Phylogeography, gene exchange, and the evolution of antibiotic resistance in *Mycoplasma hyopneumoniae*

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*Mycoplasma hyopneumoniae* is a major pathogen living in swine respiratory tracts and causes porcine enzootic pneumonia, a highly contagious and chronic disease. To explore the evolution of this pathogen, whole genomes of 117 *Mycoplasma* strains collected from pigs in four different countries between 1969 and 2011 were sequenced. Initial analyses suggested that the standard diagnostic techniques had confused *M. hyopneumoniae* with the non-pathogenic *Mycoplasma flocculare* in some cases, and also revealed evidence of gene exchange between the two species, but not with the related pathogen *M. hyorhinis*. The Bayesian phylogeographic analysis carried out on our study suggested complete clustering of *M. hyopneumoniae* within each source country, despite widespread gene exchange within, but not between countries. This is surprising given the widespread transport of pigs between these countries, and the absence of known reservoirs for the pathogen. Finally, the evolution of known antibiotic resistance genes was examined, and demonstrated repeated evolution of quinolone resistance in UK farms, consistent with use of these antibiotics in pigs in the UK. Together the results showed the utility of whole-genome sequencing, combined with evolutionary analyses, for understanding the epidemiology and emergence of infectious disease.

Biography

Fang Wang has completed her Master’s degree in Southeast University, China, 2012 at the age of 25 and is currently a second year PhD student in Welch group, Department of Genetics, University of Cambridge, UK. Her research mainly involves on studying the pathogen genome evolution, with special focus on *Staphylococcus aureus* and *Mycoplasma hyopneumoniae*. She is interested in the genomic changes for bacteria transmission between different hosts and different locations. She is also interested in understanding the genetic evolution of bacteria in antibiotic resistance.

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