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# A new species of the plume moth genus *Adaina* Tutt (Lepidoptera, Pterophoridae) from the Atacama Desert, Chile

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## Abstract

The plume moth *Adaina azapensis* **sp. nov.** (Lepidoptera, Pterophoridae, Pterophorinae, Oidaematophorini) from the transverse valleys of the Atacama Desert, northern Chile, is described and illustrated based on adults reared from florivorous larvae collected on the native shrub *Pluchea chingoyo* (Asteraceae). The morphology and larval feeding behavior of *A. azapensis* **sp. nov.** resemble those of *A. jobimi* Vargas from the Andes of northern Chile. However, the two species can be distinguished based on their wing pattern and morphological details of their genitalia. A maximum likelihood analysis based on mitochondrial DNA sequences clustered *A. azapensis* **sp. nov.** and *A. jobimi* as sister species with a genetic distance of 7.8% (Kimura 2-parameter model) and supports their adscription to *Adaina* Tutt. However, the result of the analysis also suggests that the current circumscription of this genus needs further evaluation. The discovery of *A. azapensis* **sp. nov.** highlights the need to continue searching for plume moths that remain overlooked in underexplored areas of South America.

**Key words:** Arid environments, DNA barcoding, florivory, Neotropical Region

## Introduction

The plume moth genus *Adaina* Tutt was originally proposed to include only the type species *Alucita microdactyla* Hübner (Tutt 1905), a primarily Palearctic plume moth also known from the Australian and Oriental Regions (Matthews & Maharajh 2009). After many additions, the genus currently includes 42 species described worldwide, 36 of which occur in the New World (Hobern 2024). Although genitalia morphology of *Adaina* resembles that of *Hellinsia* Tutt, the two genera can be distinguished by their forewing venation, specifically, veins $R_3$ and $R_4$ are stalked in *Adaina* species and free in *Hellinsia* species (Matthews & Maharajh 2009). The natural history of many members of *Adaina* remains unknown. However, available records suggest that their larvae are folivorous, florivorous, or gall inducers (Matthews 2006) on plants of the family Asteraceae (Matthews & Lott 2005).

Mainland South America harbors a highly diverse fauna of Oidaematophorini (Gielis 2011), including 26 species of *Adaina* (Hobern 2024), many of which have been recently described (e.g. Gielis 2016; Ustjuzhanin *et al*. 2022). Only two species of this genus have been recorded in Chile: *A. coquimboae* Gielis in the lowlands of the north-central area (Gielis 2012), and *A. jobimi* Vargas in the highlands of the Andes in the northernmost part (Vargas 2020). While the host plants of *A. coquimboae* remain unknown (Gielis 2012), two members of the family Asteraceae, *Baccharis alnifolia* and *Stevia philippiana*, have been recorded as feeding substrate for the florivorous larvae of *A. jobimi* (Vargas 2022).

The northernmost part of Chile presents a pronounced elevation gradient, extending from near sea level in the Atacama Desert to the high peaks of the Andes. Previous records of *Adaina* along this gradient were restricted to the type locality of *A. jobimi*, at an altitude of about 3400 m in the Andes of the Parinacota Province (Vargas 2022). This altitude range also harbors the highest plant diversity (Arroyo *et al*. 1988). Additional *Adaina* plume moths were recently reared from larvae collected on inflorescences of a native shrub of the family Asteraceae at an elevation of about 1000 m in the transverse valleys of the Atacama Desert in the Arica Province. Although preliminary observations suggested similarity with *A. jobimi*, a closer examination of the wing pattern and genitalia morphology,

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as well as an analysis of mitochondrial DNA sequences, revealed that the obtained plume moths belong to an undescribed species whose taxonomic description is provided here.

## Material and methods

The adult specimens examined were reared from larvae collected on inflorescences of *Pluchea chingoyo* (Asteraceae) at about 1000 m elevation in the Azapa Valley (18°34’48”S, 69°52’12”W), Arica Province, northern Chile. The abdomen of each specimen was removed and placed in hot KOH 10% for a few minutes to dissect the genitalia, which were then stained with Eosin Y and Chlorazol Black and mounted on slides with Euparal. The photos of the habitus and genitalia were respectively taken using an iPhone 11 camera attached to a Leica M125 stereomicroscope or a Leica DM1000 LED microscope. The holotype, paratypes, and their genitalia slides are deposited in the “Colección Entomológica de la Universidad de Tarapacá” (IDEA), Arica, Chile. Following Landry and Gielis (2022), the data on the labels of the holotype are recorded verbatim, with line changes indicated by vertical bars, label changes by double vertical bars, and missing information by square brackets.

Genomic DNA was extracted from two legs of the holotype using the QIAamp Fast DNA Tissue Kit, following the manufacturer’s instructions. DNA purification, PCR amplification, and sequencing of the barcode region (Hebert *et al*. 2003) with the primers LCO1490 and HCO2198 (Folmer *et al*. 1994) were performed at Macrogen Inc. (Seoul, South Korea). The PCR program included 5 min at 94°C, 35 cycles of 30 s at 94°C, 30 s at 47°C, 1 min at 72°C, and a final elongation step of 10 min at 72°C. The obtained sequence was deposited in the Barcode of Life Data System (BOLD) (Ratnasingham & Hebert 2007) under the process ID NCMIC017-25 and was subjected to a maximum likelihood (ML) analysis. The alignment also included sequences of other species of *Adaina*, other genera of Oidaematophorini, and one species of Pterophorini, which is the sister group of Oidaematophorini (Alipanah *et al*. 2011). All of these sequences were downloaded from BOLD (Table 1). Sequence alignment with the ClustalW method and assessment of sequence divergence with the Kimura 2-Parameter (K2P) method were performed with the software MEGA11 (Tamura *et al*. 2021). The substitution saturation of the alignment was assessed with the Xia test in the software DAMBE7 (Xia 2018). The ML analysis was performed using the software IQTREE 1.6.12 (Nguyen *et al*. 2015) in the web interface W-IQ-TREE (Trifinopoulos *et al*. 2016), with data partitioned according to codon position. ModelFinder (Kalyaanamoorthy *et al*. 2017) selected TIM3e+G4, F81+F, and HKY+F+G4 as the best fit models for the 1st, 2nd, and 3rd partitions, respectively. Branch support was assessed with 1000 replications of the Shimodaira-Hasegawa-like approximate likelihood ratio test (SH-aLRT) (Guindon *et al*. 2010) and ultrafast bootstrap (UFBoot) (Hoang *et al*. 2017). The unrooted tree was visualized in FigTree (Rambaut 2014) to root on the single representative of Pterophorini.

**TABLE 1.** DNA barcode sequences used in the molecular analysis.

| Tribe/Species | BOLD process ID |
|---|---|
| Oidaematophorini | |
| *Adaina ambrosiae* (Murtfeldt) | BBUSA039-09 |
| *Adaina azapensis* **sp. nov.** | NCMIC017-25 |
| *Adaina bipunctatus* (Möschler) | MNAP729-13 |
| *Adaina jobimi* Vargas | GBMNE63243-22 |
| *Adaina microdactyla* (Hübner) | ABOLA573-14 |
| *Adaina montanus* (Walsingham) | BBLPB929-10 |
| *Adaina simplicius* (Grossbeck) | BBLOB1031-11 |
| *Emmelina monodactyla* (Linnaeus) | FBLMT634-09 |
| *Gypsochares baptodactylus* (Zeller) | LON6825-18 |
| *Hellinsia osteodactylus* (Zeller) | ABOLA920-15 |
| *Oidaematophorus lithodactyla* (Treitschke) | LEATE533-13 |
| *Pselnophorus heterodactyla* (Müller) | LASTS065-14 |
| *Puerphorus olbiadactylus* (Millière) | LEASX035-21 |
| Pterophorini | |
| *Merrifieldia tridactyla* (Linnaeus) | FBLMT655-09 |

## Results

### Molecular analysis

Genetic divergence between the new species and other members of *Adaina* ranged from 7.8% (K2P) with *A. jobimi* to 17.1% with *A. montanus* (Walsingham). The index of substitution saturation of the alignment was smaller than the critical value (ISS < ISS.C; $p < 0.001$), and no evidence of stop codons was detected, suggesting that the dataset was suitable for phylogenetic analysis. The ML analysis (Fig. 1) placed five species of *Adaina* in a well-supported group (97% SH-aLRT, 97% UFBoot). Within this group, two well-supported pairs of species were found, one including the type species and *A. bipunctatus* (Möschler) (95% SH-aLRT, 98% UFBoot), and the other including the new species and *A. jobimi* (93% SH-aLRT, 95% UFBoot), while the relationships of *A. simplicius* (Grossbeck) were poorly resolved. The other two *Adaina* representatives, *A. ambrosiae* (Murtfeldt) and *A. montanus* (Walsingham), were distantly related to the five-species group.

## Taxonomy

### *Adaina azapensis* sp. nov.

urn:lsid:zoobank.org:act:45C2857E-5FA6-4575-96F2-FCF6B806C23C
Figs 1–4

**Type locality.** Chile, Arica Province, Azapa Valley (18°35'05" S, 69°52'45" W), at about 1000 m elevation in the Atacama Desert.

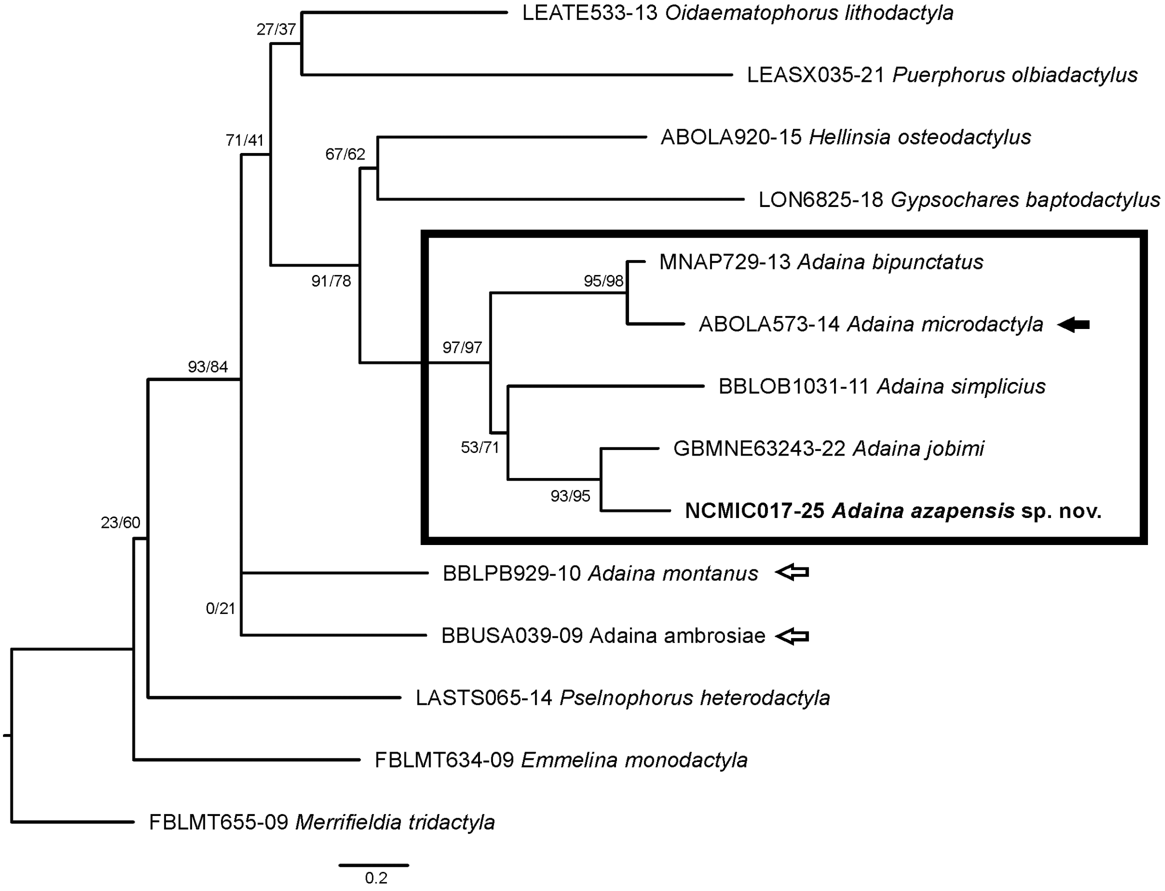

**FIGURE 1.** Maximum Likelihood tree of *Adaina azapensis* **sp. nov.** (bold) and other plume moths (Lepidoptera, Pterophoridae) based on mitochondrial DNA sequences. The BOLD Process ID is recorded to the left of each species name; the rectangle delimits a monophyletic group of representatives of *Adaina* Tutt; the closed arrow indicates the type species of this genus; open arrows indicate species currently included in *Adaina* but distantly related to the type species; numbers represent SH-aLRT/UFBoot values (1000 replicates).

**Type material.** HOLOTYPE ♂: CHILE, Arica | Azapa | February 2022 | H.A. Vargas leg. | | ex-larva | *Pluchea* | *chingoyo* | | HOLOTYPE | *Adaina* | *azapensis* | Vargas [red handwritten label] | | IDEA-LEPI-2025-01 | | HAV-1509 [genitalia slide] | | BOLD ID | NCMIC017-25. Specimen and genitalia slide deposited at IDEA.

PARATYPES: three ♂, four ♀, same data as for the holotype; IDEA-LEPI-2025-02 to IDEA-LEPI-2025-08; HAV-1572, 1682, 1683, 1845, 1846, 1847, 1848 [genitalia slides]. Specimens and genitalia slides deposited at IDEA.

**Diagnosis.** Although genitalia morphology and larval feeding behavior of *A. azapensis* **sp. nov.** resemble those of *A. jobimi*, the only congeneric species previously recorded in the northernmost part of Chile, the two species can be accurately distinguished. The forewing of *A. azapensis* **sp. nov.** is mostly creamy white with scattered greyish brown and yellowish brown scales and a well-defined C-shaped spot at the base of the cleft (Fig. 2), while that of *A. jobimi* is mostly yellowish brown with a small, not well-defined spot at the base of the cleft (Vargas 2020; fig.

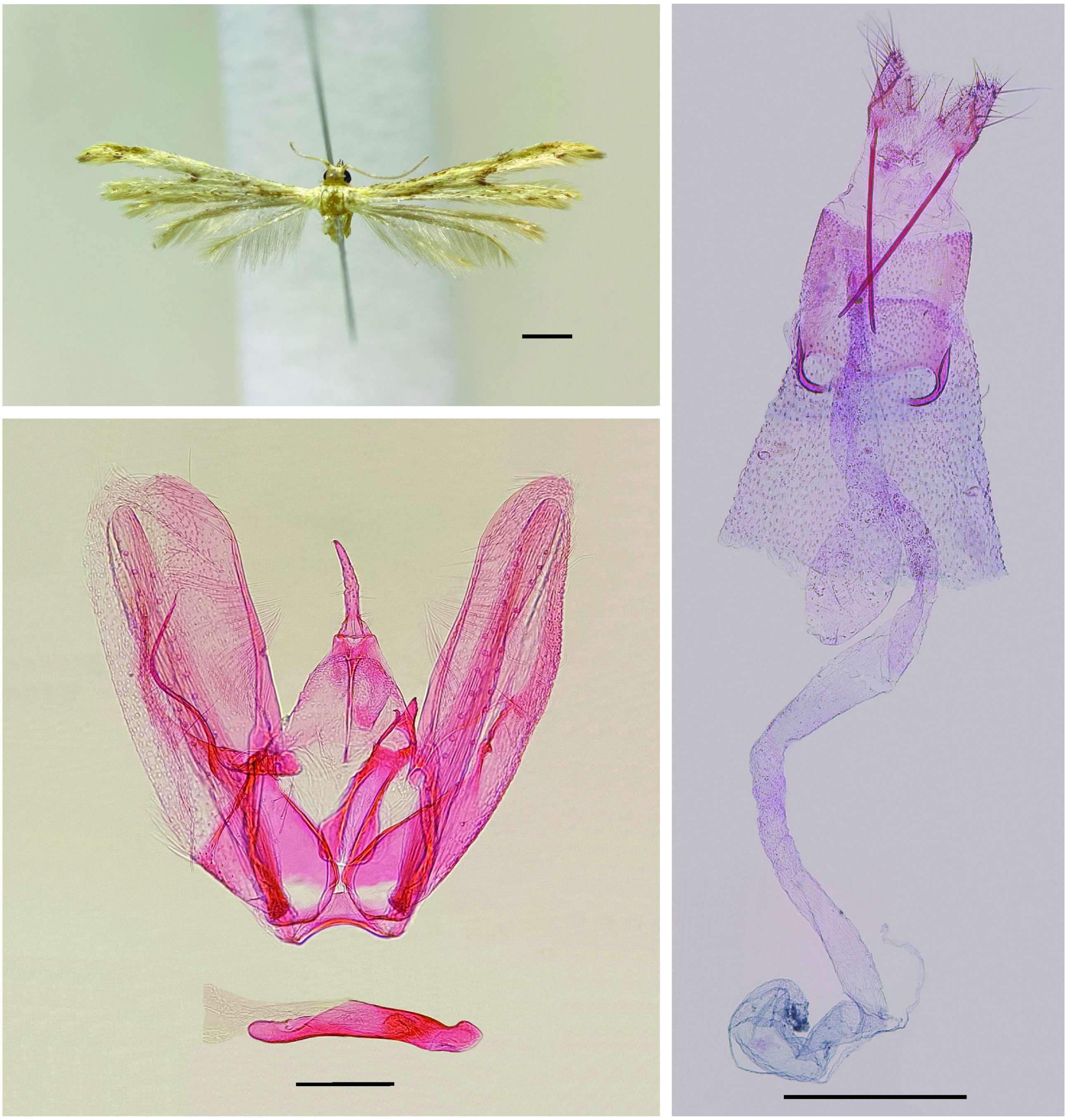

**FIGURE 2.** *Adaina azapensis* **sp. nov.** Above left: holotype male in dorsal view. Bottom left: male genitalia, phallus removed, ventral view; phallus, lateral view. Right: female genitalia, ventral view. Scale bars: 1, 0.2, 0.3 mm, respectively.

1). In male genitalia, the broadly sinuous saccular spine on the left valva, the absence of a saccular process on the right valva, and the poorly differentiated, irregular cornutus on the vesica of *A. azapensis* **sp. nov.** (Fig. 3) contrast with the almost straight medial third of the saccular spine on the left valva, the small saccular process on the right valva, and the V-shaped cornutus on the vesica of *A. jobimi* (Vargas 2020; figs 2–5). In female genitalia, the strongly inwardly curved, hook-like anterior apophyses and the convex anterior margin of the tergum VIII of *A. azapensis* **sp. nov.** (Fig. 4) contrast with the triangular anterior apophysis with slightly inwardly curved apex and the straight anterior margin of the tergum VIII of *A. jobimi* (Vargas 2020; fig. 6).

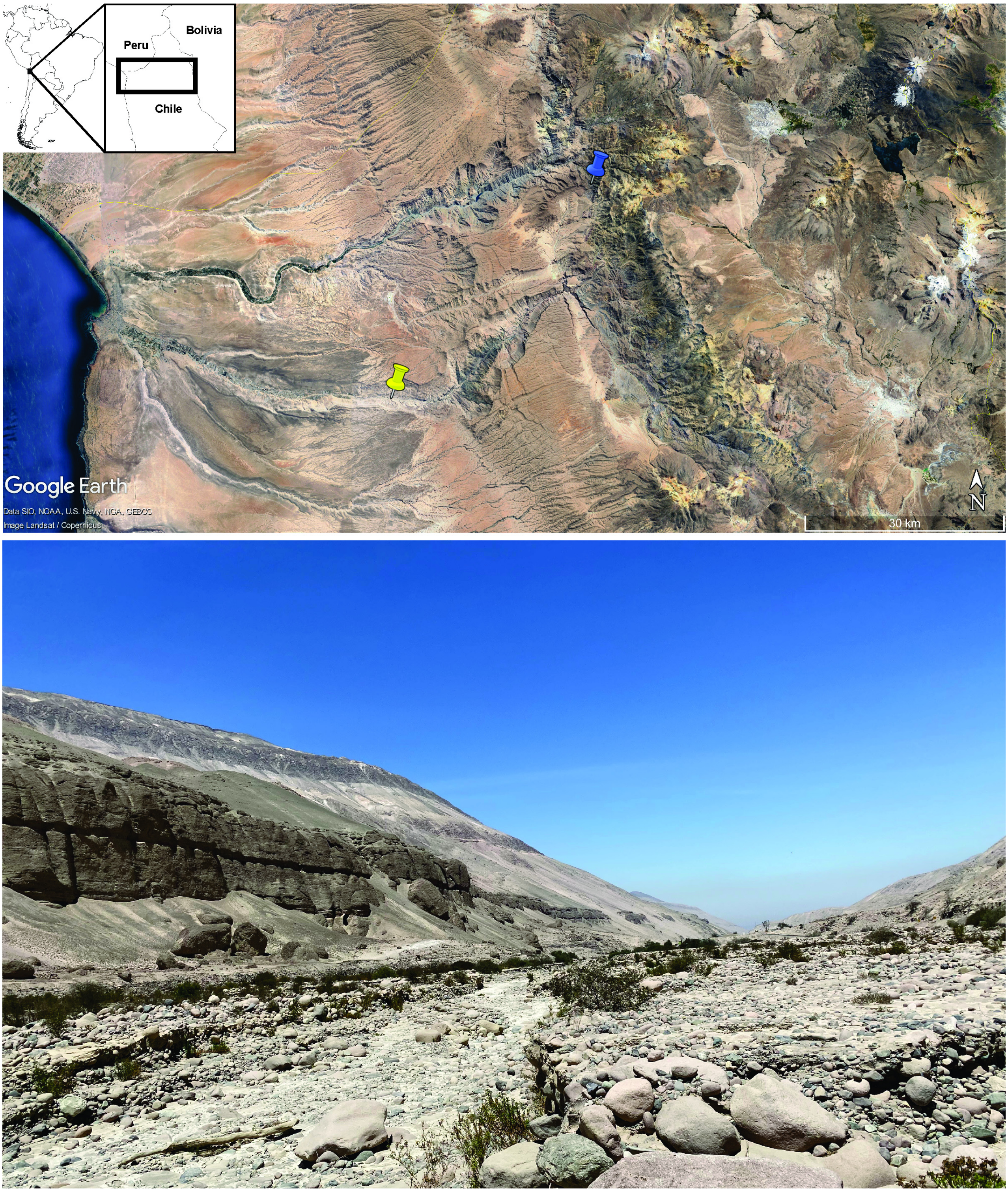

**FIGURE 3.** *Adaina* Tutt in the northernmost part of Chile. Above: documented distribution; yellow and blue marks indicate the type localities of *A. azapensis* **sp. nov.** and *A. jobimi* Vargas, respectively. Bottom: habitat of *A. azapensis* **sp. nov.** at the type locality in the Azapa Valley, Atacama Desert.

**Description. Male** (Forewing length 4.8–5.0 mm) (Fig. 2). Head. Vertex and frons whitish brown. Occiput with narrow, raised, whitish brown scales. Labial palpus porrect, short, mostly creamy white; second segment with scattered greyish brown scales; third segment greyish brown. Antenna filiform, creamy white dorsally, with short cilia ventrally. Thorax. Creamy white. Foreleg mostly creamy white; coxa, femur and tibia greyish brown anteriorly; femur with a narrow, creamy white, longitudinal stripe anteriorly; tibial epiphysis greyish brown. Midleg similar to foreleg in color; pair of tibial spurs mostly greyish brown with scattered creamy white scales. Hindleg creamy white; two pairs of tibial spurs creamy white. Forewing mostly creamy white with scattered greyish brown and yellowish brown scales; a narrow, C-shaped, greyish brown spot at base of cleft; fringe mostly creamy white, greyish brown at tip of first lobe. Hindwing greyish brown; fringe yellowish brown. Abdomen mostly creamy white with greyish brown, dorsal and lateral longitudinal stripes.

**Male genitalia** (Fig. 2). Tegumen triangular, with well-differentiated longitudinal median sulcus. Uncus hook-like, slightly curved ventrally, slightly shorter than tegumen. Vinculum narrow. Saccus as a narrow transverse stripe with slightly convex anterior margin. Juxta an elongated, asymmetrical sclerite, slightly curved to right and narrowing dorsally. Anellus arms asymmetrical; left arm finger-like, mostly straight, slightly curved near tip; right arm about 1.5× length of left arm, distal half triangular. Valvae asymmetrical; each with a tuft of filiform scales basally on external side; tuft slightly shorter than valva. Left valva wider than right valva, maximum width about one-third of length; costal and ventral margins mostly straight; apex rounded; saccular process with capsular basal section and slender, broadly sinuous saccular spine slightly shorter than half of valva. Right valva similar in length to left valva, maximum width about one-fourth length; ventral margin slightly angled at two thirds with valva tapering toward apex; apex rounded; saccular process absent. Phallus cylindrical, nearly straight, about half as long as valva, tip slightly swollen dorsally; vesica with a poorly differentiated, irregular cornutus.

**Female**. Similar to male in size and coloration.

**Female genitalia** (Fig. 2). Papillae anales lobular, slightly sclerotized, with few setae. Posterior apophyses rod-shaped, straight, about 2.5× length of papillae anales. Anterior apophyses from anterior vertex of tergum VIII, appearing as strongly inwardly curved hooks; anterior margin of tergum VIII between anterior apophyses convex. Ostium bursae displaced to left. Antrum parallel-sided, slightly sclerotized, about half as long as papillae anales. Ductus bursae membranous, about as long as papillae anales. Corpus bursae membranous, elongated, about 1.2× as

**FIGURE 4.** *Pluchea chingoyo*, the host plant of *Adaina azapensis* **sp. nov.**, in the Azapa Valley, Atacama Desert, northern Chile.

long as posterior apophyses, slightly dilated on anterior half. Ductus seminalis from base of corpus bursae, about three times as long as corpus bursae, broadly sinuous, anterior third coiled.

**Etymology**. The name of the species is derived from the type locality.

**Distribution**. *Adaina azapensis* **sp. nov.** is known only from the type locality (Fig. 3).

**Host plant**. Larvae of *A. azapensis* **sp. nov.** feed concealed within the inflorescences of *P. chingoyo* (Fig. 4). The distribution range of this shrub extends from northwestern Peru to northern Chile (Moreira-Muñoz *et al*. 2016, Vilcapoma & Beltrán 2018).

## Discussion

Although the ML analysis of this study was based on sequences of a single mitochondrial molecular marker from a reduced number of representatives of *Adaina*, the results seem consistent with the morphology and natural history of this plume moth genus, raising doubts about its monophyly. Larvae and pupae of the type species, *A. microdactyla*, lack verrucae and verruca-like tubercles, respectively (Kimber 2025), a morphological pattern also found in *A. jobimi* (Vargas 2020) and *A. simplicius* (Matthews 2006), and observed during the rearing of the type material of *A. azapensis* **sp. nov.** Regarding feeding behavior, larvae of the type species feed in the flower heads in the summer generation and bore into stems causing small gall-swellings in the overwintering generation (Matthews 2006). Like the summer generation of *A. microdactyla*, the larvae of *A. azapensis* **sp. nov.**, *A. jobimi* (Vargas 2020), and *A. simplicius* (Matthews 2006) feed on inflorescences. These three species were clustered with *A. microdactyla* and *A. bipunctatus* in a well-supported group in the ML tree (Fig. 1). In contrast, *A. ambrosiae* and *A. montanus*, both distantly related to the type species in the ML tree (Fig. 1), have larvae and pupae with verrucae and verruca-like tubercles, respectively, and their larvae feed externally on leaves (Matthews 2006). Furthermore, the male genitalia morphology of *A. ambrosiae* remarkably differs from that of the type species (Landry *et al*. 2004). Further phylogenetic studies, based on a wider taxon sampling and additional molecular markers, together with a more detailed understanding of the morphology and natural history of immature stages, are needed to assess the monophyly of *Adaina*.

While some species of Lepidoptera with high dispersal capacity have been recorded along much of the steep elevation gradient of the northernmost part of Chile (Escobar-Suárez *et al*. 2023), others with a more restricted dispersal capacity appear to have narrower elevation ranges (Vargas 2023). The distribution records of the two species of *Adaina* documented in this area include only their respective type localities, at about 3400 m elevation in the Andes and 1000 m elevation in the Atacama Desert, for *A. jobimi* and *A. azapensis* **sp. nov.**, respectively. Although the distance between these localities is only about 45 km, the elevation difference between them is notable, reaching 2400 m. Further surveys are needed to assess whether these species are restricted to different elevation belts or whether their elevation ranges are underestimated.

Like other recent taxonomic contributions (e.g. Ustjuzhanin *et al*. 2021, 2022; Landry & Gielis 2022; Kovtunovich & Ustjuzhanin 2024), the discovery of *A. azapensis* **sp. nov.** highlights the need to continue searching for plume moths that remain overlooked in underexplored areas of South America.

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