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ENVIRONMENTAL TEMPERATURE AND THE GUT MICROBIOME IN BATS: CURRENT EVIDENCE AND POTENTIAL IMPLICATIONS FOR HOST HEALTH AND INFECTION SUSCEPTIBILITY: A REVIEW

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Abstract

The physiology and gut microbiome of bats could be affected by environmental temperatures but how these factors contribute to susceptibility to infection remains unknown. This narrative review will discuss the direct evidence from bats as well as seasonal studies, hibernation studies and temperature studies in other animals. The only direct evidence available is from a field comparison which revealed no differences in overall community composition of the gut microbiomes from hibernating least horseshoe bats in different winter roosting sites, but did show correlation between winter roost temperature and gut microbiome alpha diversity. Other studies of bats report seasonality and physiological state changes in the microbiome that are also likely a consequence of changes in diet, fasting and host physiology. Individual studies have also been used to correlate bat gut microbiome patterns to immune response or infection. Bat microbiota have also influenced how mice respond to influenza, but this does not imply an effect in bats. For comparative context, experiments in other mammals have demonstrated that temperature effects on microbial communities and host physiology. Collectively, the current evidence is consistent with the possibility of a relationship between environmental temperature, bat gut microbiome and health; however, there is no evidence of any causal pathway nor proof that microbiome changes in response to environmental temperature affect infection susceptibility. Research to quantify microbiome function, immune responses and pathogen levels and bat health is required.

INTRODUCTION

Bats live in diverse habitats and have a variety of feeding niches such as insect eaters, fruit or nectar eaters. They also have different communities of gut microbiota depending on species, place and feed (Banskar et al., 2016; Carrillo-Araujo et al., 2015; Dai et al., 2024; Lutz et al., 2019). The variation is important when discussing temperature, as other aspects of a bat's life cycle like species and food could also be linked to its gut microbiome.

Environmental temperature fluctuates between roosts, within roosts and between seasons. These shifts can correspond to alterations in the behavior, diet and metabolism of the bats. Not all bats enter torpor or hibernation state in which

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body temperature and metabolic rate drops (Hosken & Withers, 1997; Liu et al., 2023; Xiao et al., 2019). Other seasonal variations in bat microbiomes have been noted as well, between active and hibernating Chinese horseshoe bats, though in these cases, it is difficult to distinguish the effect of the temperature change from the change in diet and physiology (Shao et al., 2026; Xiao et al., 2019).

There's little direct evidence that there's a connection between the environment's temperature and the bat gut microbiome. In the least horseshoe bat, *Rhinolophus pusillus*, a field study reported a significant association between the alpha diversity and the diversity of the gut microbiota and the temperature of the roosting site but no difference was reported within the overall microbial composition between the two sites (Liu et al., 2023). Current research on other bat species supports this idea, as diet has been linked to microbiome differences. Seasonal changes in diet were associated with shifts in the gut microbial community of the great evening bat (*La io*) as an example (Gong et al., 2021). Therefore, any temperature-related difference between seasons or roosts may not be a difference expected.

For comparative purposes, studies in mice are included, which showed that the gut microbial communities of mice differed between housing conditions and season-like temperature. However, in one experiment, day length and temperature varied simultaneously and cannot be separated (Chevalier et al., 2015; Hylander et al., 2023; Matsumoto et al., 2023). These results suggest a temperature microbiome relationship, but do not prove it to be the same effect in bats.

The question might have significance to bat health since research on gut microbiome patterns has been associated with immune response and infection in bats. Egyptian fruit bats (*Rousettus aegyptiacus*) were challenged with an immune stimulus (lipopolysaccharide [LPS]) followed by changes in the microbiome that were correlated with immune measures (Berman et al., 2023). For Jamaican fruit bats (*Artibeus jamaicensis*), the age-dependent variation in the gut microbial communities was linked to astrovirus infection (Wasimuddin et al., 2018). In these studies, the microbiome changes that are associated with temperature do not indicate that that changes the susceptibility to infection.

The purpose of this review is to summarize the current understanding of environmental temperature, as well as findings from direct bat studies and from other animal models relevant to the bat gut microbiome. It acknowledges a possible connection between changes in the bat microbiome due to temperature and bat health or susceptibility to infection, but that this is not yet proven.

Methodology

This narrative review basically summarizes the research performed on environmental temperature, the bat gut microbiome and potential implications for bat health and susceptibility to infection. Articles were identified by a search of PubMed and PubMed Central as well as the journals' websites and reference lists. When they looked at microbial and temperature results in other animals as well, it was helpful to give them some perspective on the scarce direct proof in bats.

The studies were divided into four research areas: temperature-related studies in bats; seasonal & hibernation-related studies; bat microbiome studies on infections or immune response; comparative studies in other animals. Due to the variations in species, methods and results, the results were compared narratively and not statistically. Evidence of cause and effect was separated from associations and microbial functions were described as predicted activity, rather than measured (Baethge et al., 2019; Liu et al., 2023; Xiao et al., 2019).

Biological Context: Environmental Temperature, Bats Physiology and the Gut Microbiome

Environmental temperature is the temperature of the surroundings, such as the surroundings of a bat's roost, not his own body temperature. Some bats can enter the torpor or hibernation state (body temperature and metabolism drop). The various responses differ between species and

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physiological condition, and it should not be assumed that all bats hibernate (Hosken & Withers, 1997; Sun et al., 2020).

The gut physiology is impacted by temperature. The gut contractions of big brown bats (*Eptesicus fuscus*) increased or decreased with an increase or decrease in the temperature of the gut tissue. This was an in vitro experiment: this demonstrated a response to the separated tissue but not a change in digestion in a living bat (Studier et al., 1976). Hibernation also means fasting and metabolic changes which affect the conditions of the gut. Gut gene expression was found to be different between torpor, arousal and active state in greater horseshoe bats (*Rhinolophus ferrumequinum*) (Sun et al., 2020).

In this instance, the gut microbiome refers to the group of microbes that live in the gut. Variation in these communities has been accounted for at the species and feeding niche level in bat studies. For instance, microbial community compositions were shown to differ between Phyllostomid bat species and between their feeding strategies, whereas a bacterial community was found to be shared between species of different feeding strategies, the authors concluded as possible dietary overlap (Banskar et al., 2016; Carrillo-Araujo et al., 2015). A comparative analysis of bats reanalyzing published sequencing data also found differences in community

structure, but only with regard to terrestrial and aquatic food resources (Corduneanu et al., 2023). In migrating bats, some core microbial features remained stable even though particular bacterial groups varied (Víquez-R et al., 2021). These studies report factors that have the potential to impact bat gut microbiomes, but do not test the effects of temperature.

Research in other animals provides comparative context. The gut microbiome composition and/or function are reportedly different depending on the temperature in mice, gerbils, and voles Chevalier et al., 2015; Khakisahneh et al., 2020; Matsumoto et al., 2023; Zhang et al., 2018; Zię tak et al., 2016). There have also been reports of differences in gastrointestinal motility and microorganisms in the gut between different temperatures in mice (Han et al., 2024; Hylander et al., 2023). Studies of hibernating ground squirrels are used to discuss alterations of gut-microbial community and gut-defense response during hibernation (Carey et al., 2013; Dill-McFarland et al., 2014). These results indicate the importance of temperature and physiology in the context of this review but do not provide any evidence of similar responses on bats. The direct comparison of bat temperature is discussed in the next section. Overall microbial community composition did not differ among the roost sites in least horseshoe bat (*Rhinolophus pusillus*). Relative abundance of gut microbial communities α-diversity was however, significantly different between roost sites (Liu et al., 2023). The microbiome of greater horseshoe bats, common noctule bats and Chinese horseshoe bats is also found to be different at various stages of the season or under physiological conditions (Popov et al., 2025; Shao et al., 2026; Xiao et al., 2019). The observations do not indicate that the changes in the microbiomes were caused by just the temperature or that the changes in the microbiomes affected the health of the bats or their susceptibility to infection.

Below is a revised version of the section. We have maintained a separate analysis of direct measurements of bat body temperature and provided supportive evidence of other species in seasonal and hibernation studies. Some of the other added bat studies are on diet or migration instead of temperature, so we have just used them as explanations as to why the seasonal microbiome patterns cannot be explained by temperature alone.

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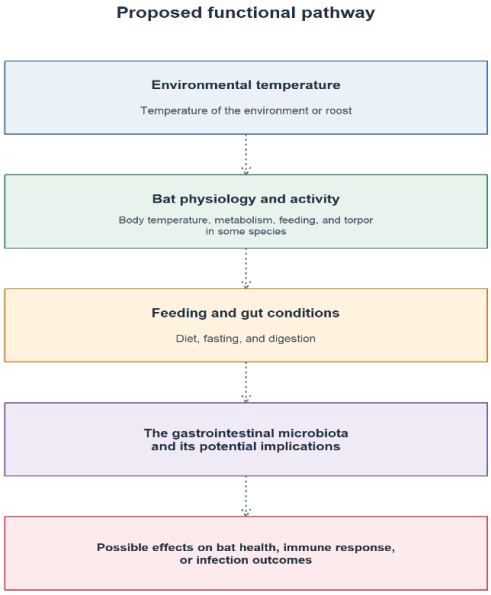


Figure 1: Proposed functional pathway between environmental temperature, bat microbiota, host health and susceptibility to infection.

Note: Dashed arrows are potential relationships that are yet to be validated.

Current Evidence for Temperature Associated Changes in the Bat Gut Microbiome

The evidence is derived from three types of study: a field comparison (measuring roost temperature and microbiome of bats), studies comparing bats between seasons or physiological states and temperature experiments in other animals. These types of evidence will answer various components of the question. Seasonal and hibernation studies reveal that bat microbiomes change, but they are unable to determine if it's due to temperature or to dietary or physiological changes.

Direct Evidence from Bat Studies

Liu et al. (2023) compared the least horseshoe bats (Rhinolophus pusillus) from two winter roosting sites in China that are within a short distance from each other. In summer, the temperatures in the roosts were similar but in winter the mean temperatures were approximately 11.9°C at the canal site and 17.1°C at the mine site. Analysis of 16S rRNA gene sequences in fecal samples of 23 of the bats revealed greater alpha diversity at the cooler site. The overall difference in community composition between groups, however, was not significantly different (beta diversity).

The Proteobacteria, the most abundant bacterial group did not show significant differences among the hibernating groups, while other groups including Firmicutes, Actinobacteria, and Tenericutes varied. The study also provided predictions of the microbial functions based on the sequencing data, which were not actually measured. Since the bats were collected from two natural roosts, instead of from roosts kept under controlled temperatures, it is not possible to conclude that the differences observed were only caused by temperature. Other site-specific factors may have also influenced and bat health and infection outcome were not tested. Bacterial sequences identified in potentially harmful groups do not necessarily mean there is infection or disease (Liu et al., 2023).

Seasonal and Hibernation-Associated Evidence

Other studies of bats have found differences in the microbial community during seasons and physiological conditions, but haven't been

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corrected for any effects of temperature, diet, fasting, or host physiology. Xiao et al. (2019) collected greater horseshoe bats (*Rhinolophus ferrumequinum*) in early spring, early summer, late summer, torpor and interbout arousal. The relative abundance of several groups of microbes varies with time and the diversity of microbes was greatest in late summer and lowest in early summer. The authors also noted seasonal variations in metabolic functions predicted from the 16S data. These predictions cannot be used as a direct measurement of the microbial activity. There was no effect on overall community structure of the torpor compared to the interbout-arousal group.

A separate study of common noctule bats (*Nyctalus noctula*) sampled before, during and after their hibernation states at a rehabilitation center. Popov et al. (2023) found a decrease in alpha diversity during the hibernation phase and variations in the composition of the communities between the three phases. The study is comparing physiological periods, since the bats were induced to hibernate at a constant temperature, and it was not testing the influence of various temperatures.

More recent work in Chinese horseshoe bats (*Rhinolophus sinicus*) also found gut microbiome differences between winter hibernation and summer activity (Shao et al., 2026). This is supporting evidence that the microbiome pattern changes with the season, but it does not prove it is caused by temperature. Combined, these bat studies demonstrate a temporal and physiological variation, but fail to separate out the temperature effect.

Diet is one of the reasons for this. Microbiome research of bats has suggested associations between microbial profiles and feeding strategies, as well as food preferences (Carrillo-Araujo et al., 2015; Corduneanu et al., 2023). The microbial community in migratory bats was stable with some variation in dietary changes during migration (Víquez-R et al., 2021). They don't account for the effect of temperature, but they reveal the importance of seasonal or site-specific differences in the microbiome data and the need to consider them in conjunction with other ecosystem shifts and changes, including diet.

Supporting Evidence from Other Animal Models

The relationship between temperature and microbiome in other animals is plausible and has been studied in other animals but is not directly applicable to bats. In mice, gut microbiome variation has been associated with housing temperature. In a study on exercise training adaptations, Raun et al. (2020) reported that housing temperature affected the microbiome; and Hylander et al. (2023) found that the microbiomes differed between mice who were kept at 22-23°C and 30°C, where diet was standardized. Matsumoto et al. (2023) also observed microbiome differences under conditions designed to mimic summer and winter, with diet held constant. Because both day length and temperature changed in that experiment, their separate effects could not be distinguished.

The cold exposure experiments in mice have moved beyond the description of the differences in community. Chevalier et al. (2015) and Zi̧tak et al. (2016) observed changes in gut microbiota during cold exposure and conducted microbiota-transfer experiments to evaluate potential metabolic effects in mice. Such findings indicate that the microbial changes associated with temperature have consequences in a specific experimental model but do not demonstrate any changes in the susceptibility to infection or in the susceptibility of bats.

Other mammal studies add evidence from different thermal conditions

Repeated exposure to low or high ambient temperatures were associated with changes in microbial community structure and thermoregulatory parameters in *Mongolian gerbils* (Khakisahneh et al., 2020). Huddling, as well as cold exposure, were both linked to changes in gut microbiota in Brandt's voles, complicating the analysis of temperature as the sole factor (Zhang et al., 2018). A rat heat-stress study also found changes in the diversity of microbiome along with relative abundance of some groups of bacteria at 35-38°C (Qu et al., 2021). The range and temperature pattern in these experimental circumstances is not the same as the range and

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pattern of temperatures bats experience in their natural roosts.

The other comparison is related to the hibernating ground squirrels, as they are studied for seasonal fasting and hibernation, and not a controlled experiment of ambient temperature as is done with the bears. Their gut microbiota shifted throughout the annual hibernation cycle and shifts in the mucosa-associated bacteria and intestinal antimicrobial responses were also associated with hibernation (Carey et al., 2013; Dill-McFarland et al., 2014). The findings are illustrative of how intertwined microbiome variation can be with physiological state and food availability.

The literature is supportive of an association between temperature and gut microbiome variation, but direct bat evidence is limited to an observational comparison of roosts only. Experiments in other animals and bat studies do provide meaningful context but they do not show that temperature driven microbiome changes alter bat health or infection susceptibility. There is a need to conduct bat studies to measure the microbiome features, temperature and health or infection outcomes together in order to establish that connection.

The evidences reviewed in the above section are summarized in Table 1. Its main purpose is to group studies into direct temperature comparisons in bats, seasonal and hibernation-associated bat studies, bat ecological findings relevant to interpretation and comparative studies in other mammals.

Table 1: Summary of Key Evidence on Temperature, Seasonal State (Seasonal state refers to seasonal changes within the year, rather than seasonal shifts between seasons) and Gut Microbiome Variation

Evidence Category	Study and Species	Comparison or study design	Main Finding and Relevance
Direct Temperature-associated evidence in bats	Liu et al. (2023), least horseshoe bat (Rhinolophus pusillus)	Comparison of bats hibernating at two close sites with differing winter temperature.	Gut microbiome alpha diversity was lower in bats at the warmer site during hibernation. No significant difference in beta diversity.
Seasonal and Hibernation associated evidence	Xiao et al. (2019), greater horseshoe bat (Rhinolophus ferrumequinum)	Samples retrieved from 5 periods including active, torpor and arousal	Diversity and composition of the gut microbiome were seasonally and physiologically opposite.
Hibernation associated evidence in bats	Popov et al. (2023), noctule bat (Nyctalus noctula)	The bacteria that live in the guts of hibernating animals were compared before and after hibernation.	The bacterial community involved in the culturing process shifted over the hibernation periods.
Seasonal and hibernation-associated evidence in bats	Shao et al. (2026), Chinese horseshoe bat (*Rhinolophus sinicus*)	The differences between gut microbiomes of animals originating from summer activities and winter hibernation.	There were differences in community composition and Faith's phylogenetic diversity but not in Chao1, Shannon and Simpson diversity.

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Bat ecology relevant to interpreting seasonal patterns	Carrillo-Araujo et al. (2015); Corduneanu et al. (2023); Víquez-R et al. (2021), multiple bat species	Research on feeding strategy, terrestrial vs. aquatic food resources and migration associated dietary changes	There were some differences in the microbiome between feeding ecology and core features were stable across migration while some taxa shifted.
Temperature evidence in mice	Hylander et al. (2023); Raun et al. (2020), laboratory mice	Different housing temperatures	Housing temperature had an impact at composition of the gut microbiome.
Cold-exposure evidence in mice	Chevalier et al. (2015); Zięta k et al. (2016), laboratory mice	Experiments for cold exposure and microbiota-transfer	The microbiota was assessed to be altered by cold exposure and these changes were correlated with the metabolic outcomes in mice through transfer experiments.
Seasonal-like conditions in mice	Matsumoto et al. (2023), laboratory mice	Light and temperature conditions during summer vs winter.	The same diet resulted in different gut microbiome composition and the temperature and day length were varied simultaneously.
Temperature fluctuations in gerbils	Khakisahneh et al. (2020), Mongolian gerbil (*Meriones unguiculatus*)	Frequent exposure to low and high temperatures	Thermoregulation related parameters were correlated with the change in the microbial community structure.
Cold and huddling in voles	Zhang et al. (2018), Brandt's vole (*Lasiopodomys brandtii*)	Cold versus warm conditions with and without huddling	Gut microbiome was altered in both cold exposure and huddling.
Heat stress in rats	Qu et al. (2021), rat	Heat stress at 35–38°C	The heat stress affected the diversity and composition of the microbiomes.
Hibernation context in ground squirrels	Carey et al. (2013); Dill-McFarland et al. (2014), ground squirrels	Active versus hibernation periods	The composition of the gut microbial community differed between the phases of the hibernation cycle and a number of aspects of intestinal immune status also varied between phases

Note: Alpha diversity measures the diversity within a sample and beta diversity is the difference in community composition between samples. There are studies relating the gut microbiome to

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temperature changes or susceptibility to infections in other animal species. These studies can be used as context but cannot be used to conclude that temperature changes the gut microbiome or susceptibility to infections in bats.

Potential Implication for Bat Health and Infection Susceptibility

The gut microbiome contributes to breaking down food and in immunity and changes in temperature can impact them and therefore lead to health implications. It is yet to be determined if they are beneficial to a bat's ability to resist infection or if they reduce the impact of infection. The bat temperature-comparison study was not conducted to measure infection or disease. Sequences for bacterial genera with species that could be pathogenic do not show that the bats were infected or more susceptible (Liu et al., 2023).

For the Egyptian fruit bat changes in gut microbiome composition have been observed following immune challenge, but not temperature. To induce inflammation (infection) the scientists applied lipopolysaccharide (LPS), which is not a living pathogen. Only a few changes in the microbiome were correlated with the immune-response marker (haptoglobin) and the sampling time was more closely correlated with the pattern. Overall, the study results indicate that there is no evidence for changes in the microbiome as a mechanism of immune response (Berman et al., 2023). In the Jamaican fruit bats, astrovirus infection was associated with microbiome changes as they aged. This demonstrates that infection can lead to shifts in the microbiome and that the direction of the shifts may differ by host age (Wasimuddin et al., 2018).

In another experiment, the researchers transferred gut bacteria from the leaf-nosed bats to mice and then infected them with H1N1 influenza. The mice with the bat microbiota also demonstrated a reduction in inflammation and an increase in survival. This suggests that infection responses in mice can be manipulated with microbes found in bats but it does not mean that the same can be achieved in bats and that temperature-mediated shifts in microbiome can influence infection outcomes in bats (Liu et al., 2022).

These studies as a whole suggest that the potential connection between temperature, the gut microbiome, host health and infection should be explored. It's not yet proven that microbiomes of bats are more or less prone to infection at various temperatures. This relationship will need some studies that quantify both the changes in the microbiome and temperature changes, the immune response and outcomes of infection, all in one. The studies discussed above along with their main findings and limitations are summarized in Table 2.

Table 2: Bat Gut Microbiome Studies Related to Immune Responses and Infection

Study and bat species	What was examined	Main Findings	Relevance & Limitation
Wasimuddin et al. (2018), Jamaican fruit bat (*Artibeus jamaicensis*)	The gut microbiome of astrovirus-positive and negative bats was separated by age.	The change in the microbiome was age-dependent with a decrease in alpha diversity in infected young bats and an increase in alpha diversity in infected mature adults.	Practices showing an infection–microbiome association; does not test temperature or determine the order of occurrence
Berman et al. (2023), Egyptian fruit bat (*Rousettus aegyptiacus*)	Immune markers and Gut microbiota after the LPS challenge	The composition of the microbiome changed following the challenge and in some instances the pattern	Connects microbiome patterns with an immune response. LPS is an immune stimulator and not a live infection.

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		was correlated with haptoglobin, whereas sampling time was more highly correlated with the pattern.	
Melville et al. (2025), Sundevall's roundleaf bat (*Hipposideros caffer* D)	Gut microbiome and body condition in wild bats with different coronavirus infections	The impacts of the Hibecovirus CoV-2B were; decreased diversity of the microbiome, altered body condition and microbiome composition.	It is a field association it does not measure temperature or determine if the microbiomes change because of infection.
Liu et al. (2022), Great Himalayan leaf-nosed bat (*Hipposideros armiger*)	Responses to H1N1 infection in mice colonized with gut microbiota from bats	Bat microbiota-fed mice showed reduced inflammation and increased survival following H1N1 challenge.	Shows an effect in a mouse model but does not demonstrate the same effect in bats.

Note: LPS = lipopolysaccharide. In the Liu et al. (2022) study, the infection outcomes were measured in mice after transfer of bat microbiota. None of these studies assessed whether temperature induced microbiome shifts impact infection outcome in bats.

Evidence Gaps and Future Research Directions

There are few studies who had directly explored the relationship between roost temperature and bat gut microbiome. This comparison is made on the basis of observation only and therefore differences in roosting sites could also have affected the results (Liu et al., 2023). Seasonal studies reveal that the microbiomes of bats evolve over time which is influenced by the temperature but also affected by other factors such as diet and hibernation states (Xiao et al., 2019). Recent study of urban bats was conducted to examine the relationship between diet, sample location and virulome, gut microbiome and resistome. It offers beneficial environmental data but doesn't differentiate temperature and identify whether microbial changes or infection outcome is due to temperature (Huang et al., 2026). Similarly, research on the association of environmental temperature and changes in microbiome to health outcomes has yet to be tested in studies of bat immune responses and infections (Berman et al., 2023; Wasimuddin et al., 2018).

Future studies could involve seasonal monitoring of roost temperatures, as well as repeated sampling of bats and incorporating other factors including diet, species, sex and physiological condition and age. The researchers need to not only pay attention to the microbes but to the action of the microbes through functional sequencing and monitoring of microbial metabolites. These data can be gathered along with immune markers, pathogen presence or load and bat condition to investigate potential health impacts. Repeated sampling will allow to see if there are microbiome changes before and after infection, if microbiome changes are correlated with resistance to infection or if there are microbiome changes correlated with a bat's resistance to the effects of infection.

Conclusion

There is a lack of direct studies on the relationship between temperature and gut microbiome in bats. In one field study, some microbiome measures changed in response to roost temperature during winter in hibernating bats but this study was not designed to test if the changes were due to the

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different temperatures (Liu et al., 2023). However, other studies have shown some of the variation in the bat gut microbiome by season and this may also be due to physiological changes and variation in food intake. It is unclear if temperature influences the composition of the gut microbiome but from a mouse study it seems that this may be the case which would not be expected to be the same for bats (Hylander et al., 2023).

It remains to be seen what changes in the bat's microbiome gut does to the health or susceptibility to infection of the bat. Microbiome changes have been observed in bat species related to immune responses or infections and recent studies have found changes in the environment and diet that have been correlated with microbiomes and virulence. But none has shown that a change in the microbiome with temperature influences the course of infection. The results suggest an association that needs to be explore but not that the susceptibility of bats increases or decreases with increasing or decreasing temperatures (Berman et al., 2023; Huang et al., 2026; Wasimuddin et al., 2018). Further research is required to evaluate the impacts of roost temperature, microbiome function, immune responses and pathogen levels and bat health together to better understand the connection.

REFERENCES

Baethge, C., Goldbeck-Wood, S., & Mertens, S. (2019). SANRA—a scale for the quality assessment of narrative review articles. *Research Integrity and Peer Review, 4*, Article 5.

Banskar, S., Mourya, D. T., & Shouche, Y. S. (2016). Bacterial diversity indicates dietary overlap among bats of different feeding habits. *Microbiological Research, 182*, 99–108.

Berman, T. S., Weinberg, M., Moreno, K. R., Czirják, G. Á., & Yovel, Y. (2023). In sickness and in health: The dynamics of the fruit bat gut microbiota under a bacterial antigen challenge and its association with the immune response. *Frontiers in Immunology, 14*, Article 1152107.

Carey, H. V., Walters, W. A., & Knight, R. (2013). Seasonal restructuring of the ground squirrel gut microbiota over the annual hibernation cycle. *American Journal of Physiology–Regulatory, Integrative and Comparative Physiology, 304*(1), R33–R42.

Carrillo-Araujo, M., Taş, N., Alcántara-Hernández, R. J., Gaona, O., Schondube, J. E., Medellín, R. A., Jansson, J. K., & Falcón, L. I. (2015). Phyllostomid bat microbiome composition is associated to host phylogeny and feeding strategies. *Frontiers in Microbiology, 6*, Article 447.

Chevalier, C., Stojanović, O., Colin, D. J., Suárez-Zamorano, N., Tarallo, V., Veyrat-Durebex, C., Rigo, D., Fabbiano, S., Stevanović, A., Hagemann, S., Montet, X., Seimbille, Y., Zamboni, N., Hapfelmeier, S., & Trajkovski, M. (2015). Gut microbiota orchestrates energy homeostasis during cold. *Cell, 163*(6), 1360–1374.

Corduneanu, A., Wu-Chuang, A., Maitre, A., Obregon, D., Sándor, A. D., & Cabezas-Cruz, A. (2023). Structural differences in the gut microbiome of bats using terrestrial vs. aquatic feeding resources. *BMC Microbiology, 23*, Article 93.

Dai, W., Leng, H., Li, J., Li, A., Li, Z., Zhu, Y., Li, X., Jin, L., Sun, K., & Feng, J. (2024). The role of host traits and geography in shaping the gut microbiome of insectivorous bats. *mSphere, 9*(4), Article e00087-24.

Dill-McFarland, K. A., Neil, K. L., Zeng, A., Sprenger, R. J., Kurtz, C. C., Suen, G., & Carey, H. V. (2014). Hibernation alters the diversity and composition of mucosa-associated bacteria while enhancing antimicrobial defence in the gut of 13-lined ground squirrels. *Molecular Ecology, 23*(18), 4658–4669.

Gong, L., Liu, B., Wu, H., Feng, J., & Jiang, T. (2021). Seasonal dietary shifts alter the gut microbiota of avivorous bats: Implication for adaptation to energy harvest and nutritional utilization. *mSphere, 6*(4), Article e00467-21.

Frontier in Medical & Health Research

ISSN: (e) 3007-1607 (p) 3007-1593

Han, A., Hudson-Paz, C., Robinson, B. G., Becker, L., Jacobson, A., Kaltschmidt, J. A., Garrison, J. L., Bhatt, A. S., & Monack, D. M. (2024). Temperature-dependent differences in mouse gut motility are mediated by stress. *Lab Animal, 53*(6), 148–159.

Hosken, D. J., & Withers, P. C. (1997). Temperature regulation and metabolism of an Australian bat, *Chalinolobus gouldii* (Chiroptera: Vespertilionidae), when euthermic and torpid. *Journal of Comparative Physiology B, 167*(1), 71–80.

Huang, L., Pu, Y.-T., Zhao, Y.-H., Sun, X.-Y., Zhu, Y., Lu, Y.-P., Leng, H.-X., Feng, J., Jin, L.-R., & Sun, K.-P. (2026). Diet and environmental factors jointly drive the gut microbiome, resistome, and virulome of urban bats. *npj Biofilms and Microbiomes, 12*, Article 61.

Hylander, B. L., Qiao, G., Cortes Gomez, E., Singh, P., & Repasky, E. A. (2023). Housing temperature plays a critical role in determining gut microbiome composition in research mice: Implications for experimental reproducibility. *Biochimie, 210*, 71–81.

Khakisahneh, S., Zhang, X.-Y., Nouri, Z., & Wang, D.-H. (2020). Gut microbiota and host thermoregulation in response to ambient temperature fluctuations. *mSystems, 5*(5), Article e00514-20.

Liu, B., Chen, X., Zhou, L., Li, J., Wang, D., Yang, W., Wu, H., Yao, J., Yang, G., Wang, C., Feng, J., & Jiang, T. (2022). The gut microbiota of bats confers tolerance to influenza virus (H1N1) infection in mice. *Transboundary and Emerging Diseases, 69*(5), e1469–e1487.

Liu, S., Xiao, Y., Wang, X., Guo, D., Wang, Y., & Wang, Y. (2023). Effects of microhabitat temperature variations on the gut microbiotas of free-living hibernating animals. *Microbiology Spectrum, 11*(4), Article e00433-23.

Lutz, H. L., Jackson, E. W., Webala, P. W., Babyesiza, W. S., Kerbis Peterhans, J. C., Demos, T. C., Patterson, B. D., & Gilbert, J. A. (2019). Ecology and host identity outweigh evolutionary history in shaping the bat microbiome. *mSystems, 4*(6), Article e00511-19.

Matsumoto, S., Ren, L., Iigo, M., Murai, A., & Yoshimura, T. (2023). Mimicking seasonal changes in light-dark cycle and ambient temperature modulates gut microbiome in mice under the same dietary regimen. *PLOS ONE, 18*(2), Article e0278013.

Melville, D. W., Meyer, M., Risely, A., Wilhelm, K., Baldwin, H. J., Badu, E. K., Nkrumah, E. E., Oppong, S. K., Schwensow, N., Tschapka, M., Vallo, P., Corman, V. M., Drosten, C., & Sommer, S. (2025). Hibecovirus (genus Betacoronavirus) infection linked to gut microbial dysbiosis in bats. *ISME Communications, 5*(1), Article ycae154.

Popov, I. V., Berezinskaia, I. S., Popov, I. V., Martiusheva, I. B., Tkacheva, E. V., Gorobets, V. E., Tikhmeneva, I. A., Aleshukina, A. V., Tverdokhlebova, T. I., Chikindas, M. L., Venema, K., & Ermakov, A. M. (2023). Cultivable gut microbiota in synanthropic bats: Shifts of its composition and diversity associated with hibernation. *Animals, 13*(23), Article 3658.

Popov, I. V., Peshkova, D. A., Lukbanova, E. A., Tsurkova, I. S., Emelyantsev, S. A., Krikunova, A. A., Malinovkin, A. V., Chikindas, M. L., Ermakov, A. M., & Popov, I. V. (2025). Gut microbiota dynamics in hibernating and active *Nyctalus noctula*: Hibernation-associated loss of diversity and anaerobe enrichment. *Veterinary Sciences, 12*(6), Article 559.

Qu, Q., Li, H., Bai, L., Zhang, S., Sun, J., Lv, W., Ye, C., Liu, C., & Shi, D. (2021). Effects of heat stress on gut microbiome in rats. *Indian Journal of Microbiology, 61*(3), 338–347.

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Raun, S. H., Henriquez-Olguín, C., Karavaeva, I., Ali, M., Møller, L. L. V., Kot, W., Castro-Mejía, J. L., Nielsen, D. S., Gerhart-Hines, Z., Richter, E. A., & Sylow, L. (2020). Housing temperature influences exercise training adaptations in mice. *Nature Communications, 11*, Article 1560.

Shao, W., Li, Y., Cheng, X., Guo, L., & Wei, L. (2026). Hibernation shifts in gut microbiota composition and metabolic function in the Chinese horseshoe bat (*Rhinolophus sinicus*). *Ecology and Evolution, 16*(2), Article e73087.

Studier, E. H., Behrend, T. A., & Freed, A. L. (1976). Effect of temperature on intrinsic intestinal motility in a hibernator. *Journal of Thermal Biology, 1*(3), 149–151.

Sun, H., Wang, J., Xing, Y., Pan, Y.-H., & Mao, X. (2020). Gut transcriptomic changes during hibernation in the greater horseshoe bat (*Rhinolophus ferrumequinum*). *Frontiers in Zoology, 17*, Article 21.

Víquez-R, L., Speer, K. A., Wilhelm, K., Simmons, N. B., Medellín, R. A., Sommer, S., & Tschapka, M. (2021). A faithful gut: Core features of gastrointestinal microbiota of long-distance migratory bats remain stable despite dietary shifts driving differences in specific bacterial taxa. *Microbiology Spectrum, 9*(3), Article e01525-21.

Wasimuddin, Brändel, S. D., Tschapka, M., Page, R. A., Rasche, A., Corman, V. M., Drosten, C., & Sommer, S. (2018). Astrovirus infections induce age-dependent dysbiosis in gut microbiomes of bats. *The ISME Journal, 12*(12), 2883–2893.

Xiao, G., Liu, S., Xiao, Y., Zhu, Y., Zhao, H., Li, A., Li, Z., & Feng, J. (2019). Seasonal changes in gut microbiota diversity and composition in the greater horseshoe bat (*Rhinolophus ferrumequinum*). *Frontiers in Microbiology, 10*, Article 2247.

Zhang, X.-Y., Sukhchuluun, G., Bo, T.-B., Chi, Q.-S., Yang, J.-J., Chen, B., Zhang, L., & Wang, D.-H. (2018). Huddling remodels gut microbiota to reduce energy requirements in a small mammal species during cold exposure. *Microbiome, 6*, Article 103.

Ziętak, M., Kovatcheva-Datchary, P., Markiewicz, L. H., Ståhlman, M., Kozak, L. P., & Bäckhed, F. (2016). Altered microbiota contributes to reduced diet-induced obesity upon cold exposure. *Cell Metabolism, 23*(6), 1216–1223.