THESIS INTRODUCTION

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1. DISCUSSION

1.1. **What I did.** In this thesis I have aimed to examine the importance of population size and structure on the accumulation of pathogen richness. I used bats as a case study throughout due to their interesting and varied social structure (Kerth 2008) and their association with a number of important, recent zoonoses (Leroy et al. 2005; Field et al. 2001; Halpin et al. 2011; Li et al. 2005; Field et al. 2001). I have studied the role of these population factors using both simulation studies and empirical comparative approaches in order to both examine the specific, epidemiological mechanisms involved in a controlled and interpretable *in silico* environment, while be able to also link these results back to real-world data. I have found the most robust evidence so far that population structure does relate to higher pathogen richness in bats. However, my simulation study testing whether newly evolved pathogens would invade more easily in a stuctured population did not recover the same relationship implying that this mechanism is not important in wild populations. Subsequently, I examined a number of intrinsically linked factors—population abundance, density and range size as well as colony size and the number of colonies—and found that contrary to beliefs commonly held in the literature, only colony size strongly promotes the invasion of newly evolved pathogens. Finally, I derived and validated a method for estimating bat abundances from acoustic data; as bat abundances are very difficult to estimate, this method fills a great need in bat ecology and zoonotic sirveillance.

1.2. **How I did it (Chapters overview).** In Chapter **??** I tested the hypothesis that bat species with more structured populations harbour more virus species. I test this hypothesis with two measurement of population structure: the number of subspecies (a novel measure and the largest dataset yet used to test this hypothesis) and gene flow. Using both meausres I found that, after controlling for phylogeny and study bias, a positive relationship between population structure and pathogen richness was very likely in the best model. This relationship was of similar strength, and at least as likely to be in the best model, as other measures (body mass and range size) which have been thought to promote pathogen richness in bats and other mammals (Kamiya et al. 2014; Arneberg 2002; Gay et al. 2014; Nunn et al. 2003; Turmelle & Olival 2009).

While the results from Chapter **??** suggest that there is a relationship between population structure and pathogen richness, comparative studies like these cannot identify by which specific mechanisms the higher pathogen richness is being maintained. To examine this I developed a model of two recently diverged—and therefore identical—pathogen lineages competing in a metapopulation based on large bat colonies with limited movement between colonies (Chapter **??**). I tested whether population structure (specifically network topology and dispersal rate) allowed a second pathogen to invade and persist in the presence of strong competition from the first, endemic pathogen. However, I found no relationship between probability of invasion and population structure, instead it appeared that if transmission rate was high enough for the invading pathogen to survive the initial, highly stochastic part of it's spread, it would then survive and spread throughout the metapopulation irregardless of how structured it was. This imples

that local dynamics, defined in part by colony size, are controlling disease invasion and that a different mechanism must be causing the relationship seen in Chapter **??**.

Group (or colony) size is one of many demographic parameters measured in comparative studies of pathogen richness. Other commonly measured parameters include population density and range size (Kamiya et al. 2014; Nunn et al. 2003; Morand & Poulin 1998; Lindenfors et al. 2007; Gay et al. 2014; Ezenwa et al. 2006) yet the intrinsic relationships between these variables are rarely acknowledged or discussed. Therefore in Chapter **??** I used the same model as Chapter **??** to test whether population density or population abundance more strongly promotes pathogen richness and whether a pathogen invades more easily into a population comprising many small colonies or few big colonies. I found that population abundance has a much stronger affect than density and that the component of abundance that has the strongest affect is colony size.

Theory (May & Anderson 1979; Anderson & May 1979), previous literature (Kamiya et al. 2014; Nunn et al. 2003; Morand & Poulin 1998) and Chapters **??** and **??** suggested that population sizes (either local group size or global population size) strongly influences the dynamics of disease and pathogen richness. However, there are very few estimates of population abundance for bats and colony counts are time consuming and costly. I therefore aimed to obtain estimates of abundance from acoustic data such as iBats (Jones et al. 2011). I developed a general method for estimating abundance and density from acoustic detectors (Chapter **??**). I used spatial simulations of animal movement to validate the method and found it to be precise and unbiased.

1.3. **What agreed/disagreed with the literature.**

- Don't find high R_0 leads to high richness in contrast to eco assumption.
- Don't find structure makes any difference in contrast to poletto and (Nunes et al. 2006) and ackleh.
- Find that colony size is more important which implies density is just proxy for group size. Group size *is* density at small scale.
- Importance of colony size agrees with nunn primate papers.

1.4. **What are the implications for research?**

- Global change and pop structure.
- Structure is not a strong enough predictor to use for zoonotic surveillance. Perhaps colony size is.
- Studies should more carefully consider density vs structure vs group size.
- Population structure should be studied in other groups other than bats.
- Can more easily estimate bat density.

1.5. **Furtherwork and limitations.**

- Collect data for colony size and test importance against structure.
- Limitations of poor data, escpecially for gene flow.
- Examine other mechanisms for richness
- Examine multi host species more carefully
- Field test gREM
- Use gREM to collect density estimates

1.6. **Conclusions.**

- Population structure does influence pathogen richness but the mechanisms are still unclear.
- Local dynamics (local density) are most important for pathogen invasions not broad scale structure.
- Data on density should be collected using the gREM.

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