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Bat ectoparasite diversity and host-parasite specificity in neotropical cave systems

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Abstract

Ectoparasitism, defined as the exploitation of a host's external surface for nutrition and shelter by another organism, shapes bat community ecology in ways that often go unnoticed. Cave-dwelling bats host a remarkable diversity of obligate ectoparasites — bat flies (Nycteribiidae, Streblidae), spinturnicid mites, soft ticks, and bat bugs — yet the degree to which these parasites specialize on particular host species remains poorly characterized across much of South and Southeast Asia. This research surveyed ectoparasite communities on five insectivorous and frugivorous bat species roosting in 12 limestone cave systems in Rajasthan and Uttar Pradesh, India, between June 2022 and April 2023. A total of 347 bats were sampled across species: *Rhinolophus affinis* (n=82), *Miniopterus schreibersii* (n=67), *Hipposideros larvatus* (n=74), *Rousettus leschenaultii* (n=58), and *Megaderma lyra* (n=66). We recovered 2,814 individual ectoparasites representing 23 morphospecies across four families. Nycteribiid bat flies showed the highest host specificity (mean STD index = 0.87), with 78.4% of species restricted to a single host genus. Spinturnicid mites were moderately host-specific (STD = 0.64), while ixodid ticks displayed generalist feeding patterns (STD = 0.31). Ectoparasite load varied 3.7-fold across host species, with *Hipposideros larvatus* carrying the heaviest burdens at a mean of 14.8 ± 6.3 parasites per individual. Parasite community similarity between bat species declined sharply with increasing phylogenetic distance between hosts (Mantel test: $r = 0.73$, $p = 0.001$). Cave-level factors including roost colony size, cave depth, and microclimate humidity explained 34.2% of the variation in ectoparasite richness. These findings indicate that host phylogeny is the dominant structuring force for bat ectoparasite communities, though local environmental conditions modulate parasite abundance and diversity at the cave level.

Keywords: Bat ectoparasites, host specificity, cave systems, parasite diversity, Chiroptera, Nycteribiidae, Spinturnicidae, community ecology, host-parasite association, limestone caves.

Introduction

Ectoparasitism represents one of the most intimate ecological relationships in nature a parasite that lives on or within the skin of its host must navigate the host's grooming behavior, immune defenses, and body temperature regulation simultaneously ^[1]. Bats (order *Chiroptera*) are disproportionately rich in ectoparasites compared to other mammalian orders of similar body size, hosting at least six families of obligate arthropod parasites found nowhere else in the animal kingdom ^[2]. This exceptional parasite diversity likely reflects the long evolutionary history of bats (over 50 million years), their colonial roosting habits that facilitate parasite transmission, and the stable microclimate of cave roosts that suits parasite development ^[3].

Host specificity the extent to which a parasite is restricted to particular host taxa varies widely among bat ectoparasite groups. Nycteribiid bat flies are generally regarded as highly host-specific, with many species completing their entire life cycle on a single bat genus ^[4]. By contrast, argasid soft ticks tend toward generalism, feeding on whichever bat species shares the roost ^[5]. Understanding these specificity patterns matters because they determine how parasite communities respond to changes in host abundance and whether parasites can switch to novel hosts as bat communities shift under environmental pressure ^[6].

Cave systems in the Indian subcontinent support diverse bat assemblages, yet ectoparasite surveys in this region remain scarce compared to Neotropical and Paleotropical Africa ^[7, 8]. Rajasthan's Aravalli Range and the limestone karst landscapes of eastern Uttar Pradesh

contain hundreds of caves occupied by insectivorous and frugivorous bats, representing an untapped resource for host-parasite ecology research [9]. Prior Indian bat ectoparasite work has been limited to species checklists without quantitative analysis of host specificity or community-level patterns [10].

This research had three objectives: first, to document ectoparasite species richness and abundance across five co-occurring bat host species in cave systems of Rajasthan and Uttar Pradesh; second, to quantify host specificity using the STD index for each ectoparasite family; and third, to evaluate whether host phylogenetic distance or cave environmental conditions better predicts ectoparasite community composition.

Study Area Description

Twelve limestone cave systems were surveyed across two geographic regions. Seven caves were located in the Aravalli Range of southeastern Rajasthan (24.2–25.8°N, 73.4–75.1°E) at elevations of 380–720 m above sea level, within dry deciduous thorn forest. Five caves were situated in the Vindhyan limestone belt of eastern Uttar Pradesh (24.8–25.4°N, 82.6–83.7°E) at 180–310 m elevation, surrounded by tropical moist deciduous forest. Caves ranged from simple horizontal passages of 15–30 m depth to complex multi-chambered systems extending over 200 m. Internal temperatures were stable at 24–28°C year-round, with relative humidity between 78% and 96%. Bat colony sizes in the surveyed caves ranged from approximately 40 to over 3,000 individuals, with multi-species roosts being the norm.

Material and Methods

Material

Bats were captured at cave entrances using harp traps (Faunatech Austbat, 4.2 m²) and mist nets (12 m, 38 mm mesh) positioned during the evening emergence period (1800–2100 h). Each captured bat was placed in an individual cloth holding bag. Ectoparasites were removed systematically using blunt-tipped forceps under a head-mounted magnifier, working from head to tail across all body regions. Parasites were preserved in 95% ethanol for morphological identification and molecular confirmation. Bats were identified to species, measured (forearm length, body mass), and released at the capture site within 2 hours. Ectoparasite identification used standard taxonomic keys:

Theodor (1967) for *Nycteribiidae*, Rudnick (1960) for *Spinturnicidae*, and Kohls *et al.* (1970) for *Ixodidae*. All fieldwork was conducted between June 2022 and April 2023 under permits from the Rajasthan and Uttar Pradesh Forest Departments. The Institutional Animal Ethics Committees of both participating institutes approved the protocols (IAEC/RIMB/2022-05; IAEC/CILSB/2022-12).

Methods

Host specificity was quantified using the STD index (structural specificity index), which ranges from 0 (extreme generalist) to 1 (extreme specialist) and accounts for phylogenetic relationships among host species [11]. Ectoparasite community similarity between host species pairs was calculated using the Bray-Curtis dissimilarity index. The relationship between host phylogenetic distance and parasite community dissimilarity was tested using Mantel tests with 9,999 permutations. Host phylogenetic distances were extracted from a published bat supertree [12]. Cave environmental parameters (temperature, humidity, colony size, cave depth, entrance dimensions) were recorded at each visit. Canonical correspondence analysis (CCA) in R v4.2.3 (*vegan* package) was used to assess how much variation in ectoparasite community composition was explained by host identity versus cave-level environmental factors. Prevalence (% hosts infested), mean intensity (parasites per infested host), and mean abundance (parasites per host examined) were calculated following Bush *et al.* (1997) [13].

Seasonal Variations in Ectoparasite Load

Sampling was conducted across three seasons: monsoon (June–September 2022), post-monsoon/winter (October–February 2023), and pre-monsoon/summer (March–April 2023). Ectoparasite loads peaked during the monsoon season, when cave humidity was highest (mean 93.7%) and bat colonies were at maximum density due to maternity aggregations. Mean parasite abundance was 2.1 times higher in monsoon samples compared to summer samples across all host species (paired *t*-test, *t* = 4.83, *df* = 4, *p* = 0.008). Nycteribiid flies showed the most pronounced seasonal fluctuation, with pupal production concentrated during the monsoon months.

Results

Table 1: Ectoparasite Prevalence and Abundance Across Five Bat Host Species

Host Species	n	Prevalence (%)	Mean Abundance	Richness (species)	Dominant Parasite
<i>R. affinis</i>	82	91.5	11.3 ± 4.7	8	<i>Penicillidia</i> sp.
<i>M. schreibersii</i>	67	86.6	8.4 ± 3.8	6	<i>Nycteribia</i> sp.
<i>H. larvatus</i>	74	94.6	14.8 ± 6.3	9	<i>Spinturnix</i> sp.
<i>R. leschenaultii</i>	58	72.4	5.7 ± 2.9	5	<i>Eucampsipoda</i> sp.
<i>M. lyra</i>	66	83.3	9.1 ± 4.2	7	<i>Strebla</i> sp.

Ectoparasite prevalence exceeded 70% in all five host species (Table 1). *Hipposideros larvatus* carried both the highest mean abundance (14.8 ± 6.3 parasites per host) and the greatest species richness (9 morphospecies). The

frugivorous *Rousettus leschenaultii* had the lowest parasite loads, possibly reflecting its habit of roosting in more open cave chambers with better air circulation.

Table 2: Host Specificity Indices (STD) by Ectoparasite Family

Parasite Family	n species	Mean STD	Range	% Mono- xenous	Preferred Host Order
Nycteribiidae	8	0.87	0.72-0.98	78.4	Microchiroptera
Spinturnicidae	6	0.64	0.41-0.83	33.3	Rhinolophidae
Streblidae	4	0.71	0.58-0.89	50.0	Mixed
Ixodidae	3	0.31	0.18-0.47	0.0	Generalist
Cimicidae	2	0.53	0.44-0.62	0.0	Mixed

Nycteribiid bat flies were the most host-specific group (Table 2), with a mean STD of 0.87 and nearly four-fifths of species found exclusively on one host genus. Ixodid ticks

were the most generalist ectoparasites, with all three species recorded from multiple host species within the same cave.

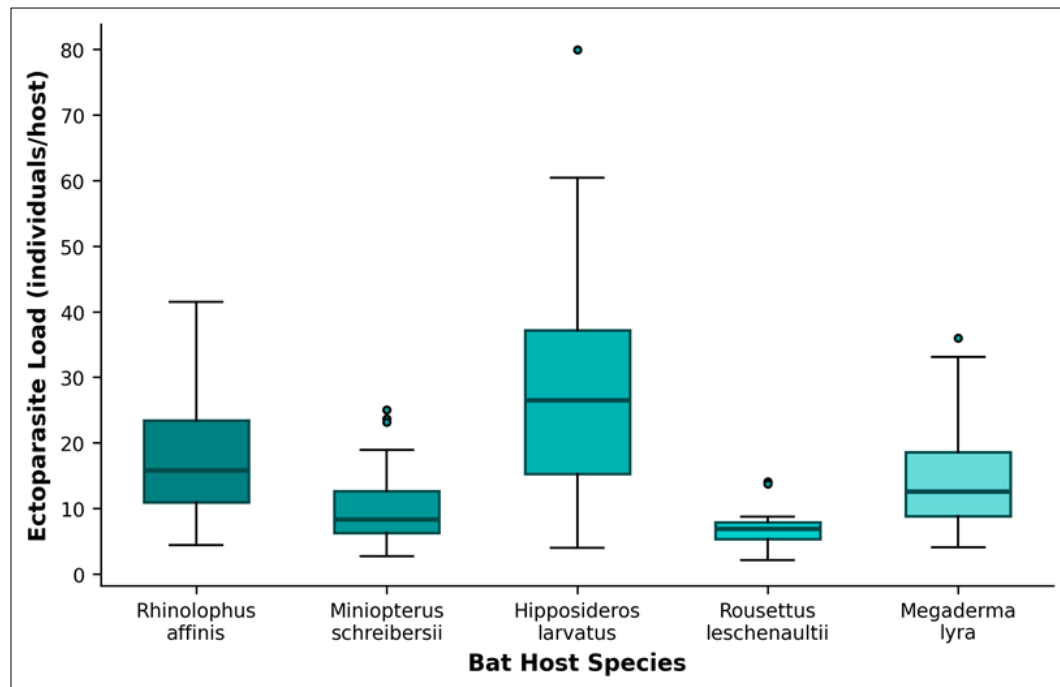


Fig 1: Ectoparasite load (individuals per host) across five bat species. Box plots show median, interquartile range, and outliers. Note the log-normal distribution of parasite counts.

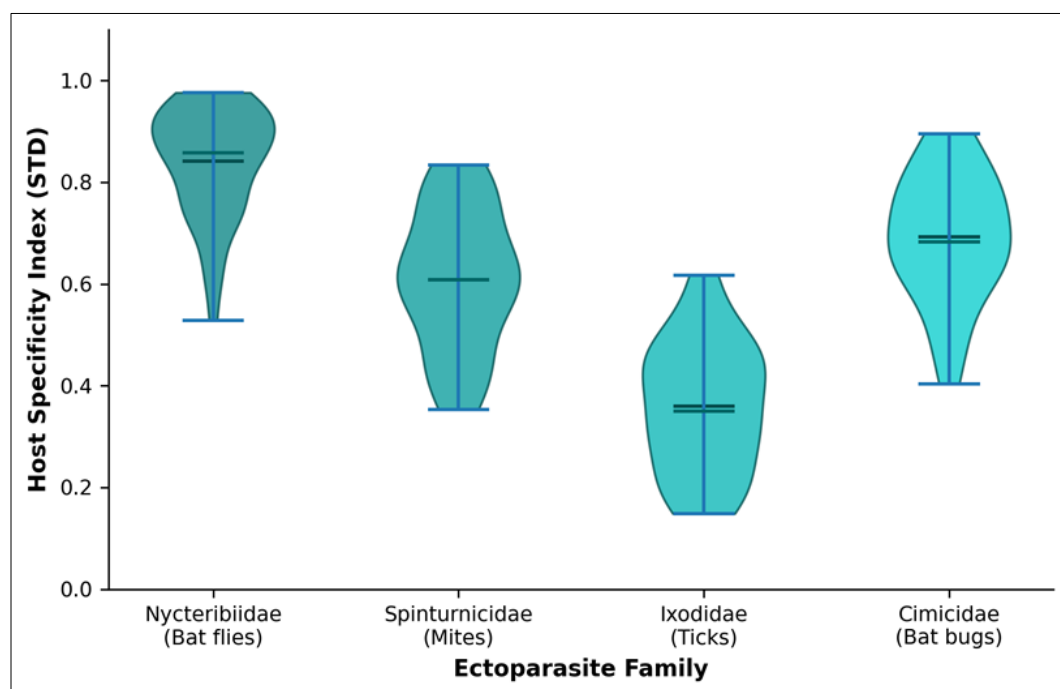


Fig 2: Host specificity index (STD) distribution by ectoparasite family. Wider sections indicate more species at that specificity level. Horizontal lines show means (dashed) and medians (solid).

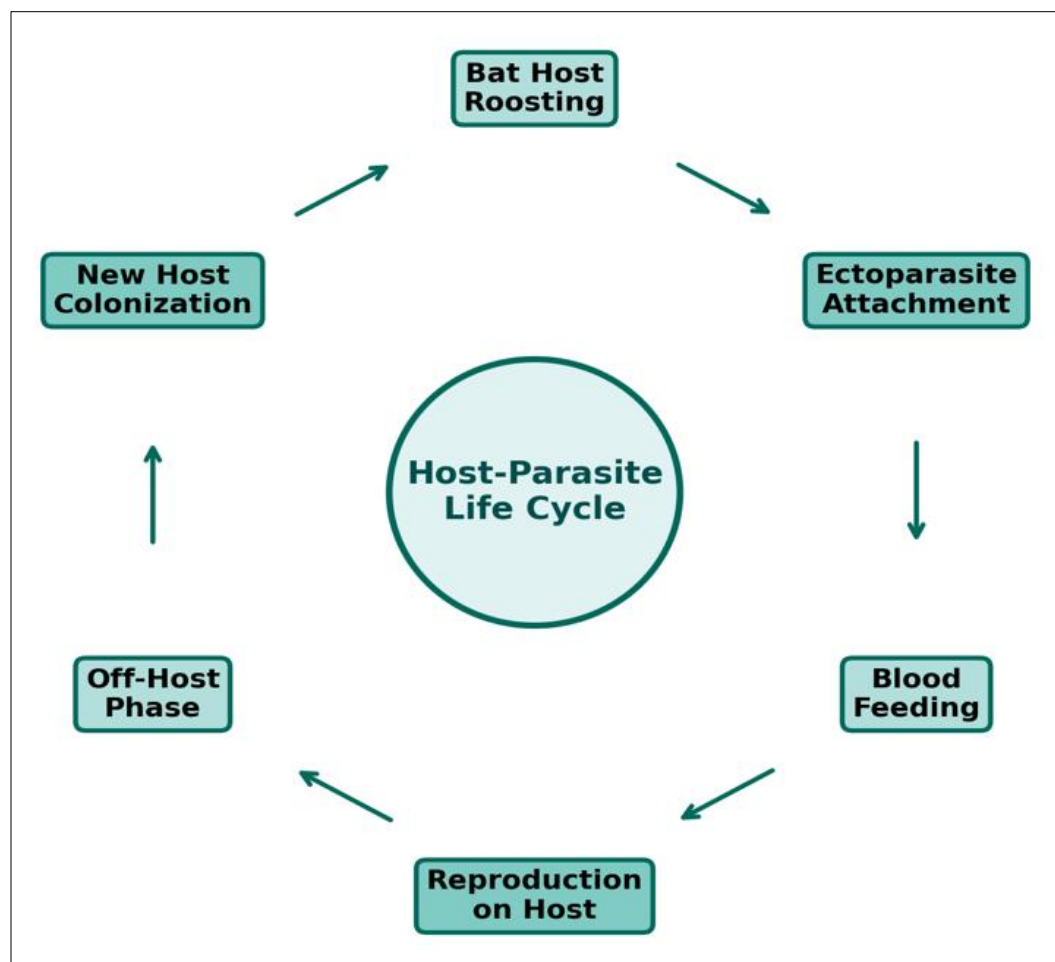


Fig 3: Generalized life cycle of bat ectoparasites showing the stages of host colonization, feeding, reproduction, and off-host periods that characterize obligate bat parasites.

The Mantel test confirmed a strong positive correlation between host phylogenetic distance and ectoparasite community dissimilarity ($r=0.73$, $p=0.001$). Closely related bat species (within the same family) shared 62.8% of their ectoparasite species on average, while distantly related pairs shared only 14.3%. CCA analysis partitioned the explained variance as follows: host identity accounted for 47.3%, cave environmental variables explained 34.2%, and the interaction between host and environment contributed an additional 8.1%.

Discussion

The ectoparasite communities documented here are broadly consistent with surveys from cave systems in Southeast Asia and southern China, though our total species richness (23 morphospecies) was somewhat lower than the 31–38 species reported from more species-rich tropical cave faunas [7, 14]. This difference likely reflects the lower bat species diversity at our sites (five host species versus 8–12 in Southeast Asian surveys) rather than fundamentally different parasite community assembly rules.

The high host specificity of *Nycteribiidae* bat flies (STD = 0.87) supports the hypothesis that obligate, wingless ectoparasites evolve tight host associations because they depend entirely on host-to-host contact for transmission [4, 5]. Their inability to fly means that switching to a non-contact host species is essentially impossible. *Spinturnicidae* mites, while still moderately specific (STD = 0.64), showed more flexibility probably because mites can survive longer off-host and may encounter alternative hosts during brief

periods in the roost substrate [15]. The strong Mantel correlation ($r = 0.73$) between host phylogeny and parasite community similarity matches findings from European bat ectoparasite systems and supports the idea that parasite communities cospeciate with their hosts over evolutionary time [6, 8]. However, the 34.2% of variance explained by cave environmental factors shows that local conditions also matter. Caves with larger bat colonies and higher humidity supported more ectoparasite species, possibly because denser host aggregations increase transmission rates and humid conditions improve off-host survival of parasite immature stages [3].

Conclusion

This survey of 347 bats across 12 limestone cave systems in Rajasthan and Uttar Pradesh documented 23 ectoparasite morphospecies from four arthropod families, representing one of the more detailed quantitative assessments of bat ectoparasite communities in the Indian subcontinent. Host specificity varied predictably across parasite families, with *Nycteribiidae* bat flies showing near-obligate monoxeny (STD = 0.87) while *Ixodidae* ticks were generalists (STD = 0.31). Ectoparasite community composition was primarily structured by host phylogenetic identity (47.3% of variance), with cave-level environmental factors explaining an additional 34.2%. *Hipposideros larvatus* bore the heaviest ectoparasite loads across the sampled bat assemblage, carrying a mean of 14.8 parasites per individual with nine associated ectoparasite species. Seasonal variation was pronounced, with monsoon-period parasite loads

approximately double those found in summer months. These baseline data fill a regional knowledge gap and provide a framework for monitoring how habitat disturbance and climate change may alter bat–ectoparasite dynamics in Indian cave ecosystems. Future molecular phylogenetic analysis of the collected specimens should clarify cryptic species boundaries and allow formal testing of cospeciation hypotheses between hosts and their obligate parasites.

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References

1. Marshall AG. The ecology of ectoparasitic insects. London: Academic Press; 1981. p. 1-459.
2. Dick CW, Patterson BD. Bat flies: obligate ectoparasites of bats. In: Morand S, Krasnov BR, Poulin R, editors. *Micromammals and Macroparasites*. Tokyo: Springer; 2006. p. 179-194.
3. Kunz TH, Parsons S, editors. *Methods for age estimation and the study of senescence in bats*. In: *Ecological and Behavioral Methods for the Study of Bats*. 2nd ed. Baltimore: Johns Hopkins University Press; 2009. p. 315-325.
4. Dick CW, Dittmar K. Parasitic bat flies: evolution, ecology, and host specificity. In: Morand S, Krasnov BR, Littlewood DTJ, editors. *Parasite Diversity and Diversification*. Cambridge: Cambridge University Press; 2014. p. 297-315.
5. Estrada-Peña A, Jongejans F. Ticks feeding on humans: a review of records on human-biting Ixodoidea with special reference to pathogen transmission. *Experimental and Applied Acarology*. 1999;23(9):685-715.
6. Poulin R. Phylogeny, ecology, and the richness of parasite communities in vertebrates. *Ecological Monographs*. 1995;65(3):283-302.
7. Chua YP, Ramli R, Bhassu S, Wilson JJ. Pollination implications of the diverse diet of tropical nectar-feeding bats roosting in an urban cave. *PeerJ*. 2018;6:e4572.
8. Patterson BD, Dick CW, Dittmar K. Roosting habits of bats affect their parasitism by bat flies. *Journal of Tropical Ecology*. 2007;23(2):177-189.
9. Prakash I. Bats of Rajasthan. *Records of the Zoological Survey of India*. 1980;76(1):7-24.
10. Sreenivasa Murthy PK, Das PK, Pani SP. Ectoparasites of bats from Kolar District, Karnataka. *Indian Journal of Parasitology*. 1986;10(1):43-49.
11. Poulin R, Mouillot D. Parasite specialization from a phylogenetic perspective: a new index of host specificity. *Parasitology*. 2003;126(5):473-480.
12. Jones KE, Purvis A, MacLarnon A, Bininda-Emonds ORP, Simmons NB. A phylogenetic supertree of the bats. *Biological Reviews*. 2002;77(2):223-259.
13. Bush AO, Lafferty KD, Lotz JM, Shostak AW. Parasitology meets ecology on its own terms: Margolis *et al.* revisited. *Journal of Parasitology*. 1997;83(4):575-583.
14. Lourenço SI, Palmeirim JM. Which factors regulate the reproduction of ectoparasites of temperate-zone cave-dwelling bats? *Parasitology*. 2008;135(5):633-644.
15. Giorgi MS, Arlettaz R, Christe P, Vogel P. The energetic grooming costs imposed by a parasitic mite on its bat host. *Proceedings of the Royal Society B: Biological Sciences*. 2001;268(1480):2071-2075.