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SYSTEMATIC POSITION AND CONSERVATION ASPECTS OF *MELINAEA MNASIAS THERA* (LEPIDOPTERA: NYMPHALIDAE: DANAINAE)

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Received: 08.10.2023. Revised: 27.11.2023. Accepted: 04.12.2023.

The tribe Ithomiini (Nymphalidae: Danainae) includes nearly 400 species of butterflies distributed from Mexico to Northern Argentina, and adults of all species are aposematic and the main models in several Neotropical mimicry rings. The subtribe Melinaeina, a small group composed of five genera of large ithomiines, is the sister group of all remaining groups in the tribe Ithomiini. With 14 recognised species, the genus Melinaea is the most species rich, and also the most widespread within the Melinaeina. From all species of the genus, Melinaea mnasias is considered very rare and a little known one. This is also true for Melinaea mnasias thera, a subspecies from the Atlantic Forest with less than 20 specimens known in all world museums. Studies combining systematics, ecology, biogeography and natural history are priority in tropical areas, especially when focusing on threatened species. Thus, the aim of this study was to compile all available knowledge on the threatened M. mnasias thera, providing information to future management plans focusing on the conservation of this butterfly and its habitats. Data were compiled from scientific collections and personal observations, and the systematics of species of Melinaea was assessed by DNA sampling and analysis. The obtained phylogeny recovered the subtribe Melinaeina organised in two clades, the first composed by Olyras + Paititia and the second by Eutresis + (Athyrtis + Melinaea). Melinaea mnasias thera was recovered as a sister to M. mnasias lucifer. A total of only 17 specimens of M. mnasias thera from four Brazilian localities were found in all revised collections. However, well-preserved forests are present only at one of these localities, in the southern Bahia state, from where a recent specimen has been collected, suggesting that the last populations of M. mnasias thera are restricted to this region. If this is true, the real conservation status of this species could be much more critical than the estimated.

Key words: Atlantic Forest, Brazil, butterfly, Ithomiini, endangered species

Introduction

The tribe Ithomiini (Lepidoptera: Nymphalidae: Danainae) includes about 400 butterfly species distributed from Mexico to Northern Argentina (Doré et al., 2023). Adults of all species are aposematic and considered the main models in many Neotropical mimicry rings (Brown & Benson, 1974; Beccaloni, 1997). In a study combining morphological and molecular data, Brower et al. (2014) recovered the tribe Ithomiini divided in ten subtribes, nine of which are well supported by both types of characters, a result congruent with subsequent molecular studies (Garzón-Orduña et al., 2015; Chazot et al., 2019). The subtribe Melinaeina is composed of five genera of large ithomiines and was recovered as a sister group of all remaining ithomiines in the listed above studies. With 14 recognised species, the genus Melinaea Hübner, 1816 is the most species rich, and also the most widespread within

the Melinaeina (Brown, 1979; McClure et al., 2018). From those 14 species, only three taxa occur in the Atlantic Forest, namely the endemic *Melinaea ethra* (Godart, 1819) and two subspecies of two widely distributed species, namely *Melinaea ludovica paraiya* Reakirt, 1866 and *Melinaea mnasias thera* C. Felder & R. Felder, 1865 (Brown, 1979).

Melinaea mnasias (Hewitson, [1856]) is divided into 11 described subspecies, and it is considered very rare and little known (Brown, 1977). Except for M. mnasias comma W. Forbes, 1927 and M. mnasias lucifer H. Bates, 1862, which are locally common, all other subspecies are scarce in collections. This is also true for the Atlantic Forest subspecies Melinaea mnasias thera, known from only 17 specimens so far (Brown & Freitas, 2008; Freitas et al., 2018; Rosa et al., 2023).

Melinaea mnasias thera occurs in a narrow region of the coastal Atlantic Forest in the Brazil-

ian state of Bahia, at only two localities. Accordingly, this taxon was included in the Brazilian Red List, being assessed as «Critically Endangered» (CR) (MMA, 2003, 2014, 2022; Freitas et al., 2018). The compiling of all available information on any threatened butterflies is an important task, especially for the species which are scarce in museum collections (Freitas & Marini-Filho, 2011). In this specific case, M. mnasias thera occurs in a critical portion of the Atlantic Forest, a global biodiversity hotspot for conservation (Myers et al., 2000). Thus, the aim of this study was to investigate the systematic position of M. mnasias thera, its conservation aspects, and compile all available information about this rare butterfly. Studies combining systematics, ecology, biogeography and natural history are priority in tropical areas, especially when focusing on threatened species. Moreover, the information obtained for a given group of herbivores can be useful in studies of diversity and health of a given plant assemblage (Gilbert, 1980; Freitas, 1996). Finally, studies like this one are important for providing information to future management plans focusing on the conservation of threatened butterflies and their habitats.

Material and Methods

Specimens of M. mnasias thera (Fig. 1a) were found in the following nine public collections: Coleção Entomológica do Instituto Oswaldo Cruz, Instituto Oswaldo Cruz, Rio de Janeiro, Rio de Janeiro, Brazil (CEIOC); Departamento de Zoologia, Universidade Federal do Paraná, Curitiba, Paraná, Brazil (DZUP); Muséum d'Histoire Naturelle, Paris, França National (MNHN); Museo de Historia Natural, Universidad Nacional Mayor de San Marcos, Lima, Peru (MUSM); Museu de Zoologia, Universidade de São Paulo, São Paulo, São Paulo, Brazil (MZUSP); Natural History Museum, London, England, United Kingdom (NHMUK); Museu Nacional, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil (MNRJ) (these specimens were lost by the fire that destroyed the Museum in 2018); Museum für Naturkunde, Berlin, Germany (ZMB); Zoological Collection, Museu de Diversidade Biológica da Universidade Estadual de Campinas, Campinas, São Paulo, Brazil (ZUEC). The search for data on M. mnasias thera followed the same databases and methods described in Rosa et al. (2023). Data labels of all specimens were compiled; they are available in Table S1.

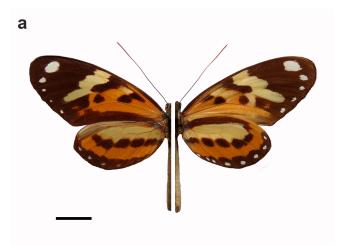




Fig. 1. Adult specimen and the habitat of *Melinaea mnasias thera*. Designations: A – *Melinaea mnasias thera* (left – dorsal view, right – ventral view); B – general view of forest habitats in Serra Bonita, Camacan, Bahia state, Brazil.

DNA sampling and analysis

All sequences used were downloaded from Genbank, except for the museum samples EB19-049 (MNHN, Muséum National d'Histoire Naturelle, Paris, France) and AHBR119 (ZUEC, Zoological Collection, Museu de Diversidade Biológica da Universidade Estadual de Campinas, Campinas, Brazil), which had their genomic DNA extracted from two legs using the QIAamp DNA MicroKit (QIAGEN®, USA) protocol, adapted with columns from MinElute PCR Purification Kit (QIAGEN®, Düsseldorf, Germany). The whole genome shotgun sequencing was performed on the two DNA extractions of museum specimens, following protocols described in Twort et al. (2021), which were modified from protocols in Meyer & Kircher (2010). Briefly, DNA was first blunt-end repaired, after which custom-made indexed Illumina adapters were ligated. The library was then pooled with 59 other Lepidoptera specimens and run on the Illumina NovaSeq platform. Raw reads were checked with FASTQC v. 0.11.8 (Andrews, 2010), and reads were cleaned with Prinseq v. 0.20.4 (Schmieder & Edwards, 2011) and Trimmomatic v. 0.38 (Bolger et al., 2014). The genome was then de novo assembled with spAdes v. 3.13.0 (Bankevich et al., 2012) with a kmer value of 21. Orthologs of the five standard genes for Lepidoptera (COI, EF1-α, CAD, wingless and GAPDH) were identified from the fragmented genome assembly using MES-PA v. 1.3 (Neethiraj et al., 2017). See Twort et al. (2021) for more detailed descriptions of the bioinformatic pipelines. For AHBR119, we were able to identify all five genes (COI, EF1- α , CAD, wingless and GAPDH). For EB19-049 we were only able to find COI. All sequences were aligned on CIPRES Science Gateway portal v. 3.1 (Miller et al., 2010) using MAFFT v. 7 (Katoh & Standley, 2013).

The final concatenated matrix comprised 37 specimens, representing most of *Melinaea* species and more close related genera, with a total of 4698 base pairs and five genes. The type species of all genera are represented in the final matrix. *Tellervo zoilus* (Fabricius, 1775) was used to root the tree (see Table S3 for voucher numbers). Analyses to find the best-fit substitution models and partition subsets for the dataset (see Table S2 for best model selected for each partition), using «merge» option, were done using ModelFinder (Kalyaanamoorthy et al., 2017) with edge-linked partition model + FreeRate heterogeneity in IQ-TREE v. 1.6.12 (Nguyen et al., 2015).

The maximum likelihood tree was inferred using ten likelihood searches in IQ-TREE v. 1.6.12. The support was calculated using the ultrafast bootstrap (UFBoot) (Hoang et al., 2018), with 2000 replications, in addition to assessing node support through 1000 replications of Shimodaira Hasegawa approximate Likelihood Ratio Test (SH-aLRT) (-alrt 1000) (Guindon et al., 2010; Hoang et al., 2018) and approximate Bayes branch test (aBayes; Anisimova et al., 2011).

Results

Systematic position

In the obtained phylogeny, the subtribe Melinaeina was organised in two clades, the first composed by *Olyras + Paititia* (type species: *Olyras crathis* E. Doubleday, 1847 and *Paititia neglecta* Lamas, 1979) and the second by

Eutresis + (Athyrtis + Melinaea) (type species: Eutresis hypereia E. Doubleday, 1847, Athyrtis mechanitis C. Felder & R. Felder, 1862 and Melinaea ludovica (Cramer, 1780)). The genus Melinaea was recovered as monophyletic and divided in two major clades, the first composed by Melinaea mnasias + Melinaea ludovica and the second formed by Melinaea ethra as the sister taxon to a large clade composed by nine species of Melinaea. The two individuals of Melinaea mnasias thera clustered together forming a clade with strong support, sister to M. mnasias lucifer (Fig. 2).

General information and conservation aspects

A total of only 17 specimens of M. mnasias thera were found in nine public collections (Table S1). These specimens represent geographical records of four localities in the Brazilian states of Rio de Janeiro, Espírito Santo, and Bahia (records from the state of São Paulo, Paraguay and Colombia are mistakes, see Rosa et al., 2023) (see Table S1, Fig. 3). Most individuals of M. mnasias thera are either very old or without any information on collecting dates, and a single individual has been collected in the XXI century (in 2016, Table S1). Morphology (mostly wing pattern) was presented and discussed by Fox (1960), and Brown (1977) presented additional data on taxonomy and distribution, anticipating by a decade the presence of M. mnasias in coastal Bahia state.

Based on the trustworthy geographical data, *M. mnasias thera* occurs in lowland coastal forests (Fig. 1b), at altitudes of 100–400 m a.s.l. (Fig. 3). At both localities, where *M. mnasias thera* was reported in the Bahia state, at least half of the area is covered by cocoa plantations locally known as «cabruca», where the cocoa trees are planted in the shade of larger trees.

The known distribution of *M. mnasias* thera is disjunct. The two localities in Bahia state (Camacan and Itapebi) are relatively close to each other (about 60 km of distance), as well as the two localities in the Espírito Santo state (Alegre) and Rio de Janeiro state (Bom Jesus do Itabapoana) are about 50 km of distance to each other. These two pairs, however, have a large gap of about 700 km between them. Based on these data, the extent of occurrence (EOO) of *M. mnasias thera* was estimated as at 7264.35 km² and its area of occupancy (AOO) as 16 km² (Rosa et al., 2023).

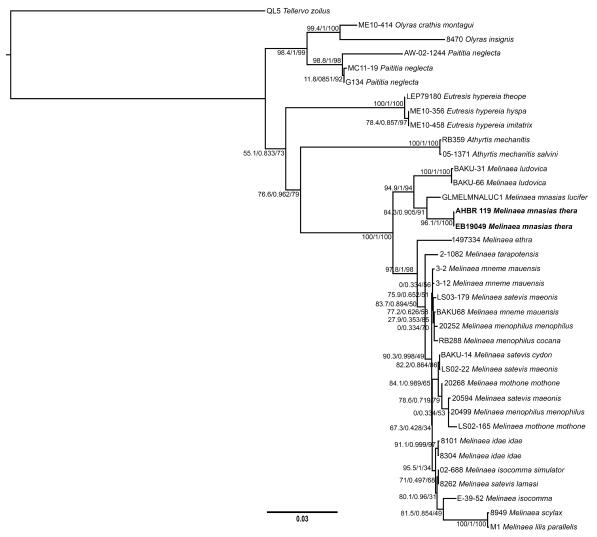


Fig. 2. Phylogenetic relationships of *Melinaea* species based on COI, EF1-α, CAD, wingless, and GAPDH genes and obtained by a maximum likelihood analysis. Numbers near the nodes are SH-aLRT/aBayes/Ultrafast bootstrap support values.

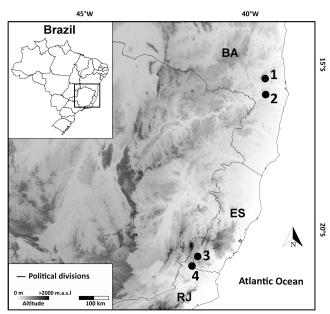


Fig. 3. Map showing the four known localities of *Melinaea mnasias thera*. Designations: 1 – Itapebi, Bahia state; 2 – Reserva Serra Bonita, Camacan, Bahia state; 3 – Alegre, Espírito Santo state; 4 – Bom Jesus de Itabapoana, Rio de Janeiro state.

Discussion Phylogeny of subtribe Melinaeina and position of M. mnasias thera

Although composed of only five genera, the internal relationships of the subtribe Melinaeina has not reached a consensus based on previous studies. Common points include the monophyly of Melinaea and the clade formed by Olyras + Paititia (Brower et al., 2006, 2014; Willmott & Freitas, 2006; Garzón-Orduña et al., 2015; Chazot et al., 2019: Fig. S2.1, Fig. S2.2). The position of the genus Athyrtis is not congruent with previous studies. Although recent molecular studies recovered it as a sister group of all remaining Melinaeina (Garzón-Orduña et al., 2015; Chazot et al., 2019), the present study recovered Athyrtis as a sister group of Melinaea. This result is similar to that obtained in the morphological study by Willmott & Freitas (2006), in combined analyses by Brower et al. (2014), and in an early molecular study by Brower et al. (2006). In addition, together with *Melinaea*, *Athyrtis* is the only other genus of Melinaeina that presents a tiger wing pattern; *Olyras*, *Paititia* and *Eutresis* have translucent wing patterns. A second divergence is the position of *Eutresis*: in the present study it was the sister group of *Athyrtis* + *Melinaea*, while it is the sister to *Olyras* + *Paititia* in previous morphological and molecular studies (Willmott & Freitas, 2006; Chazot et al., 2019).

The systematic position of *Melinaea mnasias thera* confirms the placement of this taxon as a subspecies of *M. mnasias*, as proposed by Fox (1965) based on wing patterns. In addition, the present results show that *M. mnasias* is sister to *M. ludovica* (Cramer, 1780), contrasting with the results of Chazot et al. (2019: Fig. S2.1, Fig. S2.2), where *M. mnasias* was recovered as the sister group to other *Melinaea* species. The lack of resolution among the large clade composed by nine species of *Melinaea* confirm the results found by McClure & Elias (2017), and is a result of the absence of mitochondrial divergence, suggesting a recent radiation for these nine species.

Only three species of *Melinaea* are present in the Atlantic Forest. There are no discernible reasons why none of the remaining nine taxa have reached the Atlantic Forest, as many of them are extremely common, locally abundant and present in several forested habitats (Brown, 1977; Freitas, 1996). McClure & Elias (2017) suggested that these nine taxa could have originated from a recent and rapid radiation. In fact, the dating provided by Chazot et al. (2019: Fig. S2.2) showed that this clade originated about one million year ago, and most species are much younger than that. In this case, it is possible that these species just have not had enough time to reach and colonise the Atlantic Forest domain yet.

Geographical distribution and conservation

Based on the reliable data, *M. mnasias thera* has been reported from four localities from south Bahia to north Rio de Janeiro states (Fig. 3). However, it is important to call attention to two important factors. First, most of the forests in the northern Rio de Janeiro state and southern Espírito Santo state have been destroyed and persists as small remnants (MMA, 2000), and it is hard to believe that populations of *M. mnasias thera* are still present in this region. Second, not a single individual of *M. mnasias thera* has been collected or sighted in the last large forest remnants in the

central and northern Espírito Santo state, including the low mountains near the municipality of Santa Teresa and the large tableland forests near the municipality of Linhares, both intensively censused in the last three decades (Brown & Freitas, 2000; Freitas et al., 2016). Accordingly, it is not impossible that the last populations of M. mnasias thera are restricted to the wet forests in south Bahia state. If this is true, the actual EOO should be much smaller than that presented in Rosa et al. (2023), and the estimate of EOO, which is now on the threshold to Vulnerable (VU) category, is much more optimistic than the reality. However, the fact that *M. mnasias thera* may persist in areas with cocoa plantation opens several possibilities for conservation, since there are still several areas where cocoa is cultivated in the «cabruca» system (Cocoa plantation shaded by native trees). The reasons for this can be explained in its biology. So, although the host plant and immature stages of M. mnasias thera are unknown, it likely uses Dyssochroma spp. (Solanaceae); the same host plants are used by the other two Melinaea in the Atlantic Forest (Brown, 1987; Drummond & Brown, 1987; Brown & Freitas, 1994). These plants are epiphytic, growing in tall trees near the canopy, exactly the trees that are preserved to provide the shade for the cocoa plantations in south Bahia state.

Based on this scenario, it is very important that potentially additional localities of populations of this rare butterfly should be surveyed. Suggested areas in the South Bahia state include the Serra das Lontras National Park and the region of Una Biological Reserve. In addition, the large areas of cocoa plantations in the Ilhéus-Itabuna region could harbour populations of *M. mnasias thera*. It should not be difficult to obtain eggs from wild caught females, as for other species of *Melinaea* (McClure & Elias, 2017; A.V.L. Freitas, unpublished). Details of its life cycle could provide clues to a better understanding of its rarity, as well as important information for conservation actions for this taxon.

Conclusions

The present study is the most complete concerning the threatened Brazilian butterfly *Melinaea mnasias thera*. This is one of the rarest and the most threatened *Melinaea* taxa, so far known from only 17 specimens deposited in nine museum collections. Most of the potential historical range of this species is now deforested. The species is presently restricted to the large forest remnants in

the southern part of the Bahia state, in northeastern Brazil. In fact, given this scenario, only two localities are possibly maintaining populations of *M. mnasias thera*, meaning that the current IUCN status of Vulnerable could be much more optimistic than the reality. Additional populations should be located, as these would provide more opportunities for conservation of this rare butterfly.

Acknowledgements

We thank Mirna Casagrande, Olaf Mielke, and Eduardo Carneiro (all - Universidade Federal do Paraná, Brazil) for the access to material deposited in DZUP collection; Alexandre Soares (Museu Nacional do Rio de Janeiro, Brazil) for the access to material deposited in MNRJ collection; Márcio Félix, Felipe Moreira, and Claudia Rodrigues (all – Instituto Oswaldo Cruz, Brazil) for the access to material deposited in CEIOC collection; Marcelo Duarte and Renato Silva (all – Museu de Zoologia, Universidade de São Paulo, Brazil) for the access to material deposited in MZUSP collection; Keith Willmott (Florida Museum of Natural History, University of Florida, USA) for compiling data from MUSM. We thank to Vitor O. Becker (Camacan, Brazil) helped during the field work in the Private Natural Heritage Reserve Serra Bonita, south of the Bahia state. We also thank two anonymous referees for making valuable suggestions in the submitted version of the manuscript. Augusto H.B. Rosa thanks the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, Brazil (CAPES) - Finance Code 001, for the scholarship. Eduardo P. Barbosa was supported by Fundação de Amparo à Pesquisa no Estado de São Paulo (FAPESP) (2016/15873-8, and 2018/21432-0) and the Brazilian Research Council – Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq grant 162673/2020-5) for post-doc fellowships. André V.L. Freitas thanks the Conselho Nacional de Desenvolvimento Científico e Tecnológico – CNPq (fellowship 304291/2020-0), and the FAPESP (grant 2021/03868-8). This publication is part of the RedeLep «Rede Nacional de Pesquisa e Conservação de Lepidópteros» SISBIOTA-Brasil/CNPq (563332/2010-7). This study is registered in SISGEN (ADCABAB).

Supporting Information

Additional data for the paper of Rosa et al. (2024) may be found in the **Supporting Information**.

References

- Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. Available from https://www.bioinformatics.babraham.ac.uk/projects/fastqc
- Anisimova M., Gil M., Dufayard J.F., Dessimoz C., Gascuel O. 2011. Survey of branch support methods demonstrates accuracy, power, and robustness of fast likelihood-based approximation schemes. *Systematic Biology* 60(5): 685–699. DOI: 10.1093/sysbio/syr041

- Bankevich A., Nurk S., Antipov D., Gurevich A.A., Dvorkin M., Kulikov A.S., Lesin V.M., Nikolenko S.I.,
 Pham S., Prjibelski A.D., Pyshkin A.V., Sirotkin A.V., Vyahhi N., Tesler G., Alekseyev M.A., Pevzner P.A. 2012. SPAdes: A new genome assembly algorithm and its applications to single-cell sequencing.
 Journal of Computational Biology 19(5): 455–477.
 DOI: 10.1089/cmb.2012.0021
- Beccaloni G.W. 1997. Ecology, natural history and behaviour of Ithomiine butterflies and their mimics in Ecuador (Lepidoptera: Nymphalidae: Ithomiinae). *Tropical Lepidoptera* 8(2): 103–124.
- Bolger A.M., Lohse M., Usadel B. 2014. Trimmomatic: A flexible trimmer for Illumina sequence data. *Bioinformatics* 30(15): 2114–2120. DOI: 10.1093/bioinformatics/btu170
- Brower A.V.Z., Freitas A.V.L., Lee M.M., Silva-Brandão K.L., Whinnett A., Willmott K.R. 2006. Phylogenetic relationships among the Ithomiini (Lepidoptera: Nymphalidae) inferred from one mitochondrial and two nuclear gene regions. *Systematic Entomology* 31(2): 288–301. DOI: 10.1111/j.1365-3113.2006.00321.x
- Brower A.V.Z., Willmott K.R., Silva-Brandão K.L., Garzón-Orduña I.J., Freitas A.V.L. 2014. Phylogenetic relationships of ithomiine butterflies (Lepidoptera: Nymphalidae: Danainae) as implied by combined morphological and molecular data. *Systematics and Biodiversity* 12(2): 133–147. DOI: 10.1080/14772000.2014.899650
- Brown K.S. 1977. Geographical patterns of evolution in Neotropical Lepidoptera: differentiation of the species of *Melinaea* and *Mechanitis* (Nymphalidae, Ithomiinae). *Systematic Entomology* 2(3): 161–197. DOI: 10.1111/j.1365-3113.1977.tb00368.x
- Brown K.S. 1979. *Ecological Geography and Evolution in Neotropical Forests*. Livre Docência Thesis. Campinas: Universidade Estadual de Campinas. 109 p.
- Brown K.S. 1987. Chemistry at the Solanaceae/Ithomiinae Interface. *Annals of the Missouri Botanical Garden* 74(2): 359–397. DOI: 10.2307/2399406
- Brown K.S., Benson W.W. 1974. Adaptive polymorphism associated with multiple Müllerian mimicry in *Heliconius numata*. *Biotropica* 6(4): 205–228. DOI: 10.2307/2989666
- Brown K.S., Freitas A.V.L. 1994. Juvenile stages of Ithomiinae: overview and systematics (Lepidoptera: Nymphalidae). *Tropical Lepidoptera* 5(1): 9–20.
- Brown K.S., Freitas A.V.L. 2000. Diversidade de Lepidoptera em Santa Teresa, Espírito Santo. *Boletim do Museu de Biologia Mello Leitão (Nova Série)* 11/12: 71–116.
- Brown K.S., Freitas A.V.L. 2008. *Melinaea mnasias thera* C. Felder & R. Felder, 1865. In: A.B.M. Machado, G.M. Drummond, A.P. Paglia (Eds.): *Livro Vermelho da Fauna Brasileira Ameaçada de Extinção*. Brasília, DF, Belo Horizonte, MG: Ministério do Meio Ambiente, Fundação Biodiversitas. P. 418.
- Chazot N., Willmott K.R., Lamas G., Freitas A.V.L., Piron-Prunier F., Arias C.F., Mallet J., De-Silva D.L., Elias M. 2019. Renewed diversification following Miocene

- landscape turnover in a Neotropical butterfly radiation. *Global Ecology and Biogeography* 28(8): 1118–1132. DOI: 10.1111/geb.12919
- Doré M., Willmott K.R., Lavergne S., Chazot N., Freitas A.V.L., Fontaine C., Elias M. 2023. Mutualistic interactions shape global spatial congruence and climatic niche evolution in Neotropical mimetic butterflies. *Ecology Letters* 26(6): 843–857. DOI: 10.1111/ele.14198
- Drummond B.A., Brown K.S. 1987. Ithomiinae (Lepidoptera: Nymphalidae): summary of known larval food plants. *Annals of the Missouri Botanical Garden* 74(2): 341–358. DOI: 10.2307/2399405
- Fox R.M. 1960. A monograph of the Ithomiidae (Lepidoptera). Part II. The tribe Melinaeini Clark. Transactions of the American Entomological Society 86(2): 109–171.
- Fox R.M. 1965. Additional notes on *Melinaea* Hübner (Lepidoptera: Ithomiidae). Proceedings of the Royal Entomological Society of London. Series B, Taxonomy 34(7–8): 77–82. DOI: 10.1111/j.1365-3113.1965.tb01694.x
- Freitas A.V.L. 1996. Population biology of *Heterosais edessa* (Nymphalidae) and its associated Atlantic Forest Ithomiinae community. *Journal of the Lepidopterists' Society* 50(4): 273–289.
- Freitas A.V.L., Marini-Filho O.J. 2011. Plano de Ação Nacional para Conservação dos Lepidópteros Ameaçados de Extinção. Brasília: Instituto Chico Mendes de Conservação da Biodiversidade. 124 p.
- Freitas A.V.L., Marini-Filho O.J., Mielke O.H.H., Casagrande M.M., Brown K.S., Kaminski L.A., Iserhard C.A., Ribeiro D.B., Dias F.M.S., Dolibaina D.R., Carneiro E., Uehara-Prado M., Romanowski H.P., Emery E.O., Accacio G.M., Rosa A.H.B., Bizarro J.M.S., Silva A.R.M., Guimarães M.P., Silva N.A.P., Braga L., Almeida G. 2018. *Melinaea mnasias thera* C. Felder & R. Felder, 1865. In: *Livro Vermelho da Fauna Brasileira Ameaçada de Extinção*. Vol. 7: Invertebrados. Brasília: ICMBio. P. 137–139.
- Freitas A.V.L., Brown K.S., Mielke O.H.H., Santos J.P., Vasconcellos-Neto J. 2016. Borboletas da Reserva Natural Vale, Linhares/ES. In: S.G. Rolim, L.F.T. Menezes, A.C. Srbek-Araujo (Eds.): *Floresta Atlântica de Tabuleiro: Diversidade e Endemismos na Reserva Natural Vale.* Belo Horizonte: Editora Rupestre. P. 317–328.
- Garzón-Orduña I.J., Silva-Brandão K.L., Willmott K.R., Freitas A.V.L., Brower A.V.Z. 2015. Incompatible ages for clearwing butterflies based on alternative secondary calibrations. *Systematic Biology* 64(5): 752–767. DOI: 10.1093/sysbio/syv032
- Gilbert L.E. 1980. Food web organization and the conservation of neotropical diversity. In: M.E. Soule, B.A. Wilcox (Eds.): *Conservation of neotropical biology: an evolutionary-ecological perspective*. Sunderland (MA): Sinauer. P. 11–33.
- Guindon S., Dufayard J.F., Lefort V., Anisimova M., Hordijk W., Gascuel O. 2010. New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assess-

- ing the Performance of PhyML 3.0. *Systematic Biology* 59(3): 307–321. DOI: 10.1093/sysbio/syq010
- Hoang D.T., Chernomor O., von Haeseler A., Minh B.Q., Vinh L.S. 2018. UFBoot2: Improving the ultrafast bootstrap approximation. *Molecular Biology and Evolution* 35(2): 518–522. DOI: 10.1093/molbev/msx281
- Kalyaanamoorthy S., Minh B.Q., Wong T.K.F., von Haeseler A., Jermiin L.S. 2017. ModelFinder: Fast model selection for accurate phylogenetic estimates. *Nature Methods* 14(6): 587–589. DOI: 10.1038/nmeth.4285
- Katoh K., Standley D.M. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution* 30(4): 772–780. DOI: 10.1093/molbev/mst010
- McClure M., Dutrillaux B., Dutrillaux A.M., Lukhtanov V., Elias M. 2018. Heterozygosity and Chain Multivalents during Meiosis Illustrate Ongoing Evolution as a Result of Multiple Holokinetic Chromosome Fusions in the Genus *Melinaea* (Lepidoptera, Nymphalidae). *Cytogenetic and Genome Research* 153(4): 213–222. DOI: 10.1159/000487107
- McClure M., Elias M. 2017. Ecology, life history, and genetic differentiation in Neotropical *Melinaea* (Nymphalidae: Ithomiini) butterflies from north-eastern Peru. *Zoological Journal of the Linnean Society* 179(1): 110–124. DOI: 10.1111/zoj.12433
- Meyer M., Kircher M. 2010. Illumina sequencing library preparation for highly multiplexed target capture and sequencing. *Cold Spring Harbor Protocols* 2010(6): pdb.prot5448. DOI: 10.1101/pdb.prot5448
- Miller M.A., Pfeiffer W., Schwarts T. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In: 2010 Gateway Computing Environments Workshop. New Orleans, Louisiana, USA. P. 1–8. DOI: 10.1109/GCE.2010.5676129
- MMA. 2003. *Instrução Normativa №003 de 28 de maio de 2003*. Diário Oficial da União, Brasília. DF, Seção 1:88.
- MMA. 2014. Lista Nacional Oficial de Espécies da Fauna Ameaçadas de Extinção Anexo I à Portaria №444, de 17 de dezembro de 2014. Diário Oficial da União, Brasília, DF. Seção 1. Vol. 245: 121–126.
- MMA. 2022. Portaria MMA №148, de 7 de Junho de 2022

 Atualiza o teor do Anexo da Portaria №443, de 17
 de dezembro de 2014, Lista oficial de espécies da flora
 brasileira ameaçadas de extinção. Diário Oficial da
 União, Brasília, DF. Seção 1, 108:74.
- MMA. 2000. Avaliação e ações prioritárias para a conservação da biodiversidade da Mata Atlântica e Campos Sulinos. Brasília: MMA/SBF. 40 p.
- Myers N., Mittermeier R.A., Mittermeier C.G., Fonseca G.A.B., Kent J. 2000. Biodiversity hotspots for conservation priorities. *Nature* 403(6772): 853–858. DOI: 10.1038/35002501
- Neethiraj R., Hornett E.A., Hill J.A., Wheat C.W. 2017. Investigating the genomic basis of discrete phenotypes using a Pool-Seq-only approach: New insights into the genetics

- underlying colour variation in diverse taxa. *Molecular Ecology* 26(19): 4990–5002. DOI: 10.1111/mec.14205
- Nguyen L.T., Schmidt H.A., von Haeseler A., Minh B.Q. 2015. IQ-TREE: A Fast and Effective Stochastic Algorithm for Estimating Maximum-Likelihood Phylogenies. *Molecular Biology and Evolution* 32(1): 268–274. DOI: 10.1093/molbev/msu300
- Rosa A.H.B., Ribeiro D.B., Freitas A.V.L. 2023. How data curation and new geographical records can change the conservation status of threatened Brazilian butterflies. *Journal of Insect Conservation* 27(3): 403–414. DOI: 10.1007/s10841-023-00464-0
- Schmieder R., Edwards R. 2011. Quality control and preprocessing of metagenomic datasets. *Bioinformatics* 27(6): 863–864. DOI: 10.1093/bioinformatics/btr026
- Twort V.G., Minet J., Wheat C.W., Wahlberg N. 2021. Museomics of a rare taxon: placing Whalleyanidae in the Lepidoptera Tree of Life. *Systematic Entomology* 46(4): 926–937. DOI: 10.1111/syen.12503
- Willmott K.R., Freitas A.V.L. 2006. Higher-level phylogeny of the Ithomiinae (Lepidoptera: Nymphalidae): classification, patterns of larval hostplant colonization and diversification. *Cladistics* 22(4): 297–368. DOI: 10.1111/j.1096-0031.2006.00108.x

СИСТЕМАТИЧЕСКОЕ ПОЛОЖЕНИЕ И ПРИРОДООХРАННЫЕ АСПЕКТЫ *MELINAEA MNASIAS THERA* (LEPIDOPTERA: NYMPHALIDAE: DANAINAE)

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Триба Ithomiini (Nymphalidae: Danainae) включает около 400 видов чешуекрылых, распространенных от Мексики до Северной Аргентины. При этом взрослые особи всех видов являются апосематическими и выступают основными моделями в нескольких кольцах неотропической мимикрии. Небольшая подтриба Melinaeina, состоящая из пяти родов крупных чешуекрылых, является сестринской группой всех остальных групп трибы Ithomiini. Род Melinaea, насчитывающий 14 видов, является самым крупным, а также самым распространенным в пределах подтрибы Melinaeina. Из всех видов рода Melinaea mnasias считается очень редким и малоизученным. Это справедливо и для Melinaea mnasias thera, подвида из Атлантического леса, менее 20 экземпляров которого известно во всех музеях мира. Исследования, сочетающие систематику, экологию, биогеографию и естественную историю, являются приоритетными в тропических регионах, особенно когда основное внимание уделяется видам, находящимся под угрозой исчезновения. В связи с этим целью этого исследования было собрать все доступные данные о M. mnasias thera, находящемся под угрозой исчезновения, предоставив информацию для будущих планов управления, направленных на сохранение этой бабочки и ее среды обитания. Информация была собрана на основе научных коллекций и личных наблюдений, а систематика видов Melinaea оценена путем отбора и анализа ДНК. Полученные данные о филогении восстановили подтрибу Melinaeina, организованную в две клады: первую составляют Olyras + Paititia, а вторую – Eutresis + (Athyrtis + Melinaea). Melinaea mnasias thera был обнаружен как сестринский подвид к M. mnasias lucifer. Всего во всех изученных коллекциях обнаружено 17 экземпляров M. mnasias thera из четырех местонахождений в Бразилии. Однако хорошо сохранившиеся леса присутствуют только в одном из этих мест, на юге штата Баия, откуда недавно был собран экземпляр. Это позволяет предположить, что последние популяции M. mnasias thera ограничены этим регионом. Если это действительно так, то реальный природоохранный статус этого таксона может быть гораздо более критичным, чем предполагалось.

Ключевые слова: Ithomiini, атлантический лес, бабочка, Бразилия, исчезающий вид