Genomic and epidemiologycal analyses of Manhheimia haemolytica strains

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Abstract

Mannheimia haemolytica is a gram-negative bacterium, commensal and opportunistic pathogen, and the primary agent of respiratory infections on ruminants. This bacterium causes bovine respiratory disease, a disease that generates a great economic loss in the cattle industry. Some pathogenic strains are associated to a specific serotype and the presence of integrative conjugative elements (ICEs) containing multi-drug resistance genes. To characterize the genomic features, pathogenesis, and distribution of this specie, we performed a genomic and epidemiological analyses of 113 M. haemolytica strains from diverse hosts, mostly cattle, and clinical or non-clinical status. The serotypes were classified as serotype 1 (48.67%), 2 (31.85%), 6 (13.27%) and unknown (6.19%). According to Multilocus Sequence Typing (MLST), the strains were classified as ST1 (61.94%), ST2 (30.08%), ST7 (2.26%), ST47 (1.13%), ST3 (1.13%) and unknown (3.39%). The pangenome was estimated as open. Phylogenetic analysis using whole-genome single nucleotide polymorphisms (SNPs) showed that most strains with the same serotype were clustered together. Principal Component Analysis (PCA) based on the accessory genes segregated all identified serotypes. The serotypes 1 and 6 are discretely segregated, but all strains belong to sequence type ST1, while all serotype 2 strains belong to sequence type ST2. Strains with unknown serotype did not form clusters. The integrative conjugative elements ICEPmu1 and ICEMh1 were present only in strains from USA, in both clinical and non-clinical sample, but not in all strains. The results suggest that the in silico-identified serotypes could be discriminated by SNP. In addition, the serotype 2 could be differentiated from serotypes 1 and 6 by the accessory genome. The association of genomic features with clinical or non-clinical isolates, and host species could not be evaluated due to lack of available data. Integrative conjugative elements were reported only in USA isolates, but were not specific to clinical or non-clinical isolates. Virulence factor distribution across strains will be performed in further analyses. Our findings identified genomic features that could be associated to serotypes and geographical location that could help to develop strategies for surveillance, control and prevention on respiratory infections by M. haemolytica.