Jpn. J. Infect. Dis., 66, 180-188, 2013

Original Article

Molecular Characterization of *Salmonella enterica* Serovar Typhimurium Isolated from Human, Food, and Animal Sources in Malaysia

Soo Tein Ngoi[1,2], Bjørn-Arne Lindstedt[3], Haruo Watanabe[4], and Kwai Lin Thong[1,2]*

[1]*Institute of Biological Sciences, Faculty of Science, and*
[2]*Laboratory of Biomedical Science and Molecular Microbiology, Institute of Graduate Studies, University of Malaya, Kuala Lumpur, Malaysia;*
[3]*Division of Infectious Diseases Control, Norwegian Institute of Public Health, Oslo, Norway; and*
[4]*National Institute of Infectious Diseases, Tokyo 162-8640, Japan*

(Received November 6, 2012. Accepted February 7, 2013)

SUMMARY: *Salmonella* Typhimurium is an important nontyphoidal *Salmonella* serovar associated with foodborne diseases in many parts of the world. This organism is the major causative agent of nontyphoidal salmonellosis in Malaysia. We aimed to investigate the genetic profiles of the strains isolated from clinical, zoonotic, and dietary sources in Malaysia using multilocus variable number tandem repeat analysis (MLVA) and pulsed-field gel electrophoresis (PFGE). By focusing on the 5 common variable number tandem repeat (VNTR) loci, we found that PFGE (D = 0.99) was more discriminative than MLVA (D = 0.76). The low MLVA score might be because of a lack of VNTR loci STTR6 (81.0%) and STTR10pl (76.2%). Both subtyping methods suggested that our *S.* Typhimurium strains were largely endemic with limited genetic variation. Furthermore, we observed that biphasic *S.* Typhimurium strains were dominant (99%) and multidrug resistance was prevalent (50%) within our sample pool. The most frequently observed phenotypes were resistance to compound sulfonamides (49%), tetracycline (51%), and streptomycin (52%). In this study, we documented the genetic relationship, antimicrobial resistance characteristics, and flagellar-phase dominance among *S.* Typhimurium strains found in Malaysia.

INTRODUCTION

Salmonella enterica serovar Typhimurium is one of the important nontyphoidal *Salmonella* (NTS) serovars associated with foodborne diseases. Notably, the continuous rise in the number of outbreaks of foodborne illnesses is associated with consumption of *Salmonella*-contaminated raw vegetables and fruits and poorly cooked meats (1,2). In Malaysia, *S.* Typhimurium is the most common causative agent of nontyphoidal salmonellosis (3) and is frequently found in infected patients, contaminated food, and animal sources (2,4). *S.* Typhimurium is the dominant NTS serovar (12.7%) isolated from poultry and livestock in this region (4). The prevalence of *S.* Typhimurium poses a threat to public health. In developing countries, the spread of the pathogenic *S.* Typhimurium is mainly attributed to unhygienic practices during food preparation. Evidence supporting this notion can be found in a study in which *S.* Typhimurium was isolated from ready-to-eat (RTE) food (2).

The emergence of multidrug-resistant (MDR) phenotypes of *S.* Typhimurium has been a major public health concern since the 1990s. Detection of MDR strains in animals were previously reported (5,6); presence of MDR strains in animals can often result in human infection via the consumption of contaminated processed meats (7). The prevalence of these MDR strains raised clinical issues because these strains could complicate the currently available therapeutic options.

S. Typhimurium (antigenic profile 4,[5],12:i:1,2) shows motility by means of peritrichous flagella. These flagella are made up of either of the 2 types of flagellar antigens (H:i and H:1,2), which are encoded by flagellin genes *fliC* and *fljB*, respectively (8). Phase transition of biphasic *S.* Typhimurium is achieved by switching between the expressions of the above-mentioned flagellin genes (9). However, since the mid-1990s, a worldwide increase has been observed in the prevalence of *Salmonella* 4,[5],12:i:–, a monophasic variant of *S.* Typhimurium (8,10). Similar to their biphasic counterparts, many of the monophasic variants also show multidrug resistance (10), and therefore, pose an additional threat to public health. Unfortunately, *Salmonella* 4,[5],12:i:– is antigenically similar to *S.* Typhimurium and can thus be easily misclassified as *S.* Typhimurium during conventional serotyping. In this regard, PCR serotyping is gaining increased popularity in recent years because it affords better precision than that afforded by traditional serotyping (11,12).

Detailed strain identification or strain typing is essential for successful epidemiological investigation of *S.* Typhimurium outbreaks. Currently, pulsed-field gel electrophoresis (PFGE) is considered the gold standard

*Corresponding author: Mailing address: Microbiology Division, Institute of Biological Science, Faculty of Science, University of Malaya, 50603, Kuala Lumpur, Malaysia. Tel: +603-79674437, Fax: +603-79675908, E-mail: thongkl@um.edu.my