Emergence of Multidrug Resistant Zoonotic *Salmonella* from Poultry of Savar, Bangladesh

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Abstract: *Salmonella* infection is one of the major constraints of poultry farming that hindered its development in Bangladesh. A study was conducted to investigate *Salmonellae* involved in poultry infection on the basis of five variable farm code, serotypes, resistotypes, and plasmid profiles. The study was extended towards the drug resistant profile against 28 common antibiotics and molecular characterization of *Salmonella* poultry isolates of Savar, Bangladesh. The prevalence of *Salmonella* was found to be 21.1%. A large number of plasmid-free *Salmonella* isolates were found to be resistant to 10-15 groups of antibiotics. The very high unanticipated level of multidrug resistance (MDR) of the isolated *Salmonella* against 28 commonly used therapeutic antibiotics is probably due to widespread use of and easy access to various antimicrobials in the poultry, veterinary, and public health sector in Bangladesh. PCR of 84 isolates using *Salmonella* specific primers ascertained 79, 32 and 3 isolates to be *invA* *sefA* and *fliC* gene positive. Amplified Ribosomal DNA Restriction Analysis (ARDRA) profile using *Alu* I restriction endonuclease digestion of nearly full length 16S rRNA gene of the 84 isolates gave three different restriction types indicating no single source of infection. Sequencing of representatives of each ARDRA groups detected close similarity to *S. Typhimurium*, *S. Enteritidis* and *S. Paratyphi* within the poultry samples indicating significant zoonotic hazard. Presence of identical restriction types in isolates of five different farms indicates the possibility of intrafarm transmission of these bacteria. Emergence of such multidrug drug resistant zoonotic *Salmonella* isolates is indicative of devastating situation of poultry farms in Bangladesh questioning the proper control and management of this economic sector in Bangladesh.

Key words: *Salmonella typhimurium*, *Salmonella enteritidis*, MDR, plasmids, ARDRA, 16S rRNA gene sequence.