

Human land-use change alters immunogenetic-pathogen links in a generalist rodent and zoonotic reservoir

Inhalt

Anthropogenic land use modifies landscapes and the surrounding matrix of natural habitats, alters biodiversity and increases the contact probabilities between wildlife, domestic animals and humans. Numerous lines of evidence further suggest that anthropogenically transformed environments increase the emergence of zoonoses. Wildlife species, however, respond to human disturbance differently. Generalists have high plasticity, can occupy a broad ecological niche, and thus, can adapt to human landscape modifications. Yet, whether anthropogenic disturbance modifies host-pathogen co-evolutionary relationships in generalists is unknown. We assessed pathogen diversity, neutral genome-wide (SNPs) and adaptive MHC class II diversity in a rodent generalist inhabiting three lowland rainforest landscapes with varying anthropogenic disturbance, and determined which MHC alleles co-occurred more frequently with 13 gastrointestinal nematodes, blood trypanosomes, and four zoonotic viruses. Pathogen-specific selection pressures varied between landscapes. Genome-wide diversity declined with the degree of disturbance, while MHC supertype diversity was only reduced in the most disturbed landscape. Furthermore, pristine forest landscapes had more functional important MHC-pathogen associations compared to disturbed forests. We show impoverished co-evolutionary links between host and pathogen owing to human disturbance even in generalists and suggest this may facilitate host switching by pathogens.

Keywords

Habitat disturbance, generalist species, spiny rat *Proechimys semispinosus*, genome-wide and MHC class II diversity, host-pathogen interactions, co-infections, OneHealth

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Yes, I am a Junior Scientist.

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