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Study of the avian *Salmonella* contribution to human salmonellosis in Chad: Example of the capital, N'Djamena

Djim-Adjim Tabo

University of N'djamena, Chad

Salmonella are linked to many food-borne diseases worldwide. They are also considered to be one of the main pathogens causing human gastroenteritis. The main objective of this study was to update the prevalence and antimicrobial resistance characteristics of *Salmonella* isolated from poultry and from humans experiencing gastroenteritis in N'Djamena, Chad. The results collected during this study provide the first baseline data on the prevalence of contamination by *Salmonella* in humans suffering from diarrhoea, as well as in laying hens and broiler chicken farms in N'Djamena. Samples were collected on one hand from five hospitals and on another hand from sixteen poultry farms, both over two periods of six months each: from August 2010 to January 2011 and from September 2011 to February 2012.

Diagnostic methods carried out during this study led to the isolation of one hundred and thirty nine *Salmonella* strains, belonging to forty two different serotypes. *Salmonella* Colindale was the most prevalent serovar (13.6% of the isolates belonged to this serovar), followed by *Salmonella* Minnesota (10.8%), *Salmonella* Stanleyville (5.8%), *Salmonella* Havana and *Kottbus* (5% each), *Salmonella* Idikan (4.3%), *Salmonella* Riggil and *Anatum* (3.6% each). Other serotypes were under-represented. The majority of these isolates were susceptible to all antibiotics tested (CLSI Standards), except some *Salmonella* Colindale avian isolates that exhibited a decreased susceptibility to nalidixic acid, ofloxacin and enrofloxacin, two *S. Enteritidis* human isolates resistant to nalidixic acid, ofloxacin and ciprofloxacin, a *S. limete* avian isolate resistant to three antibiotics and 15 *S. Minnesota* avian isolates resistant to five different antimicrobial classes. In order to evaluate the phylogenetic relationships and to find epidemiological links between human and avian strains isolated in the same period of time and in the same region, a total of 139 *Salmonella* isolates found in humans and poultry in this study were characterised by ERIC-PCR and IS200-PCR. The PCR analysis was followed by macrorestriction analysis (PFGE) of genomic DNA from 22 common isolates of *Salmonella* serotypes encountered in both humans and poultry with *Xba*I enzyme. PCR results demonstrated that, in the context of this epidemiological study, ERIC- and IS200-PCR methods can be used effectively to limit the number of isolates that have to be serotyped. The comparison of ERIC-PCR, IS200-PCR, PFGE and antimicrobial susceptibility profiles among isolates from human and avian origins has highlighted, on one hand, the indirect evidence of human contamination sources by *Salmonella* serovars from poultry farms, and on the other hand the diversity of sources and potential reservoirs of *Salmonella* strains in the N'Djamena city.

bekourou2000@yahoo.fr