

Genomic analysis of *Streptococcus suis* isolated from healthy and diseased birds

Inhalt

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.

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Streptococcus suis, birds, sequencing, genome analysis

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Postdoc

Junior Scientist Status

Yes, I am a Junior Scientist.

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