ABSTRACTS SUBMISSION

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A bacteria-phage system for the investigation of virus host shifts

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Host shifts, where a pathogen jumps to and establishes onward transmission in a new host species, are a major source of emerging infectious diseases. However, little is known about what determines the ability of viruses to infect some hosts but not others. We have established a bacteria-phage system, using a diverse panel of Staphylococcus aureus isolates and a broad host range bacteriophage (ISP), to investigate the evolutionary factors that influence virus host shifts. Our initial work aimed to characterise the most appropriate method for assessing phage host range. The methods tested were: spot tests, where the presence of plaques indicates susceptibility; liquid media assays, where bacterial growth (optical density) is measured over time and compared between infected and uninfected samples; and qPCR, where susceptibility is measured as the increase in viral load over time. Comparison of these methods has shown that the reported host range of a bacteriophage is likely to be biased by the method used to determine it, with different methods either over- or under-estimating host range. We found weak positive correlations between some of these methods, although these relationships deteriorate below certain thresholds. Accurate assessments of phage host ranges are especially important in the context of phage therapy, where treatment regimens can be designed to target specific pathogenic bacteria. Our results therefore have important implications for the future study and application of these treatments.

1. What is your pathogen? Multiple options possible (e.g. if working on coinfections)

Other viruses : Bacteriophage, ISP
Bacteria : Staphylococcus

2. On a scale of 1-5 is your work mostly eco/epidemiological or evolutionary? 3

3. On a scale of 1-5 is your work mostly theoretical or experimental/empirical?
5 (100% empirical)