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Genome Sequences of Three Highly Copper-Resistant *Salmonella enterica* subsp. I Serovar Typhimurium Strains Isolated from Pigs in Denmark

Yanan Qin, a Henrik Hasman, b Frank M. Aarestrup, b Hend A. Alwathnani, c Christopher Rensing a,d

Department of Plant and Environmental Science, University of Copenhagen, Frederiksberg, Denmark; a National Food Institute, Technical University of Denmark, Lyngby, Denmark; c Department of Botany and Microbiology, King Saud University, Riyadh, Saudi Arabia; d Institute of Urban Environment, Chinese Academy of Sciences, Xiamen, China.

*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 Monitoring (DANMAP) surveillance program (4). The sequences also revealed genes encoding the *Salmonella*-specific P-type ATPase, GoT, golBS, and gesABC (17, 18, 19) 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 JRGR00000000, JRGX00000000, JRGX00000000. 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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