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New larval host plant records for wild silkmoths from Arunachal Pradesh in the Indian Eastern Himalaya

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Abstract

Silkmoths are both ecologically significant and economically valuable insects, with larval host plant associations playing a crucial role in shaping their development, survival, and silk yield. Arunachal Pradesh, a biodiversity hotspot in the Eastern Himalayas, harbours diverse silk moth species. However, comprehensive documentation of their host plants remains limited. Through extensive field surveys conducted in various parts of Arunachal Pradesh, we recorded 14 species of wild silkworms, and documented seven species of new host plant associations for three wild silkmoth species in addition to the previous records. The new records include *Gunda ochracea* Walker (Bombycidae) on *Ficus rumphii* Blume (Moraceae), *Antheraea frithi* Moore on *Terminalia chebula* Retz, *Terminalia myriocarpa* Van Heurck & Müll. Arg, *Combretum pilosum* Roxb. ex G.Don (Combretaceae), *Lagerstroemia speciosa* (L.) Martyn (Lythraceae), *Castanopsis lanceifolia* (Oerst.) Hickel & A.Camus (Fagaceae) and *Samia canningii* (Hutton, 1859) on *Litsea monopetala* (Roxb.) Pers. (Lauraceae). These results fill a major gap in the ecological knowledge of wild silkmoths in the Eastern Himalayas. Additionally, it supports sericultural applications of the documented larval host plants.

Keywords: Arunachal Pradesh, Bombycidae, host plant associations, Saturniidae, sericulture, wild silkmoths

Introduction

Silk is one of the most ancient and highly valuable, prized biomaterials, appreciated for its protein-based composition, tensile strength and lustre (Ki *et al.,* 2009). While many arthropods produce silk, it is primarily the cocoons of lepidopteran larvae — especially those from Bombycidae and Saturniidae — that are utilised in sericulture. Both families belong to the superfamily Bombycoidea, noted for its capacity to produce robust silk-fibres during pupation (Zwick, 2008; Sutherland *et al.,* 2010; Zwick *et al.,* 2011).

The Bombycidae includes about 202 species across 27 genera, with *Bombyx mori* being the most domesticated and studied for mulberry silk production. Whereas Saturniidae is a highly diverse family with over 3,400 species and approximately 180 genera globally, known for wild silk varieties like tasar, muga and eri (Kitching *et al.,* 2018). India, particularly the northeastern region, including Arunachal Pradesh, is a centre of silkmoth diversity. Arunachal Pradesh alone had a record of 27 saturniid and 10 bombycid species (Gogoi *et al.,* 2014; Kumar *et al.,* 2016), before the present survey.

Despite rich taxonomic data, larval host plant associations — critical for silkmoth development and silk yield — are, however, inadequately recorded in this region. Host plant selection influences not only larval survival but also cocoon quality (Vijayan, 2013; Das *et al.,* 2020). Therefore, the introduction of new host plants could be beneficial to the sericulture sector. Furthermore, the relationship between herbivorous insects and host plants conveys the tale of coevolution and evolutionary radiation (Farrell & Mitter, 1990; Fordyce, 2010). Thus, understanding these associations can pave the way for further studies on ecological specialiszation and co-evolutionary dynamics among wild silkmoths and native host plants.

Materials and Methods

Field surveys were undertaken in different locations of Arunachal Pradesh between 2023 and 2024, covering elevations ranging from 150 to over 3,000 m above mean sea level (Figure 1). The survey locations included both planted and natural forest covers. The natural forest cover in the studied area was comprised of tropical evergreen, semi-evergreen, moist deciduous, pine, or subalpine forests.

Host plants were identified based on three key observations:

1. Presence of larval excreta under host trees,
2. Evidence of partial leaf consumption,
3. Direct visual confirmation of larvae feeding in the wild.
4. Search for cocoons, followed by a search for larvae in the same host plant

Only those host plant records with active larval feeding were considered valid. Some of the areas were visited multiple times to monitor the cocoon formation of the larvae. Some larvae were also raised in both outdoor and indoor conditions to validate the identification of the moths that developed from the larvae.

Plant voucher specimens were collected and pressed to prepare a herbarium. Plants were identified based on local floras (Kanjilal *et al.,* 1934-1940; Hajra *et al.,* 1996; Giri *et al.,* 2008), and the present status of nomenclature was verified from www.plantsoftheworldonline.org (POWO, 2025). Moth identification was carried out when adult moths developed from the corresponding larva and cocoon (Peigler & Naumann 2003, Gogoi *et al.,* 2014, Sondhi & Kunte 2014; Sondhi *et al.,* 2025).

Results and Discussion

During the survey, the following 14 species of wild silkmoths were recorded:

(A) Saturniidae: *Tasar* silkworm *Antheraea frithi* Moore, 1859 and *Antheraea mylitta* (Drury, 1773); wild race of *muga* silkworm *Antheraea assamensis* Helfer, 1837, wild *eri* silkworm *Samia canningii* (Hutton, 1859), Emperor moth *Rinaca cidosa* (Moore, 1865) (=*Saturnia cidosa*), *Rinaca thibeta* (Westwood, 1854) (=*Saturnia thibeta*), moon moths *Actias selene* (Hübner, 1807), *Actias maenas* Doubleday, 1847, *Actias parasinensis* Brechlin, 2009, atlas moth *Attacus atlas* (Linnaeus,1758) and *Archaeoattacus edwardsii* (White 1859), *plain golden* emperor moth *Loepa katinka* (Westwood, 1848), Cricula moth *Cricula trifenestrata* (Helfer, 1837)

(B) Bombycidae: *Gunda ochracea* Walker, 1862

Out of these, *Rinaca cidosa* was recorded from West Siang district and Eaglenest Wildlife Sanctuary (West Kameng district), *Rinaca thibeta* from West Siang district, *Cricula trifenestrata* and *Antheraea mylitta* from Lower Siang district and all others from Papum Pare district. All larval stages, cocoons and moths were recorded for *Antheraea frithi* and the wild race of *Antheraea assamensis*. Only the fifth instar larva, cocoon and adult stages were recorded for the wild race of *Samia canningii* and the *Rinaca cidosa*. Only moth stages were recorded for the rest. Therefore, in this investigation, host plants were not assigned to these silkworms.

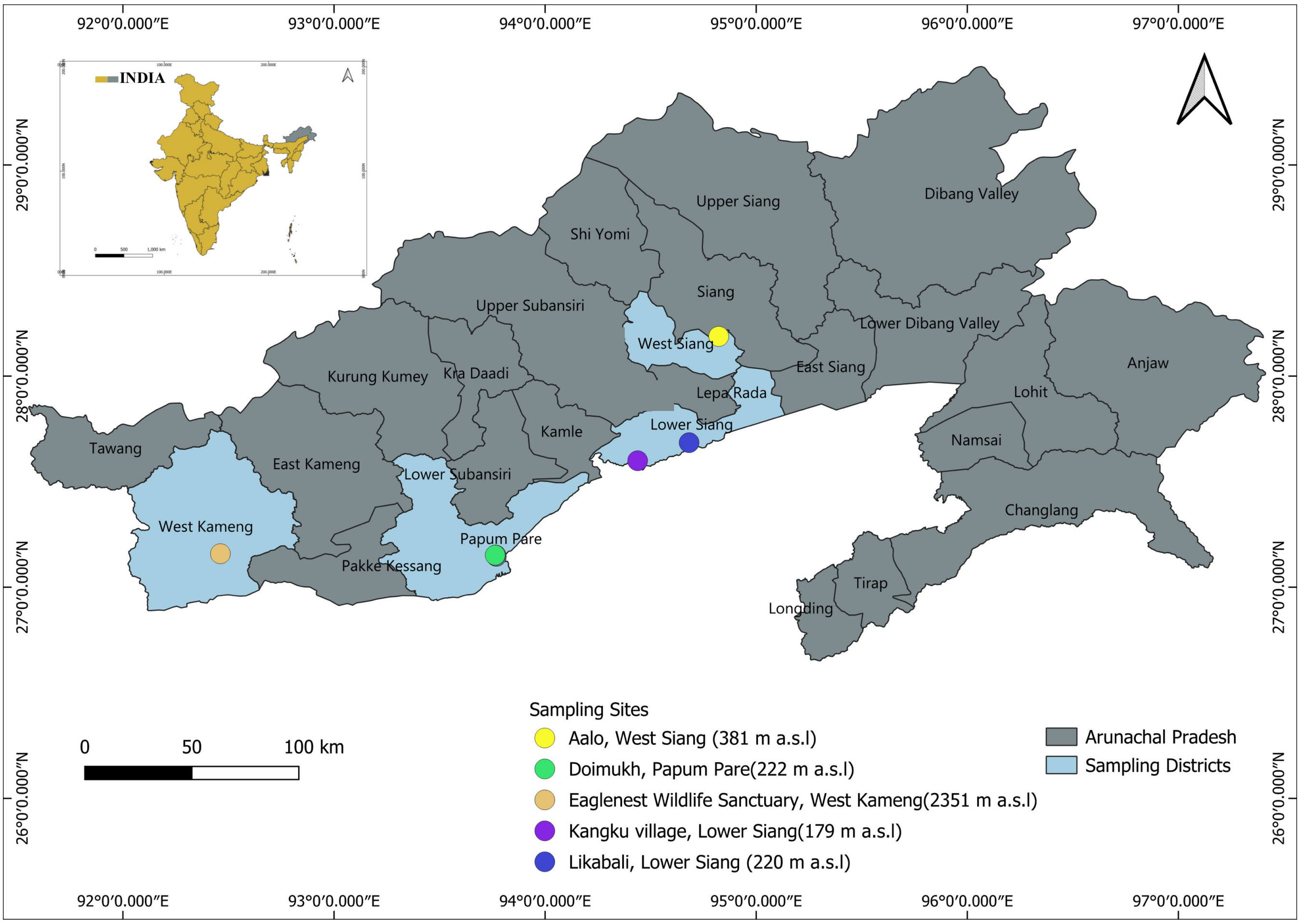

Fig. 1: A map of Arunachal Pradesh, India showing the locations where the silkworms and host plants are recorded.

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We report new host plant for the species as follow (Figure 2):

(A) *Gunda ochracea* on *Ficus rumphii* Blume (Rosales: Moraceae)

(B) *Antheraea frithi* on *Terminalia chebula* Retz., *Terminalia myriocarpa* Van Heurck & Müll. Arg, *Combretum pilosum* Roxb. ex G. Don (Myrtales: Combretaceae), *Lagerstroemia speciosa* (L.) Martyn (Myrtales: Lythraceae), and *Castanopsis lanceifolia* (Oerst.) Hickel & A.Camus (Fagales: Fagaceae)

(C) *Samia canningii* on *Litsea monopetala* (Roxb.) Pers. (Laurales: Lauraceae)

We also observed previously recorded and known host plants (Figure 2):

(A) Wild race of *Antheraea assamensis* on *Litsea monopetala* (Roxb.) Pers. and *Machilus gamblei* King ex Hook.f. (=*Machilus bombycina* King ex Hook.f.) (Laurales: Lauraceae)

(B) *Antheraea frithi* on *Terminalia arjuna* (Roxb. ex DC.) Wight & Arn., (Combretaceae)

(C) *Antheraea mylitta* on *Ziziphus mauritiana* Lam. (Rosales: Rhamnaceae)

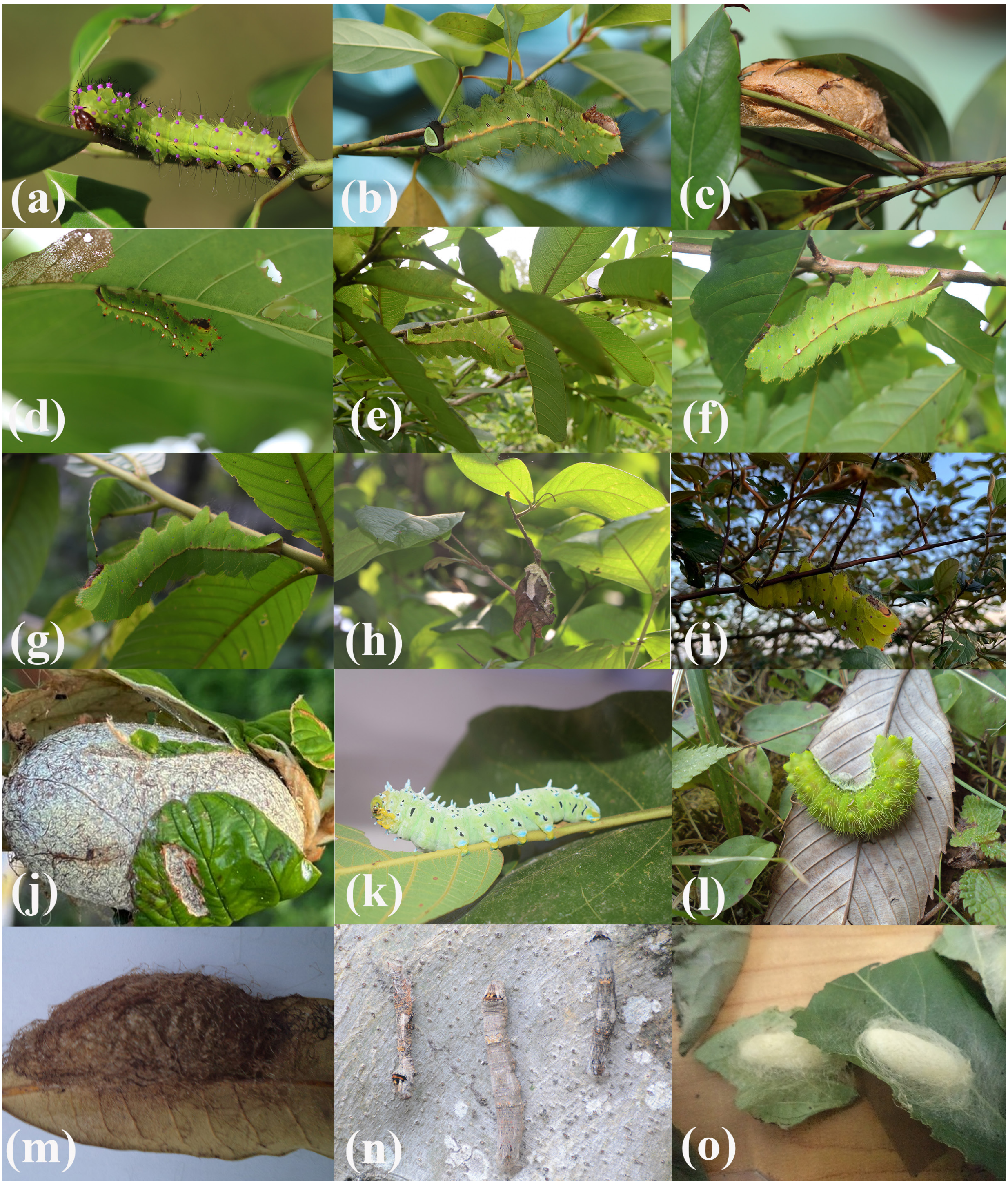

Fig. 2: (a-c) Wild race of (a) third and (b) fifth instar larva of muga silkworm, *Antheraea assamensis* and (c) its cocoon on Som tree, *Machilus gamblei*; (d-h) Larva of *tasar* silkworm *Antheraea frithi* on (d) Indian crape myrtle, *Lagerstroemia speciosa*, (e) Arjun tree, *Terminalia arjuna*, (f) Myrobalan tree, *Terminalia chebula*, (g) Hollock tree, *Terminalia myriocarpa*, (h) its cocoon on *Combretum pilosum*; (i, j) Tasar silkworm, *Antheraea mylitta* and its cocoon on Ber tree, *Zizyphus mauritiana*; (k) Wild *eri* silkworm, *Samia canningii* on Soalu plant, *Litsea monopetala*; (l, m) Larva of *Rinaca* moth and its cocoon; (n) Larvae of wild bombycid moth, *Gunda ochracea* on banyan fig tree *Ficus rumphii*; (o) Cocoon of *Gunda ochracea.*

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Further, we documented the cocoon properties of selected wild silkworm species raised on particular host plants (Table 1).

Table 1. Cocoon morphometric parameters of selected wild silkworms reared on various host plants.

Sl. No.	Host plant used for rearing	No. of cocoon measured (N)	Cocoon weight with pupa (g) ± SD	Cocoon length (mm) ± SD	Cocoon breadth (mm) ± SD
A. *Antheraea frithi*					
1.	*Terminalia chebula*	3	4.18 ± 1.43	42.91 ± 1.44	20.11 ± 0.81
2.	*Terminalia arjuna*	4	7.19 ± 1.32	43.20 ± 1.92	21.90 ± 1.10
3.	*Terminalia myriocarpa*	3	10.91 ± 2.48	48.05 ± 5.06	21.64 ± 3.34
4.	*Lager-stroemia speciosa*	3	7.95 ± 1.73	45.37 ± 3.53	22.34 ± 1.55
B. *Antheraea assamenseis* (wild race)					
5.	*Machilus gamblei*	3	9.20 ± 0.29	51.79 ± 1.15	23.49 ± 0.70
C. *Samia canningii*					
6.	*Litsea monopetala*	3	3.03 ± 0.39	42.51 ± 1.24	17.09 ± 3.36
D. *Gunda ochracea*					
7.	*Ficus rumphii*	5	0.55 ± 0.12	25.25 ± 1.71	12.39 ± 2.54

Prior reports showed that *Antheraea frithi* primarily feeds on species of *Terminalia* and members of Dipterocarpaceae and Fagaceae (Chutia *et al.,* 2016; Singh *et al.,* 2022). The inclusion of *Lagerstroemia speciosa* is a novel observation in this study. Similarly, *Litsea monopetala*, known as a host of semi-domesticated *Antheraea assamensis*, was here reported as a natural host for *Samia canningii*, expanding its ecological associations. As per a previous study, *Samia canningii* can be reared on *Ricinus communis* L. (Malpighiales: Euphorbiaceae) and *Heteropanax fragrans* (Roxb.) Seem. (Apiales: Araliaceae) — host plants it shares with the domesticated *Samia cynthia* (Taba & Gogoi, 2019). The current record from Lauraceae introduces a new host family for this species. The present study also shows that the larvae of *Samia canningii* that feed on *Litsea monopetala* are larger in diameter (length: ca. 58.60 mm, breadth: ca. 17.75 mm) and cocoons are larger in length and breadth (length 42.51, breadth 17.09 mm) compared to those reared on *Ricinus communis* and *Heteropanax fragrans* (length 62–65 mm, width 9–10 mm; Cocoon length 27–33 mm, breadth 12–14 mm) (Taba & Gogoi 2019). Therefore, it may be hypothesised that *Litsea monopetala* could be a better host plants for the purpose of the sericulture industry compared to other plants known for hosting *Samia canningii*. Phylogenetic proximity exists among Rosales, Fagales, Malpighiales and Myrtales, which are associated with *Bombyx mori*, *Gunda ochracea*, *Antheraea frithi*, *Antheraea mylitta* and *Samia cynthia*. In contrast, Laurales (host to *Antheraea assamensis* and *Samia canningii*) and Apiales (host to *Samia cynthia*) are more distantly related (Figure. 3) (Li *et al.,* 2021). This divergence in host plant phylogeny may reflect adaptations of silkworms driven by domestication and ecological specialisation. These patterns suggest that *Antheraea assamensis* and *Samia canningii* may share evolutionary host plant lineages adapted to Lauraceae, diverging from other Saturniids and Bombycids whose host plants (in the family such as Lythraceae, Combretaceae, Moraceae, Fabaceae, Euphorbiaceae) are more closely related phylogenetically (Li *et al.,* 2021).

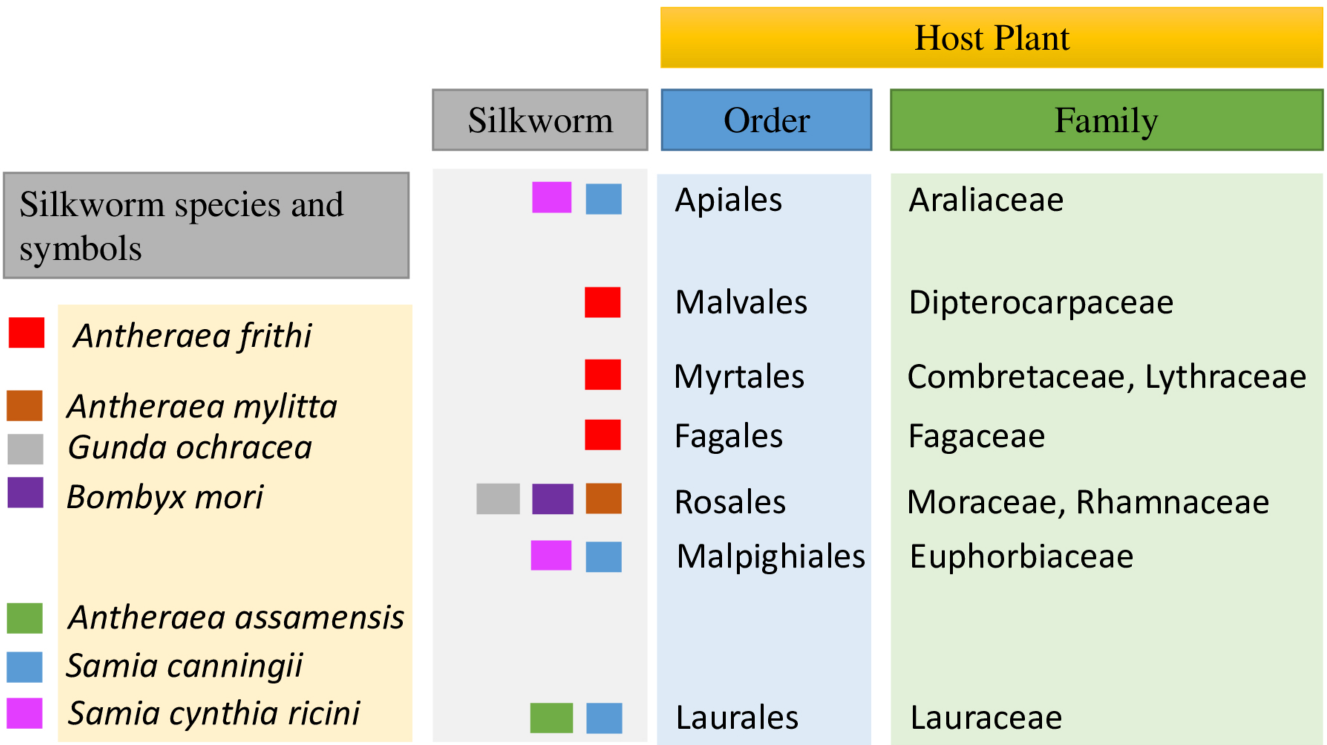

Fig. 3: Hypothetical grouping of the silkworms based on larval host plant phylogeny (Li *et al.,* 2021).

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Conclusion

This study expands our knowledge of silkmoth – host plant interactions, revealing new larval host associations for key wild silkmoth species. These findings have broad implications for evolutionary biology, conservation ecology and the development of sustainable sericultural practices in the Indian East Himalayan regions. Protecting both the moths and their host plants is essential for conserving the intricate ecological web and supporting rural livelihoods dependent on wild silk.

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CONFLICT OF INTEREST

There is no actual or potential conflict of interest.

DATA AVAILABILITY

Data are available with the corresponding author on request.

AUTHOR CONTRIBUTIONS

HG, TD, SS- Survey and manuscript writing. APD-Identification of plants and manuscript writing.

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