Oral Presentation (MP-3)

Antimicrobial Resistance of *Streptococcus suis* and *Salmonella* sp. Isolates from Selected Swine and Poultry Farms in Regions III and IV in the Philippines

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INTRODUCTION

Swine and poultry industries are significant contributors to the agricultural sector in the Philippines. Specifically, the provinces in Regions III and IV have registered the highest number of pigs and chickens raised and also the highest production of pork, chicken and eggs in the Philippines (1). Despite the increasing trend in chicken and pork production, these agricultural sectors are beset with animal health concerns, particularly, the occurrences of bacterial diseases and indiscriminate use of antimicrobial compounds. The widespread practice of antimicrobial use provides an environment conducive for selection, spread and persistence of antimicrobial-resistant bacteria (2).

Antimicrobial resistance is being encountered in swine and poultry industry with the common respiratory and gastrointestinal diseases of bacterial causes. In this research, the commonly observed opportunistic agent, *Streptococcus suis* was detected in pigs, while the enteric bacteria, *Salmonella enterica* was isolated from chickens. Antimicrobials are important for the control of infectious diseases. However, several studies have shown that the use of antimicrobials has resulted in resistance, making AMR a worldwide concern (3).

MATERIALS AND METHODS

Lungs were collected from pigs in swine farms and slaughter houses from selected provinces in Regions III and IV in the Philippines and a small section of each lung sample was streaked on blood agar plates. The growth of alpha-hemolytic colonies suggestive of *S. suis* was observed. These bacterial samples were later confirmed as *S. suis* through PCR using specific primers. On the other hand, chickens were obtained from different farms in the same Regions in the Philippines and organ samples such as spleen, liver and intestine were collected for bacterial culture. The bacterial colonies showing black centers on XLD were later confirmed as *Salmonella* sp. through PCR. The confirmed *S. suis* and *Salmonell*a sp. isolates were subjected to antimicrobial sensitivity testing (AST) using 13 commercially available antimicrobial discs (ampicillin, gentamycin, tetracycline, trimethoprim-sulfamethoxazole, trimethoprim, erythromycin, spectinomycin, chloramphenicol, ciprofloxacin, ceftriaxone, clindamycin, penicillin, and enrofloxacin) and the antimicrobial resistance (AMR) genes were subsequently identified through PCR.

RESULTS AND DISCUSSION

A total of 56 isolates of *Streptococcus suis* and 28 isolates of *Salmonella enterica* were obtained. Based on AST, the *S. suis* isolates showed highest resistance to tetracycline (94.64%), followed by clindamycin (87.5%), trimethoprim (78.5%), sulfamethoxazole -trimethoprim (75%) and erythromycin (66.07%). As reported in other literature, the most common antibiotics utilized for the treatment of streptococcal infections are macrolides and tetracyclines. Therefore, increased resistance to both of these antibiotics has been observed among pathogenic and commensal Streptococci (4). Specific primer pairs were used to detect the antimicrobial resistance (AMR) genes present in *S. suis* isolates. *erm*B was present in 33 isolates (58.92%) while *mef*A was detected in five of the isolates (8. 92%), both encoding for erythromycin resistance. Tet genes (*tet*L, M, O) encode for tetracycline resistance through ribosomal protection proteins. Thirty-seven (37) isolates (66.07%) were positive for *tet*M, 21 (37.5%) were positive for *tet*O and two (3.575%) for *tet*L. *fex*A encodes for efflux system for phenicols and two isolates (3.57%) were positive for this gene. *lin*B confers lincosamide resistance and 11 isolates (19.64%) were positive for this gene. Resistance to aminoglycosides was attributed to the presence of *aph*(3")- IIIa, *aac*(6')-Ie-aph(2")-Ia, or a combination of both genes. The former was present in 14 isolates (25%) and the latter was detected in 6 isolates (10.71%).

AST results showed that all the 28 *Salmonella* sp. isolates were resistant to clindamycin and erythromycin while all were sensitive to gentamicin, chloramphenicol,

ciprofloxacin and enrofloxacin. The isolates showed relatively high resistance to tetracycline (75%) and penicillin (71.43%). *Salmonella* sp. isolates were also tested for AMR genes. The bla_{TEM} and bla_{CMY2} genes encode for the resistance to beta-lactam antibiotics such as ampicillin and penicillin. Three isolates were positive for bla_{CMY2} and one for bla_{TEM}. Tet genes in *Salmonella* sp. commonly encode for efflux system. In *Salmonella* spp., tetracycline resistance is usually mediated by the *tet*A and *tet*B genes which are the genetic determinants encoding efflux pumps resulting to the removal of the drug from the bacterial cell (5). Among the isolates, 17 (60.71%) were positive for *tet*A and six (21.43%) for *tet*B. *Salmonella* sp. is one of the most frequently isolated bacteria in poultry production. The increasing antimicrobial-resistant *Salmonella* strains isolated from human cases of salmonellosis have been linked with the widespread use of antimicrobial agents in food animal production. This may pose a public health risk due to the transfer of resistant *Salmonella* strains to humans through the consumption of contaminated food and food products (6).

CONCLUSION

The study demonstrated the susceptibility patterns and the resistance genes present in swine pathogens *Streptococcus suis* and the enteric bacterium in avian, *Salmonella enterica*. The rampant use or misuse of antimicrobials may result to the occurrence and spread of antimicrobial resistance since most of these genes can easily be transferred from one organism to another. This phenomenon represents a global concern for both veterinary and public health sectors. Thus, to address these problems, proper antibiotic administration should be practiced like accurate dosing, correct route of administration, observance of withdrawal periods and strict compliance to instructions (7).

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