

## **Linking space use and individual traits to parasite infection in free-roaming sheep**

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Individual and spatial heterogeneity shape host-parasite dynamics. The liver fluke is an ideal model for understanding how space use drive parasite infection, as its intermediate host, a mud snail, requires water-land interface habitats for survival, which serves as a proxy for parasite risk.

In this study, we examined how space use and internal state traits in free-roaming sheep in Northwestern Patagonia (Argentina) drove liver fluke infection patterns across a landscape with variable infection risk. We measured reproductive status and body condition (traits) of individual sheep (n = 23) and we treated them with flukicide (Triclabendazole) in January 2024 to remove liver flukes, then collected faecal samples at 3-week intervals throughout the year to measure faecal egg counts (FEC). Space use in risky habitat (snail habitat) was inferred from GPS collars deployed on each sheep. We modelled individual sheep-parasite dynamics using Ordinary Differential Equations within a Bayesian framework, allowing us to estimate the rate of consumption of metacercariae (infective stage) per day when using risky habitat, while accounting for reproductive status and body condition. We found that consumption rate in risky habitat varied per individual. Individuals that were lactating had higher consumption rates compared to non-lactating individuals, and individuals with better body condition had higher consumption rates compared to individuals with poor body condition. In sheep, it has been previously observed that lactating individuals have a higher energetic demand and, thus, spend more time foraging; and that individuals with better body condition also spend more time foraging, which help explain these results. In summary, variation in observed FEC could be explained by the use sheep make of risky habitat, and by individual traits (reproductive status and body condition). However, unexplained variation in FEC may be related to unmeasured differences in susceptibility, immune function or fine scale variation in fluke infection risk. By integrating GPS, parasite infection data, traits of individuals, and Bayesian mechanistic modelling, our work provides a framework for linking host space use and internal state traits to infection dynamics in free-ranging or wild systems.