Molecular epidemiology of zoonotic Streptococcus suis on pig farms

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Research area: Infectious disease evolutionary genomics

Project outline:

Streptococcus suis is a highly diverse, Gram-positive bacterial species, which is asymptomatically carried as a commensal of the pig upper respiratory tract. However, S. suis can also cause pneumonia, meningitis, septicaemia, and arthritis, particularly in piglets. S. suis is also an emerging zoonotic pathogen that can cause disease in humans, with those who come into contact with pigs and pork products at high risk.

Due to the disease's public health concern as well as the resulting high economic losses and animal welfare issues, methods to understand and limit the spread of S. suis on pig farms are critical.

Molecular epidemiology uses molecular markers to trace the origin and transmission of disease during outbreaks. So far, molecular epidemiology of S. suis on pig farms has used multi locus sequencing typing and serotyping, which limits the resolution of tracking transmission.

This project will use phylodynamic methods, metagenomics methods and whole genome sequences of S. suis taken from samples of clinically-infected and asymptomatic pigs to understand S. suis spread on farms. We will investigate transmission of the same strains between and within farms, to understand where intervention will be most effective.

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Marois, C et al. (2007). Detection and molecular typing of Streptococcus suis in tonsils from live pigs in France. Canadian journal of veterinary research, 71(1), 14.

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