Genome sequences of three highly copper-resistant Salmonella enterica subsp. I serovar typhimurium strains isolated from pigs in Denmark
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Salmonella enterica subsp. I serovar Typhimurium is one of the most important food-borne bacterial pathogens, with a broad host range, including food animals and humans, infecting 21.7 million people and causing 217,000 deaths annually (1–3). In addition, the magnitude of multidrug resistance in Salmonella and other pathogens at the human-animal and ecosystem interface has been a major concern globally.

Three S. typhimurium (S7, S15, S23) strains were isolated from copper-fed pigs as part of the Danish Integrated Antimicrobial Resistance and the five-gene pcoEDAPTR merEDAPTR arsRDABC cluster. The resulting contigs were uploaded into the RAST server (6,7) and analyzed using the Clusters of Orthologous Groups (COGs) database. The sequences also revealed genes encoding the Salmonella-specific pcoEDAPTR merEDAPTR arsRDABC cluster. The three S. typhimurium genomes contain several copper-resistance genes, including the Cu(I)-translocating P-type ATPase CopA, multicopper oxidase CueO, and a copper-responsive MerR-family transcriptional regulator CueR (9–11), which were also reported in S. typhi strains Ty2 and CT18 (12–14). All three strains contained a mobile 20-gene copper resistance determinant that contained the previously described pco and sil determinants (15, 16). There are two additional genes between these two determinants; pcoG encodes a putative M23B metallophotoprotein, and pcoJ encodes a putative copper binding protein.

The sequences also revealed genes encoding the Salmonella-specific P-type ATPase, GoIT, golsB, and gesABC genes. Most Salmonella strains lack an RND-type CusCFBA system; instead, CueP sequesters copper to neutralize toxicity (20–23). However, S. typhimurium (S7, S15, S23) contained both an RND type system and CueP. In addition, the genome also revealed a six-gene cluster merEDAPTR encoding proteins conferring mercury resistance and the five-gene ars operon arsRDABC (24).

Nucleotide sequence accession numbers. These whole-genome shotgun projects have been deposited in DDBJ/EMBL/GenBank under the accession numbers JRGS00000000, JRGR00000000, JRGT00000000. The version described in this paper is the first version. The BioProject designations for those projects are PRJNA260777, PRJNA260771, and PRJNA260778.

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