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Bacteriological and Molecular Studies on Multiple Antibiotic Resistance Among *Salmonella* Species Isolated From Chicken and its Products

A Thesis Presented by

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8. English Summary

Salmonella Enterica serotype Enteritidis and Typhimurium are considered two of the most interesting foodborne pathogens. The difference in the Antigenic profile of *Salmonella* is accompanied by more disease syndromes.

Rapid monitoring and discrimination of *Salmonella* serovars is an effective means of preventing infection. The use of the traditional serotyping technique is inaccurate to identify strains with rough lipopolysaccharides structure.

Due to a lack of information regarding molecular relatedness among *Salmonella* species in Egypt. This study aimed to elucidate data about the genetic diversity, evolutionary level, and prevalent genotype of the most popularity isolates of *Salmonella* (*S.* Enteritidis and *S.* Typhimurium). Using one of the advances molecular recognition techniques, Multi-locus variable number of tandem repeat analysis (MLVA), to decipher the dynamics and spread of *S.* Enteritidis and *S.* Typhimurium.

A total number of 200 chicken samples, comprising chicken meat products (n=75) and fresh tissue samples from slaughtered boiler chicken (n=125), were collected From Alexandria governorate along the period of December 2017 to December 2019. And cultured for *Salmonella* isolation. 52 samples 26% (52/200) show different bacterial isolates on XLD, which were isolated from pure cultures of chicken organs and chicken product samples. The isolated *Salmonella* were: 17.31% (9/52 isolates) *Salmonella* Enteritidis, 5.77% (3/52 isolates) *Salmonella Typhimurium*.

PCR based IE-1 and flic-C identification revealed that 75% (n=9) of the *Salmonella* were *S.* Enteritidis and 25% (n= 3) were *S. Typhimurium*. Six markers Sal02, Sal04, Sal06, Sal10, Sal20, and Sal23 were applied to 12 samples of extracted DNA from *Salmonella* isolates. The six locus showed allelic diversity. The most discriminatory heterogenic locus for *S.* Enteritidis was Sal20, while Sal04 and Sal23 in the case of *S. Typhimurium*. Results of VNTR allelic profiles analysis reveal 9 unique genotypes for *S.* Enteritidis and 3 for *S. Typhimurium*.