Genomic characterization, phylogenetic analysis, and identification of virulence factors in Aerococcus sanguinicola and Aerococcus urinae strains isolated from infection episodes - DTU Orbit (06/11/2018)

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Aerococcus sanguinicola and Aerococcus urinae are emerging pathogens in clinical settings mostly being causative agents of urinary tract infections (UTIs), urogenic sepsis and more seldomly complicated infective endocarditis (IE). Limited knowledge exists concerning the pathogenicity of these two species. Eight clinical A. sanguinicola (isolated from 2009 to 2015) and 40 clinical A. urinae (isolated from 1984 to 2015) strains from episodes of UTIs, bacteremia, and IE were whole-genome sequenced (WGS) to analyze genomic diversity and characterization of virulence genes involved in the bacterial pathogenicity.

A. sanguinicola genome sizes were 2.06–2.12 Mb with a 47.4–47.6% GC-contents, and 1783–1905 genes were predicted whereof 1170 were core-genes. In case of A. urinae strains, the genome sizes were 1.93–2.44 Mb with 41.6–42.6% GC-contents, and 1708–2256 genes of which 907 were core-genes.

Marked differences were observed within A. urinae strains with respect to the average genome sizes, number and sequence identity of core-genes, proteome conservations, phylogenetic analysis, and putative capsular polysaccharide (CPS) loci sequences. Strains of A. sanguinicola showed high degree of homology. Phylogenetic analyses showed the 40 A. urinae strains formed two clusters according to two time periods: 1984–2004 strains and 2010–2015 strains.

Genes that were homologs to virulence genes associated with bacterial adhesion and antiphagocytosis were identified by aligning A. sanguinicola and A. urinae pan- and core-genes against Virulence Factors of Bacterial Pathogens (VFDB). Bacterial adherence associated gene homologs were present in genomes of A. sanguinicola (htpB, fbpA, lmb, and ilpA) and A. urinae (htpB, lap, lmb, fbp54, and ilpA). Fifteen and 11–16 CPS gene homologs were identified in genomes of A. sanguinicola and A. urinae strains, respectively. Analysis of these genes identified one type of putative CPS locus within all A. sanguinicola strains. In A. urinae genomes, five different CPS loci types were identified with variations in CPS locus sizes, genetic content, and structural organization.

In conclusion, this is the first study dealing with WGS and comparative genomics of clinical A. sanguinicola and A. urinae strains from episodes of UTIs, bacteremia, and IE. Gene homologs associated with antiphagocytosis and bacterial adherence were identified and genetic variability was observed within A. urinae genomes. These findings contributes with important knowledge and basis for future molecular and experimental pathogenicity study of UTIs, bacteremia, and IE causing A. sanguinicola and A. urinae strains.

General information

State: Published
Organisations: Department of Bio and Health Informatics, Metagenomics, Slagelse Hospital, Roskilde University, Statens Serum Institut
Contributors: Carkaci, D., Højholt, K., Nielsen, X. C., Dargis, R., Rasmussen, S., Skovgaard, O., Fuursted, K., Andersen, P. S., Stegger, M., Christensen, J. J.
Pages: 327-340
Publication date: 2017
Peer-reviewed: Yes

Publication information
Journal: Microbial Pathogenesis
Volume: 112
ISSN (Print): 0882-4010
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.36 SJR 0.751 SNIP 0.849
Web of Science (2017): Impact factor 2.332
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.12 SJR 0.781 SNIP 0.746
Web of Science (2016): Impact factor 2.009
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.99 SJR 0.906 SNIP 0.755
Web of Science (2015): Impact factor 1.888
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.89 SJR 0.929 SNIP 0.76
Web of Science (2014): Impact factor 1.794