

Comparative and Functional Genomic Studies of

Histophilus somni (Haemophilus somnus)

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in

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ABSTRACT

Histophilus somni is a commensal of the mucosal surfaces of respiratory and reproductive tracts of cattle and sheep. However, as an opportunistic pathogen, *H. somni* can cause diseases such as pneumonia, myocarditis, abortion, arthritis, and meningo-encephalitis. Previously, several virulence factors/mechanisms had been identified in *H. somni* of which the phase-variable lipooligosaccharide, induction of host cell apoptosis, intraphagocytic survival, and immunoglobulin Fc binding proteins were well characterized. To further understand the biological properties of *H. somni*, the genomes of pneumonia strain 2336 and preputial strain 129Pt have been sequenced. Using the genome sequence data and comparative analyses with other members of the *Pasteurellaceae*, putative genes that encode proteases, restriction-modification enzymes, hemagglutinins, glycosyltransferases, kinases, helicases, and adhesins have been identified in *H. somni*. Most of the *H. somni* strain-specific genes were found to be associated with prophage-like sequences, plasmids, and/or transposons. Therefore, it is likely that these mobile genetic elements played a significant role in creating genomic diversity and phenotypic variability among strains of *H. somni*. Functional characterization of *H. somni luxS* in the genomic context revealed that the gene encodes S-ribosylhomocysteinase that can complement biosynthesis of AI-2 quorum sensing signal molecules in *Escherichia coli* DH5 α . It was also found that several pathogenic isolates of *H. somni* form a prominent biofilm and that *luxS* as well as phosphorylcholine expression can influence biofilm formation by *H. somni*. In conclusion, comparative analyses of the genomes and functional characterization of putative genes have shed new light on the versatility and evolution of *H. somni*.

Dedication:

To the Purposeful Ingenuity and Resourceful Mystery of Nature

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