Genomic traits of Aeromonas hydrophila isolated from humans and foods in different countries

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Aeromonas hydrophila (*A. hydrophila*) is an emerging and neglected waterborne and foodborne pathogen in many countries, commonly associated with gastroenteritis in humans. However, information on the genomic traits of strains of this pathogen isolated worldwide is scarce. Therefore, this study aimed to analyze the presence of antimicrobial resistance (AMR), stress, and virulence genes, plasmids, and the genetic diversity of *A. hydrophila* isolated from humans and foods in diverse countries. A total of 64 *A. hydrophila* genomes of strains isolated from humans (n=61) and food (n=3), from 10 countries, and publicly available at NCBI Pathogen Detection were selected. For all 64 strains, AMR and stress-related genes were identified through AMRFinder Plus and ResFinder, virulence genes through VFAnalyzer, and plasmid incompatibility groups (Inc) through PlasmidFinder 2.1. The genetic diversity was assessed by Multi-Locus Sequence Typing (MLST), and by the Single-Nucleotide Polymorphism (SNP) clusters determined by NCBI Pathogen Detection. A total of 50 out of the 64 genomes were also selected for core-genome MLST (cgMLST) and fragmented genome analyses. The studied genomes harbored 131 AMR genes conferring resistance to aminoglycosides, beta-lactams, bleomycin, colistin, fosfomycin, macrolides, phenicols, quinolones, rifamycin, streptogramin, streptothricin, sulfonamide, tetracycline, and trimethoprim, in frequencies ranging from 1.6 to 98.4%. A genotypic multi-drug resistance profile was found in 37.5% of the genomes. Genes for arsenic and mercury tolerance and quaternary ammonium and heat resistance were also found in frequencies ranging from 1.6 to 85.9%. Virulence genes encoding pilli, fimbriae and flagella-mediated adhesion, secretion systems of types II, III and VI, and toxins were found in frequencies ranging from 0.4 to 100%. Only 13 genomes harbored six types of plasmid replicons, being ColKP3, IncC and IncU the most frequent ones, in four genomes each. The majority of the studied genomes (n=35) were not assigned to a Sequence Type (ST), while the rest was assigned to 19 STs, with ST1172 and ST1824 being the most frequent ones (n=4, each). Also, 34 genomes were assigned to 21 SNP clusters, with PDS000074337.3 being the most frequent (n=4). Phylogenomic analyses of cgMLST and fragmented genomes also demonstrated the high genomic diversity among these genomes, with no distinction in the generated phylogenetic trees regarding the isolation years and countries. In conclusion, the high diversity and frequency of clinically relevant antimicrobial resistance and virulence genes associated to diverse genomic profiles among *A. hydrophila* reinforced the potential hazard of infections caused by this pathogen, and the need for more effective monitoring and surveillance by public health authorities.

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