

Discerning the antimicrobial resistance, virulence, and phylogenetic relatedness of *Salmonella* isolates across the human, poultry and food materials sources in Malaysia

ABSTRACT

Salmonella enterica subspecies *enterica* serovar *Enteritidis* is one of the major foodborne zoonotic pathogens globally. It has significantly impacted human health and global trade. In this investigation, whole-genome sequencing was employed to determine the antimicrobial resistance (AMR) pattern of a collection of *Salmonella Enteritidis* isolated from humans, poultry, and food sources. The study also investigated the virulence genes profile of the isolates as well as the phylogenetic relationships among strains. Illumina NextSeq technology was used to sequence the genome of 82 *Salmonella Enteritidis* strains isolated over 3 years (2016-2018) in Peninsular Malaysia. The pattern of resistance showed that tetracycline had the highest frequency (37/82, 45.12%), and isolates from food samples showed the highest rate of 9/18 (50.00%), followed by human 17/35 (48.57%) and then poultry 11/29 (37.93%). The second drug with the highest resistance rate is ampicillin with 5/29 (17.24%) for poultry, 4/35 (11.43%) for human, and 0/18 (0.00%) for food isolates respectively. Similarly, a total of 19 antimicrobial resistance (AMR) genes corresponding to the nine drugs used in the disc diffusion assay were evaluated from the whole genome sequence data. The aminoglycoside resistance gene *aac(6)-ly* was detected in 79 of the 82 isolates (96.34%). While the phylogenetic analysis revealed distinct lineages isolated, the three sources indicating possible cross-contamination. In conclusion, the results showed that the genomic profile of *Salmonella Enteritidis* isolated from humans, poultry, and food samples share genetic traits, hence the need to institute measures at controlling the continuous spread of these resistant pathogens.

Keyword: *Salmonella*; *Salmonella enteritidis*; Antimicrobial resistance; Foodborne infections; Phylogenetic studies; Virulence gene profile; Whole-genome sequencing