MULTI-DRUG RESISTANCE AND GENETIC RELATEDNESS AMONG MALAYSIAN SALMONELLA ENTERICA SEROVAR TYPHIMURIUM ISOLATED FROM FOOD AND ANIMALS

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Salmonella Typhimurium is one of the important non-typhoidal salmonellae commonly isolated from live stocks and poultry products in Malaysia. The emergence and expansion of multidrug resistant phenotypes among the Salmonella Typhimurium strains raised public health concern as this may complicate therapeutic options. The purpose of this study was to determine the prevalence of multi-drug resistant (MDR) phenotypes in Salmonella Typhimurium isolated from zoonotic and food sources in Malaysia and their genetic relatedness. A total of 38 strains isolated from zoonotic (n=17) and food (n=21) sources between 1998 and 2009 were examined for resistance to 16 antimicrobial agents. The Kirby-Bauer disk diffusion method was adopted and inhibitory zone was interpreted according to Clinical and Laboratory Standards Institute guidelines. The genetic relationship among the strains was determined by pulsed-field gel electrophoretic separation of XbaI digested bacterial chromosomal DNA. Twenty-nine percent (n=11) of the strains were sensitive to all antimicrobial agents tested. There was a high prevalence (50%) of MDR phenotypes among the strains, isolated over the ten-year period. This indicates the persistence of the MDR phenotypes among Salmonella Typhimurium in Malaysia as early as 1998. A high rate of resistance to sulfonamide (61%), streptomycin (58%), and tetracycline (55%) were observed. Simultaneous resistance to these three antimicrobials constituted the most common (44%) resistance pattern, R-type SSuT, with or without additional resistance to other antimicrobials tested. None of the strains was resistant to third-generation cephalosporins, suggesting these drugs are still useful therapeutic options for invasive salmonellosis. The high genetic similarity between the food and zoonotic strains as shown by PFGE analysis indicates dissemination of MDR Salmonella Typhimurium strains from food animals to human via consumption of contaminated food. In summary, the high prevalence of MDR phenotypes reiterates the need for stricter control of use of antibiotics in animal feeds as food animals indeed play an important role as the reservoir of MDR salmonellae.