PREVALENCE OF MCR-HARBORING *SALMONELLA* SPP. AND ENTEROBACTERIACEAE ISOLATED FROM MEAT PRODUCTS, FOOD-PRODUCING ANIMALS, AND THEIR ENVIRONMENTS FROM DIFFERENT LOCATIONS IN THE DOMINICAN REPUBLIC

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I. OBJECTIVES

Estimate the prevalence of the *mcr* genes in gram-negative bacteria recovered from retailed meat, food-producing animals, and their production environment in the Dominican Republic.

II. MATERIALS AND METHODS

A total of 80 raw beef, 94 chicken, and 88 pork samples were obtained from various types of meat markets from touristic and production areas in the Dominican Republic. In addition, 330 samples from cattle, swine, and poultry farming operations, animal feces, feed, and water were collected. Each sample was enriched overnight at 37°C in 90 mL of Buffered Peptone Water, using 3 different colistin conditions (0 mg/L, 1 mg/L or 2 mg/L). Real-time polymerase chain reaction was performed to detect *mcr* genes in DNA extractions from the 0 mg/L-colistin overnight enrichment. All *mcr*-positive samples were subjected to Enterobacteriaceae and *Salmonella* spp. isolation procedures. For Enterobacteria, overnight enrichments were streaked on Violet Red Bile Glucose Agar with concentrations of 0 mg/L, 1 mg/L, and 2 mg/L. For *Salmonella* spp., one aliquot from the overnight enrichment of Buffered Peptone Water 0 mg/L colistin was transferred to Brilliant Green Sulfa and Xylose Lysin Tergitol 4 without colistin. Isolated colonies were screened by real-time polymerase chain reaction to detect genes *mcr*-1 through *8*. Positive *mcr* isolates were further characterized using whole genome sequencing.

III. RESULTS

Of the samples, 60.3% (357/592) were found to carry one or more *mcr* genes, 142 from swine, 128 from poultry, and 87 from beef cattle. From the *mcr*-positive samples, a total of 1,940 isolates were tested for *mcr* gene, from which 45.9% (34/74) were presumptive *Salmonella* spp. and 54.1% (40/74) were presumptive Enterobacteriaceae. Overall, multiplex analysis showed that 3.8% (74/1,940) were positive for at least 1 of 8 *mcr* genes. By grouping the *mcr*-positive isolates per animal of origin, it was observed that 53 (71.6%) came from swine, 10 (13.5%) from poultry, and 11 (14.9%) from beef cattle. A total of 27 *mcr*-positive isolates were analyzed by whole genome sequencing. Results showed that only 5 (18.5%) of the 27 isolates were colistin resistant, from which 4 isolates were *Escherichia coli* carrying *mcr*-1 and 1 *Enterobacter cloacae* carrying *mcr*-9.

IV. CONCLUSION

Results showed a high *mcr* sample prevalence (60.3%) compared to a very low *mcr* isolate (3.8%). This is perhaps due the elevated bacterial background on the samples and isolation protocols only focused on *Salmonella* and Enterobacteriaceae. Media used for the latter may not be fully selective for specific members of this family. It is also possible that naked DNA or injured cells carrying the genes were present in the samples.

Keywords: antimicrobial resistance, colistin, Enterobacteriaceae, *mcr* genes