How social network affects disease transmission in social lizards?

The infection of bacterial strains differed between sampling points. It seemed that most of the bacterial strains were randomly distributed among lizards. However, among strains having significant interaction, most of which were positively co-occurred with each other. We detected negative interaction between some strains, but whether these strains avoided or segregated with each other remained unknown. Co-infection of bacterial strains was significantly affected by which of the previous sampling point.

Known: variation of strains, co-occurrence of strains

Unknown: distribution of the strain among lizards, relationship between infection and social connection

Focus on the lizards

Variation of bacterial infection on lizards. The co-occurrence and inhibition.

The battery changing and fortnight swapping were conducted every two weeks.

Hypotheses that we can address

Big question with some appended small questions

Start with (1) the variation in bacterial infection (2) the dynamic of social network

Bacteria distribution <- - ? - -> phylogenetic group

* Budget

1. Field work
2. Conference (ASH 2018)
3. Laptop stand (keyboard)

* Project

Hierarchical structure should move

* Abstract for the workshop (29/6)
* Away 17/6~20/6

Hypothesis:

# The variation in bacterial infection of lizards

The bacterial infection could vary from one individual to another. Hypotheses were proposed to explain the non-random distribution of pathogens in wild animal’s population. Within-host competitive interaction suggests that the presence of bacteria could be affected by the existence of other strains (Gordon & FitzGibbon 1999). The competition between different bacterial taxon was rarely studied, yet it was important in predicting the non-random distribution of bacteria in wild animal population. Some bacteria form a biofilm that can facilitate the infection (Hall-Stoodley et al. 2004), while others inhibit the presence of other bacteria (Blyton et al. 2014). Tackling the interaction between different strains can improve our understanding in enteric bacteria community among wild animals. ­Additional opportunities are to gain a better understanding of the survival rate of bacteria in external environment, where bacteria have higher tolerance to extreme condition could have higher chance to infect hosts (Jackson & Tinsley 2002; Parsons et al. 2015). **In this chapter, I will quantify the variation of bacterial infection through time** and I aim to **investigate what causes the variation** in bacterial infection among sleepy lizards. The questions that I want to ask are:

How do different bacterial strains affect each other’s infection? Is there any bacterial strain could facilitate or inhibit the infection?

Hypothesis:

# The dynamic of disease model in relation to social network

Social network arises as a novel tool to investigate pathogen transmission through social animals, such as mammals (Hamede et al. 2009; Macintosh et al. 2012) and lizards (Godfrey et al. 2009; Fenner et al. 2011). Most of the researches only focus on one pathogen or one pathway at a time. However, animals are often infected by multiple bacteria or parasites in the wild. Our dataset contains over a hundred bacteria strains and the infectious status every fortnight across the year. The GPS data were collected to evaluate their movement patterns, which combined with the bacterial infection could investigate the dynamic of social network through time. We hypothesized that the bacteria could transmit through social and spatial route. Researches have shown that bacteria differed in their survival abilities in the wild (Bergholz et al. 2011; Parsons et al. 2015). Those cannot survive in the wild were more likely to transmit through direct contact. For example, transmission of *E. coli* was more related to social network than spatial network in giraffe. Individuals that engaged in frequent contact would be more likely to share the same bacteria subtype (VanderWall et al. 2014). On the other hand, how does the network change after being infected was rarely studied because of the lack of empirical data. Sah et al. (2018) pointed out that the structure of social network has a strong effect on disease outbreak frequency and time. It is possible that primitive social structure forms under the selection for resistance to disease transmission. In this chapter, I aim to test the hypothesis that the behavioural change of infected individuals would alter the social network. The question I want to ask are:

1. How do gut bacteria infect the lizards in the wild? I will compare the differences in transmission pathway between bacterial strains.
2. What characters would make an individual/a habitat become a superspreader/hotspot? How strong is the effect of individual’s position on the disease transmission? How many bacteria can a hotspot carry?
3. How does the social network change through time after the lizards are infected? Will modular structure be formed to prevent the spread of certain bacteria? Are there any bacteria could transmit in spite of the network structure?

Hypotheses:

# The effect of the architecture of the social network

The structure of social network has been proved to have strong effect on the disease transmission, especially the modular structure which forms small groups in the population. Social network theory predicts that different structures of network can have variation in pathogen transmission (Sah et al. 2017). Either with a more connected position or a more hierarchic structure, the distribution of pathogens differs from clustered to prevalent in the network (Bull et al. 2012; Sah et al. 2018). However, most of the efforts were addressed on social species, the understanding on social network of relatively solitary species was considerably scarce.

How strong is the influence of social hierarchy or network architecture on bacterial transmission? Does infection differ between solitary and social individuals?

Which species can be used to manipulate the effect of infection in captivity