Genomic analysis of Streptococcus suis isolated from healthy and diseased birds

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Streptococcus suis is a respiratory commensal of pigs, with some lineages causing serious swine disease and zoonotic disease in humans. In recent years, S. suis has also been isolated from cats, dogs, cattle, sheep, wild boars, and different bird species, including chicken. It is generally assumed that, as in humans, these infections are due to "spillovers" from pigs, but no genomic investigation of respective isolates has yet been performed. Over the last six years, we collected and whole-genome sequenced S. suis samples from birds in the veterinary diagnostics department of the Freie Universität Berlin. Most of these birds were diseased and S. suis was isolated as the causative pathogenic agent. We combined these samples with published genomes of Vietnamese chicken isolates and compared them to S. suis lineages isolated from pigs and wild boars. All the bird isolates clustered phylogenetically within a group of largely commensal isolates of pigs, and distinct from the lineage responsible for most zoonoses. Bird isolates also lacked most known virulence genes but were often multi-drug resistant. We detected a significant overrepresentation of unique genomic islands within bird isolates, suggestive of S. suis adaptation to birds. Taken together, our results imply that S. suis could be persisting in bird populations independently of pigs, at least for short periods, but that birds are unlikely to be a source of zoonotic infection in humans.

Keywords

Streptococcus suis, birds, sequencing, genome anlysis

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Professional Status of the Speaker

Postdoc

Junior Scientist Status

Yes, I am a Junior Scientist.

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