Microbiology Congress 2018: Prevalence, antibiotic resistance and molecular characterization of Salmonella serovars in Lebanese broiler chickens: Focus on Salmonella Kentucky - Rima El Hage - Holi Spirit University of Kaslik

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Non-typhoidal Salmonella sp. of chicken origin has always been the major causative pathogen of food poisoning worldwide. Furthermore, non-responsible use of antibiotics promotes the development of multidrug-resistant bacteria. Since data on Salmonella in poultry industry in Lebanon are scarce, this study was conducted to determine the prevalence of Salmonella at different stages of the production chain, their antibiotic resistance profile and molecular patterns. Over a period of 3 years, samples of feces were collected by a sock method from local Lebanese farms (n=237), poultry meat from slaughterhouses (n=100) and from retail (n=1600).

In parallel, ceca (n=100) and neck skins (n=100) were collected from two major slaughter plants. Isolated Salmonella strains (n=663) were serotyped from which 500 were analyzed for antimicrobial resistance (panel of 29 drugs) using the standard disk diffusion and MIC Method (CLSI guideline). Pulsed-field gel electrophoresis (PFGE) using the macro-restriction enzyme Xbal was used to define the molecular patterns of the main serovars.

The results highlighted a high prevalence in poultry with 30% of positive farms and almost 55% of the samples from slaughterhouses and retail. A large diversity of serotypes was identified with Salmonella infantis (33%), Salmonella enteritidis (28%) and Salmonella kentucky (22%) the most predominant ones. High resistance to Nalidixic acid was shown in all Salmonella strains. No remarkable resistance was detected in Salmonella enteritidis. In addition, Salmonella infantis was resistant to both Streptomycin, Tetracycline at a rate of 100% and 97%, respectively.

However, the most prominent resistance was exhibited in Salmonella kentucky, where all strains (n=133) were multidrug resistant (MDR) and showed 100% resistance to Nalidixic acid, Ciprofloxacin, Norfloxacin and Enrofloxacin and at a significant rate to Ampicillin (72%), Tetracycline (61%), Amoxicillin (59%) and Gentamycin (50%).

Salmonella kentucky were differentiated by PFGE into 10 pulso-types from which six (n=96) showing 94, 2% pattern similarity index. Similar genomic profile and antibiotic-resistance phenotypes were detected between farms, slaughterhouses and retail suggesting the circulation and transmission of identical clones. Furthermore multidrugresistant Salmonella kentucky CIPR (n=9) to 3rd Cephalosporin antibiotics recovered from both slaughterhouse and retail market displayed an identical PFGE pattern. This study reported for the 1st time in Lebanon the high prevalence of Salmonella sp. and the detection of multi-resistant Salmonella Kentucky in poultry. This work highlighted the interconnectedness between different ecologies, through a 'Farm to fork' approach, which urge to establish a strategic plan on Salmonella and the use of antimicrobials in Lebanese poultry industry to protect consumer health. Salmonella represents a large genus of global public health significance and is the leading cause of foodborne illnesses responsible for thousands of deaths worldwide. Salmonella is Gram-negative, rod-shaped bacteria, and facultative anaerobes belonging to the family Enterobacteriaceae.

The genus Salmonella belongs to two broad species namely Salmonella enterica and Salmonella bongori. So far, more than 2600 serovars belonging to S. enterica have been described worldwide, and many of these serovars are capable of causing illnesses in both humans and animals. The SG and SP are associated with clinical disease in poultry, and they cause considerable economic losses – due to the replacement of infected flocks and associated treatment costs – to poultry farmers, especially in developing countries of the world.

In general, the genus has a predilection limited to the digestive tracts of both humans and animals hosts. Thus, the presence of Salmonella in other habitats such as the water, environment, and food represents fecal contamination. Recent data from the United States, European countries, and low- and middle-income countries (LMICs) indicate that Salmonella cases are the most commonly encountered cause of bacterial foodborne disease globally and hence supporting the fact that the control programs aimed at reducing the Salmonella contamination along the food chain have not been successful Consequently, there will be increased frequency and persistence of S. enterica in the intestinal tracts of food animals and this situation creates chronic or non-symptomatic carriers that continue to shed the organism in their feces.

Thus, these carriers serve as reservoirs for future contamination and spread of Salmonella by contaminated milk, meat, eggs and other agricultural products fertilized and grown in Salmonella contaminated manure.