Risk assessments of antimicrobial resistance in enterobacteria in Thailand and evaluation of control measures of bovine viral diarrhea -mucosal disease in Japan

Norikazu Isoda

Unit of Risk Analysis and Management
Research Center for Zoonosis Control, Hokkaido University

The antimicrobial resistance (AMR) is one of the most important public health issues at global level. As misuse and overuse of antibiotics at husbandry, which are considered to be associated with the risk of emergence and spread of AMR, widely occur in developing countries, monitoring of antimicrobial resistant pathogens in meat production processes is necessary so as to decrease the burden of public health. We surveyed enterobacteria in pig feces to assess the risk of spread of antimicrobial resistant pathogens at commercial farms and to identify risk factors for pathogen spread in Thailand. In 2015, a total of 20 pig farms were selected to be surveyed. Among 235 pigs, 26, 231, and 99 pigs were positive for parasite oocysts, *E.coli,* and *Salmonella* spp., respectively. Resistance rates of the two bacterium species to each of ampicillin, chloramphenicol, cefotaxime, sulfamethoxazole/trimethoprim, tetracycline, streptomycin, and nalidixic acid were similar to those previously reported in Thailand. Resistance to tetracycline, doxycycline, and oxytetracycline was confirmed in 50% of the antimicrobial resistant *E. coli*. Resistance to tetracycline, doxycycline, oxytetracycline, ampicillin, and streptomycin was confirmed in 43% of the antimicrobial resistant *Salmonella spp.* In both bacterium species, resistance rates were strongly correlated among three tetracycline families but not those among three aminoglycoside families. The univariate analysis revealed that decreased appetite in pigs was commonly confirmed as a positive risk factor for infection with parasite oocysts and/or *Salmonella spp.*, and that number of visitors from feed companies to the farms was commonly confirmed as a negative risk factor for infection with *E. coli* and/or *Salmonella spp.*

Bovine viral diarrhea – mucosal disease (BVD-MD) is caused by BVD virus (BVDV) infection in cattle. Infection of pregnant cattle with BVDV often delivers persistently infected calves, which become a major source of BVDV spread throughout their lives. A scenario tree model was developed to propose efficient control measures for BVD-MD using the field data in the eastern Hokkaido where the risk of BVDV infection in cattle has been reduced by an eradication program including mass vaccination, individual test prior to communal pasture grazing, herd screening test using bulk milk, and outbreak investigation of newly infected herds. Since this model enabled us to simulate BVD-MD endemic situations, these 4 activities were then used as hypothesized control measures in the simulation. In each simulation, the number of BVD cattle detected by clinical signs and the diagnosis tests and that of BVD cattle missed by all of the diagnosis tests were calculated, and these numbers were used as indicators to be compared for the efficacy of the control measures. The model outputs indicated that the adoption of mass vaccination surely decreased the number of missed BVD cattle though it did not increase the numbers of detected BVD cattle. Under implementation of mass vaccination, the efficacy of individual tests selected from 20% of the young and adult cattle was equal to that of the herd screening test performed in all the herds. Taken the model outputs together, the scenario tree model developed in our study was useful to compare the efficacy of the control measures for BVD-MD.

Furthermore, the activities for infectious disease control through my carrier at World Health Organization and the current position will be introduced to encourage young colleagues who are interested in activities and works in international organizations.