Short Communication

**Tropical Tasar Silkworm *Antheraea mylitta* Drury: A Propitious Ecological Indicator of Forest Ecosystems in India**

**Abstract**

Anthropogenic activities have increasingly led to habitat fragmentation and biodiversity loss across ecosystems worldwide, severely impacting species such as Lepidopterans, which act as ecological indicators. Among them, the Tropical Tasar Silkmoth (*Antheraea mylitta* Drury), a unique species endemic to India, which has been deeply woven into the lives and traditions of Scheduled Tribe and Scheduled Caste communities, has suffered heavy population losses as its natural habitats continue to shrink. This study investigates the distribution and genetic diversity of *A. mylitta* ecoraces across Odisha, where seven historical ecoraces have dwindled to five, with signs of local extinction in some regions. Through Cytochrome b as a mitochondrial molecular marker, phylogenetic analyses revealed the gene flow patterns consistent with geographical proximity but also uncovered unexpected genetic similarities, suggesting historical population mixing. Habitat degradation, primarily from mining and deforestation, has severely impacted tasar host plant availability, leading to a decline in the tasar silk production and threatening the wild ecorace survival. The findings highlight the critical need for conservation strategies focusing on habitat protection, genetic monitoring, and sustainable management to preserve *A. mylitta* populations and the forest ecosystems they symbolize.

Keywords: Cytochrome b, Ecoraces, Tasar, Habitat degradation, Mitochondrial marker

**Introduction**

Numerous human-induced activities have significantly contributed to the fragmentation of natural habitats and the subsequent decline of biodiversity across various ecosystems. These disturbances have disrupted ecological balance, isolated species populations, and hindered the natural interactions necessary for the survival and sustainability of diverse life forms on Earth. Lepidopterans, particularly those that function as ecological indicator species and serve as vital monitors of local biodiversity health, have not been spared from the relentless cycle of environmental degradation. Despite their critical role in maintaining ecosystem balance and signalling ecological changes, these species are also increasingly threatened by habitat loss, climate change, pollution, and other anthropogenic pressures. Environmental degradation not only impacts Lepidopteran species but also affects the human communities closely linked to them. For instance, economically important Lepidopterans like silkmoths, particularly wild varieties such as the Tropical Tasar Silkmoth (*Antheraea mylitta* Drury), which are intricately connected to the livelihoods of Scheduled Tribe and Scheduled Caste populations in India, especially in the states of Odisha, Jharkhand, Chhatisgarh, West Bengal etc., as tribal families, primarily women, rear the silkworms in semi-wild conditions to produce Tasar silk, where they have been proven to be milestone for rural and tribal development along with sustainable livelihood (Roychoudhury et al., 2011)

1. **Distribution status of the Tropical Tasar silkmoth *Antheraea mylitta* Drury in India and Odisha:**

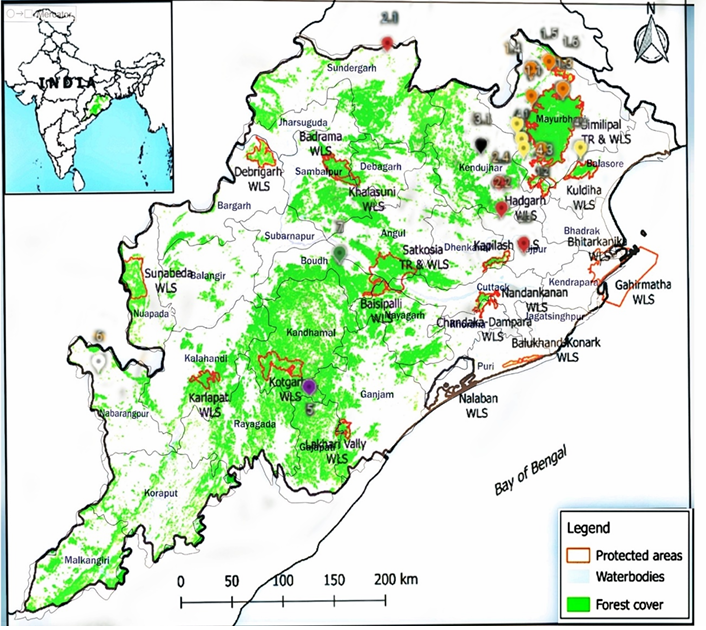
This particular species, which is endemic to India only, been found to be distributed across the states of West Bengal, Bihar, Odisha, Jharkhand, Chhattisgarh, Madhya Pradesh, Uttar Pradesh, Maharashtra, Rajasthan, Andhra Pradesh, Karnataka, Kerala, Himachal Pradesh, Nagaland, Assam, Meghalaya, Manipur, including two of the Union territories, Jammu and Kashmir and Dadar Nagar Haveli (Singh and Srivastava, 1997; Srivastava and Sinha, 2002). Anthropogenic habitat degradation has directly affected the distribution of the distribution of this species, leading to its fragmentation into 44 distinct population pockets, commonly referred to as “Ecoraces” (Hansda et al., 2008 and Reddy 2010). These ecoraces have been found to be phenotypically and behaviourally different from each other. In Odisha, seven ecoraces of tasar silkworms have been previously documented; namely, Modal, Nalia, Sukinda, Jata-Daba, Boudh, Adaba, and Umerkote (Renuka and Shamitha 2015). However, Adaba and Umerkote have not been reported in the past decade, indicating a possible local extinction of these ecoraces from the region. To assess the current geographical distribution of the existing ecoraces in Odisha, we collected and analysed both primary and secondary data regarding their respective ecozones and present-day availability. This information has been consolidated into a comprehensive point map of Odisha, highlighting the key ecozones associated with each major tasar ecorace (Ray and Barala 2023) (refer Fig 1 and Table 1).

1. **Overview of Previous Research on *Antheraea mylitta* and Knowledge Gaps in Odisha Ecoraces**

Previous and recent researches on *Antheraea mylitta* has been predominantly focused on various biological and biochemical aspects of commercially important ecoraces. Studies have explored oviposition behaviour (Soundappan et al., 2021), host plant preference (Thirupam et al., 2023), and the impact of avian predation (Reddy et al., 2020). On the biochemical front, significant attention has been given to the characterisation of midgut microbial symbionts using metagenomic approaches (Baig et al., 2023), histamine neuropeptide localization through immunohistochemistry (Barsagade et al., 2022), and enzymatic as well as protein studies, including cocoonase (Rani et al., 2024) and sericin (Jena et al., 2021), particularly in widely reared ecoraces like Daba, Railey, and Andhra Local. Recent molecular investigations have led to the development of RAPD-SCAR markers (Prabhu et al., 2023), analysis of arylphorin proteins (Dutta et al., 2020), and protocols for DNA isolation and quantification across several commercial strains (Manda et al., 2019). Advanced genomic tools such as Next Generation Sequencing (NGS) have also been applied to ecoraces like Andhra Local and Daba (Renuka & Shamitha, 2021). However, Odisha’s native ecoraces, Modal, Nalia, Jata-Daba, Sukinda, and Boudh, remain largely uncharacterized at the molecular level, despite their high potential in tasar silk productivity. This gap highlights the urgent need for focused genetic and genomic studies on these underrepresented ecoraces.

**Table 1: Ecoraces of Antheraea mylitta Drury found in Odisha and their respective ecozones**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **ECORACE NAME** | **LOCATION NAME** | **LOCATION ON MAP** | **AVERAGE ELEVATION ASL**  **(IN METERS)** | **DISTRICT** |
| **MODAL** C:\Users\BARSHA\Desktop\724-7245648_google-maps-marker-transparent-clipart-jpg-black-and.png | * 1. Gudgudia | 21°52'59"N  86°15'19"E | 379 | Mayurbhanj  (Similpal National Forest) |
| * 1. Sarat | 21°26’39”N  86°20’38”E | 203 | Mayurbhanj  (Similpal National Forest) |
| * 1. Lulung | 21°56’42”N  86°33’20”E | 300 | Mayurbhanj  (Similpal National Forest) |
| * 1. Arjunvilla Village | 22°06’14”N  86°15’24”E | 335 | Mayurbhanj  (Similpal National Forest) |
| * 1. Khadambeda | 22°10’55”N  86°25’34”E | 358 | Mayurbhanj  (Similpal National Forest) |
| * 1. Kitabeda | 22°10'07"N  86°25'16"E | 350 | Mayurbhanj  (Similpal National Forest) |
| **SUKINDA**  C:\Users\BARSHA\Desktop\drop-pin-png-png-image-720561.png | 2.1 Ankurpali | 22°19'21"N  84°53'36"E | 242 | Jajpur |
| 2.2 Sukaran | 20°57'30"N  85°57'57"E | 223 | Jajpur |
| 2.3 Kundal | 20°39'52"N  86°10'28"E | 72 | Jajpur |
| 2.4 Kansa | 21°91'54"N  85°56'53"E | 63 | Jajpur |
| **NALIA**  C:\Users\BARSHA\Desktop\215-2158499_map-marker-icons-transparent-background-location-logo.png | 3. Raghubeda Forest Range | 21°28'52"N  85°46'33"E | 434 | Keonjhar |
| **JATA-DABA**  C:\Users\BARSHA\Desktop\21-214357_pin-google-earth-png.png | 4.1 Thakurmunda | 21°31'24"N  86°09'39"E | 329 | Mayurbhanj |
| 4.2 Kendujuiani | 21°39'03"N  86°07'03"E | 346 | Mayurbhanj |
| 4.3 Mahuldiha | 21°26'55"N  86°10'39"E | 268 | Mayurbhanj |
| 4.4 Kuldiha | 21°27'04"N  86°42'56"E | 91 | Mayurbhanj |
| **ADABA**  Purple Location Pin Png - Free Transparent PNG Clipart ... | 5. Adava | 19°40'21"N  84°10'25"E | 386 | Gajapati |
| **UMERKOTE** C:\Users\BARSHA\Desktop\48-480379_thin-line-google-map-pin-point-location-icon.png | 6. Umerkote/Umarkote | 19°40'21"N  82°12'09"E | 612 | Nabarangpur |
| **BOUDH**  C:\Users\BARSHA\Desktop\196-1963827_landmark-map-marker-green-location-google-maps-landmark.png | 7. Satkosia Range | 20°35'12"N  84°27'06"E | 320 | Boudh |



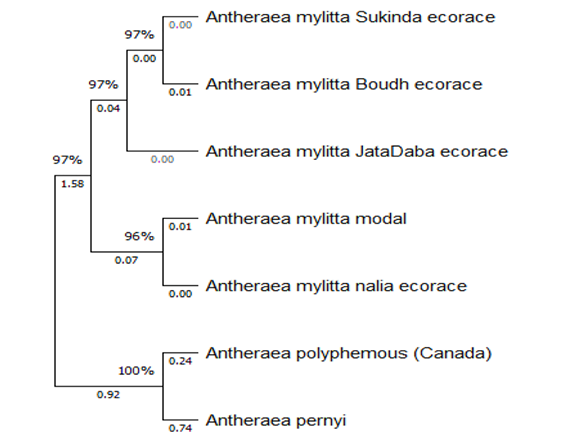
**Fig 1: Geographical distribution of the Ecoarces of Tropical Tasar Silkmoth *Antheraea mylitta* Drury in Odisha (©Ray and Barala, 2024)**

1. **Analysis of Gene Flow among Ecoraces across Distinct Ecozones of Odisha, Using Cytochrome b as a Molecular Marker:**

The mtDNA in most animals evolves 5-10 times faster than nuclear DNA (Brown et al., 1979; Wilson et al., 1985); hence, this provides greater resolution in distinguishing closely related species or populations. The maternal inheritance and lack of recombination in the mitochondrial genes allow for the tracing of matrilineal ancestry without the complexity of recombination seen in nuclear DNA (Avice et al., 1987). Along with that, the high copy number of mitochondrial gene as compared to the nuclear genes makes it easier to isolate and purify high-quality of DNA (Simon et al., 1994) and presence of conserved genes (e.g., 12s, 16s rRNA, COI, COII etc.) and hypervariable regions (like the control region/D-loop), making it suitable for analysing both deep and recent divergences (Boore 1999). The availability of the universal markers for these genes, not only makes it cheaper as compared to specifically designed primers of the nuclear genes, but also gives scope to Phylogeny and population-level studies (Hajibabaei et al., 2006; Yang and Li 2008). The mtDNA in animals is relatively small, approximately 16.5 kb in length, and notably lacks introns. Its compact, circular structure and conserved gene order make it particularly easy to amplify, sequence, and perform comparative genomic analysis (Anderson et al., 1981; Cameron, 2014). These structural and molecular features have facilitated the widespread application of mtDNA in evolutionary and phylogenetic studies. In insects, especially within Lepidopterans, the mitochondrial markers such as COI, Cyt b, and 16S rRNA have been extensively employed to resolve interspecific and intraspecific relationships, assess genetic diversity, and to detect cryptic speciation (Hebert et al., 2004). The use of mtDNA thus provides a robust framework for understanding evolutionary processes and species boundaries in insect taxa.

Hence to understand the dwindling population of the native ecoraces of the *A. mylitta* of Odisha and their phylogeny a study was conducted by Ray and Barala in 2024, using Cyt b as a mitochondrial molecular marker to estimate the phylogeny among the ecoraces of *Antheraea mylitta* of Odisha and across other Lepidopteran species as well. A total of around 50 healthy cocoons were randomly sampled from all the five major ecozones of Odisha (Modal-Similpal Biosphere Reserve; Nalia- Keonjhar; Sukinda- Mangalpur,Jajpur; JataDaba-Thakurmunda,Mayurbhanj; and Boudh-Patora Dam, Nuapada) across their respective ecoraces (Ref. Table 1). The pupae of the samples were extracted from the cocoons and subjected to mitochondrial DNA isolation. The Cyt b gene was then amplified through PCR using Cytb\_mcb 398 (TACCATGAGGACAAATATCATTCTG) and Cytb\_mcb 869 (CCTCCTAGTTTGTTAGGGATTGATCG) primers (Ray et al., 2024). The sequences obtained from the amplicon were subjected to Neighbour-Joining analysis in MEGA 11 software, as this particular method is quite helpful while working on the Lepidoptera phylogeny using mitochondrial markers such as Cyt b, or COI (which are widely used in Lepidopteran study) Neighbour-Joining is particularly suitable for building initial trees to explore species boundaries, genetic divergence, or cluster species groups before applying more complex methods like ML or Bayesian inference. The Neighbour joining tree using Kimura-2 Parameters with 1000 robust bootstraps, yielded high bootstrap values (96%. 97%, 100%), suggesting strong confidence in the grouping of closely related ecoraces like Sukinda, Boudh, and JataDaba, as well as species like *A. pernyi* and *A. polyphemous.* Genetic distance values ranging from 0.00 to 0.92 reflect varying degrees of sequence divergence, with minimal differences among *A. mylitta ecoraces* and greater divergence between *A. mylitta* and other *Antheraea* outgroup species.

The Sukinda and Boudh ecorace cluster with the almost identical sequence (0.00) indicates towards the very recent divergence or minimal evolutionary distance. Similarly, pairwise distance between Boudh and JataDaba (0.01) very low amount divergence suggests genetic similarity and likely gene flow or recent separation. The Modal and Nalia cluster with Slightly more divergence with 0.07 pairwise distance, may indicate a little more ecological or geographical isolation as compared to other clusters. As for Interspecific clusters, 0.24 Pairwise distance between *A. mylitta* clade and *A. polyphemous* indicates moderate divergence, suggesting species-level differentiation.



**Fig 2: Interspecific Phylogenetic tree using Neighbour Joining Method using Kimura-2 Parameters in MEGA 11**

(The Percentage on the lines indicates Bootstrap Support, whereas the Numerical Values on Branches indicate the Genetic Distance)

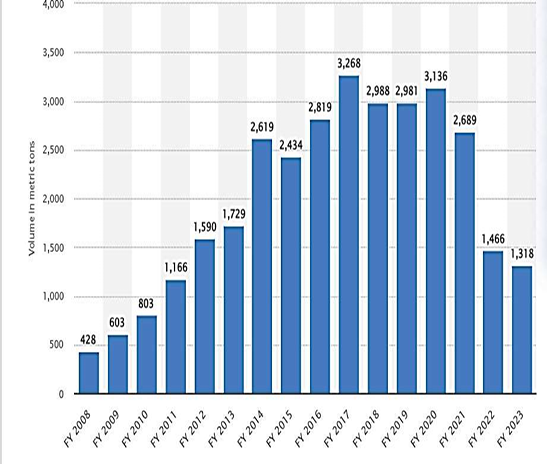
**(Ray et al. 2024)**

The genetic patterns largely correspond with geographical proximity, i.e, ecoraces from closer ecozones, like Nalia and Modal in the Similipal Biosphere Reserve, exhibit higher

gene flow than those from distant regions, such as Boudh from Sunabeda Forest Range. An anomaly was observed between Jata-Daba (native to Similipal) and Sukinda (from Jajpur), which showed unexpectedly high genetic similarity. This may indicate towards the historical mixing of populations or misclassification of one as a distinct ecorace. Interspecific phylogenetic analysis using MEGA 11 showed that Modal and Nalia clustered with *Antheraea pernyi* (China), Sukinda with *A. polyphemus* (USA), and Boudh with *Saturnia pavonia* (Europe). These outgroup species share ecological similarities with *A. mylitta*, such as tropical or subtropical habitats and polyphagous feeding behaviour. Host plant diversity, like Sal, Arjun, Asan, and Oak, might have some influence on the genetic divergence within *A. mylitta* ecoraces. Similarly, outgroups that have been found in the phylogeny also feed on a wide range of plants, including Oak, Maple, Birch, and Willow, further supporting ecological and genetic parallels between ecoraces of *A. mylitta* and other out groups. As demonstrated by Safran and Nosil (2012), populations feeding on similar host plants tend to show ecological convergence, possibly explaining the observed phylogenetic clustering in the following. The Jata-Daba and Sukinda ecorace’s ecozones, Thakurmunda and Sukindagarh of Jajpur, respectively been revealed as “Hybrid Zones” of the ecoraces as the intermixing of the ecorace’s population is higher in the given regions owing to the wild nature of the insect (unlike other domesticated silkmoths like *Bombyx* or *Philosamia*) and mixing of the ecoraces by the rearers for better quality of cocoon. However, drawing absolute conclusions about gene flow between the ecoraces based solely on a single mitochondrial marker (Cyt b) is insufficient. Empirical validation would require the inclusion of additional primary markers, such as COI or COII, in future studies (Ray et al., 2024).

**Habitat degradation, Tasar silkmoth ecoraces and Biodiversity:**

Unlike domesticated silk-producing species like *Bombyx mori* (Mulberry silk), which can be reared indoors, the tropical tasar silkmoth *Antheraea mylitta* Drury is entirely wild. It depends on forest ecosystems to complete its life cycle, earning it the name “forest insect”. This species primarily feeds on Sal (*Shorea robusta*), Arjun (*Terminalia arjuna*), and Asan (*Terminalia tomentosa*), which together form the core of its natural habitat. Notably, Sal trees alone constitute about 86.9% of the total tasar flora in India, while Arjun and Asan collectively make up the remaining 13.1% (Lokesh et al., 2016), predominantly within the tropical moist and dry deciduous forests of the Indian Tasar belt.



**Fig 3: Statistical Data representation on the Tasar Silk Production from 2008-2023**

**Table 2: Production of tasar silk**

**Source: Ministry of textiles, Govt. of India**

|  |  |
| --- | --- |
| Financial year | Tasar host Plantation (in Ha) |
| 2019-20 | 1812 |
| 2020-21 | 1231 |
| 2021-22 | 660 |

In recent years, there has been a significant decline in both total forest cover and the area under tasar host plant plantations, leading to a corresponding drop in tasar silk production. These wild tasar ecoraces do not only play an important role economically but ecologically as well. The decline in silk production serves as a clear indicator that tasar host plant habitats are increasingly under threat across the country. It has also been observed that the tasar belt regions of India overlap significantly with major mining zones across several states. Activities such as over-mining and infrastructure development have caused substantial anthropogenic disturbances, adversely impacting forest ecosystems. These disruptions are increasingly reflected in the declining populations and diversity of *Antheraea mylitta* ecoraces.

Among the five wild ecoraces currently viable in Odisha, the Modal ecorace shows the highest productivity, even though it is univoltine. This success can be largely attributed to the relatively undisturbed forest cover within the Similipal Biosphere Reserve. In contrast, ecoraces like Nalia (endemic to Keonjhar) and Sukinda (endemic to Jajpur) are facing significant challenges due to intense mining activities near their natural tasar habitats. As a result, over the past few years, tasar silk production from these bivoltine and trivoltine ecoraces has remained consistently low. Additionally, the phylogenetic analysis using the Neighbor-Joining (N-J) method revealed that the Jata-Daba population is of hybrid origin, thereby challenging and effectively nullifying its recognition as a distinct ecorace (Ray et al. 2024). Similarly, the Boudh ecorace is now found only in the Sunabeda forest range, which raises concerns about its validity as a separate ecorace. The declining population, reduced productivity, and poor-quality cocoon yield are alarming indicators, pointing toward the possible extinction of this ecorace in the future.

**Conclusion:**

The presence of multiple “ecoraces” of *Antheraea mylitta* Drury, now fragmented into 44 isolated pocket populations, is a significant cause for concern. These smaller, scattered populations are inherently more susceptible to extinction than a single, large, and well-distributed population. Furthermore, the polyphyletic nature of the species suggests a potential for future speciation, provided that the species survives long enough and anthropogenic disturbances in these regions are mitigated in time. Along with that, since this species is an integrated part of the forest ecosystem, the population’s behaviour is an indication of the native forest ecosystem as well, for which it has gained its name as “Ecological indicator”. Therefore, along with the integration of improved Tasar Silkworm Rearing Technologies for better commercial rearing (Gedam et al., 2023), monitoring key aspects such as population dynamics, productivity, and voltinism of these ecoraces is crucial. It will enable conservationists to develop more effective strategies, not only for the preservation of *Antheraea mylitta* itself and the population that depends on it, but also for the protection and sustainability of the entire forest ecosystem.

Conflict of Interest: There is No Conflict of Interest between the Authors

Disclaimer (Artificial intelligence): Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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