Multi-host pathogens and multi-parasitised hosts: an individual-level approach to understanding transmission of two pathogens (*Batrachochytrium dendrobatidis* and Ranavirus) across three amphibian host species.

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The notable, global decline of amphibians has largely been attributed to parasitism; the two pathogens of greatest conservation concern being Ranavirus and Batrachochytrium dendrobatidis (Bd). While both pathogens have been studied extensively the majority of these studies have taken a one-host, one-pathogen approach. In nature, things are rarely that simple; pathogens often infect multiple host species and hosts can be parasitised by multiple pathogen species. Increasingly, we are seeing field studies reporting co-infection occurring in multiple host species. Yet our understanding of these complex host-pathogen interactions and the implications on disease transmission and persistence maintenance within a host community remains limited.

To help unpick the tangled dynamics of this multi-host, multi-pathogen system we empirically tested how susceptibility, infectiousness and burden of disease changed with infection scenario (single vs coinfection) across a panel of host species (Bufo bufo, Rana temporaria and Alytes muletensis) that range in their reported susceptibility. We demonstrate that disease prevalence and infection burden is context dependent. Pathogen prevalence appears to be particularly linked to the exposure scenario whereas host species determined endpoint pathogen burden, in particular, Bufo bufo exhibited higher Bd load regardless of exposure regimes.

\*\*\*While Bd was detected in all host species across treatment groups, the exposure sequence determined the extent of ranaviral infection with, significantly higher disease prevalence in co-infection scenarios. \*\*\*

Understanding the susceptibility and infectiousness of each host at an individual level allows us to predict how host species community composition influences the establishment and persistence of both pathogens, singularly and as coinfections, at the community level. Our study provides previously lacking empirical evidence of within-host dynamics influencing disease outcome under different exposure scenarios (single vs co-infection).