

Molecular Analysis of *Salmonella enterica* Serotype Typhimurium and Enteritidis Isolated in Malaysia

B. Douadi¹, N. Ahmad², R.M. Yasin², S.D. Puthuchery³, K.L. Thong¹

¹ Institute of Biological Sciences, Faculty of Science, University of Malaya

² Institute of Medical Research, Kuala Lumpur, Malaysia,

³ Department of Medical Microbiology, Faculty of Medicine, University of Malaya

Salmonella enterica serovars are among the most important agents of food-borne infections throughout the world. Poultry, pigs, and cattle rank as the major sources of *Salmonella*-contaminated food products that cause human Salmonellosis. Currently there are global pandemics of *Salmonella enterica* subsp. *enterica* serovars Enteritidis and Typhimurium. However, from time to time less common serovars emerge and can cause outbreaks in humans or animals. In this study 106 strains of *Salmonella* samples, including 47 *S. Typhimurium* (33 zoonotic, 14 clinical) and 59 *S. Enteritidis* (zoonotic) were tested with 22 antibiotic discs. Overall, 29.24% of strains were multi-drug resistant (resists to more than 3 antibiotics). Besides resistance towards cephalosporin antibiotic, 13.21% of the isolates were resistant to cephalothin, 10.4% to amoxicillin acid, 9.44% to cephradine and 8.5% to cephalexin. In PCR detection of resistant genes (*bla-TEM*, *strA*, *sul*, *aad* and *tet*), antimicrobial resistance genes have been detected among the samples and are thought to be responsible for the emergence of MDR strains. Pulsed-field Gel Electrophoresis (PFGE), repetitive extragenic palindromes (REP) and enterobacterial repetitive intergenic consensus (ERIC) were used to determine the genetic diversity of strains. The results showed wide genetic diversity observed among the analysed strains of *S. Typhimurium* (40 patterns) and also high similarity in *S. Enteritidis* (11 patterns). In conclusion, an emergence of MDR *Salmonella* to 3rd generation of cephalosporin was observed and high heterogeneity was found among the serotypes.