

Title: Effect of co-habitation on gastrointestinal parasite prevalence and burden in wild and domestic herbivores in Maasai Mara National Reserve, Kenya.

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Parasite transmission between wildlife and livestock is common. Of great importance are ubiquitous gastrointestinal nematodes and coccidia, which are associated with livestock production losses and can interfere with natural ecological processes in wildlife. These parasites are of growing concern, especially in places where livestock-wildlife interactions are increasing, such as the Maasai Mara ecosystem in Kenya. To determine the occurrence of gastrointestinal parasites and cross-species transmission in this region, we quantified nematode egg (*Strongyles spp.*, *Strongyloides spp.*) and coccidia oocyst (*Eimeria spp.*) counts and nematode infective larvae from ~1000 faecal samples of wild and domestic herbivores (>10 kg) across mixed livestock-wildlife and single-occupancy pastures. Through generalised linear models, individual parasite prevalence and intensity were analysed as functions of 'area type' (single vs. mixed occupancy) and 'species type' (livestock vs wildlife) to explore (a) whether wildlife and livestock differed in parasite infection levels, and (b) whether those infection levels for each animal type differed depending on whether they shared pastures with animals of the other type. We generally found wildlife to have significantly higher parasite prevalence and intensities than livestock, likely reflecting the impact of management practices on reducing infection risks in livestock. We found no area type effect on the prevalence of nematodes in both wildlife and livestock. However, animals browsing or grazing on mixed pastures had significantly higher intensities of nematodes than those on single-occupancy pastures. For coccidia, we found the opposite: prevalence and infection intensities were significantly lower for animals on communal grasslands. These results suggest that livestock-wildlife co-habitation could have community-wide implications for cross-species transmission of parasites. A next step is to identify individual nematode species through next-generation sequencing of the larval nemabiome and use this to develop a multi-host epidemiological model, to determine the directions of transmission for the different parasite species within these wildlife-livestock communities.