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Land use shapes host–pathogen associations and disease hazard in small mammal communities

Inhalt

Human-driven land-use change is recognized as a major driver of zoonotic disease emergence by altering interactions among hosts, vectors, and pathogens. In the Netherlands, landscapes are expected to undergo substantial transitions in response to population growth, biodiversity conservation, and societal well-being. To assess the potential impact of future landscape transitions, it is necessary to first understand how disease hazard is currently distributed across dominant land-use types.

We investigated host–pathogen associations and disease hazard across three Dutch land-use types representing different levels of anthropogenic disturbance: forests, farmlands, and urban areas. We characterized host communities and evaluated the contribution of individual host species to pathogen circulation. We also quantified variation in disease hazard and pathogen infection probability among land-use types at both the community level and within *Apodemus sylvaticus*, a widespread habitat-generalist rodent.

We captured 1,621 small mammals belonging to 10 species. Although *A. sylvaticus* was associated with the greatest number of pathogens, *C. glareolus* was disproportionately important in maintaining pathogen communities in forests, while *Microtus arvalis* played a similar role in urban habitats. Disease hazard for tick-borne pathogens was highest in forests, whereas *Leptospira* spp. and *Toxoplasma gondii* were more prevalent in anthropogenic habitats.

Keywords

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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