

Investigation on the occurrence of antimicrobial resistance in enteric pathogens, *Salmonella* Typhi and *S. Paratyphi*, *Shigella* and Shiga toxin-producing *Escherichia coli* (STEC) worldwide

According to WHO, *Salmonella enterica* serovars Typhi (typhoid fever) and Paratyphi A, B or C (paratyphoid fever) infect more than 27 million people annually worldwide, resulting in high rates of morbidity and mortality (over 200,000 deaths per year). Shigellosis is also endemic throughout the world where it is held responsible for some 120 million cases of severe dysentery. About 1.1 million people were estimated to die from *Shigella* infection each year, with 60% of the deaths occurring in children under 5 years of age. Finally, more than 200 *E. coli* serotypes are known to produce Shiga toxins (Stx), and greater than 50 of these serotypes have been associated with bloody diarrhea (i.e., hemorrhagic colitis [HC]) or hemolytic uremic syndrome (HUS) in humans. The most commonly isolated STEC serotypes are O26, O111, and O103, and especially O157:H7. *E. coli* O157:H7 is the most common, even predominant, cause of HUS in most of the world, the STEC most likely to cause epidemics, and the STEC serotype most commonly associated with human gastrointestinal infection.

These infection diseases are mainly transmitted via humans-to-humans by the faecal-oral route, via contaminated food and water, or through person-to-person contact, and are generally associated to developing countries where sanitation and hygiene conditions are poor.

Due to the worldwide importance of these diseases and the impact that the emergence of multi-drug resistant enteric pathogens have in clinical settings, it would be of global benefit to acquire a better understanding on their epidemiology, occurrence and persistence.

Therefore, we encourage all scientists to take part on this global survey by reporting **summarised annual data** on **antimicrobial resistance** in *S. Typhi* and *S. Paratyphi A, B* and *C* (excluding *S. Paratyphi B* serovar **Java**), **STEC** and *Shigella* isolated in your countries **from 2003 to 2007**. This epidemiological study would help to clarify the incidence and distribution of these diseases from a global perspective. The data obtained from this survey intends to draw attention to initiate programmes for prevention and control of these invasive diseases, and to take actions to minimise the level of antimicrobial resistance. Furthermore, these data may also provide guidelines to improve the empiric treatment in order to minimise the usage of critical important antimicrobials for human health.

Please, find attached in this email the protocol and two MS Excel spreadsheet for collection of the relevant epidemiological data. We would be grateful if you could complete the form by the **30th of September** and send it to entericpathogens@food.dtu.dk.

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Protocol:

Two MS excel files has been attached to this email. One of them compiles data for *S. Typhi* and *S. Paratyphi* and the second for Shiga toxin producing *E. coli* (STEC) and *Shigella*.

Each MS excel file contains five sheets, one per each year, from 2003 to 2007. Please, carefully fill out the five sheets with the data you have collected from your country. If you do not have information for one or more fields just leave them blank. We have also included space for some additional information, such as percentage of female affected, median of the age affected and seasonal variations if you have them. For the seasonal variation field we would appreciate if you could provide the percentage of cases isolated during the different seasons.

If you have any further comments you would like to include, there is a “comment” field on the first sheet of each of the MS excel files you are welcome to use.

If you do not wish to participate in the study please reply to this email by writing ”not participating” on the subject of the email.

We would very much appreciate your collaboration and we hope with this study we can contribute to minimize emergence and spread of multi-drug resistant enteric bacteria.