Diversity and Population Overlap between Avian and Human Escherichia coli Belonging to Sequence Type 95 - DTU Orbit (06/03/2019)

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Avian-pathogenic Escherichia coli (APEC) is a subgroup of extraintestinal pathogenic E. coli (ExPEC) presumed to be zoonotic and to represent an external reservoir for extraintestinal infections in humans, including uropathogenic E. coli (UPEC) causing urinary tract infections. Comparative genomics has previously been applied to investigate whether APEC and human ExPEC are distinct entities. Even so, whole-genome-based studies are limited, and large-scale comparisons focused on single sequence types (STs) are not available yet. In this study, comparative genomic analysis was performed on 323 APEC and human ExPEC genomes belonging to sequence type 95 (ST95) to investigate whether APEC and human ExPEC are distinct entities. Our study showed that APEC of ST95 did not constitute a unique ExPEC branch and was genetically diverse. A large genetic overlap between APEC and certain human ExPEC was observed, with APEC located on multiple branches together with closely related human ExPEC, including nearly identical APEC and human ExPEC. These results illustrate that certain ExPEC clones may indeed have the potential to cause infection in both poultry and humans. Previously described ExPEC-associated genes were found to be encoded on ColV plasmids. These virulence-associated plasmids seem to be crucial for ExPEC strains to cause avian colibacillosis and are strongly associated with strains of the mixed APEC/human ExPEC clusters. The phylogenetic analysis revealed two distinct branches consisting of exclusively closely related human ExPEC which did not carry the virulence-associated plasmids, emphasizing a lower avian virulence potential of human ExPEC in relation to an avian host. IMPORTANCE APEC causes a range of infections in poultry, collectively called colibacillosis, and is the leading cause of mortality and is associated with major economic significance in the poultry industry. A growing number of studies have suggested APEC as an external reservoir of human ExPEC, including UPEC, which is a reservoir. ExPEC belonging to ST95 is considered one of the most important pathogens in both poultry and humans. This study is the first in-depth whole-genome-based comparison of ST95 E. coli which investigates both the core genomes as well as the accessory genomes of avian and human ExPEC. We demonstrated that multiple lineages of ExPEC belonging to ST95 exist, of which the majority may cause infection in humans, while only part of the ST95 cluster seem to be avian pathogenic. These findings further support the idea that urinary tract infections may be a zoonotic infection.

**General information**

State: Published
Organisations: Bacteriology & Parasitology, National Veterinary Institute, University of Copenhagen, Statens Serum Institut, George Washington University, Bisgaard Consulting, University of Georgia
Contributors: Jørgensen, S. L., Stegger, M., Kudirkienė, E., Lilje, B., Poulsen, L. L., Ronco, T., Pires Dos Santos, T., Kiil, K., Bisgaard, M., Pedersen, K., Nolan, L. K., Price, L. B., Olsen, R. H., Andersen, P. S., Christensen, H.
Number of pages: 12
Publication date: 16 Jan 2019
Peer-reviewed: Yes

**Publication information**

Journal: mSphere
Volume: 4
Issue number: 1
Article number: e00333-18
ISSN (Print): 1535-9786
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SJR 2.03 SNIP 0.985
Web of Science (2017): Impact factor 3.575
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 3 SJR 1.576 SNIP 1.043
Web of Science (2016): Impact factor
Web of Science (2016): Indexed yes
Scopus rating (2015): CiteScore 3.12 SJR 1.873 SNIP 0.852
Web of Science (2015): Impact factor 2.946
Scopus rating (2014): CiteScore 3.13 SJR 1.784 SNIP 0.9
Web of Science (2014): Impact factor 2.82
Scopus rating (2013): CiteScore 3.58 SJR 2.073 SNIP 0.997
Web of Science (2013): Impact factor 3.179