

## Evolutionary and mechanistic basis of virus host shifts

### Supervisory team:

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### Project description:

Virus host shifts – where a virus jumps from one host species to another – are a major source of emerging infectious diseases. For example, Ebola, HIV and SARS coronavirus have all jumped into humans from other species. Despite the importance of emerging viral diseases, we have a limited understanding about what determines the ability of a virus to infect some groups of hosts but not others, or how viruses will evolve in different hosts (Longdon et al. 2014, <https://doi.org/10.1371/journal.ppat.1004395>). Understanding these processes is vital to predict when and where diseases will emerge in the future.

### BACKGROUND

Viruses are disproportionately responsible for emerging infectious diseases, with RNA viruses that normally infect multiple host species considered the most likely to emerge. Additionally, host shifts appear to occur most often between closely related host species. However, evidence for these hypotheses largely come from comparative data (i.e. observations with no experimental manipulation). Therefore, they point us toward interesting areas for investigation, but cannot tease apart the complex processes explaining the observed patterns.

Experimental studies have highlighted some of the important host-virus interactions that result in successful host shifts (e.g. parvoviruses from cats to dogs (Parrish et al. 2008 <http://doi.org/MMBR.00004-08>) but the majority of these studies have been limited to two host systems. Therefore, experimental studies using a wide breadth of host species that vary in their relatedness are essential to make broadly applicable conclusions. Our previous work has used up to 50 species of *Drosophila*, and their naturally occurring RNA viruses (Longdon et al. 2011 and 2015 <https://doi.org/10.1371/journal.ppat.1002260> and <https://doi.org/10.1371/journal.ppat.1004728>) to examine host shifts (video here [www.goo.gl/sXBiv5](http://www.goo.gl/sXBiv5)). By using a large number of different host species we are able to find general patterns that apply across host species with varying relatedness.

This project will ask fundamental questions about disease emergence using a bacteria-virus system to study the consequences of virus evolution on host shifts. We will use a panel of over 50 different *Staphylococcus* species and a broad host range bacteriophage. This model offers a unique opportunity to perform experiments that would not be possible in a vertebrate-system, and critically will allow us to use experimental evolution to ask fundamental questions about pathogen host shifts.

This interdisciplinary project integrates expertise on pathogen host shifts (Ben Longdon, Exeter) and bacteria-phage co-evolution (Angus Buckling, Exeter).