTCTATTTTTGATCCAGCCGGAGGAGGAGACCCTATTTTATACCAACATTTATTT
```

Type material. Holotype: ♀ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 167–168, bears the following five rectangular labels, four white: [Jan.29, 1989 | Carret del Mar | to Dapa Rd., 1800 m | Valle, Colombia | J. B. Sullivan], [Genit. Vial | SRS-3248], [DNA sample ID: | NVG-19021G09 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532704], and one red [HOLOTYPE ♀ | *Lychnuchus (Enosis) valle* Grishin]. **Paratype:** 1♀ NVG-22035H06 Colombia: Valle, San Antonio, above Cali, 1900 m, 2-Feb-1987, J. B. Sullivan leg., genitalia SRS-3224 [USNM].

Type locality. Colombia: Valle, Carret del Mar to Dapa Rd., elevation 1800 m.

Etymology. The name is for the type locality and is a noun in apposition.

Distribution. Eastern Colombia.

Lectotype designation for *Eutyichide ochus* Godman, 1900

Eutyichide ochus Godman, 1900, currently a subspecies of *Eutyichide subcordata* (Herrich-Schäffer, 1869), was described from a series of specimens collected at multiple localities: Mexico: Veracruz, Nicaragua, and Brazil: Amazonas. Due to the polytypic type series and to define the type locality more precisely, N.V.G. hereby designates a male syntype in the Natural History Museum, London, UK, that according to its label, was illustrated by Godman (1899–1901) and bears the following 11 rectangular (except the first three, which are round and with a red circle on the upper side, and the 9th which is round and yellow) white labels: (Type), (Type), (Type | H. T.), [Atoyac, | Vera Cruz. | May. H.H.S.], [♂], [Sp. figured.], [B.C.A.Lep.Rhop. | *Eutyichide* | *ochus*, | Godm.], [Godman-Salvin | Coll. 1912.—2.], (13), [16 { genitalia glued to this label }], and [PHOTO | AA], as the **lectotype** of *Eutyichide ochus* Godman, 1900. The type locality of *E. ochus* becomes Mexico: Veracruz, Atoyac.

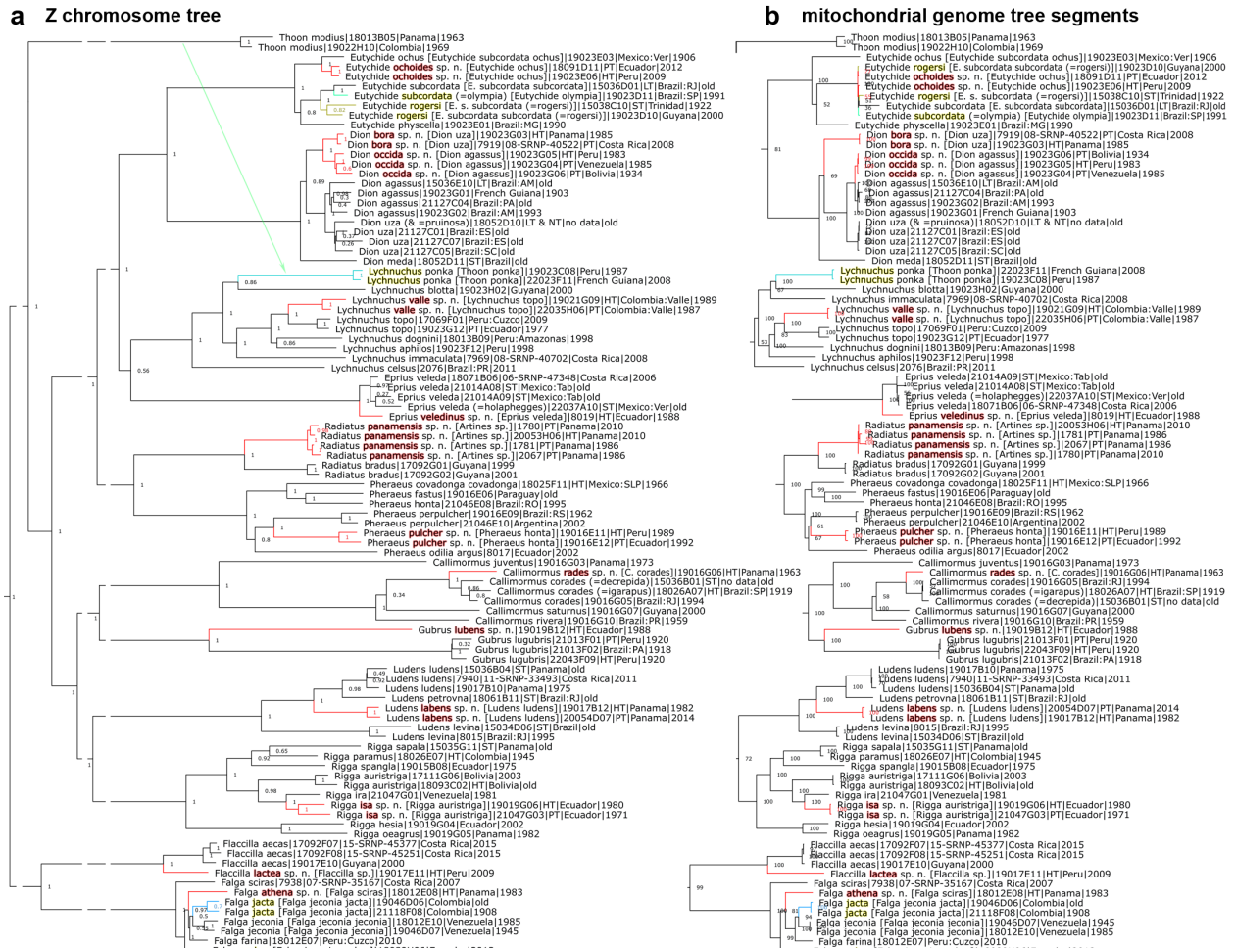


Figure 7. Phylogenetic trees of Moncina (part 3) and Flagina inferred from protein-coding regions in a) the Z chromosome and b) the mitochondrial genome (in segments). See Fig. 1 legend for other notations.

Hesperia olympia Plötz, 1882 is a junior subjective synonym of *Eutychide subcordata* (Herrich-Schäffer, 1869) and a lectotype designation

Genomic sequencing of a syntype of *Cobalus subcordata* Herrich-Schäffer, 1869 (type locality not specified, probably Brazil: Rio de Janeiro per Plötz (1882)) reveals that Evans (1955) misidentified this species. This specimen is a syntype because it agrees with the original description, is from the Herrich-Schäffer collection, and bears a label in likely Herrich-Schäffer’s handwriting “subcordata | m”, where ‘m’ stands for ‘mih’ (Latin for ‘of me’), placed after a species name as an attribution of the new species to the writer. This notation was common over a century ago, instead of the author’s name being written directly. This ‘m’ confirms that the label was written by Herrich-Schäffer and offers additional evidence that this specimen is a syntype.

To define this species objectively, N.V.G. hereby designates the sequenced male syntype in the Museum für Naturkunde, Berlin, Germany, that bears the following ten rectangular labels (the first and the fourth are purple, others are white): [Origin.], [Co subcordata | m], [Coll. H.—Sch.], [syn- t. | volesus Mab.], [912.], [Coll. | Staudinger], [subcordata | H. Sch.], [Caryst. | subcordata | HS.], [{QR Code} http://coll.mfn-berlin.de/u/ | 449f81], and [DNA sample ID: | NVG-15036D01 | c/o Nick V. Grishin] as the **lectotype** of *Cobalus subcordata* Herrich-Schäffer, 1869, currently in the genus *Eutychide* Godman, 1900 (type species *Hesperia physcella* Hewitson, 1866). While the lectotype lacks a locality label, the genomic tree places the lectotype with a specimen from

Southeast Brazil, thus suggesting that the type locality of *Eutyichide subcordata* is in Southeast Brazil, in agreement with Plötz (1882), who stated that the type locality was “Rio”.

According to genomic comparison (Fig. 7) and phenotypic characters, the lectotype of *Eutyichide subcordata* is conspecific with *Hesperia olympia* Plötz, 1882 (type locality in Brazil) as the latter species was identified by Draudt (1921–1924), who already used the combination *Cobalus subcordata* form *olympia*, and later treated as a species by Evans (1955), who misidentified *E. subcordata*. Therefore, we propose that *Hesperia olympia* Plötz, 1882 is a **new junior subjective synonym** of *Eutyichide subcordata* (Herrich-Schäffer, 1869).

***Eutyichide ochus* Godman, 1900 and *Eutyichide rogersi* (Kaye, 1914) are valid species-level taxa**

Placed as a subspecies of *Eutyichide subcordata* (Herrich-Schäffer, 1869) (type locality likely in Brazil: Rio de Janeiro) by Evans (1955), *Eutyichide ochus* Godman, 1900 (type locality in Mexico: Veracruz) is not conspecific with the former because Evans misidentified *E. subcordata*, which instead, as shown above, is conspecific with and a senior name for *Hesperia olympia* Plötz, 1882 (type locality in Brazil). Therefore, the senior name for the species Evans misidentified as *E. subcordata* is *E. ochus*, and a senior name for the subspecies Evans misidentified as *E. subcordata subcordata* is *Cobalopsis rogersi* Kaye, 1914 (type locality in Trinidad, syntype sequenced as NVG-15038C10) (Fig. 7). However, Evans (1955) mentioned male genitalia differences between his subspecies of “*E. subcordata*” and genomic sequencing suggests that these “subspecies” are species-level taxa. Therefore, we **reinstate** these two taxa as species: *Eutyichide ochus* Godman, 1900 and *Eutyichide rogersi* (Kaye, 1914).

***Eutyichide ochooides* Grishin, new species**

<https://zoobank.org/972EB90E-A40C-45F1-8ED0-F796092C18B9>

(Fig. 7 part, 169–170, 399–401)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Ecuador and Peru identified as *Eutyichide ochus* Godman, 1900 (type locality in Mexico: Veracruz) show prominent genetic differentiation from it (Fig. 7): e.g., their COI barcodes differ by 7.3% (48 bp), and therefore represent a new species. This new species keys to “*Eutyichide subcordata ochus*” (J.50.3(a)) in Evans (1955) but differs from it by more contrasty hindwing with submarginal area paler than discal area and typically larger subapical forewing spots of about equal size. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly5.7.1:T1986A, aly5.7.1:A2066G, aly1249.21.19:T39C, aly1036.5.4:C96T, aly851.2.8:C43T, and COI barcode: T92C, 157C, T287C, 346A, T436C, T568A.

Barcode sequence of the holotype. Sample NVG-19023E06, GenBank OR837699, 658 base pairs:

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AAC TTTATATTTTATTTTGGTATTTGAGCAGGAATATTAGGAACCTCTTAAAGATTATTAATTCGAACAGAATTAGGAAATCCTGGTTCACATAATT
GGAGATGATCAAATTTATAATACTATTGTAAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTATAATGGAGGATTTGGAAATT
GATTAGTACCTTTAATATTAGGAGCACCTGATATAGCTTTCCACGAATAAACAATATAAGATTTTGAATATTACCCCTTCATTAATATTACTAAT
TTCTAGAAGAATTGTTGAAAATGGTGCAGGTACAGGATGAACAGTTTACCCCTTTCATCTAATATTGCTCACCAAGGTTCTTCAGTTGATCTA
GCAATTTTCTCCCTACACTTAGCAGGAATTTCTTCTATTTAGGAGCCATTAACCTTTATTACTACAATTTAATATACGAATTAGAAATTTATCAT
TTGATCAAATACCTTTATTTGTATGATCTGTAGGTATTACAGCCCTATTATTATTATTATCATTACCTGTATTAGCAGGTGCAATTACAATACTTTT
AACCGACCGAAATTTAAATACTTTCTTTTTTTGATCCAGCTGGAGGAGGATCCTATTTTATACCAACATTTATTT
```

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 169–170, bears the following four rectangular labels, three white: [PERU: Cuzco:Cosñipata Valley | San Pedro vicinity 1,373m. | 13°03'30"S, 71°32'64"W | 11 August 2009 Brian Harris], [DNA sample ID: | NVG-19023E06 | c/o Nick V. Grishin], [USNMNT | {QR Code} | 01532848], and one red [HOLOTYPE ♂ | *Eutyichide* | *ochooides* Grishin]. **Paratype:** 1♂ NVG-18091D11 Ecuador: Morona-Santiago, Mendez, 800 m, GPS –2.42, –78.20, 9-Nov-2012, J.-C. Petit leg., [EBrockmann].

Type locality. Peru: Cuzco, Cosñipata Valley, near San Pedro, elevation 1373 m, GPS –13.0583, –71.5483.

Etymology. The name reflects a similarity to *E. ochus*. It is longer to signify a more southern distribution. The name is an adjective.

Distribution. Ecuador and Peru.

***Dion bora* Grishin, new species**

<https://zoobank.org/75DE2A48-50F7-4D25-8E27-F1F95CCD0CE4>

(Fig. 7 part, 171–172, 402–403)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Costa Rica and Panama identified as *Dion uza* (Hewitson, 1877) (type locality not specified, lectotype sequenced as NVG-18052D10) show prominent genetic differentiation from it (Fig. 7): e.g., their COI barcodes differ by 3.6% (24 bp), and therefore represent a new species. This new species keys to “*Enosis pruinosa pruinosa*” (K.4.3(a)) in Evans (1955), which was misidentified by Evans, see Zhang et al. (2022b), and differs from its relatives by a combination of the following characters: ventral hindwing with broader blue metallic overscaling in posterior half and partly along forewing outer margin, similar to *D. uza*, but hindwing discal cyan-blue spots are more prominent on the blue ground color (Fig. 172) and less developed than in another new species described below, tube-like arched upcurved process from near the base of harpe is thinner and longer, harpe is broader, with two humps on its dorsal margin, costa straighter, less concave (Fig. 403). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly6954.4.5:G69A, aly6954.4.5:C91T, aly527.12.3:T74C, aly103.13.2:C60T, aly103.13.2:A78G, and COI barcode: T49C, T91A, T325C, A553G, C539T, T601C.

Barcode sequence of the holotype. Sample NVG-19023G03, GenBank OR837700, 658 base pairs:

```
AACTTTATATTTTATTTTGGTATTTGAGCAGGAATATTAGGAACTTCCTTAAGTTTATTAATTCGAACAGAAATTAGGTAATCCTGGCTCATTAAATT
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATGGAGGATTTGGTAATT
GATTAGTTCCCTCTAATATTAGGAGCACCTGATATAGCTTTCCCCCGAATAAATAATAAGATTTGAATACTACCCCTTCCCTTATACTATTAAC
TTTTAGAAGAATTGTAGAAAATGGTGCAGGTACCGGATGAACAGTTTACCCCCCTTTCTTCTAATATTGCCATCAAGGTTCTTCAGTTGATTTA
GCAATTTTTCATTACATTTAGCAGGAATTTCTTCTATTTAGGTGCTATTAATTTTATTACAACAATTTAATATACGAATTAATAATTTATCAT
TTGATCAAATACCTTTATTTGTTGATCTGTAGGTATTACAGCTTTATTATTATTATTATCTTTACCGGTATTAGCAGGAGCTATTACAATACTTCT
CACTGATCGAAATTTAAACACTTCTTTTTTTGATCCAGCAGGAGGAGAGATCCAATTTTATATCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 171–172, bears the following four rectangular labels, three white: [PANAMA: Darien | Rio Tuira at | Rio Pucuro | 16–17 Feb. 1985 | J. Louton], [DNA sample ID: | NVG-19023G03 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532867], and one red [HOLOTYPE ♂ | *Dion bora* | Grishin]. **Paratype:** ♂ NVG-7919, 08-SRNP-40522 Costa Rica: Area de Conservación Guanacaste, Alajuela Prov., Sector Rincon Rain Forest, Laureles, 95 m, GPS 10.9332, –85.25335, genitalia NVG170207-04 [USNM].

Type locality. Panama: Darien Province, Rio Tuira at Rio Pucuro.

Etymology. The name is formed from the Latin *borealis*, meaning northern. It signifies it is the northernmost species within the *D. uza* group. The name is a noun in apposition.

Distribution. El Salvador to Panama.

***Dion occida* Grishin, new species**

<https://zoobank.org/0458BF11-8AEB-4AF2-8B02-A4F6DF108B58>

(Fig. 7 part, 173–174, 404–406)

Definition and diagnosis. Phylogenetic trees reveal that several specimens identified as *Dion agassus* (Mabille, 1891) (type locality type locality Brazil: Amazonas, Massauary, lectotype sequenced as NVG-15036E10) show prominent genetic differentiation from it in the Z chromosome and are sister to *Dion bora* new species (Fig. 7), but their COI barcodes differ from *D. bora* by 4.1% (27 bp) while being closer to sympatric *D. agassus*, probably due to introgression: 1.1% (7 bp). Therefore, these specimens represent a new species that keys to “*Enosis pruinosa agassus*” (K.4.3(a)) in Evans (1955) and differs from its relatives by a combination of the following characters: ventral hindwing with comparatively reduced blue metallic overscaling and on forewing replaced by purple tint overscaling, similar to *D. agassus*, but hindwing discal cyan-blue spots are most prominent on the blue ground color, and blue overscaling is framing the inner margin (Fig. 174), the tube-like arched upcurved process from near the base of harpe is thicker and shorter, harpe is narrower, rounder, with a straight or convex dorsal margin that bears a small hump directed partly inward and anteriad, costa more concave (Fig. 405–406). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the

following base pairs is diagnostic in the nuclear genome: aly87.2.2:C44T, aly1259.30.6:C96T, aly2130.12.1:C174T, aly349.2.5:A264G, aly2130.9.3:C120T, and COI barcode: T59C, T322G, T373C, T533C, T616T.

Barcode sequence of the holotype. Sample NVG-19023G05, GenBank OR837701, 658 base pairs:

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AACCTTATATTTTATTTTGGTATTTGAGCAGGAATATTAGGAACTTCTTAAAGTTTACTAATTCGAACAGAATTAGGTAATCCTGGCTCTTTAATT
GGAGACGATCAAATTTATAACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTCATAGTTATACCTATTATAATGGAGGATTTGGTAATT
GATTAGTCCCTCTAATACTAGGAGCACCTGATATAGCTTTCCCCCGAATAAATAAATAAGATTTTGAATACTACCACCTCACTTATACTATTAAC
TTTTAGTAGAATTGTAGAAAATGGAGCAGGGACTGGATGAACAGTTTACCCCTCTTTCTTCTAATATTGCTCATCAAGGCTCTTCAGTTGATTTA
GCAATTTTTTCTTACATTTAGCAGGAATTTCTTCTATTTTAGGCGCTATTAATTTTATTACAACAATTTATAATATACGAATAAAACTTATCAT
TTGATCAAATACCTTTATTTGTGTGATCTGTAGGTATTACAGCCTTACTGTTACTACTATCTTTACCAGTATTAGCAGGAGCTATTACAATACTTCT
CACTGATCGAAATTTAAATACTTCTTTTTTTGATCCAGCAGGAGGAGAGATCCAATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 173–174, bears the following six rectangular labels, five white: [PERU 300m | 30 Km S. W. | Pro. Maldonado | 27 Oct. '83 | S. S. Nicolay], [♂ genitalia | slide/vial # | H790 | Prep. S.S. Nicolay], [Enosis ♂ | pruinosa | Det. pruinosa | S.S. Nicolay], [DNA sample ID: | NVG-19023G05 | c/o Nick V. Grishin], [USNM | {QR Code} | 01532869], and one red [HOLOTYPE ♂ | Dion occida | Grishin]. **Paratypes:** 2♂♂ [USNM]: NVG-19023G04, USNM_01532868 Venezuela: Amazonas, Cerro de la Neblina basecamp, 140 m, GPS 0.8333, -66.1667, 10–20-Feb-1985, P. J. and P. M. Spangler, R. A. Faitoute, W. E. Steiner leg. and NVG-19023G06 with a single label “17o46-55. S. Lat. 63-5-34 Long.”, which we interpreted as Bolivia: Santa Cruz department, Santa Cruz de la Sierra, GPS -17.7819, -63.0928.

Type locality. Peru: Madre de Dios Region, 30 km SW of Puerto Maldonado, elevation 300 m.

Etymology. In Latin, *occidentalis* means western. The name signifies the westernmost species of the *D. uza* group and is a noun in apposition.

Distribution. Currently known from Venezuela, Peru, and Bolivia.

Eprius (Eprius) veledinus Grishin, new species

<https://zoobank.org/C135FD94-6DC9-4C82-9C2E-8A62D34DA640>

(Fig. 7 part, 175–176, 407–409)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Ecuador identified as *Eprius veleda* (Godman, 1901) (type locality in Mexico: Veracruz and Tabasco, Guatemala, Honduras, and Panama, syntypes sequenced as NVG-21014A08 and NVG-21014A09) shows prominent genetic differentiation from it (Fig. 7): e.g., their COI barcodes differ by 2.7% (18 bp), and therefore represents a new species. This new species keys to “*Epeus veleda veleda*” (J.5.(a)) in Evans (1955) but differs from the true *E. veleda* by less extensive white overscaling on the abdomen beneath, which is present in the form of two stripes rather than the entire ventral side white with a narrow dark stripe in the middle (Fig. 176) and harpe more expanded dorsad into a small lobe (Fig. 409). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly276665.5.1:A864G, aly276665.5.1:A912G, aly2790.11.3:T489G, aly2487.46.1:T39G, aly2487.46.1:T45C, aly770.26.3:A73A (not C), aly860.3.1:T690T (not C), aly860.3.1:C723C (not T), aly3241.2.5:G289G (not A), aly86.14.6:C90C (not T), and COI barcode: T25C, G34C, T100G, T479C, T583C.

Barcode sequence of the holotype. Sample NVG-8019, GenBank OR837702, 658 base pairs:

```
AACCTTATATTTTATTTTGGTATCTGAGCTGGCATACTAGGAACATCCTTAAGATTATAATTCGTACAGAATTAGGTAATCCTGGATCTTTAATT
GGGGATGATCAAATTTATAACTATTGTAACAGCTCACGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATGGAGGTTTTGGTAATT
GATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCCCGAATAAATAAATAAGATTTTGGATACTACCACCTTCTTTAATATTATTAAT
CTCAAGAAGAATTGTTGAAAATGGTGTGGAAGCTGGATGAACCTTTTATCCCCCTTTCATCTAATATTGCTCACCAAGGTTCTTCTGTAGATTTA
GCAATTTTTTCTTACATTTAGCAGGAATTTCTTCTATTTTAGGAGCTATTAATTTTATTACTACAATTTATAATATACGAATAAAACTTATCAT
TTGATCAAATACCTTTATTTGTGTTGATCTGTAGGTATTACAGCCTTATTGTTATTATTATCTTTACCTGTATTAGCTGGGGCTATTACAATATTACT
CACTGATCGAAATTTAAATACTTCAATTTTTTGACCCAGCAGGAGGAGGAGACCAATTTTATATCAACACTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 175–176, bears the following five rectangular labels, four white: [ECUADOR Pichincha | Alluriquin 700m | 26 May '88 | S. S. Nicolay], [DNA sample ID: | NVG-8019 | c/o Nick V. Grishin], [genitalia | NVG170208-04 | Nick V. Grishin], [USNM | {QR Code} | 01321859], and one red [HOLOTYPE ♂ | *Eprius (Eprius) veledinus* Grishin].

Type locality. Ecuador: Pichincha Province, Alluriquin, elevation 700 m.

Etymology. The name is formed from the name of its northern sister species (*E. veleda*), which is made longer to indicate southern origin. The name is an adjective.

Distribution. Currently known only from the holotype collected in Ecuador.

Radiatus panamensis Grishin, new species

<https://zoobank.org/FF987ADB-7F20-4972-9BFE-C5B24701E914>

(Fig. 7 part, 177–178, 410–412)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Panama that someone associated with *Artines* Godman, 1901 (type species *Hesperia aquilina* Plötz, 1882) are sister to South American *Radiatus bradus* O. Mielke, 1968 (type locality in Brazil: Distrito Federal) while being genetically differentiated from it (Fig. 7): e.g., their COI barcodes differ by 4.6% (30 bp), and therefore represent a new species of *Radiatus* O. Mielke, 1968 (type species *R. bradus*). This new species differs from its only close relative *R. bradus* by the presence of forewing discal and sometimes subapical spots, longer, dash-like postdiscal spots between veins on ventral hindwing, less prominent pale area by dorsal forewing inner margin (Fig. 177–178), more extended harpe, longer process of ampulla, longer saccus, narrower undivided uncus, wider separated gnathos arms, and stronger bent aedeagus (Fig. 410–412). This species is not cryptic. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly318.14.8:A156T, aly361.13.3:G40C, aly2379.4.3:T30C, aly2011.1.3:C117T, aly2011.1.3:C192G, and COI barcode: A70G, A130T, T212C, T337C, T799A.

Barcode sequence of the holotype. Sample NVG-20053H06, GenBank OR837703, 658 base pairs:

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AAC TT TATATTTTATTTTFFGGAATTTGAGCAGGAATATTAGGAACTTCATTAAGTTTATTAATTCGAACGGAATTAGGTAACCCAGGCTCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTAACTGCTCACGCTTTTATTATAATTTTTTTTATAGTAATACCTATTATAATTTGGAGGATTTGGAAATT
GATTAGTTCCTTTAATACTAGGAGCTCCTGATATAGCTTTCCACGAATAAATAACATAAGATTTTGAATATTACCACCTTCTTTAATATTTAAT
TTCAAGAAGAATTGTTGAAAATGGTGCAGGTAAGTGGATGAAGTGTCTATCCCCCTTTCTTCTAATATGCTCACCAAGGATCTTCAGTTGACTTA
GCAATTTTTTCATTACATTTAGCAGGTATTTCTTCAATTTTAGGAGCTATTAATTTTACTACTACAATTTAATATACGAATTAGAAATTTATCAT
TTGATCAAATACCATTATTTGTTGATCTGTAGGAATTACAGCATTATTAATTTTACTTCTTTTATCTTTACCTGTTTTAGCTGGAGCTATTACAATACTTCT
TACAGACCGAAATTTAAATACTTCATTTTTTTGATCCTGCTGGAGGAGGGATCCAATTTTATATCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the Mississippi Entomological Museum, Starkville, MS, USA (MEM), illustrated in Fig. 177–178, bears the following three rectangular labels, two white: [Panama: Panama | Cerro Jefe | “elfin forest” | ca. 950 m. | N 09° 13' 27.1" | W 079° 22' 32.9" | July 31, 2010 | J. R. MacDonald], [DNA sample ID: | NVG-20053H06 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | *Radiatus panamensis* | Grishin].

Paratypes: 2♂ and 1♀ from Panama, John R. MacDonald leg. in MEM: 1♂ NVG-2067 Panama: Cocle, El Valle, 800–850 m, 7-Jan-1986, John R. MacDonald leg., genitalia vial no. RAA 0212; 1♂ NVG-1781 Cocle, El Valle, 800–850 m, 7-Jan-1986, John R. MacDonald leg.; 1♀ NVG-1780 Panama, Cerro Jefe, ca. 950 m, GPS 9.22419, –79.37581, 31-Jul-2010, John R. MacDonald leg.

Type locality. Panama: Panama Province, Cerro Jefe, elevation ca. 950 m, GPS 9.22419, –79.37581

Etymology. The name is given for the type locality and is an adjective.

Distribution. Known only from Panama but may be present in western Colombia.

Comment. A significant extension of the range of this formerly monotypic genus known only from South America.

Pheraeus pulcher Grishin, new species

<https://zoobank.org/309A87AC-194F-4AC8-BA2A-4E489BA69D46>

(Fig. 7 part, 179–180, 413–414)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Ecuador and Peru that look superficially similar to *Pheraeus honta* Evans, 1955 (type locality in Peru) are not monophyletic with it and show prominent genetic differentiation from it (Fig. 7): e.g., their COI barcodes differ by 5.5% (36 bp), and therefore represent a new species. This new species is a distant sister to *Pheraeus perpulcher* (Hayward, 1934) (type locality in Argentina), while not being very similar to it in ventral wing patterns and differs by 6.1% (40 bp) in the COI

barcode. This new species keys (incompletely and as the best overall compromise) to *P. honta* (L.11.1.) in Evans (1955) but has an orange tinted with brown at the tip tuft of long scales near the inner hindwing margin above. The holotype was misidentified as *Pheraeus rumba* Evans, 1955 (type locality in Brazil) but differs from it by the lack of yellow and hyaline spots in forewing cells M_1 - M_2 and M_2 - M_3 and the lack of submarginal brown “shading” of ventral hindwing postmedian spots: these white spots are encircled by relatively well-defined blackish frames and the submarginal area is of orange-yellow ground color, similar to *P. honta*. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly536.17.10:C39T, aly166.5.1:C267T, aly166.5.1:G282A, aly594.8.2:G80C, aly1454.4.1:A246G, and COI barcode: T38C, A100G, T121C, C220A, T548C.

Barcode sequence of the holotype. Sample NVG-19016E11, GenBank OR837704, 658 base pairs:

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AACTTTTATATTTTATTTTGGTATTTGAGCAGGAATACTAGGAAGTTCATTAAGTTTATTAATTCGAAGTGAATTAGGAAACCCAGGTTCTTTAATT
GGGGATGATCAAATTTATAATACCATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTTATACCTATTATAATCGGAGGATTTGGTAATT
GATTAGTTCCTCTTATATTTAGGTGCACCTGATATAGCTTTCCACGAATAAATAATATAAGATTTGAATATTACCTCCTCTTTAATATTTAAT
CTCAAGAAGAATTGTTGAAAATGGTGCAGGAAGTGGATGAACAGTTTACCCTCCTTTTCTTCTAATATTGCCCATCAAGGTTCTTCAGTTGATTTA
GCAATTTTCTTTACATTTAGCAGGAATTTTCATCAATTTTAGGAGCTATCAATTTTATTACAACAATTTAATATACGAGTTAAAACTTATCTT
TTGATCAAATACCTTTATTTGTATGATCTGTAGGATTTACAGCATTACTATTACTTCTATCTTACCTGTTTTAGCAGGAGCTATTACTATACTTCT
TACTGATCGAAATTTAATACTTCTATTTTGTATCCAGCAGGAGGAGATCCAATTTTATATCAACATTTATTT
```

Type material. **Holotype:** ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 179–180, bears the following five rectangular labels, four white: [PERU Madre De Dios | Rio La Torre 300m | Tambopata Res. | 27 Sept. ‘89 | S. S. Nicolay], [*Pheraeus* | *rumba* ♂ | Det. | S.S. Nicolay], [DNA sample ID: | NVG-19016E11 | c/o Nick V. Grishin], [USNMENT | {QR Code} | 01532334], and one red [HOLOTYPE ♂ | *Pheraeus* | *pulcher* Grishin]. **Paratype:** 1♀ Ecuador: Napo Province, Jatun Sacha Biological Reserve, elevation 450 m, GPS –1.0667, –77.6167, 7-Nov-1992, S. S. Nicolay leg. [USNM].

Type locality. Peru: Madre de Dios, Tambopata National Reserve, Rio La Torre, elevation 300 m.

Etymology. In Latin, *perpulcher* means very beautiful. Even after removing the prefix “per”, we still have a beautiful species. A shorter name signifies a more northern distribution of this species. The name is a noun in apposition.

Distribution. The upper Amazonian region, known from Ecuador and Peru.

Callimormus rades Grishin, new species

<https://zoobank.org/6B68354B-2C44-4669-8A87-E093C704272A>

(Fig. 7 part, 181–182, 415–417)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Panama identified as *Callimormus corades* (C. Felder, 1862) (type locality in Brazil: Rio de Janeiro) shows prominent genetic differentiation from it (Fig. 7): e.g., their COI barcodes differ by 3% (20 bp) and, therefore, represents a new species, provided that we sequenced primary type specimens of taxa treated as synonyms of *Callimormus corades* and show that they are distinct from the new species (Fig. 7). This new species keys to *C. corades* (J.2.7) in Evans (1955) but differs from it by discal spot in ventral hindwing cell $Sc+R_1$ -RS slightly more offset basad, rounder discal spots on forewing, and generally more prominent yellow overscaling of veins on the ventral side, more evident as a yellow bar at the end of discocellular vein (Fig. 181–182). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly2041.16.10:C33T, aly159.20.1:C99G, aly814.17.1:G105A, aly4007.2.5:G48A, aly1631.11.9:T43G, aly50.38.2:G177G (not C), aly686.17.2:G54G (not A), aly60.25.7:C69C (not A), aly26.25.5:C138C (not T), aly6847.3.5:C54C (not T), and COI barcode: T212C, 271A, C334T, T337A, T574C.

Barcode sequence of the holotype. Sample NVG-19016G06, GenBank OR837705, 658 base pairs:

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AACTTTATATTTTATTTTTCGGAATTTGAGCAGGAATAATGGTACTTTCATTAAGTTTATTAATTCGTACAGAATTAGGTAATCCAGGTTCTTTAATT
GGAGATGATCAAATTTATAATACCATTGTACTGCTCATGCCTTTATTATAATTTTTTTTATAGTTATACCAATTATAATGGAGGATTTGGTAATT
GATTAGTTCCTTAACTAGGAGCTCCTGATATAGCTTTCCACGAATAAATAATATAAGATTTCTGAATACTTCCACCATCATTAACACTTTTAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGACTGGTTGAACTGTATACCCCTCTTTCTTCTAATATTGCTCATCAAGGATCTTCAGTTGATTTA
GCAATTTTTCATTACATCTTGCAGGAATTTCTTCTATTTTAGGAGCTATTAATTTTATTACAACATTTAATATACGAAATAAAACTTTCTTCTT
TTGATCAAATACCTTTATTTGTATGATCAGTTGGTATTACAGCTTTACTTCTACTTTTATCTTTACCAGTTTTAGCTGGAGCTATTACCATACTTTT
AACAGATCGTAATCTTAATACTTTCATTTTGTATCTGCAGGAGGAGACCAATTCCTTTATCAACATTTATTT
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Type material. Holotype: ♀ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 181–182, bears the following five rectangular labels, four white: [Farfan, | Panama C. Z. | 17 Feb. '63 | S. S. Nicolay], [Callimormus | corades | Felder | DET.BY S.S.NICOLAY], [DNA sample ID: | NVG-19016G06 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532350], and one red [HOLOTYPE ♀ | Callimormus | rades Grishin].

Type locality. Panama: Panama Province, Farfan.

Etymology. The name is formed from its sister species name (*C. corades*). By shortening the name, we specify a more northern distribution of this species. The name is a noun in apposition.

Distribution. Currently known only from the holotype collected in Panama.

***Gubrus lubens* Grishin, new species**

<https://zoobank.org/AEEFAD08-1F9A-406F-8AD7-AD386BBA716D>

(Fig. 7 part, 183–184, 418–420)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Loja, Ecuador, placed in the USNM collection among possible new species of “*Vehilius*” is a distant sister of *Gubrus lugubris* (Lindsey, 1925) (type locality in Peru) that was previously in the genus *Vehilius* Godman, 1900 (type species *Cobalus illudens* Mabilbe, 1891, a subspecies of *Pamphila stictomenes* Butler, 1877) (Fig. 7): e.g., their COI barcodes differ by 10.8% (71 bp), a large divergence likely caused by an elevated evolutionary rate in this lineage and its sister genus *Callimormus* Scudder, 1872 (type species *Callimormus juvenus* Scudder, 1872), and therefore represents a new species in the previously monotypic genus *Gubrus*. This new species is distinct in its appearance and is recognized among small brown HesperIIDae by rounder hindwing, without produced tornus in males, uniformly colored wings without paler veins and on the forewing with three pale-yellow spots in a line near the bases of forewing cells CuA₁-CuA₂, M₃-CuA₁, and M₂-M₃ and a small paler area instead of a developed spot in cell R₅-M₁; fringes are paler and indistinctly checkered. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly349.39.4:A117G, aly824.21.1:T348C, aly824.21.1:G351C, aly770.22.2:T84G, aly770.22.2:T120C, aly536.107.1:A129A (not C), aly536.107.1:G135G (not A), aly595.10.1:G801G (not A), aly9855.3.1:C140C (not T), aly1405.20.4:T18T (not C), and COI barcode: T22G, A79C, A379G, A529C, T619A.

Barcode sequence of the holotype. Sample NVG-19019B12, GenBank OR837706, 658 base pairs:

```
AACTTTATATTTTATTTTGGGATTTGAGCAGGAATATTAGGAACCTTCATTAAGATTATTAATTCGTACAGAATTAGGCAATCCTGGATCTTTAATT
GGGGATGACCAAATTTATAATACTATTGTTACAGCCCATGCTTTTATTATAATTTCTTTATAGTTATACCTATTATAAATGGAGGTTTTGGTAATT
GATTAGTCCCTTTAATACTAGGAGCCCTGATATAGCATTTCCTCGAATAAATAATATAAGATTTTGAATATTGCCCCCTCACTAATATTATTAAT
TTCTAGAAGAATTGTAGAAAATGGTGCAGGAACAGGTTGAACAGTTTATCCCCCTCTTTCTTCTAATATTGCCCATCAAGGTTTCATCGGTTGATTTA
GCAATTTTTCCTTCATTTAGCAGGAATTTCACTATTTTAGGAGCTATTAATTTTACTACTATCATTAAACATACGAATTAATAATCTTTTCAT
TTGATCAAATACCTTTATTTGTTGATCAGTAGGATTACAGCCTTACTTTTACTTTTATCTTTACCAGTATTAGCTGGAGCTATTACTATACTTCT
AACAGATCGAAATTTAATACTTCTTTTGTGATCCAGCTGGAGGAGGTGACCCAATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 183–184, bears the following six rectangular labels, five white: [ECUADOR Loja | Loja-Catamayo Rd. | Km 28 1800m | 16 May '88 | S. S. Nicolay], [♂ genitalia | slide/vial # | H989 | Prep. S.S. Nicolay], [*Vehilius* | n. sps. | Det. | S.S. Nicolay], [DNA sample ID: | NVG-19019B12 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532564], and one red [HOLOTYPE ♂ | *Gubrus lubens* | Grishin].

Type locality. Ecuador: Loja Province, km 28 of Loja–Catamayo road.

Etymology. In Latin, *lugubris* means sad, and *lubens* means happy, merry, joyful, willing, ready, or eager. This new species is happy to be the second species of this genus and is eager to be described here. The name is a masculine adjective.

Distribution. Currently known only from the holotype collected in Ecuador.

***Ludens labens* Grishin, new species**

<https://zoobank.org/7B83772E-AFB1-4A3F-995A-363407AD85FC>

(Fig. 7 part, 185–186, 421–422)

Definition and diagnosis. Phylogenetic trees reveal that several specimens from Panama identified as *Ludens ludens* (Mabille, 1891) (type locality in Panama, syntype sequenced as NVG-15036B04) are not monophyletic with it and show prominent genetic differentiation from it (Fig. 7): e.g., their COI barcodes differ by 8.4% (55 bp), and therefore represent a new species. This new species is sister to the species pair *L. ludens* and *Ludens petrovna* (Schaus, 1902) (type species Brazil: Rio de Janeiro) (Fig. 7). This new species keys to *Ludens ludens* (J.7) that included *L. petrovna* as its synonym in Evans (1955) but differs from these species by the lack of postdiscal spots that connect yellow veins on the ventral hindwing (Fig. 186), longer harpe than in *L. ludens* that is more similar to *L. petrovna*, shorter (compared to the length of costa) “thumb”-like expansion of the ampulla, and more concave ventral margin of harpe in lateral view (Fig. 422). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly216.51.3:T66C, aly890.73.2:C99T, aly890.73.2:G111A, aly600.14.2:G80A, aly1493.4.5:C60T, and COI barcode: T118A, T163A, C346A, A391T, A565G.

Barcode sequence of the holotype. Sample NVG-19017B12, GenBank OR837707, 658 base pairs:

```
AACATTATATTTTATTTTGGAAATTTGAGCAGGAATATTAGGTACATCATTAAGAATATTAATTCGTAATAGGTAATCCAGGATCTTTAATT
GGAGATGATCAAATTTATAACACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATGGTAATAACCAATTATAATTTGGCGGATTCGGTAATT
GATTAGTCCCATTAAATATTAGGAGCCCCAGATATAGCTTTTCCCTCGTATAAATAAATAAGATTTTGAATATTACCCCATCATTAAACATTATTAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGAACAGGATGAACTGTATATCCCCACTTTCATCCAATATGTCACATCAAGGATCCTCTGTTGATTTA
GCTATTTTCTCCCTTCATTTAGCAGGAATTTCTTCTATTTTAGGAGCTATTAATTTTATCACCCTATTTAATATACGAATAAAAACCTATCTT
TCGATCAAATACCTTTTATTTGATGATCTGTAGGTATTACAGCTTTATTATTATTATTATCATTACCTGTTCTAGCTGGGCCATTACTACTATTTT
AACAGATCGAAATTTAAATACTTCATTTTTTTGATCCTGCTGGAGGGGGGACCTATTTTATATCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 185–186, bears the following four rectangular labels, three white: [PANAMA:Darien | Cana 1200m | 7°56'N 77°43'W | 22 September 1982 | leg. G.B.Small], [DNA sample ID: | NVG-19017B12 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532848], and one red [HOLOTYPE ♂ | *Ludens labens* Grishin]. **Paratype:** 1♂ NVG-20054D07 Panama: Panama Province, Cerro Jefe, elevation ca. 880 m, GPS 9.2242, -79.3758, 17-Feb-2014, J. R. MacDonald leg. [MEM].

Type locality. Panama: Darien Province, Cana, elevation 1200 m, GPS 7.9333, -77.7167.

Etymology. In Latin, *ludens* means playful. An antonym for play is work. In Latin, *labor* means work, and the name derived from this word, similarly to *ludens*, is *labens*, which actually means slipping, gliding, or flowing. The name is treated as a noun in apposition.

Distribution. Panama.

***Rigga isa* Grishin, new species**

<https://zoobank.org/82DE66CF-AF62-4C68-9D1F-3ABCEBCFD07E>

(Fig. 7 part, 187–188, 423–424)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Ecuador similar in appearance to *Rigga auristriga* (Draudt, 1923) (type locality in Bolivia, holotype sequenced as NVG-18093C02) are not monophyletic with it and show prominent genetic differentiation from it (Fig. 7): e.g., their COI barcodes differ by 5.5% (36 bp), and therefore represent a new species. This new species is sister to *Rigga ira* (A. Butler, 1870) (type locality not given, possibly in Venezuela) and differs from it by 3.2% (21 bp) in the COI barcode. The hindwing of the new species is uniformly colored above, lacking yellow rays of *R. ira*, ventral hindwing veins are overscaled with approximately uniform thickness (except M_2 , which is weaker), and there is no appearance of a ray along the radius and vein M_1 as in *R. ira*. The new species differs from *R. auristriga*, which frequently has similar uniform overscaling of veins, by wider forewing spots and wider lower section of stigma. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly2284.14.4:G85C, aly4778.18.1:C946T, aly4778.18.1:T1398C, aly1937.17.47:C39A, aly1019.14.1:A84T, and COI barcode: A100G, C343A, T397C, T463C, T556C.

Barcode sequence of the holotype. Sample NVG-19019G06, GenBank OR837708, 658 base pairs:

AACTTTATATTTTATTTTGGTATTTGAGCAGGTATATTAGGAACTTCTTTAAGTATACTAATTCGAACAGAATTAGGTAACCCAGGATCTTTAATT
GGGGATGATCAAATTTATAATACTATTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTTGGAGGATTTGGTAATT
GATTAGTCCCCCTTATACTAGGAGCCCCAGATATAGCTTTCCACGAATAAATAATATAAGATTTGAATGCTTCCCCCTTCTTTAACACTTTTAAT
TTCTAGAAGAATTGTTGAAAATGGAGCAGGTACTGGTTGAACAGTTTACCACCTCTTTCTTCTAATATTGCCACCAAGGTTCTTCTGTGATTTA
GCAATTTTCTCCCTTCATTTAGCAGGTATTTCTTCTATTTTAGGAGCTATTAATTTTATTACTACAATTTAATACATACGAGTTAGAAAATTTATCAT
TTGATCAAATACCTTTATTTGTTGATCAGTAGGTATTACAGCATTATTATTACTTTTATCTTTACCTGTCTTAGCAGGAGCTATTACTATACTTCT
TACAGATCGAAATTTAAATACTTCTTTTTTTGACCCTGCTGGAGGAGGAGACCAATTTTATACCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 187–188, bears the following five rectangular labels, four white: [ECUADOR Napo | Baeza 2000m | 6 July '80 | S. S. Nicolay], [Parphorus | hesia ♂ | Det. Hew. | S.S. Nicolay], [DNA sample ID: | NVG-19019G06 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532617], and one red [HOLOTYPE ♂ | Rigga isa | Grishin]. **Paratype:** 1♀ NVG-21047G03 Ecuador: Napo, El Chaco, 1500 m, Nov-1971, R. de Lafebre leg. [MGCL].

Type locality. Ecuador: Napo Province, Baeza, elevation 2000 m.

Etymology. The name is formed from the Greek ίσος (isos), meaning equal. It reflects the equal overscaling of nearly all veins and signifies a more uniform appearance than *R. ira* and other congeners. The name is a noun in apposition.

Distribution. Ecuador.

Subtribe Falgina Grishin, 2019

Flaccilla lactea Grishin, new species

<https://zoobank.org/CB051F7E-A99E-4DE6-B233-993276D1F393>

(Fig. 7 part, 189–190, 425–426)

Definition and diagnosis. Sequencing of an unusual specimen of *Flaccilla* Godman, 1901 (type species *Papilio aecas* Stoll, 1781) from Peru with largely cream-colored ventral hindwing confirms its expected prominent genetic differentiation from *F. aecas* (type locality in Surinam) (Fig. 7): e.g., their COI barcodes differ by 7% (46 bp), and therefore it represents a new species. This new species (incompletely) keys to “*Aecas aecas*” (J.13.1) in Evans (1955) but differs from it by the lack of purple sheen on the ventral side and hindwing cream in color with discal brown spots and brown marginal spots nearly fused into a band. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly123.8.1:A51T, aly123.8.1:T72G, aly1779.16.4:C84T, aly1779.16.4:G111A, aly13170.2.2:A27G, aly1139.48.20:T97T (not C), aly1139.48.20:G102G (not A), aly499.35.1:G419G (not A), aly2096.12.3:A137A (not C), aly2096.12.3:T155T (not G), and COI barcode: A35T, T142C, A241T, 484C, T580C.

Barcode sequence of the holotype. Sample NVG-19017E11, GenBank OR837709, 658 base pairs:

AACTTTATATTTTATTTTGGTATTTGAGCAGGATTATTAGGAACTTCATTAAGATTATAAATTCGGACAGAAGTAGGAAACCCAGGTTCTTTAATC
GGAGATGATCAAATTTATAATACTATTGTAACAGCTCATGCTTTTATTATAATTTTTTTTATAGTAATACTATTATAATCGGAGGATTTGGAAAT
GATTAGTTCATTAATATTAGGAGCTCCTGACATAGCCTTCCACGTATAAATAATATAAGATTTGAATACTACCCCATCATTAACTTTATTAAT
TTCAAGAAGAATTGTAGAAAATGGGGCAGGAACAGGATGAACCTGTTTATCCGCCCTTTCTCTAATATTGCCCATCAAGGTTCTTCTGTGATTTA
GCAATTTTTCATTACATTTAGCTGGAATTTCTTCTATTTTAGGAGCTATTAATTTTACTACTACAATTTAATATACGAATTAATAATATATCCT
TTGATCAAATACCATTATTTGTTGATCTGTAGGAATTACAGCATTATATTACTTTTTATCTTTTACCTGTTTTAGCTGGAGCTATTACATACTCCT
TACTGATCGAAATTTAAATACATCATTTTTTTGATCCTGCAGGAGGAGGAGACCTATTTTATACCAACATTTATTT

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 189–190, bears the following five rectangular labels, four white: [PERU: Cuzco: Cosñipata Valley | Quebrada Quitacalzón 1,050m. | 13° 01' 13"S, 71° 29' 50"W | 12 August 2009 Brian Harris], [*Flaccilla* sp. n.], [DNA sample ID: | NVG-19017E11 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01532369], and one red [HOLOTYPE ♂ | *Flaccilla* | *lactea* Grishin].

Type locality. Peru: Cuzco Region, Cosñipata Valley, Quebrada Quitacalzón, elevation 1050 m, GPS –13.020278, –71.497222.

Etymology. In Latin, *lacteus* means milky. The name is given for the milky-colored hindwing and is a feminine adjective.

Distribution. Currently known only from the holotype collected in the Cosñipata Valley, Peru.

***Falga mirabilis* Evans, 1955 (with *Falga jeconia odol* Evans, 1955 as its subspecies), *Falga jacta* Evans, 1955, and *Falga ombra* Evans, 1955 are species distinct from *Falga jeconia* (A. Butler, 1870)**

Genomic sequencing taxa currently treated as subspecies of *Falga jeconia* (A. Butler, 1870) (type locality in Venezuela), namely: *Falga mirabilis* Mabilie, 1898 (type locality in Bolivia), *Falga jeconia jacta* Evans, 1955 (type locality in Colombia), and *Falga jeconia ombra* Evans, 1955 (type locality in Ecuador) show substantial genetic differentiation from it and each other (Fig. 7): e.g., the smallest barcode difference among them is 2.1% (14 bp), between *F. jeconia* and *F. j. jacta*, with the next being 2.6% (17 bp) between *F. mirabilis* and *F. j. ombra*. Therefore, we propose a **new status** of species for *Falga mirabilis* Evans, 1955, *Falga jacta* Evans, 1955, and *Falga ombra* Evans, 1955. The phylogenetic tree reveals that *Falga jeconia odol* Evans, 1955 (type locality in southern Peru) is closely related to *Falga mirabilis* (Fig. 7). Therefore, we propose to treat the former as a subspecies of the latter: *Falga mirabilis odol* Evans, 1955, **new combination**.

***Falga athena* Grishin, new species**

<https://zoobank.org/E9BA59DB-2467-42BA-9C5F-BEB41F8CF500>

(Fig. 7 part, 191–192, 427–429)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Panama resembling a darker *Falga sciras* Godman, 1901 (type locality in Honduras) is not monophyletic with it and shows prominent genetic differentiation from it (Fig. 7): e.g., their COI barcodes differ by 5.9% (39 bp). This specimen also differs from all other species of *Falga* Mabilie, 1898 (type species *Carystus jeconia* Butler, 1870) and, therefore, represents a new species. This new species (incompletely) keys to *Falga jeconia jeconia* (I.1.2(b)) in Evans (1955). It differs from *F. sciras* by lacking a discal brown spot at the end of discal cell on the ventral hindwing and orange spots on the dorsal forewing not reaching the wing base. It differs from other species by orange, rather than yellow or yellow-orange spots and patches on the dorsal side and brown around the tornus on the ventral hindwing. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly2423.6.2:G57A, aly1838.37.5:T96C, aly666.26.4:A100C, aly542.3.12:C99T, aly1651.8.4:A153T, aly2548.20.5:C27C (not T), aly725.21.1:A114A (not G), aly208.47.15:T281T (not C), aly7689.2.1:T36T (not C), aly11945.4.1:T2088T (not C), and COI barcode: T250C, T352C, T355A, T530C, A565T.

Barcode sequence of the holotype. Sample NVG-18012E08, GenBank OR837710, 658 base pairs:

```
AAC TT TAT ATTTT ATTTT TGGT ATTTG AGCAGGA ATATTAG GAAC TCTTTAAGTATATTAATTCGTACTGAATTAGGAATCCAGGATTTTAAATT
GGAGATGATCAAATTTATAACTATTTGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATAACCAATTATAATTGGAGGATTTGGAAATT
GATTAGTCCATTAATATTAGGAGCTCCTGATATAGCTTTTCCCTCGAATAAATAACATAAGATTTTGAATATTGCCTCCTCCCTAACATTATTAAT
TTCAAGAAGAATTGTTGAAAATGGTGCAGGAAC TGGATGAACAGTTTATCCCCCTCTTTCCTCAAATATGCTCATCAAGGATCTTCTGTTGATTTA
GCAATTTTCTCTTCAATTTAGCTGGAATTTCTTCTATTCTTGGAGCTATTAAC TTTATTACTACAATTTATAATATACGAATTAATAATAGATCAT
TTGATCAAATACCAATTTGTTATGATCTGTGGGAATTACAGCACTTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCTATTACTACTTCT
TACAGATCGAAATCTTAATACATCTTTTTTTTGGATCCTGCAGGAGGAGGGGATCCAATTTTATATCAACATTTTATTT
```

Type material. **Holotype:** ♀ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 191–192, bears the following four rectangular labels, three white: [PANAMA: Darien | Cana 1550m | 23.III.1983 | leg. G.B.Small], [DNA sample ID: | NVG-18012E08 | c/o Nick V. Grishin], [USNMEN | {QR Code} | 01450279], and one red [HOLOTYPE ♀ | *Falga athena* | Grishin].

Type locality. Panama: Darien Province, Cana, elevation 1550 m.

Etymology. *Sciras* is the surname of Athena, an Olympian goddess. The name *athena* signifies that the new species is closest in wing pattern to *F. sciras*. The name is a noun in apposition.

Distribution. Currently known only from the holotype collected in eastern Panama.

Subtribe Calpodina A. Clark, 1948

***Panoquina jay* Grishin, new species**

<https://zoobank.org/B6EEC7CF-A0A4-4AB2-BB1D-14F036CB0D20>

(Fig. 8 part, 193–194, 430–431)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Peru with a general appearance of

Panoquina bola Bell, 1942 (type locality in Bolivia) shows prominent genetic differentiation from all named relatives without strong affinity to any of them (Fig. 8): e.g., their COI barcodes differ by 6.5% (43 bp) and, therefore, represents a new species. This new species keys to *P. bola* (O.2.9) in Evans (1955) but differs from it and other relatives by broader ventral hindwing discal band of uniform width and extending into the cell CuA₂-1A+2A on chestnut ground color and a smaller forewing spot in the cell M₂-M₃. Due to the lack of additional specimens and unknown phenotypic variation, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1041.32.2:T54C, aly1019.32.2:A169C, aly221.7.14:A63T, aly10226.12.4:A54G, aly971.2.12:C129G, aly481.23.3:C109C (not A), aly481.23.3:T117T (not C), aly927.1.16:C177C (not T), aly171.7.2:C69C (not T), aly531.29.1:A138A (not G), and COI barcode: T49C, A67G, A251T, A433G, A550G.

Barcode sequence of the holotype. Sample NVG-8064, GenBank OR837711, 658 base pairs:

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AACTTTATATTTTATTTTGGAAATTTGAGCAGGTATATTAGGTACTTCCTTAAGTTTATTAATTCGGACAGAATTAGGAAATCCTGGATCTTTAATT
GGAGATGATCAAATTTATAATACCATCGTTACAGCTCATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATGGAGGATTTGGTAATT
GATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTCCCTCGTATAAATAATTTAAGATTTTGAATACTACCTCCTTCTTAACCTTTATTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCAGGTACAGGTTGAACCTGTTTATCCCCCTTCTTCTAATATTGCTCATCAAGGAGCTTCTGTTGATTTA
GCAATTTTTTCCCTTCATTTAGCAGGTATTTCAACAATCTTAGGGCTATTAATTTTATTACTACAATTTAATATACGAATTAATAAATTTATCAT
TTGATCAAATACCTTTATTTGTATGATCCGTTGGAATTTACAGCCTTATTATTACTTTTTATCTTTGCCAGTTTTAGCTGGAGCTATTACTATACTTTT
AACTGATCGAAATTTAATACTTCATTTTTTGACCCTGCTGGAGGGGGGATCCAATTTTATATCAACATTTATTT
```

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 193–194, bears the following five rectangular labels, four white: [PERU: Loreto Prov. | Rio Amazonas, 200m | Explorama Lodge | 50 mi E Iquitos | 12-16 Sept. 1990 | Brian P. Harris], [DNA sample ID: | NVG-8064 | c/o Nick V. Grishin], [genitalia | NVG170208-49 | Nick V. Grishin], [USNMENT | {QR Code} | 01321904], and one red [HOLOTYPE ♂ | Panoquina | jay Grishin].

Type locality. Peru: Loreto Province, 50 mi E Iquitos, Amazon River, Explorama Lodge, elevation 200 m.

Etymology. The name reflects the white band on the ventral hindwing, which reminds us of the letter J (jay). The name is a noun in apposition.

Distribution. Currently known only from the holotype collected in northeastern Peru.

Calpodes salianus Grishin, new species

<https://zoobank.org/9916050C-DBCE-4EDA-A05C-6BB74C2BD7B3>

(Fig. 8 part, 195–196, 432–434)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Peru identified as *Calpodes salius* (Cramer, 1775) (type locality in Suriname) is not monophyletic with and shows prominent genetic differentiation from it (Fig. 8): e.g., their COI barcodes differ by 5.2% (34 bp), and therefore represents a new species. This new species keys to “*Saliana salius*” (O.14.17) in Evans (1955) but differs from it by longer costal shoulder of the discal cell spot that has an appearance of a separate spot shifted distad (at the base too) but joined with the lower spot (instead of a single spot with a flatter base and irregular outer margin), and the lack of ash-gray overscaling at the base of ventral hindwing (this area is maroon-colored instead with violet sheen) (Fig. 195–196), ampulla more protruding dorsad, and more convex costa near ampulla (Fig. 434). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly276558.9.2:A84G, aly276558.9.2:A150G, aly2258.12.5:G486C, aly272.25.11:T84C, aly1660.4.4:C157T, aly638.8.1:G327G (not A), aly638.8.1:A369A (not G), aly827.13.1:C42C (not G), aly827.13.1:C75C (not T), aly525.2.6:G186G (not A), and COI barcode: T19C, A44T, T121C, A175G, T596C.

Barcode sequence of the holotype. Sample NVG-18112H11, GenBank OR837712, 658 base pairs:

```
AACTTTATATTTTATTTTCGGTATTTGAGCAGGAATATTAGGTCTTCATTAAGTTTATTAATTCGTACAGAATTAGGTAATCCTGGTTTCATTAATT
GGAGATGACCAAATTTATAATACCATTGTTACAGCTCAGCTTTTATTATAATTTTTTTTATAGTAATACCTATTATGATTGGAGGATTTGGAAAT
GATTAGTACCATTAATATTAGGAGCCCCAGATATAGCTTTTCCCTCGAATAAATAATATAAGATTTTGAATACTCCCCCTTCATTAACCTTTATTAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGAACAGGTTGAACAGTTTATCCCCCTTTCAGCTAATATCGCCCATCAAGGATCTTCAGTTGATCTA
GCAATTTTTTCTTTCATTTAGCAGGAATTTCAACAATTTTAGGAGCTATTAATTTTATTACTACAATTTAATATACGAATTAGAAAATTTAATAT
TTGACCAAATACCATTATTTGTTGATCTGTAGGAATTACAGCATTATTATTACTATTATCATTACCAGTTTTAGCAGGAGCTATTACAATACTTCT
TACTGACCGAAATCTAAATACATCTTCTTTTGACCCTGCAGGAGGAGGTGACCCTATTTTATACCAACATTTATTT
```

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 195–196, bears the following four rectangular labels, three white: [PERU 300m | 30 Km S.W. | Pto. Maldonado | 26 Oct. '83 | S. S. Nicolay], [DNA sample ID: | NVG-18112H11 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01531430], and one red [HOLOTYPE ♂ | Calpodes | salianus Grishin].

Type locality. Peru: Madre de Dios Region, 30 km SW of Puerto Maldonado, elevation 300 m.

Etymology. The name reflects its somewhat similar appearance to *C. salius*. Made longer, the name signifies it is a more southern relative. The name is treated as a noun in apposition.

Distribution. Currently known only from the holotype collected in the Amazonian region of Peru.

Calpodes stingo Grishin, new species

<https://zoobank.org/C1F403E7-718A-427C-9882-2C56D6D2B124>

(Fig. 8 part, 197–198, 435–437)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Ecuador identified as *Calpodes placens* (A. Butler, 1874) (type locality Colombia: Bogota) shows prominent genetic differentiation from it (Fig. 8): e.g., their COI barcodes differ by 3.6% (24 bp), and therefore represents a new species. This new species keys to “*Saliana placens*” (O.14.9) in Evans (1955) but differs from it by much reduced orange overscaling between the pale base and brown tornus of ventral hindwing with that area being more brown than pale or orange (in *C. placens*, pale basal color intrudes into the brown area and is framed with yellow and orange), as well as darker and more restricted rusty overscaling on forewing above. Due to the lack of additional specimens and unknown phenotypic variation, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1603.82.16:T51C, aly1603.82.16:A54G, aly84.57.9:A48T, aly671.7.4:T54C, aly619.9.1:T48C, aly4305.15.6:T303T (not C), aly1041.22.3:G133G (not A), aly2103.6.1:A392A (not G), aly144.20.2:T57T (not A), aly18882.2.3:G48G (not T), and COI barcode: A34C, A58G, A373T, 220C, T653C.

Barcode sequence of the holotype. Sample NVG-18112H02, GenBank OR837713, 658 base pairs:

```
AACTTTATATTTTATTTTGGTATTTGAGCAGGCATATTAGGTACTTTCATTAAGTTTGTAAATTCGTACTGAATTAGGTAACCCCTGGTTCATTAATT
GGAGATGACCAAATTTATAATACTATTGTTACAGCTCATGCCTTATTATAATTTTTTTTATAGTTATACCTATTATAATTTGGAGGATTTGGAAATT
GATTAGTTCATTAAATATTAGGTGCCCCGTGATATAGCTTTCCCGAATAAATAAATAAGATTTTGAATACTCCCCCTTCATTAACCTTTATTAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGAACAGGTTGAACGGTTTACCCCCCTTTCATCCAATATGCCCACCAAGGTTTCATCTGTGATTTA
GCAATTTTTTCTTTACATTTAGCAGGAATCTCATCAATTTTAGGAGCTATTAATTTTATTACTACAATTATTAATATACGAATTAATAATTTAATAT
TTGATCAAAATACCATTATTTGTTGATCTGTAGGAATTACAGCATTATTACTTTTATCATTACCTGTTTGTAGCAGGAGCTATTACTATATTACT
TACTGATCGAAATTTAAATACATCTTTTTTTGATCCTGCAGGAGGAGGTGATCCTATTTTATATCAACATCTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 197–198, bears the following four rectangular labels, three white: [ECUADOR: Sucumbíos, | Cerro Lumbaquí Norte, | 0° 01'70" N, 77° 19'22" W | 800–950 m, 18–22 Aug 2002 | J.P.W. Hall & M.A. Solis], [DNA sample ID: | NVG-18112H02 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01531422], and one red [HOLOTYPE ♂ | Calpodes | stingo Grishin].

Type locality. Ecuador: Sucumbíos Province, Cerro Lumbaquí Norte, elevation 800–950 m, approx. GPS 0.0283, –77.3203

Etymology. In Latin, *placens* means pleasing, and *stinguō* means to put out or extinguish. The name *stingo* is given to this species with a “pleasing” orange streak removed from the ventral hindwing. The name is a noun in apposition.

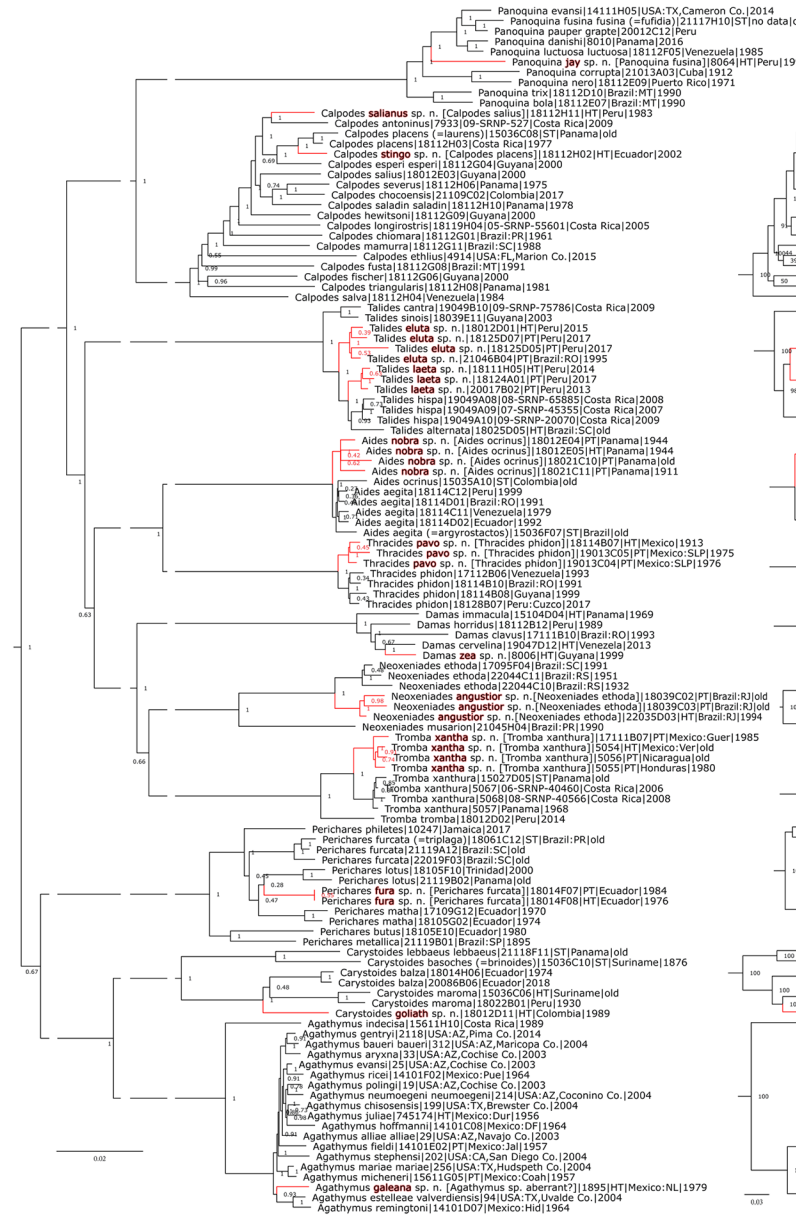
Distribution. Currently known only from the holotype collected in north-central Ecuador.

Subscribe Carystina Mabilie, 1878

Hesperia ocrinus Plötz, 1882 is a junior subjective synonym of *Aides aegita* (Hewitson, 1866)

Genomic sequencing of a single syntype of *Hesperia ocrinus* Plötz, 1882 (type locality in Colombia, NVG-15035A10) in MFNB, currently a valid species in the genus *Aides* Billberg, 1820 (type species *Papilio epitus* Stoll,

a Z chromosome tree



b mitochondrial genome tree segments

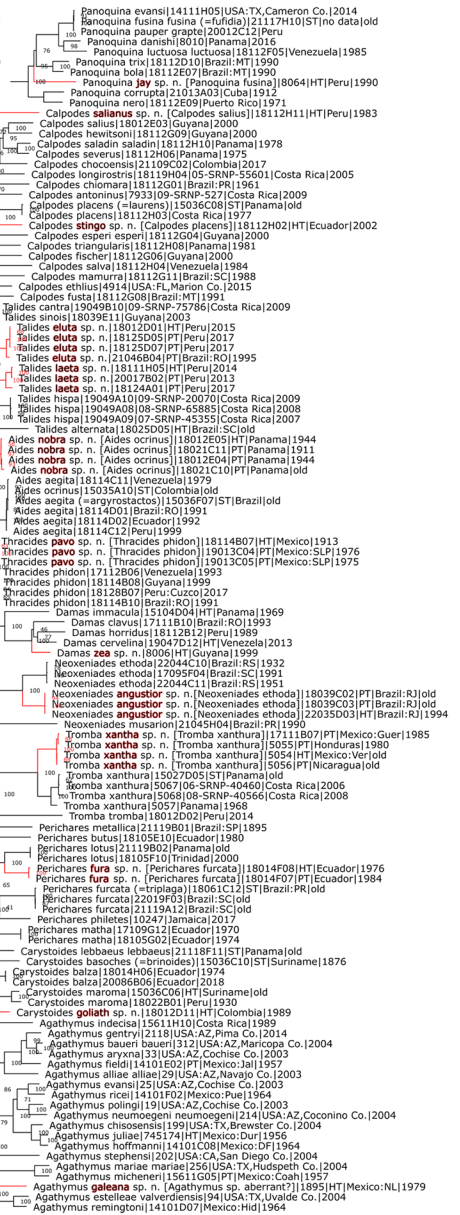


Figure 8. Phylogenetic trees of several Hesperii subtribes inferred from protein-coding regions in **a**) the Z chromosome and **b**) the mitochondrial genome (in segments). See Fig. 1 legend for other notations.

1781, a homonym, the valid name for this species is *Aedes duma argyrina* Cowan, 1970) reveals that it is *Aedes aegita* (Hewitson, 1866) (type locality in Brazil: Para) (Fig. 8). Indeed, inspection of the *H. ocrinus* syntype, a male, reveals bands on the wings that are characteristic of *A. aegita* and its junior subjective synonyms. Therefore, we propose to treat *Hesperia ocrinus* Plötze, 1882 as a junior subjective synonym of *Aedes aegita* (Hewitson, 1866). *Hesperia ocrinus* was misidentified by Evans (1955), and the species without bands that Evans called “*Aedes ocrinus*” does not have a name and is described next as new.

***Aides nobra* Grishin, new species**

<https://zoobank.org/3466088D-C59F-48E0-BEE9-4231E4D349A7>

(Fig. 8 part, 199–200, 438–439)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Panama identified as *Aides ocrinus* show prominent genetic differentiation from a syntype of *Hesperia ocrinus* Plötz, 1882 (type locality in Colombia, NVG-15035A10, see above for its synonymization) (Fig. 8): e.g., their COI barcodes differ by 3.6% (24 bp), and therefore represent a new species. This new species keys to “*Aides ocrinus*” (O.12.6) in Evans (1955), which he misidentified, and specimens he identified as “*A. ocrinus*” are probably this species. Differs from its relatives by the lack of brands in males, redder (instead of more olive in color) ventral wing coloration, and harpe with broad and rounded end. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly1222.14.21:A112T, aly1222.14.21:A228G, aly7999.4.21:G189A, aly19602.6.1:G288A, aly19602.6.1:G574T, and COI barcode: T10C, T154C, T171C, T367C, A628T.

Barcode sequence of the holotype. Sample NVG-18012E05, GenBank OR837714, 658 base pairs:

```
AACTTTTACTTTTATTTTTGGAAATTTGAGCAGGTATATTAGGAACTTCCTTAAGTTTATTAATTCGAACAGAATTAGGTAATCCAGGATCATTAAATT
GGAGATGATCAAATTTATAATACTATTGTTACTGCTCATGCTTTTATTATAATTTCTTTATAGTAATACCTACTATAAATGGAGGATTTGGAAATT
GACTAGTCCCTCTAATACTAGGAGCCCCGTGATATAGCATTTCCCTCGAATAAATAAATAAGATTTTGATTATTACCTCCCTCACTTACTTTACTAAT
TTCAAGAAGAATTGTAGAAAATGGTGCAGGAACGGATGAACAGTTTATCCCCCTCTTTCATCTAATATGCTCACCAGGATCATCAGTTGATTTA
GCAATTTTTCTCTTCACTTAGCAGGTATTTTCATCAATTTTAGGAGCAATTAATTTTATTACTACAATTTAATAATACGAATTAATAATTTATCTT
TTGACCAATACCTTTTATTTGTATGATCTGTAGGAATTACAGCTTTATTACTTTTATCATTACCAGTATTAGCCGGAGCCATTACAATACTCCT
TACTGATCGAAATTTAAATACTTCAATTTTTGATCCAGCTGGAGGTGGTGATCCAATTTTATACCAACATTTATTT
```

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 199–200, bears the following four rectangular labels, three white: [COCO SOLO | PANAMA CANAL ZONE | 1 APRIL 1944 | W. M. WAGNER, JR.], [DNA sample ID: | NVG-18012E05 | c/o Nick V. Grishin], [USNMENT | {QR Code} | 01450333], and one red [HOLOTYPE ♂ | *Aides nobra* | Grishin]. **Paratypes:** 3♂♂ and 3♀♀ from Panama, Canal Zone: 1♂ NVG-18012E04, USNMENT_01450332 the same data as the holotype but collected on 30-Mar-1944; 1♂ Gulf of Panama nr. Cape Mala, 30-Sep-1024 [BMNH]; 1♂ Pedro Miguel, G. Tryhane leg. [BMNH]; 1♀ 1-Feb-1913, A. Hall leg. [BMNH]; 2♀♀ [AMNH]: NVG-18021C10 no other data than “Panama”; and NVG-18021C11 May-1911, collection F. E. Watson.

Type locality. Panama: Colón Province, Cativá [formerly Coco Solo].

Etymology. The name reflects the lack of brands: *no* + *bra*[nds] and is a noun in apposition.

Distribution. Currently known only from central Panama.

***Thracides pavo* Grishin, new species**

<https://zoobank.org/14FC64FB-D37D-43E1-8764-08D112459C19>

(Fig. 8 part, 201–202, 440–441)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Mexico identified as *Thracides phidon* (Cramer, 1779) (type locality in Suriname) show prominent genetic differentiation from it in the Z chromosome (Fig. 8) and, therefore, represent a new species. Curiously, despite the prominent differentiation in the Z chromosome, their COI barcodes differ by only 1.1% (7 bp). This new species keys to *T. phidon* (O.15.7) in Evans (1955) but differs from it by typically longer segments of stigma, by lacking or vestigial subapical white spots on ventral forewing (many *T. phidon* specimens have these spots), especially in males, yellower and more extensive overscaling at the forewing apex beneath, less extensive blue overscaling on dorsal hindwings (Fig. 201–202), longer saccus, and broader rounded distal end of harpe (Fig. 441). Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly38.8.4:C87A, aly423.2.7:A162T, aly214.15.4:G34A, aly1074.2.19:G51A, aly1074.2.19:C66T, and COI barcode: T5A, T118T, 127A, T442T, A508G, T533T.

Barcode sequence of the holotype. Sample NVG-18114B07, GenBank OR837715, 658 base pairs:

```
AACTCTATATTTTATTTTTGGAAATTTGAGCAGGAATATTAGGAACATCTTTAAGATTATTAATTCGAACCTGAATTAGGTAACCCAGGATCTTTAATT
```

GGAGATGATCAAATCTATAAATACTATTGTAACCTGCTCATGCTTTTATTATAAATTTTTTTTATAGTAATACCTATTATAAATGGAGGATTGGAAATT
 GATTAGTTCCTTTAATATAGGAGCTCCCGATATAGCTTTCCCCCGAATAAATAAATAAGTTTTTGAATGCTACCCCTTCATTAACCTCTTTAAT
 TTCAGAAGAATTGTAGAAAATGGTGCAGGAACAGGATGAACAGTTTACCCCTTTATCCTCTAATATTGCTCATCAAGGATCTCAGTAGATTTA
 GCCATTTTTCTCTTCATTTAGCCGGAATTTCTCAATTTAGGAGCTATTAATTTTATACTACAATTATAATATACGAATTAATAAATTTATCTT
 TCGATCAAATACCTTTATTTGTGTGATCAGTAGGAATTACAGCTTTATTATTACTTTTATCTCTACCAGTATTAGCAGGTGCTATTACTATACTTCT
 TACAGATCGAAATTTAAATACATCTTTTTTTGATCCTGCTGGAGGAGATCCTATTCTTTATCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 201–202, bears the following seven rectangular labels, six white: [Teapa | Tabasco | Mexico], [March | 1913], [RMuller | Collector], [3708], [DNA sample ID: | NVG-18114B07 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01531463], and one red [HOLOTYPE ♂ | Thracides | pavo Grishin]. **Paratypes:** 2♀♀: Mexico: San Luis Potosi, Sierra Madre O., El Salto Falls, Roy O. Kendall and C. A. Kendall leg., larval foodplant: *Heliconia latispatha* Benth. [TAMU]: NVG-19013C04 4-Feb-1976 and NVG-19013C05 14-Feb-1975.

Type locality. Mexico: Tabasco, Teapa.

Etymology. In Latin, *pavo* means peacock. The name is given for the colorful wings of this species and is a noun in apposition.

Distribution. Currently recorded from Tabasco and San Luis Potosi in Mexico.

Talides eluta Grishin, new species

<https://zoobank.org/900BB006-C1DB-4CC9-ADD3-B2393A6B4539>

(Fig. 8 part, 203–204, 442–443)

Definition and diagnosis. Phylogenetic trees reveal that several specimens of *Talides* Hübner, [1819] (type species *Talides sinois* Hübner, [1819]) from Peru and Brazil show prominent genetic differentiation from named species of this genus (Fig. 8): e.g., their COI barcodes differ from that of *Talides alternata* E. Bell, 1941 (type locality in Brazil: Santa Catarina, holotype sequenced as NVG-18025D05) by 5.6% (37 bp), and therefore represent a new species. This new species keys to *T. alternata hispa* (K.13.3(b)) in Evans (1955) but differs from it by less rounded wings and less contrasting patterns of ventral side, shorter and not as bright orange fringes, straighter and shorter upper segment of stigma, and a more elongated and thinner apical spot in the cell R_5-M_1 . Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly1244.8.2:G99A, aly927.2.7:G49T, aly927.2.7:G128A, aly596.8.4:C10A, aly35002.7.1:C96T, and COI barcode: T247C, T373C, T436A, T482A, A622G.

Barcode sequence of the holotype. Sample NVG-18012D01, GenBank OR837716, 658 base pairs:

AACTTTATATTTTATTTTGGAAATTTGAGCAGGAATATTAGGAACTTCTTTAAGATTATAAATTCGAACAGAATTAGGTAATCCAGGATTTTAAAT
 GGAGATGATCAAATTTATAAATACTATTGTAACAGCTCATGCTTTTATTATAAATTTTTTTTATAGTAATACCAATTATAAATGGAGGATTGGAAATT
 GATTAGTTCCTCTTATACTTTGGAGCCCTGATATAGCTTTCCCCCGAATAAACAATATAAGATTCTGAATACTTCCCTTCTTTAACATTATTAAT
 TTCAGAAGAATTGTAGAAAATGGTGTGCTGGTACAGGATGAACCTGTATAATCCCTCTTTTCAGCTAATATTGCTCATCAAGGCTCATCTGTGATTTA
 GCAATTTTTTCCCTTCATTTAGCAGGAATTTCTTCTATTTTAGGAGCAATTAACCTTTATTACAACAATTTATAATATACGAATTAGAAATTTAATAT
 TTGATCAAATACCTCTATTTGTATGATCTGTGGGAATTACAGCTTTATTATTATTATTCTTTACCTGTTTTAGCAGGAGCTATTACTATACTTCT
 TACTGATCGTAATTTAAATACTTCAATTTTTGACCCTGCGGGTGGAGGAGATCCTATTTTATACCAACATTTATTT

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 203–204, bears the following four rectangular labels, three white: [PERU:Cuzco 540 m. | Villa Carmen | Pilcopata 4057 | 03-V-2015 Kinyon], [DNA sample ID: | NVG-18012D01 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01450290], and one red [HOLOTYPE ♂ | *Talides* | *eluta* Grishin]. **Paratypes:** 3♂♂: 1♂ NVG-21046B04 Brazil: Rondônia, 5 km S Cacaulandia, linha C-10 (at Rio Pardo) off B-65, 18-Apr-1995, O. Gomes leg., genitalia GTA-7238 [MGCL]; 2♂♂: Peru: Madre de Dios, Alto Madre de Dios at Pantiacolla Lodge, 400 m, GPS –12.6500, –71.2167 W. Dempwolf leg. [WRDempwolf]: NVG-18125D05, WRD 14975 4-Nov-2017; and NVG-18125D07, WRD 14981 7-Nov-2017.

Type locality. Peru: Cuzco, Pilcopata, Villa Carmen Biological Reserve, elevation 540 m.

Etymology. In Latin, *elutus* means washed out. The name is given to signify the reduced coloration and duller appearance of this species compared to the new species described next. The name is an adjective.

Distribution. Currently known from Peru (Cuzco and Madre de Dios) and Brazil (Rondônia).

***Talides laeta* Grishin, new species**

<https://zoobank.org/61A18EF8-BC80-4CF3-9143-26179E53CECA>

(Fig. 8 part, 205–206, 444–445)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Peru identified as *Talides alternata* E. Bell, 1941 (type locality in Brazil: Santa Catarina, holotype sequenced as NVG-18025D05) show prominent genetic differentiation from it and other species in the genus (Fig. 8): e.g., their COI barcodes differ by 6.4% (42 bp) and from *Talides eluta* **new species** by 4.9% (32 bp), and therefore represent a new species. This new species keys to *T. alternata alternata* (K.13.3(a)) in Evans (1955) but differs from it by a broader, nearly square-shaped yellow spot in the forewing discal cell and the broader area of ventral forewing with submarginal pale overscaling. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly536.106.3:C159T, aly444.1.12:C24T, aly444.1.12:G45A, aly444.1.12:G138A, aly971.9.9:C61T, and COI barcode: A34T, A67G, T133A, C271A, 499C.

Barcode sequence of the holotype. Sample NVG-18111H05, GenBank OR837717, 658 base pairs:

```
AACTTTATATTTTATTTTGGAAATTTGAGCAGGTATATTAGGAACCTTCATTAAGATTATTAATTCGGACAGAATTAGGTAATCCAGGATTTTAAATC
GGAGATGATCAAATCTATAATACTATTGTAACAGCACATGCTTTTATTATAATTTTTTTTATAGTAATAACCAATTATAATGGAGGATTTGGAAAT
GATTAGTTCCCTCTTATACCTGGAGCTCCTGATATAGCTTTTCCCTCGAATAAATAATATAAGATTTTGAATACTCCACCCTCTTTAACATTATTAAT
TTCAAGAAGAATTGTAGAAAATGGTGCTGGTACAGGATGAACTGTATACCCCCCTCTTTCAGCTAATATTGCCCATCAAGGTTCTCTGTGATTTA
GCAATTTTTTCACTTCATTTAGCAGGAATTTCTTCTATTTTGGGAGCTATTAATTTTTATTACAACAATTTAATATACGAATTAGAAATTTATTAT
TTGATCAAATACCCCTATTTGTATGATCTGTAGGAATTACAGCTTTATGTTATTATTATCTTTTACCTGTTTTAGCAGGAGCTATTACAATACTTCT
TACAGATCGAAACTTAATACTTTCATTTTTTGTATCCTGCAGGTGGAGGAGATCCTATCTTATACCAACATTTATTT
```

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 205–206, bears the following four rectangular labels, three white: [PERU:Cuzco, 1375m | San Pedro Lodge | Cosnipata Valley 3756 | 21.IX.2014 Kinyon], [DNA sample ID: | NVG-18111H05 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01531341], and one red [HOLOTYPE ♂ | *Talides laeta* | Grishin]. **Paratypes:** 2♂♂ NVG-18124A01, WRD 14984 at the type locality, GPS –13.05, –71.55, 1-Nov-2017, W. Dempwolf leg. [WRDempwolf] and NVG-20017B02, 2019-043 Peru: Madre de Dios, Amazonia Lodge, 491m, 24-Oct-2013, M. McInnis leg. [MUSM].

Type locality. Peru: Cuzco Region, Cosnipata Road, San Pedro Lodge, elevation 1375 m.

Etymology. In Latin, *laetus* means colorful, joyful, glad, pleasing, or vivid. The name is given to signify this species is more brightly colored than the previous one (*Talides eluta* **new species**). The name is an adjective.

Distribution. Currently known from Peru.

***Neoxeniades angustior* Grishin, new species**

<https://zoobank.org/AD9B121F-E94F-4090-A0FF-339601F78275>

(Fig. 8 part, 207–210, 446–450)

Definition and diagnosis. Phylogenetic trees reveal that some specimens identified as *Neoxeniades ethoda* (Hewitson, 1866) (type locality in Brazil: Rio de Janeiro) show prominent genetic differentiation from it (Fig. 8): e.g., their COI barcodes differ by 4% (26 bp), and therefore represent a new species. This new species keys to “*Xeniades ethoda*” (O.13.4) in Evans (1955) but differs from it by smaller forewing hyaline yellow spots: e.g., the spot in cell CuA₁-CuA₂ does not overlap with the discal cell spot, the presence of subapical forewing hyaline spots (small in some males), a differently shaped hindwing white band: gets very thin, intermittent, or disappears towards vein Sc+R1-RS, and more olive in color in contrast to redder *N. ethoda*. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly318.10.1:A2253G, aly318.10.1:T2289C, aly133.4.1:C446T, aly133.4.1:G456A, aly159.20.1:C63G, and COI barcode: T46C, T56C, T133C, T340C, T364C, 500C.

Barcode sequence of the holotype. Sample NVG-22035D03, GenBank OR837718, 658 base pairs:

```
AACTTTATATTTTATTTTGGAAATTTGAGCAGGAATACTAGGAACCTCTTAAAGACTATTAATTCGTACAGAATTAGGAAATCCTGGATTTTAAAT
GGAAATGATCAAATTTATAATACCATTTGTAACAGCCCATGCTTTTATTATAATTTTTTTTATAGTAATACTATTATAATGGAGGATTCGGAAAT
GATTAGTTCCATTAATATTAGGTGCTCCTGATATAGCATTTTCCCTCGAATAAATAATATAAGATTTTGATTATTACCACCTTCATTAATATTATTAAT
TTCAAGAAGAATTGTAGAAAATGGAGCTGGAACAGGTTGAACTGTTTACCACCTCTTCTTCTAATATTGCCCATCAAGGATCTTCTGTAGATTTA
GCAATTTTTTCCCTTCATTTAGCAGGAATTTCTTCTATTTTAGGAGCTATTAATTTTTATTACTACCATTATTAATATACGAATTAAAAATTTATCAT
```

TTGATCAAATACCTCTATTTGTTTGATCTGTAGGAATTACAGCTTTACTTTTATTATTATCTCTCCAGTATTAGCAGGAGCAATTACAATACTTCT
TACTGATCGTAATCTTAATACTTCATTTTTTGATCCTTCAGGAGGAGGAGATCCAATTTTATATCAACATTTATTT

Type material. Holotype: ♂ currently deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 207–208, bears the following four rectangular labels, three white: [BRAZIL, RJ, RJ | P. N. da Tijuca | Morro de Dona Marta | 22°56.7'S, 43°11.4'W | 7 May 1994, 362 m | Leg. Robbins/Caldas], [Territorial | Behavior | Time: 0715], [DNA sample ID: | NVG-22035D03 | c/o Nick V. Grishin], and one red [HOLOTYPE ♂ | Neoxeniades | angustior Grishin]. **Paratypes:** 1♂ and 2♀♀: Brazil: Rio de Janeiro, old (around 1900) [FMNH]: 1♂ NVG-18039C02 and 1♀ NVG-18039C03; and 1♀ NVG-21119A09, #5243 Brazil, prior to 1876 [MFNB] (Fig. 209–210).

Type locality. Brazil: Rio de Janeiro, Tijuca National Park, Morro de Dona Marta, elevation 362 m, GPS –22.945, –43.190.

Etymology. In Latin, *angustior* means narrower, limited, or constructed. The name is given to signify both its wing pattern and distribution and is treated as a noun in apposition.

Distribution. Currently only known from around Rio de Janeiro in Brazil.

Damas zea Grishin, new species

<https://zoobank.org/60CBF52F-A78C-4AA8-8C6C-5E47E7638F4D>

(Fig. 8 part, 211–212, 451–453)

Definition and diagnosis. Phylogenetic trees reveal that a specimen from Guyana that is similar in appearance to *Damas cervelina* Orellana and Costa 2019 (type locality in Venezuela) shows prominent genetic differentiation from it (Fig. 8): e.g., their COI barcodes differ by 4.1% (27 bp), and therefore represents a new species. This new species differs from its sister *D. cervelina* by forewing spots being rounder and subapical spots lacking. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly393.18.11:A61G, aly860.2.2:G81T, aly1772.7.1:T522G, aly1772.7.1:T732A, aly1405.1.1:T303C, aly499.36.2:C202C (not A), aly499.36.2:A240A (not G), aly16540.2.1:C225C (not T), aly16540.2.1:A289A (not T), aly2700.18.3:G117G (not A), and COI barcode: T133C, T136C, T337C, T406C, A562G.

Barcode sequence of the holotype. Sample NVG-8006, GenBank OR837719, 658 base pairs:

AAC TTTATATTTTATTTTGGTATTTGAGCAGGATTATTAGGAACTTCTTTAAGTATATTAATTCGAACAGAAATTAGGAAATCCTGGATCTTTAATT
GGAGATGATCAAATTTATAATAACAATTGTTACAGCCCACGCCTTATTATAAATTTCTTTATAGTTATACCTATTATAAATGGAGGATTTGGTAATT
GATTAGTACCTTTAATATTAGGTGCTCCTGATATAGCTTTCCCTCGAATAAATAAATAAGATTTTGAATATTACCTCCATCTTTAATCTTATTAAT
TTCAAGAAGAATCGTAGAACTGGAGCAGGAAC TGGTTGAACTGTCTATCCCCCTCTTTCCCTCCAATATGCTCACCAAGGAGCTTCAGTAGATTTA
GCTATTTTTTCTTACACTTAGCAGGAATTTCTTCCATTTTAGGAGCAATTAATTTTATTACCACAATCATTAATATACGTGTGAAGAAATTTATCTT
TTGATCAAATACCTTTATTTGTATGATCAGTAGGAATTACAGCCCTATTATTACTTTTATCTTTACCAGTTTGTAGCGGGAGCTATTACTATATTACT
TACTGATCGAAATCTTAATACTTCTTTTTTTGACCCAGCTGGAGGAGGATCCTATTTTATATCAACATTTATTT

Type material. Holotype: ♀ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 211–212, bears the following six rectangular labels, five white: [Guyana: Region 7 | Mt. Ayanganna | 4500' - 5500' | 5°24.1'N 59°57.4'W | 13 - 18 Apr 1999 | leg. S. Fratello, R. Hanner, | W. Prince, R. Williams.], [{QR Code} | USNM ENT 00232408], [DNA sample ID: | NVG-8006 | c/o Nick V. Grishin], [genitalia | NVG170207-91 | Nick V. Grishin], [USNM ENT | {QR Code} | 01321846], and one red [HOLOTYPE ♀ | *Damas zea* | Grishin].

Type locality. Guyana: Cuyuni-Mazaruni Region, Mt. Ayanganna, elevation 4500–5500 ft, GPS 5.4017, –59.9567.

Etymology. The name reflects wing pattern similarity to the Old World species *Unkana mythea* (Hewitson, 1877), which is the type species of the genus *Zea* Distant, 1886, currently regarded as a junior subjective synonym of the genus *Unkana* Distant, 1886. The name is a noun in apposition.

Distribution. Currently known only from the holotype collected in Guyana.

Lectotype designation for *Thracides xanthura* Godman, 1901

Thracides xanthura Godman, 1901, currently a species of *Tromba* Evans, 1955 (type species *Tromba tromba* Evans, 1955), was described from a series of specimens collected at multiple localities: Belize, Honduras, Panama, and

Colombia. Due to the polytypic type series and to define the type locality more precisely, N.V.G. hereby designates a male syntype in the Natural History Museum, London, UK, that according to its label, was illustrated by Godman (1899–1901), and bears the following five rectangular white labels: [Bugaba, | 800-1,000 ft. | Champion.], [Sp. figured.], [B.C.A.Lep.Rhop. | *Thracides xanthura*, | Godm.], [Godman-Salvin | Coll. 1914.—5.], [{QR Code} | BMNH(E) 1669777], and a genitalia mini-slide number 111 that is pinned with the labels, as the **lectotype** of *Thracides xanthura* Godman, 1901. The lectotype had scales of left wings removed to study venation. The type locality of *Thracides xanthura* becomes Panama: Chiriquí Province, Bugaba.

Tromba xantha Grishin, new species

<https://zoobank.org/8A465187-542D-43AA-B5DA-BF3B8DB19614>

(Fig. 8 part, 213–214, 454–455)

Definition and diagnosis. Phylogenetic trees reveal that a number of specimens identified as *Tromba xanthura* (Godman, 1901) (type locality in Panama) show prominent genetic differentiation from it (Fig. 8): e.g., their COI barcodes differ by 3.6% (24 bp), and therefore represent a new species. This new species keys to *T. xanthura* (K.14.2) in Evans (1955) but differs from it by male genitalia with deeper separation of harpe from ampulla, which is only slightly notched in *T. xanthura*, but in some specimens of the new species (including the holotype, Fig. 454–455) is separated by a groove, more prominent serrations towards distal end of the dorsal margin of harpe, and less bulky ventral margin on harpe near its fusion with the body of valva. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly2672.7.10:C117T, aly1295.7.1:A156T, aly133.6.8:G260A, aly4592.2.4:G73A, aly4592.2.4:A74T, and COI barcode: 49G, 238C, T340C, T367C, T640C.

Barcode sequence of the holotype. Sample NVG-5054, GenBank OR837720, 658 base pairs:

```
AACTTTATATTTTATTTTCGGTATTTGAGCAGGAATATTAGGAACATCGTTAAGATTATTAATTCGAACGAATTAGGTAATCCAGGATCTTTAATT
GGAGATGATCAAATTTATAATACCATTGTAACAGCTCATGCCTTTATTATAATTTTTTTTATAGTAATACCTATTATAATTTGGAGGTTTTGGAAAT
GATTAGTACCATTAATATTAGGAGCACCAGATATAGCTTTCCCCCGAATAAATAATATAAGATTTGAATATTACCTCCTTCATTAACCTTTATTAAT
CTCAAGAAGAATTGTAGAAAATGGTGACAGGAACAGGATGAACGTGTTTACCCCTTTATCTTCTAATATGCTCACCAAGGATCTTCAGTAGATTTA
GCAATTTTTCTCTTCATTTAGCAGGATTTCTTCTATTTTAGGAGCAATTAATTTTACTACTACAATTTAATATACGAATTATAAATTAATCTT
TTGACCAAATACCTTTATTTGTTTGATCTGTAGGAATTACAGCTTTATATTATTATTATCTTTACCTGTATTAGCTGGAGCTATTACAATATTACT
TACTGATCGAAATTTAAATACTTCTTTTTTTGATCCTGCAGGAGGTGGAGATCCAATCTTATATCAACATTTATTT
```

Type material. **Holotype:** ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 213–214, bears the following five rectangular labels, four white: [Paso San Juan, | V. Cruz.], [*Thracides xanthura* | Godm. | comp. type.], [DNA sample ID: | NVG-5054 | c/o Nick V. Grishin], [genitalia | NVG151102-09 | Nick V. Grishin], and one red [HOLOTYPE ♂ | *Tromba xantha* | Grishin]. **Paratypes:** 3♂♂: 1♂ NVG-17111B07 Mexico: Guerrero, Ixtapa, 5-Mar-1985, Benjamin Landing leg. [LACM]; 1♂ NVG-5055 Honduras: 18 km W of La Ceiba, 17-Apr-1980 Robert D. Lehman leg., genitalia NVG151102-10 [USNM]; and 1♂ NVG-5056 Nicaragua: San Marcos, old specimen ca. 1900, Coll. Baker, genitalia NVG151102-11 [USNM].

Type locality. Mexico: Veracruz, Paso de San Juan.

Etymology. The name is derived from *T. xanthura*, the southern counterpart of this species. It has been shortened to indicate this is a more northern species. The name is a feminine adjective.

Distribution. From Mexico to Nicaragua.

Tribe Pericharini Grishin, 2019
Subtribe Pericharina Grishin, 2019

Perichares fura Grishin, new species

<https://zoobank.org/2FD4A73B-7AC8-4B32-BC27-CB0F8F5FE674>

(Fig. 8 part, 215–216, 456–458)

Definition and diagnosis. Phylogenetic trees reveal that specimens from Ecuador identified as *Perichares furcata* (Mabille, 1891) (type locality in Brazil: São Paulo) are not monophyletic with it and show prominent genetic

differentiation from it (Fig. 8): e.g., their COI barcodes differ by 6.7% (44 bp), and therefore represent a new species. This new species is a distant sister to *Perichares lotus* (A. Butler, 1870) (type locality in Venezuela), differing from it by 4.9% (32 bp) in COI barcode, but has remarkably different ventral wing pattern, being nearly identical to *Perichares furcata* instead. This new species keys to “*Alera furcata*” (K.32.3) in Evans (1955) but differs from it by a brown spot in the humeral area of ventral hindwing that is missing in *P. furcata* and a more diffuse boundary between the darker discal forewing area and paler apex, particularly towards costa that is rather sharp in *P. furcata*. Due to the cryptic nature of this species, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly525.25.7:G450T, aly15656.2.3:G461A, aly275209.10.4:C66G, aly173.49.2:C33T, aly2012.16.4:T135A, and COI barcode: T55A, T241C, T250C, T394C, T484C.

Barcode sequence of the holotype. Sample NVG-18014F08, GenBank OR837721, 658 base pairs:

```
AAC TTTATATTTTATTTTGGTATTTGAGCAGGAATATTAGGAACATCTCTAAGATTATTAATTCGTACTGAATTAGGAAATCCAGGATCTTTAATT
GGAGATGATCAAATTTATAATACTATTGTTACTGCCCATGCTTTTATTATAATTTTTTTTATAGTTATACCCATTATAATTGGAGGATTCGGAAATT
GACTTGTCCCTCTTATATTAGGAGCTCCTGATATAGCTTTTCCCTCGCATAAATAACATAAGATTTTGAATATTACCCCATCATTAACCTCTTTTAAT
TTCAAGAAGAATCGTTGAAAACGGTGTGGAACCTGGATGAACAGTTTACCCCCACTTTTCATCTAATATTGCCCATCAAGGATCTTCAGTTGATTTA
GCAATCTTTCCCTTCATTTAGCAGGAATTTCCCTCTATTCTAGGAGCTATTAATTTTATTACTACAATTTAATATACGAATTATAAATTTATCCT
TTGACCAAATACCTTTATTTGTTTGTATGATCAGTAGGTATTACAGCCTTATTATTACTACTATCTTTACCAGTATTAGCAGGAGCTATTACAATACTTCT
TACAGATCGAAATTTAAATACCTCATTTTTTGATCCTGCAGGAGGAGGAGATCCAATTTTATATCAACATTTATTT
```

Type material. Holotype: ♀ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 215–216, bears the following five rectangular labels, four white: [Alluriquin 700 m | PICHINCHA ECUADOR | 14 Sept. '76 | S. S. Nicolay], [Perichares | lotus ♀ | Det. Btlr. | S.S. Nicolay], [DNA sample ID: | NVG-18014F08 | c/o Nick V. Grishin], [USNMMENT | {QR Code} | 01450684], and one red [HOLOTYPE ♀ | Perichares | fura Grishin]. **Paratype:** 1♀ NVG-18014F07, USNMMENT_01450683 Ecuador: Pichincha, 10 mi E of Santo Domingo de los Colovados, Tinalandia Grounds/Trails, 16–21-Apr-1984, Brian Harris leg. [USNM].

Type locality. Ecuador: Pichincha, Alluriquin, elevation 700 m.

Etymology. The name reflects a strong superficial similarity to *Perichares furcata* (Mabille, 1891) but does not reflect a close relationship. The name is a non-Latinized noun in apposition.

Distribution. Currently known only from Pichincha Province, Ecuador.

Tribe Megathymini Comstock and Comstock, 1895
Subtribe Carystoidina Grishin, 2022

Carystoides (Balma) goliath Grishin, new species

<https://zoobank.org/A2EA2056-49E6-4315-A42C-A9FF87A5C1A3>

(Fig. 8 part, 217–218, 459–464)

Definition and diagnosis. Phylogenetic trees reveal that a unique in appearance specimen from Colombia belongs to the subgenus *Balma* Grishin, 2022 (type species *Carystoides balza* Evans, 1955) of the genus *Carystoides* Godman, 1901 (type species *Hesperia basoches* Latreille, [1824]) and differs prominently from both species of the subgenus: *C. balza* (type locality in Ecuador) and *Carystoides maroma* Möschler, 1877 (type locality in Suriname) (Fig. 8): by 8.1% (52 bp) and 5.5% (36 bp) in COI barcodes, respectively, and therefore represents a new species. This new species differs from all others by a pale yellow spot at the base of forewing cell CuA_1-CuA_2 above and a unique for a male arrangement of three forewing hyaline spots with the spot in cell CuA_1-CuA_2 basad of the spot in the discal cell without overlapping it. This species is not cryptic and is diagnosed reliably by phenotype. In DNA, a combination of the following base pairs is diagnostic in the nuclear genome: aly1146.46.3:T206C, aly1139.84.1:A2445G, aly923.1.5:T72C, aly215.21.1:A1036C, aly215.21.1:A1078C, aly85.38.8:G72G (not T), aly85.38.8:A81A (not T), aly128.26.2:A160A (not C), aly4778.18.1:A394A (not C), aly1282.12.2:T204T (not C), and COI barcode: A37G, T115C, T142C, T487C, A577G, T637C.

Barcode sequence of the holotype. Sample NVG-18012D11, GenBank OR837722, 658 base pairs:

```
AAC TTTATATTTTATTTTGGAAATTTGAGCAGGAATGTTAGGAACATCATTAAAGTTTAAATAATTCGTACAGAATTAGGAAATCCTGGATCTTTAATT
```

GGAGATGACCAAATTTACAATACTATTGTCACAGCCCATGCTTTCATTATAATTTTTTTTATAGTTATACCTATTATAAATGGAGGATTGGAAATT
 GACTTGTACCTTTAATACTAGGAGCTCCTGATATAGCATTCCTCCGAATAAATAAATAAGTTTTTGAATACTACCCCTCATTAACTTTATTAAT
 TTCAGAAGAATTGTAGAAAATGGTGCCTGGTACAGGATGAAGTGTCTATCCCCCTTTCATCTAATGTAGCTACCAAGGATCATCTGTAGATTTA
 GCTATTTTTTCTTTACATTTAGCAGGTATTTCTCAATTTAGGAGCTATTAATTTTATTACTACTATTATAATATACGAATTAATAAATTTATCAT
 TCGACCAAATACCTTTATTTATTTGATCTGTAGGAATTACTGCTTTATTATTATTATTATCTTTACCTGTTTTAGCGGGAGCTATTACTATGCTTCT
 TACTGATCGAAATTTAATACTCTTTTTTTGACCCAGCGGGAGGAGACCCCATCTTTTCAACATTTATTT

Type material. Holotype: ♂ deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC, USA (USNM), illustrated in Fig. 217–218, bears the following five rectangular labels, four white: [FEB. 1 1989 | Anchicaya, 650m | Valle, Colombia | J. Bolling Sullivan], [Genit. Vial | SRS-3255], [DNA sample ID: | NVG-18012D11 | c/o Nick V. Grishin], [USNMENT | {QR Code} | 01450298], and one red [HOLOTYPE ♂ | *Carystoides* (Balma) | goliath Grishin].

Type locality. Colombia: Valle, Anchicaya, elevation 650 m.

Etymology. The name is given for the large size of this species and is a noun in apposition.

Distribution. Colombia.

Subtribe Megathymini Comstock and Comstock, 1895

Agathymus galeana Grishin, new species

<https://zoobank.org/1705C581-B49C-4679-9A6C-B1ACDD11F9CB>

(Fig. 8 part, 219–220)

Definition and diagnosis. Phylogenetic trees reveal that a specimen of *Agathymus* H. Freeman, 1959 (type species *Megathymus neumoeni* W. H. Edwards, 1882) from Nuevo Leon Mexico is not closely related to any of the known species of the genus and is a distant sister to both *Agathymus estelleae* (D. Stallings and Turner, 1958) (type locality in Mexico: Nuevo Leon) and *Agathymus remingtoni* (D. Stallings and J. Turner, 1958) (type locality in Mexico: Hidalgo) (Fig. 8): COI barcode differences from them are 6.2% (41 bp), and 5.3% (35 bp), respectively, while being phenotypically dissimilar to them. This new species is more similar to *Agathymus hoffmanni* (H. Freeman, 1952) (type locality in Mexico: “Valle de Mexico”), among others, in its orange coloration and pattern of spots but differs from it and other species by rounder wings, uniformly gray ventral hindwing without any spots and blotches, relatively narrow dorsal hindwing orange postdiscal band contrasting with broader orange spots on forewing overscaled with orange at its base, and orange along the cubitus in forewing discal cell. Due to the lack of additional specimens and unknown phenotypic variation, most reliable identification is achieved by DNA and a combination of the following base pairs is diagnostic in the nuclear genome: aly5773.3.3:C118T, aly5773.3.3:T428C, aly2874.12.6:C66T, aly3850.2.2:T84A, aly2041.8.3:T41G, aly2012.46.3:A132A (not G), aly5729.2.6:A854A (not C), aly536.163.5:T18T (not G), aly798.8.13:G48G (not C), aly16.30.9:A241A (not G), and COI barcode: A37G, T59A, T136C, T346C, 581C.

Barcode sequence of the holotype. Sample NVG-1895, GenBank OR837723, 658 base pairs:

TACTTTATATTTTATTTTGGTATTTGAGCAGGTATGTTAGGAACATCTTTAAGATTAATAATTCGTACTGAATTAGGAAATCCAGGATCATTAAAT
 GGAGATGATCAAATTTATAATACCATTGTAACAGCTCACGCTTTTATTATAATTTTTTTCATAGTTATACCTATTATAAATGGAGGATTGGTAATT
 GATTAGTACCTTTAATATTAGGAGCACCTGATATAGCTTTTCCCGTATAAATAACATAAGATTTTGAATATTACCCCTCATTAAATATTACTAAT
 CTCAGAAGAATTGTAGAAAATGGTGCAGGAACAGGATGAAGTGTATACCTCCCTATCTTCTAATATTGCACATCAAGGTTCTTCAGTTGATTTA
 GCAATTTTTTCCCTTTCATTAGCAGGTATCTCTCTATTTTAGGAGCTATTAATTTTATTACTACAATTATAATATACGAATTAATAAATTTATCAT
 TTGATCAAATACCTCTATTTGTATGATCTGTTGGAATTACTGCTTTATTATTATTATTATCTCTACCTGTTTTAGCTGGAGCTATTACTATACTTCT
 AACAGATCGAAATTTAATACTCTTTTTTTGACCCTGCTGGAGGAGGAGATCCAATTTTATATCAACACTTATTT

Type material. Holotype: ♀ deposited in the Texas A&M University Insect Collection, College Station, TX, USA (TAMU), illustrated in Fig. 219–220, bears the following six rectangular labels, five white: [MEXICO: | NUEVO LEON | ± 40 Km. WSW | Linares], [♂], [coll. | 21-IX-1977 | Roy O. Kendall | & C. A. Kendall], [DNA sample ID: | NVG-1895 | c/o Nick V. Grishin], [NVG140104-44], and one red [HOLOTYPE ♀ | *Agathymus* | *galeana* Grishin].

Type locality. Mexico: Nuevo Leon, ca 40 km WSW of Linares.

Etymology. The name is given for the type locality of this species near Galeana in Mexico and is a noun in apposition.

Distribution. Currently known only from the holotype collected in Nuevo Leon, Mexico.

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Literature Cited

- Austin GT. 2000.** HesperIIDae of Rondônia, Brazil: “*Antigonus*” genus group (Pyrginae), with taxonomic comments and descriptions of new species from Brazil and Guatemala. *Journal of the Lepidopterists’ Society* 54(1): 1–28.
- Austin GT. 2008.** HesperIIDae of Rondônia, Brazil: Taxonomic comments on ‘night’ skippers, with descriptions of new genera and species (Lepidoptera: Eudaminae). *Insecta Mundi* 29: 1–36.

- Austin GT, Mielke OHH. 1998.** HesperIIDae of Rondônia, Brazil: *Aguna* Williams (Pyrginae), with a partial revision and descriptions of new species from Panama, Ecuador, and Brazil. *Revista brasileira de Zoologia* 14(4): 889–965.
- Buchfink B, Xie C, Huson DH. 2015.** Fast and sensitive protein alignment using DIAMOND. *Nature Methods* 12(1): 59–60.
- Burns JM, Janzen DH, Hajibabaei M, Hallwachs W, Hebert PD. 2008.** DNA barcodes and cryptic species of skipper butterflies in the genus *Perichares* in Area de Conservacion Guanacaste, Costa Rica. *Proceedings of the National Academy of Sciences of the United States of America* 105(17): 6350–6355.
- Cong Q, Shen J, Zhang J, Li W, Kinch LN, Calhoun JV, Warren AD, Grishin NV. 2021.** Genomics reveals the origins of historical specimens. *Molecular Biology and Evolution* 38(5): 2166–2176.
- Cong Q, Zhang J, Grishin NV. 2019a.** Genomic determinants of speciation. bioRxiv BIORXIV/2019/837666. Available at <https://doi.org/10.1101/837666> (Last accessed November 2023.)
- Cong Q, Zhang J, Shen J, Grishin NV. 2019b.** Fifty new genera of HesperIIDae (Lepidoptera). *Insecta Mundi* 0731: 1–56.
- Dolibaina DR, Mielke OH, Casagrande MM. 2014.** Taxonomic revision of *Cumbre* Evans, 1955 (HesperIIDae: HesperIIDae: Moncini), with the description of two new species. *Zootaxa* 3841(1): 47–66.
- Dolibaina DR, Mielke OHH, Casagrande MM. 2017.** Taxonomy of *Rufocumbre* gen. nov., a new Moncini skipper genus (Lepidoptera: HesperIIDae: HesperIIDae). *Zootaxa* 4365(2): 196–216.
- Draudt MWK. 1921–1924.** B. Grypocera, breitköpfige Tagfalter. p. 833–1011, 1046–1139, pl. 113B, 160–193. *In*: Seitz A (Ed.). *Die Gross-Schmetterlinge der Erde*. Alfred Kernen; Stuttgart. 1141 p.
- Evans WH. 1937.** A catalogue of the African HesperIIDae indicating the classification and nomenclature adopted in the British Museum. The Trustees of the British Museum (Natural History); London. xii + 212 p., 30 pl.
- Evans WH. 1949.** A catalogue of the HesperIIDae from Europe, Asia, and Australia in the British Museum (Natural History). The Trustees of the British Museum (Natural History); London. xix + 502 p., 53 pl.
- Evans WH. 1951.** A catalogue of the American HesperIIDae indicating the classification and nomenclature adopted in the British Museum (Natural History). Part I. Introduction and Group A Pyrrhopyginae. The Trustees of the British Museum (Natural History); London. x + 92 p., pl. 1–9.
- Evans WH. 1952.** A catalogue of the American HesperIIDae indicating the classification and nomenclature adopted in the British Museum (Natural History). Part II. Pyrginae. Section I. The Trustees of the British Museum (Natural History); London. v + 178 p., pl. 10–25.
- Evans WH. 1953.** A catalogue of the American HesperIIDae indicating the classification and nomenclature adopted in the British Museum (Natural History). Part III. Pyrginae. Section 2. The Trustees of the British Museum (Natural History); London. v + 246 p., pl. 26–53.
- Evans WH. 1955.** A catalogue of the American HesperIIDae indicating the classification and nomenclature adopted in the British Museum (Natural History). Part IV. HesperIIDae and Megathyminae. The Trustees of the British Museum (Natural History); London. v + 499 p., pl. 54–88.
- Fernandez-Triana JL, Shimbori EM, Whitfield JB, Penteado-Dias AM, Shaw SR, Boudreault C, Sones J, Perez K, Brown A, Manjunath R, Burns JM, Hebert PDN, Smith MA, Hallwachs W, Janzen DH. 2023.** A revision of the parasitoid wasp genus *Alphomelon* Mason with the description of 30 new species (Hymenoptera, Braconidae). *ZooKeys* 1175: 5–162.
- Fernandez-Triana JL, Whitfield JB, Rodriguez JJ, Smith MA, Janzen DH, Hallwachs WD, Hajibabaei M, Burns JM, Solis MA, Brown J, Cardinal S, Goulet H, Hebert PD. 2014.** Review of *Apanteles* sensu stricto (Hymenoptera, Braconidae, Microgastrinae) from Area de Conservacion Guanacaste, northwestern Costa Rica, with keys to all described species from Mesoamerica. *ZooKeys* 383: 1–565.
- Godman FD. 1899–1901.** HesperIIDae. p. 457–782. *In*: Godman FD, Salvin O. *Biologia Centrali-Americana*. Insecta. Lepidoptera-Rhopalocera. Vol 2. Dulau & Co., Bernard Quaritch; London. 782 p.
- Godman FD. 1907.** Notes on the American species of HesperIIDae described by Plötz. *Annals and Magazine of Natural History* (7)20(16): 132–155.
- Godman FD, Salvin O. 1893–1899.** *Biologia Centrali-Americana*. Insecta. Lepidoptera-Rhopalocera. Vol 2. Dulau & Co., Bernard Quaritch; London. 782 p.
- Hebert PD, Cywinska A, Ball SL, deWaard JR. 2003.** Biological identifications through DNA barcodes. *Proceedings of the Royal Society B: Biological Sciences* 270(1512): 313–321.
- Hewitson WC. 1867.** Descriptions of one hundred new species of HesperIIDae 1. John Van Voorst; London. ii+25 p.
- Hewitson WC. 1868.** Descriptions of one hundred new species of HesperIIDae 2. John Van Voorst; London. p. 25–56.
- Li W, Cong Q, Shen J, Zhang J, Hallwachs W, Janzen DH, Grishin NV. 2019.** Genomes of skipper butterflies reveal extensive convergence of wing patterns. *Proceedings of the National Academy of Sciences of the United States of America* 116(13): 6232–6237.
- Lukhtanov VA, Sourakov A, Zakharov E. 2016.** DNA barcodes as a tool in biodiversity research: testing pre-existing taxonomic hypotheses in Delphic Apollo butterflies (Lepidoptera, Papilionidae). *Systematics and Biodiversity* 14: 599–613.

- Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution* 32(1): 268–274.
- Pazhenkova EA, Lukhtanov VA. 2021. Genomic introgression from a distant congener in the Levant fritillary butterfly, *Melitaea acentria*. *Molecular Ecology* 30(19): 4819–4832.
- Plötz C. 1881. Die Hesperiiinen-Gattung *Eudamus* und ihre Arten. *Stettiner entomologische Zeitung* 42(10/12): 500–504; 43(1/3): 87–101.
- Plötz C. 1882. Die Hesperiiinen-Gattung *Hesperia* Aut. und ihre Arten. *Stettiner entomologische Zeitung* 44(1/3): 26–64.
- Plötz C. 1883. Die Hesperiiinen-Gattung *Hesperia* Aut. und ihre Arten. *Stettiner entomologische Zeitung* 44(4/6): 195–233.
- Rambaut A. 2018. FigTree, version 1.4.4. Available at <http://tree.bio.ed.ac.uk/software/figtree/> (Last accessed November 2023.)
- Rubinoff D, Cameron S, Will K. 2006. A genomic perspective on the shortcomings of mitochondrial DNA for “barcoding” identification. *Journal of Heredity* 97(6): 581–594.
- Sharkey MJ, Janzen DH, Hallwachs W, Chapman EG, Smith MA, Dapkey T, Brown A, Ratnasingham S, Naik S, Manjunath R, Perez K, Milton M, Hebert P, Shaw SR, Kittel RN, Solis MA, Metz MA, Goldstein PZ, Brown JW, Quicke DLJ, van Achterberg C, Brown BV, Burns JM. 2021. Minimalist revision and description of 403 new species in 11 subfamilies of Costa Rican braconid parasitoid wasps, including host records for 219 species. *ZooKeys* 1013: 1–665.
- Shen J, Cong Q, Borek D, Otwinowski Z, Grishin NV. 2017. Complete genome of *Achalarus lyciades*, the first representative of the Eudaminae subfamily of skippers. *Current Genomics* 18(4): 366–374.
- Siewert RR, Mielke OHH, Casagrande MM. 2020. Taxonomic revision of the Neotropical genus *Telemiades* Hubner, [1819] (Lepidoptera: Hesperiiidae: Eudaminae), with descriptions of fourteen new species. *Zootaxa* 4721(1): 1–111.
- Steinhauser SR, Austin GT. 1993. New species of Hesperiiidae from Costa Rica. *Tropical Lepidoptera* 4(Suppl. 2): 12–20.
- Wikipedia contributors. 2023. Corax of Syracuse. Wikipedia, The Free Encyclopedia. August 2, 2023, 07:50 UTC. Available at https://en.wikipedia.org/w/index.php?title=Corax_of_Syracuse&oldid=1168349841 (Last accessed November 2023.)
- Zhang J, Cong Q, Burns JM, Grishin NV. 2022a. Checking the checkered taxonomy of Plötz’s checkered skippers (Hesperiiidae: Pyrgini). *The Taxonomic Report of the International Lepidoptera Survey* 10(5): 1–31.
- Zhang J, Cong Q, Grishin NV. 2023a. Supplementary information to “Descriptions of one hundred new species of Hesperiiidae.” Table S1 and DNA sequences of exons with diagnostic characters. Available at <https://osf.io/hq7g4/> (Last accessed December 2023.)
- Zhang J, Cong Q, Grishin NV. 2023b. Thirteen new species of butterflies (Lepidoptera: Hesperiiidae) from Texas. *Insecta Mundi* 0969: 1–58.
- Zhang J, Cong Q, Shen J, Brockmann E, Grishin NV. 2019a. Genomes reveal drastic and recurrent phenotypic divergence in firetip skipper butterflies (Hesperiiidae: Pyrrhopyginae). *Proceedings of the Royal Society B: Biological Sciences* 286(1903): 20190609.
- Zhang J, Cong Q, Shen J, Brockmann E, Grishin NV. 2019b. Three new subfamilies of skipper butterflies (Lepidoptera, Hesperiiidae). *ZooKeys* 861: 91–105.
- Zhang J, Cong Q, Shen J, Grishin NV. 2022b. Taxonomic changes suggested by the genomic analysis of Hesperiiidae (Lepidoptera). *Insecta Mundi* 0921: 1–135.
- Zhang J, Cong Q, Shen J, Opler PA, Grishin NV. 2020. Genomic evidence suggests further changes of butterfly names. *The Taxonomic Report of the International Lepidoptera Survey* 8(7): 1–40.
- Zhang J, Cong Q, Shen J, Song L, Grishin NV. 2022c. Genomic DNA sequencing reveals two new North American species of *Staphylus* (Hesperiiidae: Pyrginae: Carcharodini). *The Taxonomic Report of the International Lepidoptera Survey* 10(4): 1–13.
- Zhang J, Cong Q, Shen J, Song L, Grishin NV. 2023c. Butterfly classification and species discovery using genomics. *The Taxonomic Report of the International Lepidoptera Survey* 11(3): 1–93.
- Zhang J, Dolibaina DR, Cong Q, Shen J, Song L, Mielke CGC, Casagrande MM, Mielke OHH, Grishin NV. 2023d. Taxonomic notes on Neotropical Hesperiiidae (Lepidoptera). *Zootaxa* 5271(1): 91–114.
- Zhang J, Shen J, Cong Q, Grishin NV. 2019c. Genomic analysis of the tribe Emesidini (Lepidoptera: Riodinidae). *Zootaxa* 4668(4): 475–488.

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Supplemental Data

Table S1. Data for 833 sequenced Hesperiiidae specimens, available at <https://osf.io/hq7g4/> (Zhang et al. 2023a).



Figures 9–16. Holotypes, data in text. In Fig. 9–220, dorsal and ventral sides are denoted by odd and even numbers, respectively. 9–10) *Drephalys (Drephalys) diovalis* sp. n. 11–12) *Euriphellus panador* sp. n. 13–14) *Euriphellus panamicus* sp. n. 15–16) *Cecropterus (Thorybes) viridissimus* sp. n.



Figures 17–24. Holotypes, data in text. 17–18) *Cecropterus (Murgaria) dariensis* sp. n. 19–20) *Urbanus (Urbanus) mericuti* sp. n. 21–22) *Telegonus (Telegonus) pastus* sp. n. 23–24) *Autochton (Autochton) dora* sp. n.



Figures 25–32. Holotypes, data in text. 25–26) *Astraptes centralis* sp. n. 27–28) *Aguna claxonica* sp. n. 29–30) *Aguna esmeralda* sp. n. 31–32) *Aguna lata* sp. n.



Figures 33–48. Holotypes, data in text. 33–34) *Ridens angulinea* sp. n. 35–36) *Pythonides lera* sp. n. 37–38) *Pythonides latemarginatus* sp. n. 39–40) *Gindanes variegatus* sp. n. 41–42) *Milanion (Milanion) virga* sp. n. 43–44) *Milanion (Milanion) furvus* sp. n. 45–46) *Milanion (Milanion) larius* sp. n. 47–48) *Charidia ronda* sp. n.



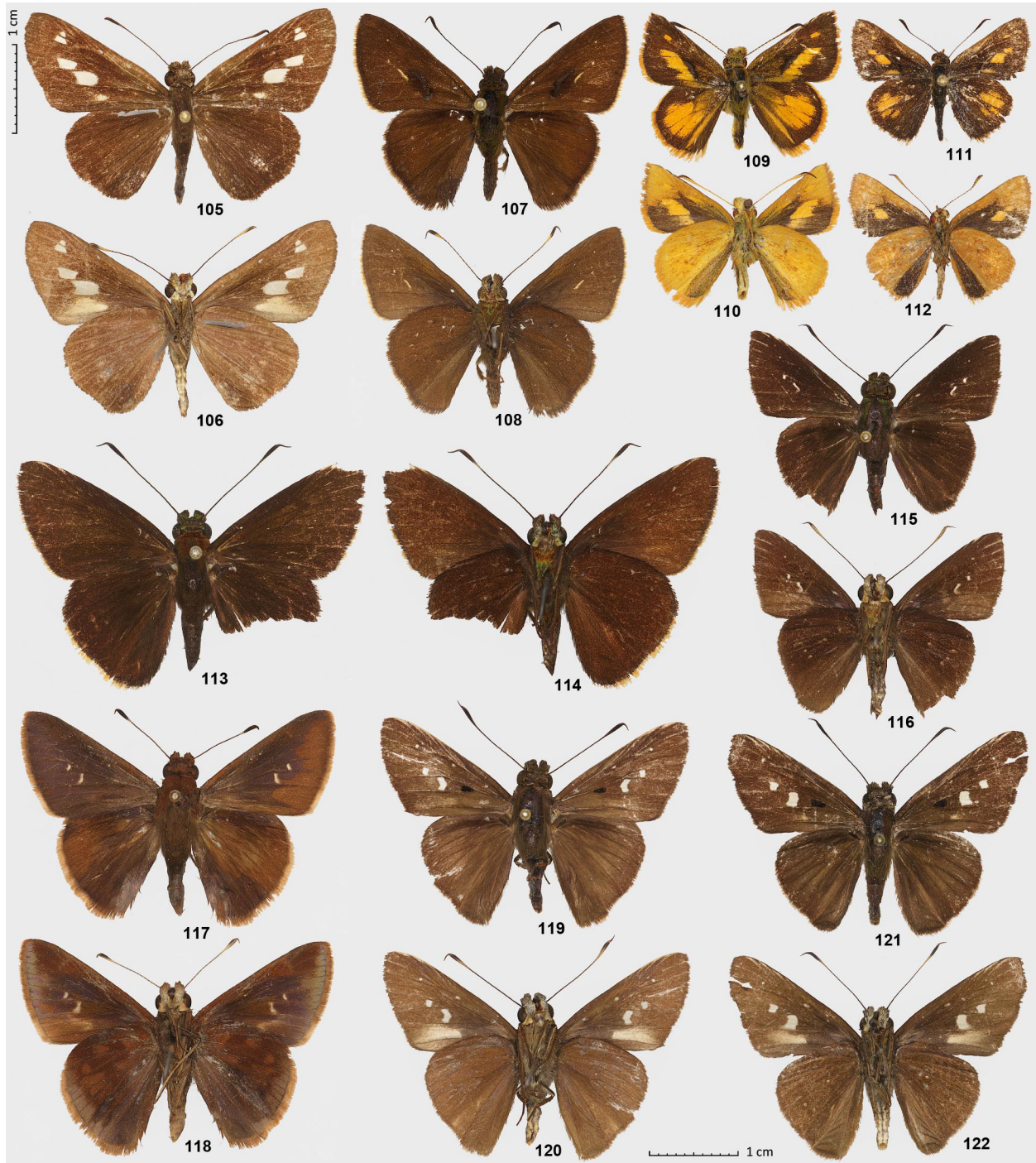
Figures 49–62. Holotypes (unless indicated), data in text. 49–52) *Pseudodrephalys tinas* sp. n.: 51–52) paratype ♀ NVG-19039F11. 53–54) *Pseudodrephalys argus* sp. n. 55–56) *Achlyodes calvus* sp. n. 57–58) *Spioniades artemis* sp. n. 59–60) *Spioniades artemidoides* sp. n. 61–62) *Myrinia orieca* sp. n.



Figures 63–84. Holotypes, data in text. 63–64) *Myrinia aragua* sp. n. 65–66) *Myrinia maculosa* sp. n. 67–68) *Myrinia manchada* sp. n. 69–70) *Polycitor (Fenops) lamperus* sp. n. 71–72) *Nisoniades (Nisoniades) lutum* sp. n. 73–74) *Bolla (Stolla) vena* sp. n. 75–76) *Staphylus (Vulga) vula* sp. n. 77–78) *Staphylus (Vulga) vulga* sp. n. 79–80) *Staphylus (Staphylus) rotundalus* sp. n. 81–82) *Staphylus (Staphylus) yucatanus* sp. n. 83–84) *Heliopetes (Heliopetes) lana* sp. n.



Figures 85–104. Holotypes, data in text. 85–86) *Canesia ella* sp. n. 87–88) *Paches (Paches) loxeca* sp. n. 89–90) *Clito congruens* sp. n. 91–92) *Cycloglypha corax* sp. n. 93–94) *Festivia peruvia* sp. n. 95–96) *Decinea notata* sp. n. 97–98) *Pompeius fuscus* sp. n. 99–100) *Vernia clara* sp. n. 101–102) *Oligoria (Oligoria) obtena* sp. n. 103–104) *Thespieus mandal* sp. n.



Figures 105–122. Holotypes, data in text. 105–106) *Psoralis (Saniba) magnamacus* sp. n. 107–108) *Alychna ayonis* sp. n. 109–110) *Wahydra banios* sp. n. 111–112) *Wahydra cuzcona* sp. n. 113–114) *Cynea (Cynea) aureofimbria* sp. n. 115–116) *Cynea (Nycea) quada* sp. n. 117–118) *Cynea (Quinta) achirae* sp. n. 119–120) *Eutus amazonicus* sp. n. 121–122) *Eutus incus* sp. n.



Figures 123–148. Holotypes (unless indicated), data in text. **123–124** *Eutus septemaculatus* sp. n. **125–126** *Godmia viridicapita* sp. n. **127–128** *Rhomba pulla* sp. n. **129–130** *Niconiades victoria* sp. n. **131–134** *Lancephallus purpurus* sp. n.: **133–134** Paratype ♀ NVG-19024B11. **135–136** *Mnasicles (Remella) ecua* sp. n. **137–140** *Amblyscirtes (Amblyscirtes) aera-tus* sp. n.: **139–140** Paratype ♀ NVG-19122A02. **141–144** specimens of *Amblyscirtes (Amblyscirtes) fluonia*: from Mexico: Oaxaca, J. Kemner leg. [USNM]: **141–142** ♂ NVG-19112A03 3-Aug-1992; **143–144** ♀ NVG-19112A04 13-Aug-1991. **145–146** *Amblyscirtes (Mastor) chrysoplea* sp. n. **147–148** *Amblyscirtes (Mastor) chrysomisa* sp. n. “F” indicates mirror image (i.e., flipped, left-right inverted).



Figures 149–172. Holotypes, data in text. 149–150) *Amblyscirtes (Flor) meridus* sp. n. 151–152) *Rectava chiriquensis* sp. n. 153–154) *Cobalopsis adictys* sp. n. 155–156) *Cybaenes melaporphyrus* sp. n. 157–158) *Lerema (Morys) ecuadorica* sp. n. 159–160) *Saturnus obscurior* sp. n. 161–162) *Cantha zoirodicta* sp. n. 163–164) *Cantha meiodicta* sp. n. 165–166) *Phlebodes duplex* sp. n. 167–168) *Lychnuchus (Enosis) valle* sp. n. 169–170) *Eutyche ochoides* sp. n. 171–172) *Dion bora* sp. n.



Figures 173–194. Holotypes, data in text. 173–174) *Dion occida* sp. n. 175–176) *Eprius* (*Eprius*) *veledinus* sp. n. 177–178) *Radiatus panamensis* sp. n. 179–180) *Pheraeus pulcher* sp. n. 181–182) *Callimormus rades* sp. n. 183–184) *Gubrus lubens* sp. n. 185–186) *Ludens labens* sp. n. 187–188) *Rigga isa* sp. n. 189–190) *Flaccilla lactea* sp. n. 191–192) *Falga athena* sp. n. 193–194) *Panoquina jay* sp. n.



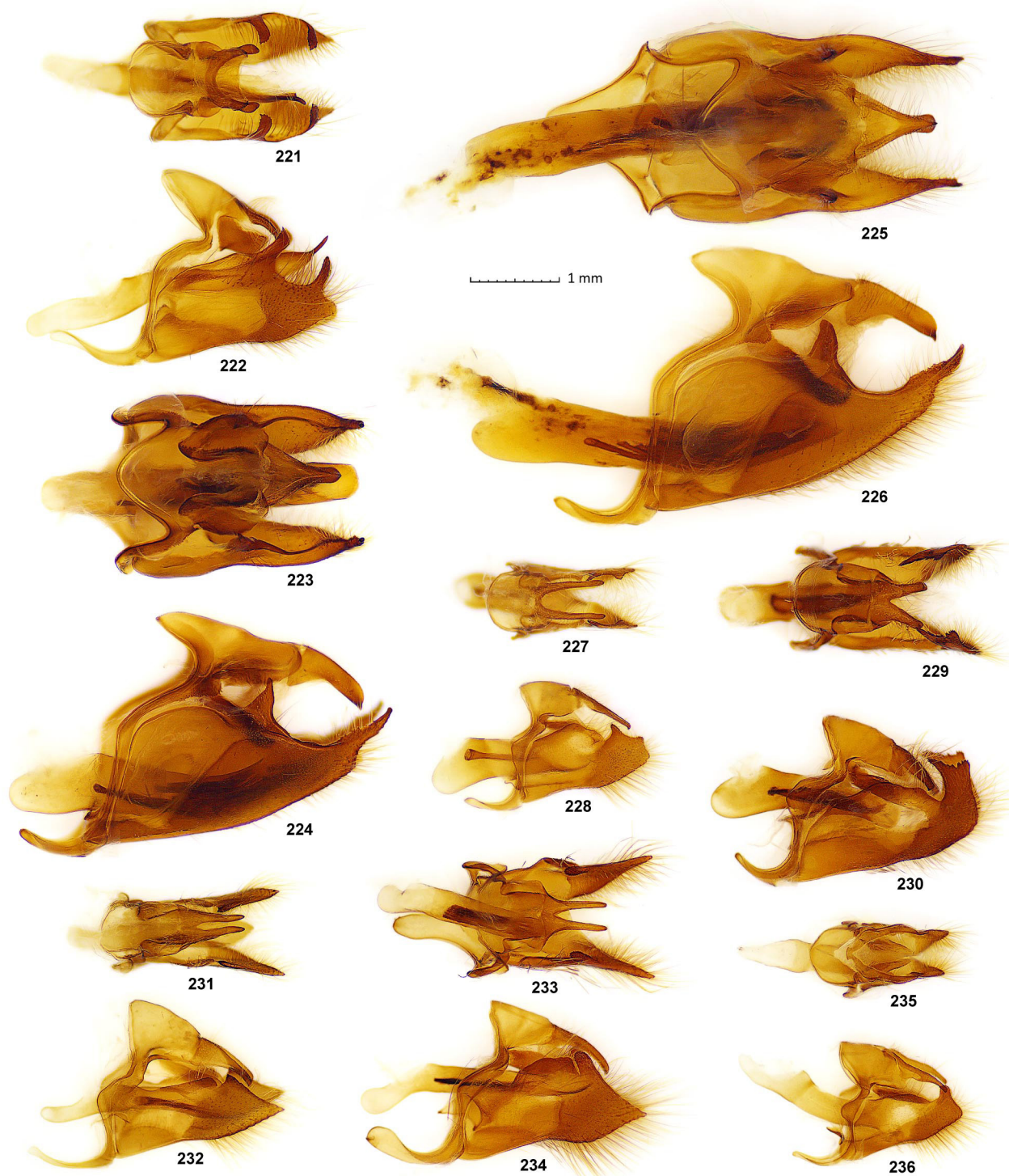
Figures 195–202. Holotypes, data in text. 195–196) *Calpodus salianus* sp. n. 197–198) *Calpodus stingo* sp. n. 199–200) *Aides nobra* sp. n. 201–202) *Thracides pavo* sp. n.



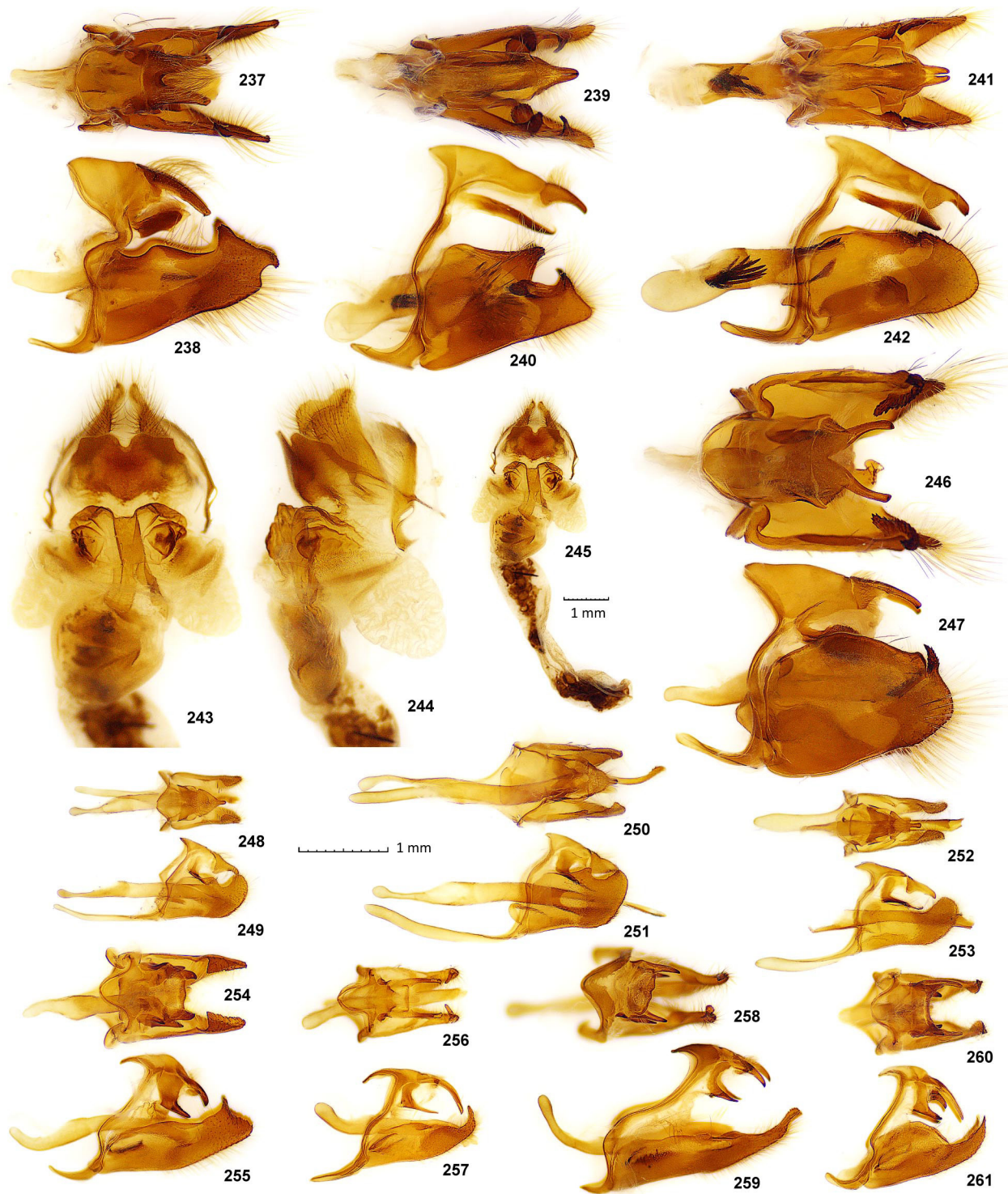
Figures 203–212. Holotypes (unless indicated), data in text. 203–204) *Talides eluta* sp. n. 205–206) *Talides laeta* sp. n. 207–210) *Neoxeniades angustior* sp. n.: 209–210) Paratype ♀ NVG-21119A09. 211–212) *Damas zea* sp. n.



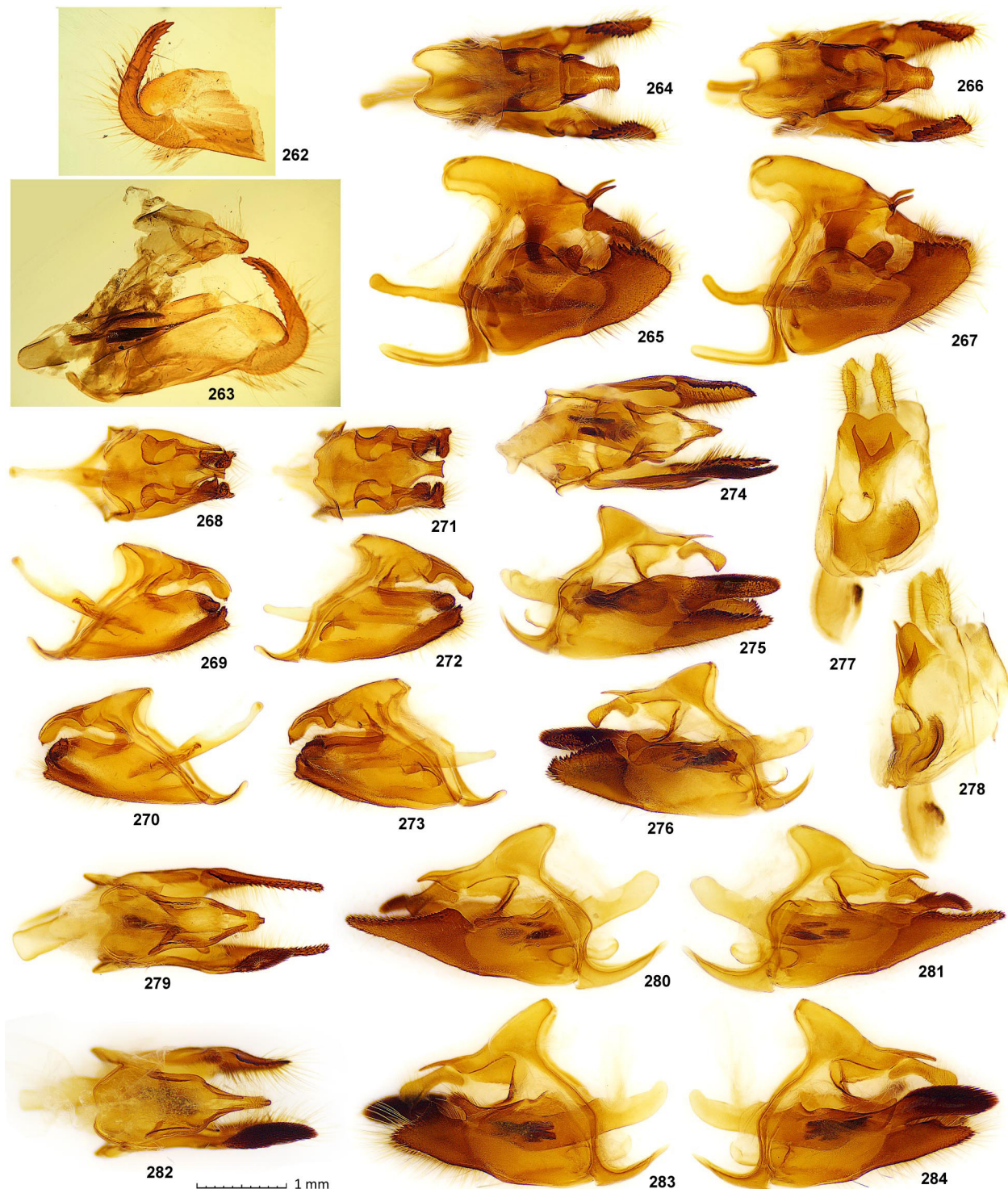
Figures 213–220. Holotypes, data in text. 213–214) *Tromba xantha* sp. n. 215–216) *Perichares fura* sp. n. 217–218) *Carystoides (Balma) goliath* sp. n. 219–220) *Agathymus galeana* sp. n.



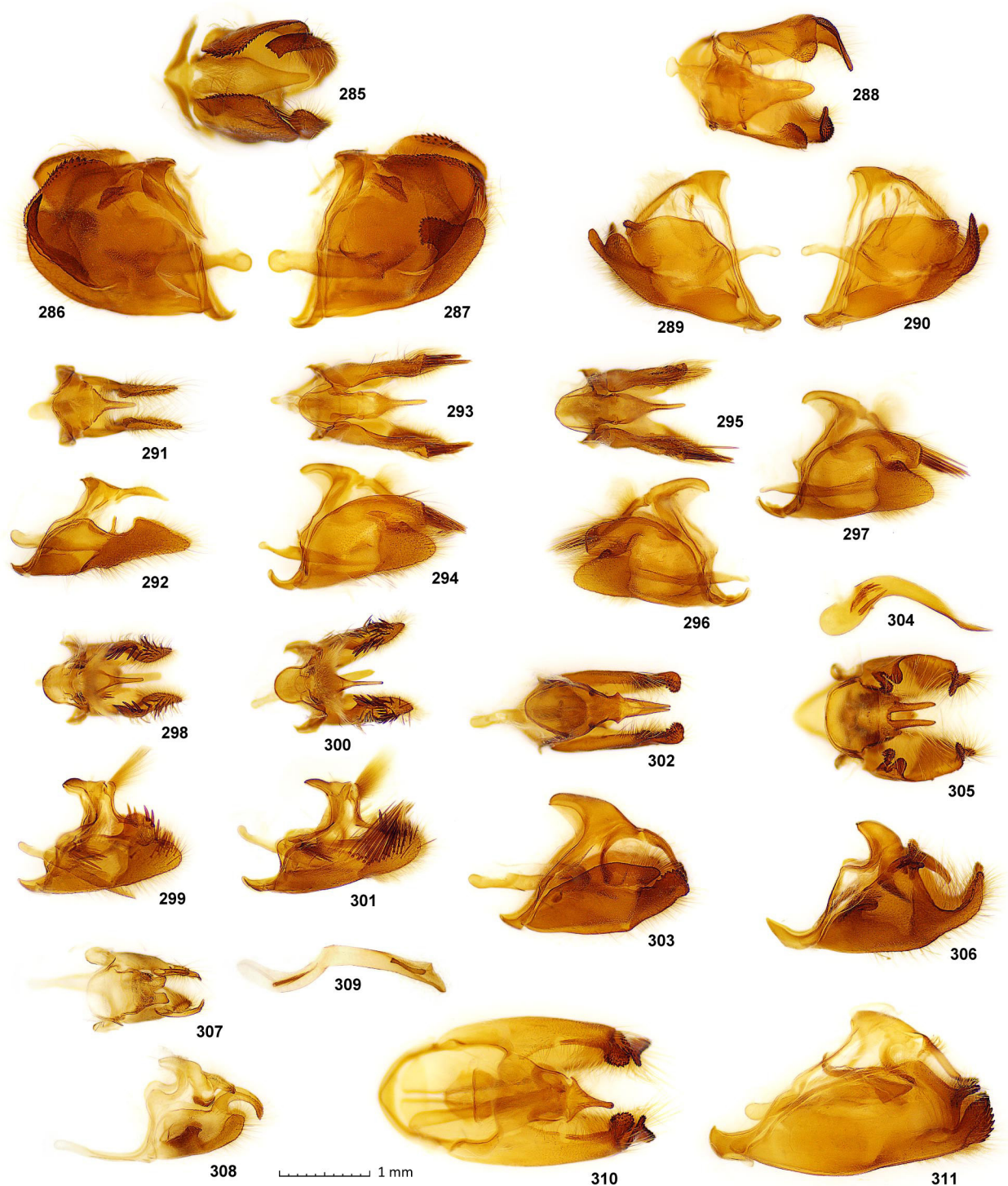
Figures 221–236. Genitalia of holotypes (unless indicated), data in text. In Fig. 221–464, complete genitalia are illustrated, in some cases with parts removed and shown separately (as indicated); for females, only sterigma is shown to scale, and complete genitalia (including ducts and corpus bursae) are reduced in size, as indicated by smaller scale bars. **221–222** *Drephalys* (*Drephalys*) *diovalis* sp. n. **223–224** *Euriphellus panador* sp. n. **225–226** *Euriphellus panamicus* sp. n. **227–228** *Cecropterus* (*Thorybes*) *viridissimus* sp. n. **229–230** *Cecropterus* (*Murgaria*) *dariensis* sp. n. **231–232** *Urbanus* (*Urbanus*) *mericuti* sp. n. paratype ♂ NVG-8078. **233–234** *Telegonus* (*Telegonus*) *pastus* sp. n. **235–236** *Autochton* (*Autochton*) *dora* sp. n. Views: dorsal (odd number), left lateral (even numbers).



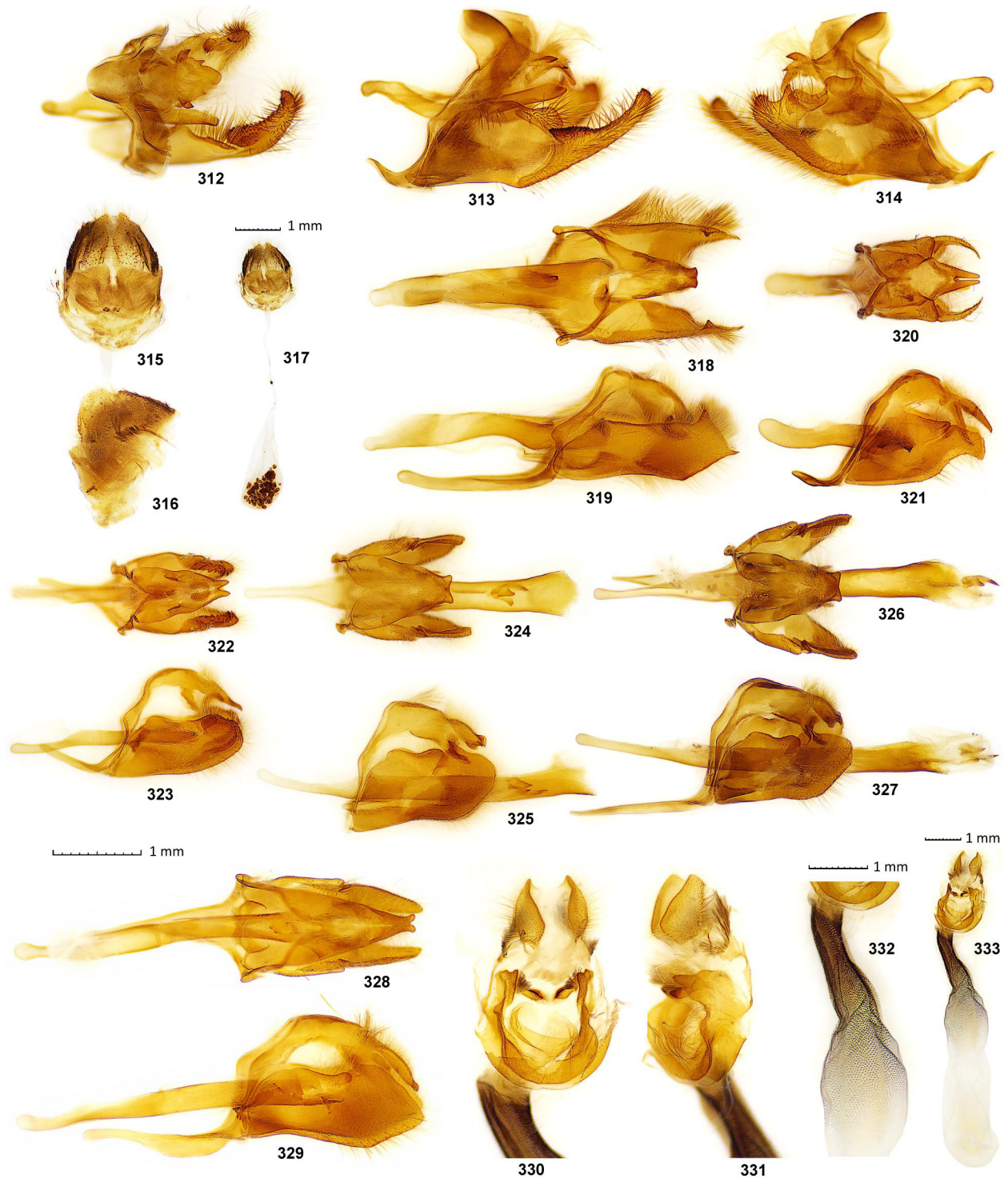
Figures 237–261. Genitalia of holotypes, data in text. 237–238) *Astraptus centralis* sp. n. 239–240) *Aguna claxonica* sp. n. 241–242) *Aguna esmeralda* sp. n. 243–245) *Aguna lata* sp. n. 246–247) *Ridens angulinea* sp. n. 248–249) *Pythonides lera* sp. n. 250–251) *Pythonides latemarginatus* sp. n. 252–253) *Gindanes variegatus* sp. n. 254–255) *Milanion (Milanion) virga* sp. n. 256–257) *Milanion (Milanion) furvus* sp. n. 258–259) *Milanion (Milanion) laricus* sp. n. 260–261) *Charidia ronda* sp. n. Views: dorsal (237, 239, 241, 246, 248, 250, 252, 254, 256, 258, 260), left lateral (238, 240, 242, 247, 249, 251, 253, 255, 257, 259, 261), ventral (243, 245), right ventrolateral (244). Smaller scale refers to 245.



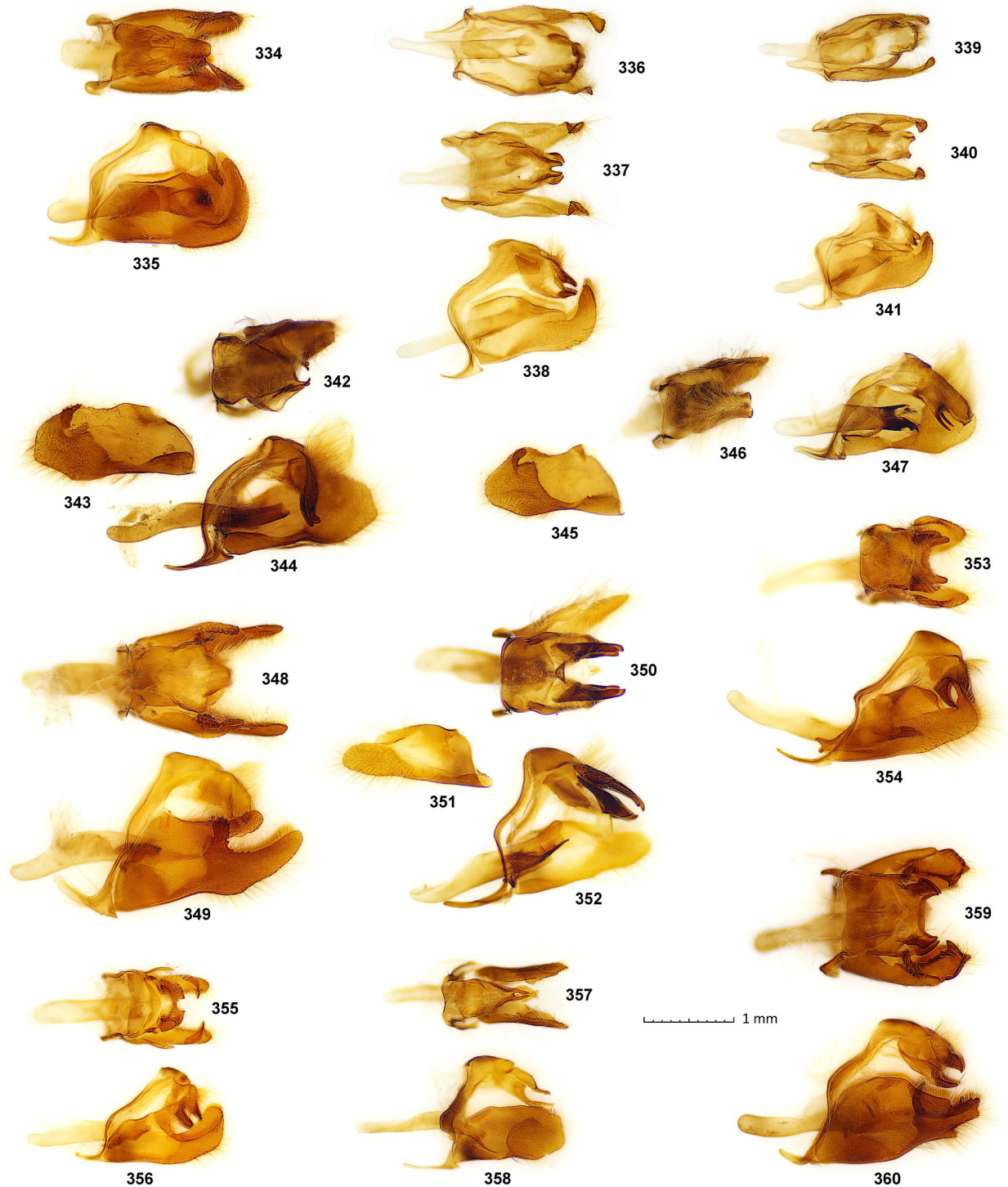
Figures 262–284. Genitalia of holotypes (unless indicated), data in text. **262–263)** *Pseudodrephalys tinas* sp. n. **264–265)** *Achlyodes busirus rioja* ♂ specimen NVG-22019A04. **266–267)** *Achlyodes calvus* sp. n. paratype ♂ NVG-22019A03. **268–270)** *Spioniades artemis* sp. n. **271–273)** *Spioniades artemidoides* sp. n. **274–276)** *Myrinia orieca* sp. n. **277–278)** *Myrinia aragua* sp. n. **279–281)** *Myrinia maculosa* sp. n. **282–284)** *Myrinia manchada* sp. n. Views: dorsal (264, 266, 268, 271, 274, 279, 282), left lateral (263, 265, 267, 269, 272, 275, 281, 284), right lateral (262 left valva, 270, 273, 276, 280, 283), ventral (277), right ventrolateral (278).



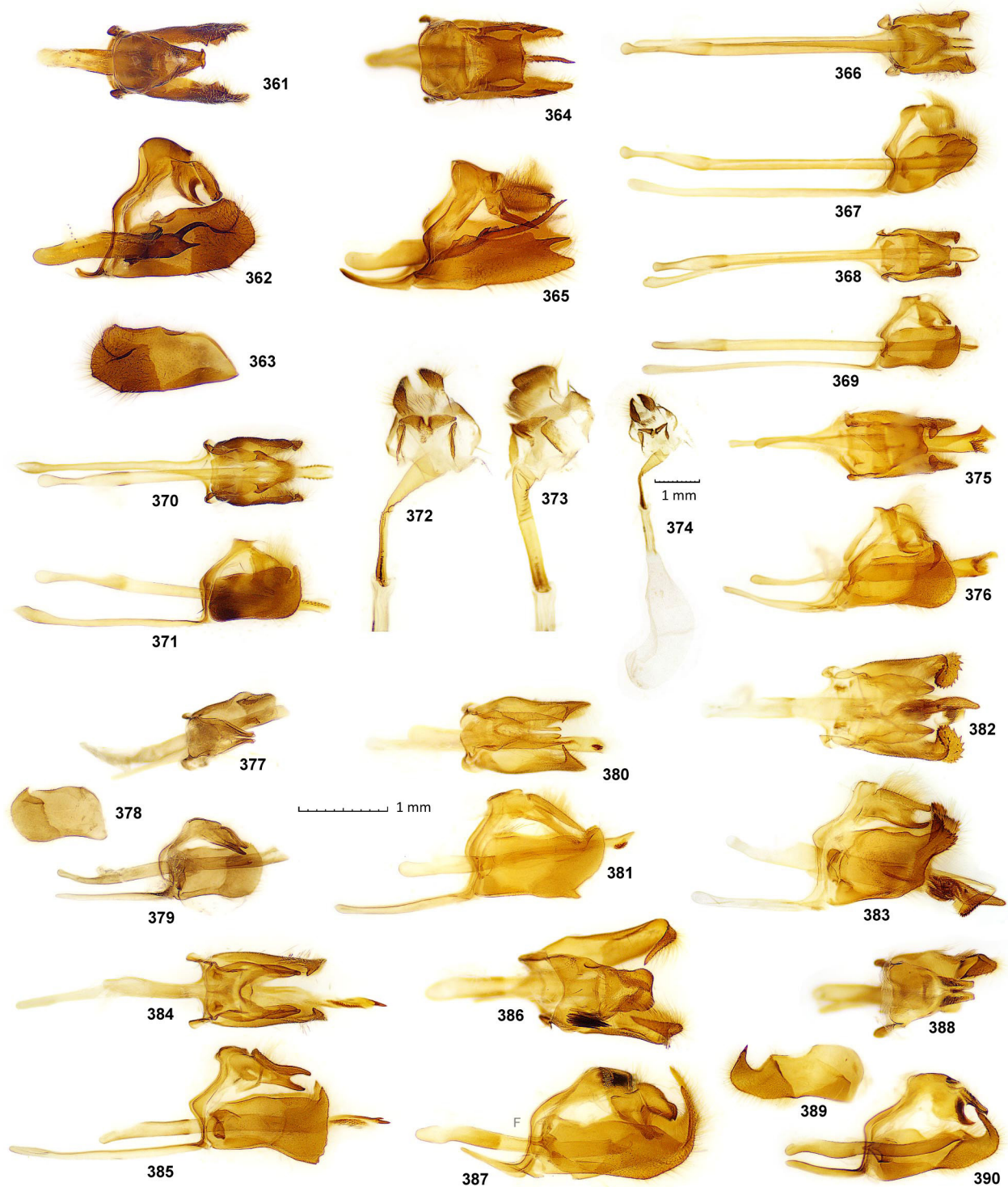
Figures 285–311. Genitalia of holotypes (unless indicated), data in text. **285–287** *Polyctor (Fenops) lamperus* sp. n. **288–290** *Nisoniades (Nisoniades) lutum* sp. n. **291–292** *Bolla (Stolla) vena* sp. n. **293–294** *Staphylus (Vulga) vula* sp. n. **295–297** *Staphylus (Vulga) vulga* sp. n. **298–299** *Staphylus (Staphylus) rotundalus* sp. n. **300–301** *Staphylus (Staphylus) yucatanus* sp. n. paratype ♂ NVG-20063A08. **302–303** *Heliopetes (Heliopetes) lana* sp. n. paratype ♂ NVG-20062H06. **304–306** *Canesia ella* sp. n. **307–309** *Paches (Paches) loxeca* sp. n. **310–311** *Clito congruens* sp. n. Views: dorsal (285, 288, 291, 293, 295, 298, 300, 302, 305, 307, 310), left lateral (287, 290, 292, 294, 297, 299, 301, 303, 304 aedeagus, 306, 308, 309 aedeagus, 311), right lateral (286, 289, 296).



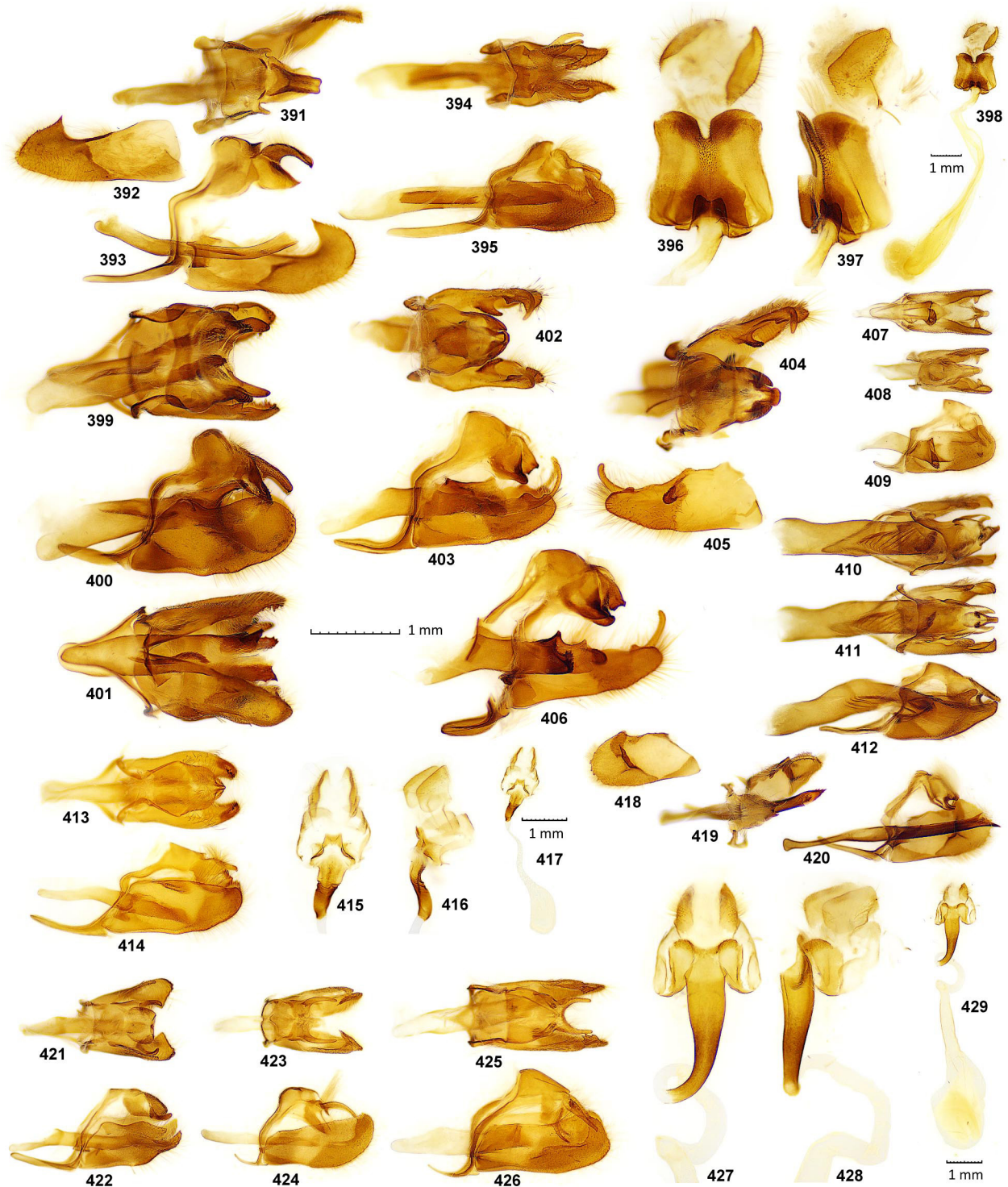
Figures 312–333. Genitalia of holotypes (unless indicated), data in text. **312–314** *Cycloglypha corax* sp. n. **315–317** *Festivia peruvia* sp. n. **318–319** *Decinea notata* sp. n. **320–321** *Pompeius fuscus* sp. n. **322–323** *Vernia clara* sp. n. **324–327** *Oligoria (Oligoria) obtena* sp. n.: **324–325** Paratype ♂ NVG-18118B07. **328–329** *Thespieus mandal* sp. n. **330–333** *Psoralis (Saniba) magnamacus* sp. n. Views: dorsal (312, 318, 320, 322, 324, 326, 328), left lateral (313, 319, 321, 323, 325, 327, 329), right lateral (314), ventral (315, 317, 330, 332, 333), right ventrolateral (316, 331). Smaller scales refer to the images below them.



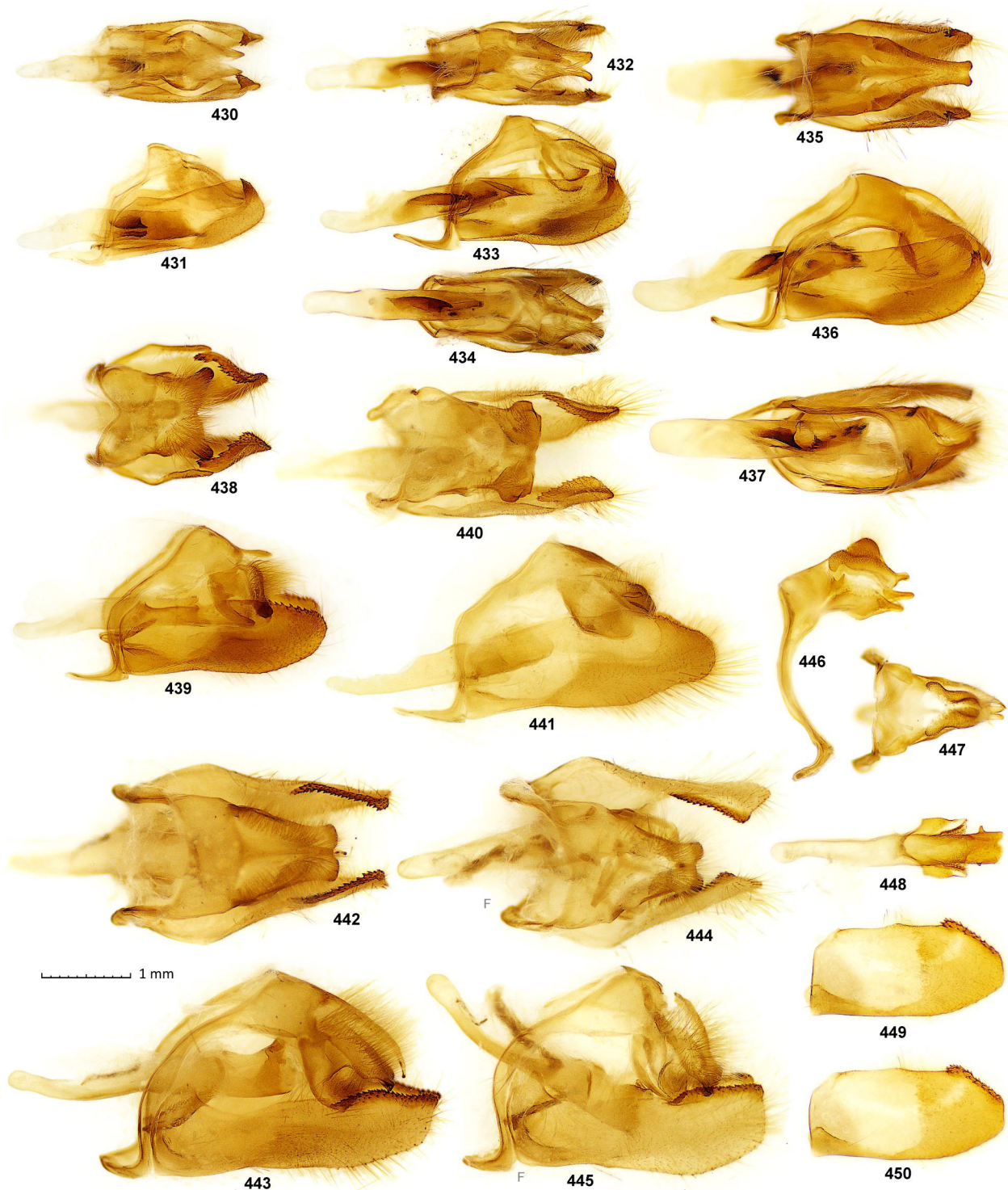
Figures 334–360. Genitalia of holotypes (unless indicated), data in text. 334–335) *Alychna ayonis* sp. n. 336–338) *Wahydra banios* sp. n. 339–341) *Wahydra cuzcona* sp. n. 342–344) *Cynea (Cynea) aureofimbria* sp. n. 345–347) *Cynea (Nycea) quada* sp. n. 348–349) *Cynea (Quinta) achirae* sp. n. paratype ♂ NVG-22035B12. 350–352) *Eutus amazonicus* sp. n. 353–354) *Eutus incus* sp. n. 355–356) *Eutus septemaculatus* sp. n. 357–358) *Godmia viridicapita* sp. n. 359–360) *Rhomba pulla* sp. n. Views: dorsal (334, 337, 340, 342, 346, 348, 350, 353, 355, 358, 359), left lateral (335, 338, 341, 344, 347, 349, 352, 354, 356, 358, 360), right lateral of left valva (343, 345, 351), dorsoanterior (336, 339).



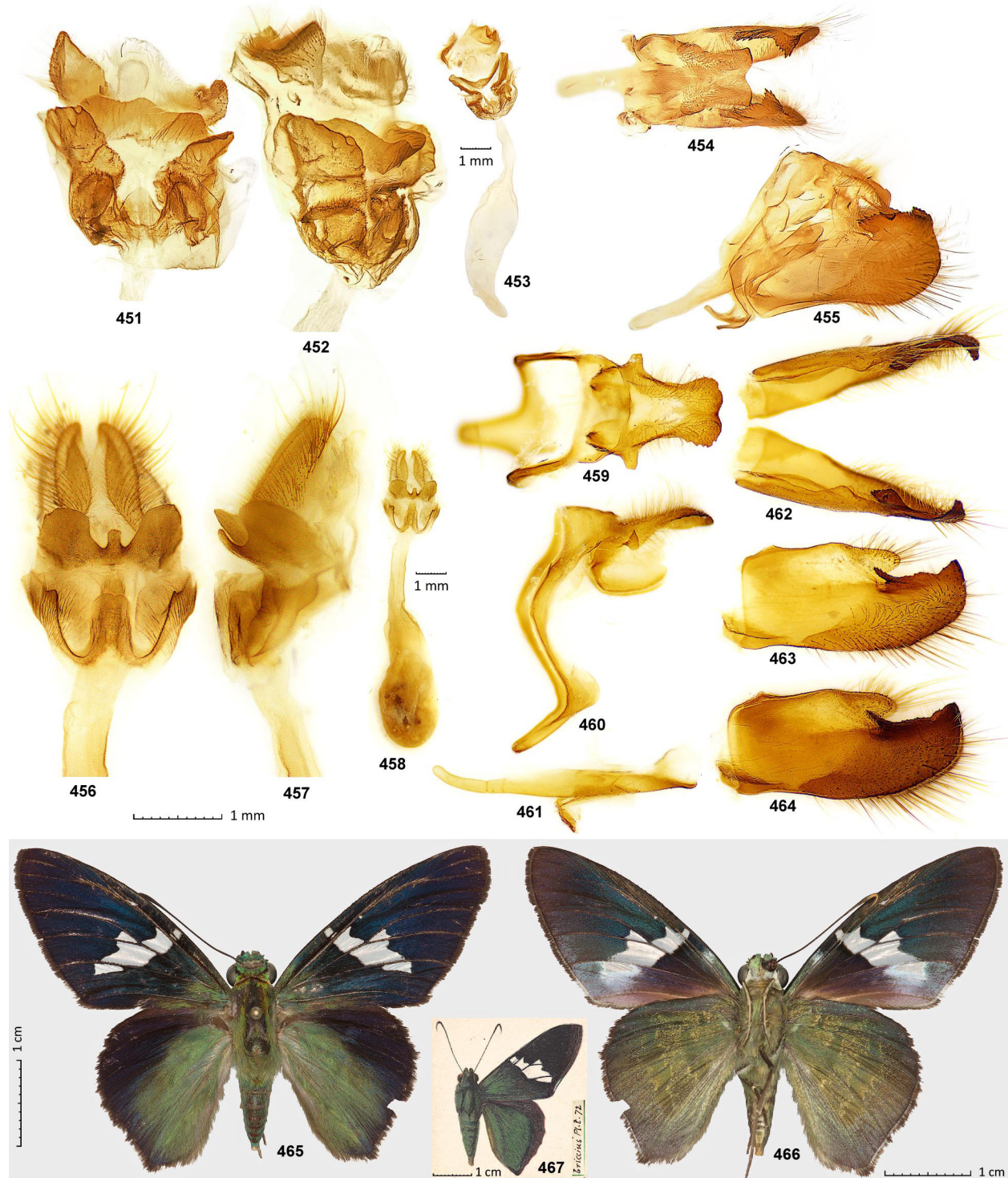
Figures 361–390. Genitalia of holotypes (unless indicated), data in text. **361–363** *Niconiades victoria* sp. n. paratype ♂ NVG-20057B04. **364–365** *Lancephallus purpurus* sp. n. **366–367** *Mnasicles (Remella) ecua* sp. n. **368–369** *Amblyscirtes (Amblyscirtes) aeratus* sp. n. **370–371** *Amblyscirtes (Mastor) chrysoptera* sp. n. **372–374** *Amblyscirtes (Mastor) chrysomisa* sp. n. **375–376** *Amblyscirtes (Flor) meridus* sp. n. **377–379** *Rectava chiriquensis* sp. n. **380–381** *Cobalopsis adictys* sp. n. **382–383** *Cymaenes melaporphyrus* sp. n. **384–385** *Lerema (Morys) ecuadorica* sp. n. **386–387** *Saturnus obscurior* sp. n. **388–390** *Cantha zoirodicta* sp. n. Views: dorsal (361, 364, 366, 368, 370, 375, 377, 380, 383, 384, 386, 388), left lateral (362 left valva removed, 365, 367, 369, 371, 376, 379, 381, 383, 385, 390), right lateral of left valva (363, 378, 389) and genital capsule, a flipped image (i.e., left-right inverted) as indicated by F (387), ventral (372, 374), right ventrolateral (373). The smaller scale refers to 374.



Figures 391–429. Genitalia of holotypes, data in text. **391–393)** *Cantha meiodicta* sp. n. **394–395)** *Phlebodes duplex* sp. n. **396–398)** *Lychnuchus (Enosis) valle* sp. n. **399–401)** *Eutychide ochoides* sp. n. **402–403)** *Dion bora* sp. n. **404–406)** *Dion occida* sp. n. **407–409)** *Eprius (Eprius) veledinus* sp. n. **410–412)** *Radiatus panamensis* sp. n. **413–414)** *Pheraeus pulcher* sp. n. **415–417)** *Callimormus rades* sp. n. **418–420)** *Gubrus lubens* sp. n. **421–422)** *Ludens labens* sp. n. **423–424)** *Rigga isa* sp. n. **425–426)** *Flaccilla lactea* sp. n. **427–429)** *Falga athena* sp. n. Views: dorsal (391, 394, 399, 402, 404, 408, 411, 413, 419, 421, 423, 425), left lateral (393, 395, 400, 403, 406, 409, 412, 414, 420, 422, 424, 426), right lateral of left valva (393, 405, 418), ventral (396, 398, 401, 407, 415, 417, 427, 429), right ventrolateral (397, 416, 428), dorsoanterior (410). Smaller scales refer to images next to them.



Figures 430–450. Genitalia of holotypes, data in text. **430–431)** *Panoquina jay* sp. n. **432–434)** *Calpodes salianus* sp. n. **435–437)** *Calpodes stingo* sp. n. **438–439)** *Aides nobra* sp. n. **440–441)** *Thracides pavo* sp. n. **442–443)** *Talides eluta* sp. n. **444–445)** *Talides laeta* sp. n. **446–450)** *Neoxeniades angustior* sp. n. Views: dorsal (430, 432, 435, 438, 440, 442, 444, 447 tegumen and uncus), left lateral (431, 433, 436, 439, 441, 443, 446 valvae and aedeagus removed, 449 right valva, 450 left valva), right lateral (445 a flipped image, i.e., left-right inverted, as indicated by F), ventral of aedeagus (448), dorsoanterior (434, 437).



Figures 451–467. Genitalia of holotypes (top) and spread specimens (bottom), data in text. **451–453** *Damas zea* sp. n. **454–455** *Tromba xantha* sp. n. **456–458** *Perichares fura* sp. n. **459–464** *Carystoides (Balma) goliath* sp. n. Views: dorsal (454, 459 valvae and aedeagus removed, 462 valvae), left lateral (455, 463 right valva, 464 both valvae, 461 aedeagus), ventral (451, 453, 456, 458), left ventrolateral (452), right ventrolateral (457). Smaller scales refer to images next to them. **465–466** Neotype of *Eudamus briccius*. **467** A drawing of *E. briccius* in ZSMC (with a smaller scale).

