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**Ecological dynamics of host-vector-pathogen relationships in sika deer and brown bears
in Hokkaido**

(エゾシカおよびエゾヒグマにおける宿主・ベクター・病原体の生態学的関係)

Tick-borne diseases arise from complex interactions among hosts, vectors, and pathogens. In Hokkaido, large mammals, such as sika deer (*Cervus nippon yesoensis*) and brown bears (*Ursus arctos yesoensis*), serve as primary hosts for various tick species and are infected with diverse tick-borne pathogens. Understanding transmission dynamics requires an integrated ecological analysis of tripartite relationships among hosts, vectors, and pathogens. However, ecological studies that comprehensively examine host-vector-pathogen relationships remain limited. This study aimed to elucidate host-vector-pathogen relationships in sika deer and brown bears using three interrelated research components to examine these complex ecological interactions from multiple perspectives.

Chapter I tested the hypothesis that tick species exhibit species-specific attachment site preferences influenced by interspecific interactions. Detailed investigations of tick infestation patterns were conducted using sika deer from the Shiretoko Peninsula between June and October 2022. Four tick species were identified: *Ixodes ovatus*, *I. persulcatus*, *Haemaphysalis japonica*, and *Ha. megaspinosa*. Results revealed distinct attachment site preferences and seasonal variations for each species. *Ixodes ovatus* and *I. persulcatus* preferred attachment to pinnae, while *Ha. japonica* showed seasonal variation, shifting from body and legs in summer to pinnae in autumn. *Haemaphysalis megaspinosa* was widely distributed across head, pinnae, and body. Co-occurrence analysis revealed positive associations within the same species and genera, and negative associations between different genera, particularly between *I. ovatus* and *Haemaphysalis* spp. These results suggest that tick attachment site selection is influenced by inter- and intraspecific interactions.

Chapter II examined how environmental and host factors influence pathogen infection rates and tick infestation patterns across four regions of Hokkaido from April

2021 to February 2024. The study investigated transmission dynamics of *Anaplasma* sp. AP-sd (AP-sd) in sika deer and *Hepatozoon ursi* in brown bears, representing two pathogen systems with different transmission characteristics. AP-sd infection rates corresponded closely with vector distribution, showing high prevalence in South and East Hokkaido where multiple *Ixodes* and *Haemaphysalis* spp. coexist, while North Hokkaido showed markedly low infection rates corresponding to *Haemaphysalis* absence. In contrast, *He. ursi* exhibited more complex dynamics, with unexpectedly low infection rates in East Hokkaido despite abundant *Haemaphysalis* vectors and similarly low rates in North Hokkaido, compared to high rates in South and Central Hokkaido. This pattern suggests involvement of multiple limiting factors including recent vector range expansion and host-acquired immunity.

Chapter III evaluated the vector potential of deer keds (*Lipoptena fortisetosa*), an ectoparasite different from ticks. *Theileria* sp. Thrivae, AP-sd, and *Borrelia* sp. were detected in both sika deer and deer keds. Importantly, pathogens were detected in deer keds collected from PCR-negative deer, suggesting acquisition from previously infected hosts. However, no pathogens were detected in unfed deer keds from the environment, indicating potential roles as mechanical rather than biological vectors.

The integration of these three chapters revealed complex ecological interactions among hosts, vectors, and pathogens in Hokkaido's large mammals. Transmission dynamics create unique epidemiological patterns through multilayered interactions that cannot be predicted by studying individual components in isolation. This study provides crucial foundations for developing effective, pathogen-specific management strategies to promote wildlife and human health.