Emergence and clonal dissemination of Salmonella enterica serovar Enteritidis causing salmonellosis in Mauritius

Introduction: For decades, Salmonella enterica serovar Enteritidis has been among the most prevalent serovars reported worldwide. However, it was rarely encountered in Mauritius until 2007; since then the number of non-typhoidal Salmonella serogroup O:9 (including serovar Enteritidis) increased. A study was conducted to investigate the genetic relatedness between S. Enteritidis isolates recovered in Mauritius from food and clinical specimens (stool, blood, and exudate).

Methodology: Forty-seven isolates of S. Enteritidis obtained in 2009 from human stools, blood cultures and exudates, and from food specimens were characterized by antimicrobial susceptibility testing and Multiple-Locus Variable-number tandem Repeat Analysis (MLVA).

Results: With the exception of a single isolate which demonstrated intermediate susceptibility to streptomycin, all isolates were pansusceptible to the 14 antimicrobials tested. Thirty seven out of the 47 isolates (78.7%) exhibited an indistinguishable MLVA profile which included isolates from ready-to-eat food products, chicken, and human clinical isolates from stool, blood and exudate.

Conclusions: The presence of highly related strains in both humans and raw chicken, and the failure to isolate the serovar from other foods, suggests that poultry is the main reservoir of S. Enteritidis in Mauritius and that the majority of human cases are associated with chicken consumption which originated from one major producer. Stool isolates were indistinguishable or closely related to blood and exudate isolates, indicating that, besides gastroenteritis, the same strain caused invasive infections. Control of S. Enteritidis by poultry breeders would lower the financial burden associated with morbidity in humans caused by this organism in Mauritius.