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Monitoring of antimicrobial resistance and genetic analysis of bacteria from meat and sea food in Korea

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Distribution of antimicrobial resistant bacteria among agricultural, livestock and fishery products of domestic production and imported primary products in Korea was assessed. From the total 200 cases domestic food products analyzed in 2014, 77 *E. coli*, 55 *S. aureus*, 7 *Enterococcus spp.* and 9 *Salmonella spp.* were isolated. Imported 285 samples were analyzed and 29 *E. coli*, 13 *S. aureus* and 9 *Enterococcus spp.* were isolated. For *E. coli*, from domestic primary products, tetracycline, ampicillin, nalidixic acid resistance was relatively high compared to the other antimicrobials. And for imported products streptomycin, tetracycline, ampicillin resistance was relatively higher. In case of *S. aureus* penicillin resistance was higher in domestic products, but in imported products it was lower than results of previous studies. In case of *Enterococcus spp.* overall resistance decreased and continuous monitoring was required in future as number of isolated strains were so few. 2 MRSA strains were isolated from domestic beef and chicken meat and 2 ESBL producing *E. coli* from domestic chicken meat, 1 ESBL producing *E. coli* from imported chicken meat and 5 ESBL producing *Salmonella spp.* from domestic chicken meat were isolated. Tetracycline resistance of *E. coli* from domestic products that was slightly decreased from 57.9% (2013) to 51.9% in 2014 managed decreased level of resistance from resistance levels in 2006. Tetracycline resistance of *E. coli* from imported products showed lower resistance than that of previous year. In case of *S. aureus*, strains from domestic products had lower resistance than previous year and from imported products showed much lower resistance ever. PFGE and rep-PCR based comparative analysis was conducted against isolates of major resistant bacteria, which showed genetic similarity in 2 *Salmonella spp.* strains. Via MLST analysis, one MRSA strain from beef was determined as ST72 and one strain from chicken meat was ST692 and that was similar to precedent study in Korea.

In silico analysis of gene encoding catechol 2,3-dioxygenase (XylE) in *Pseudomonas sp.* degrading crude oil bacteria

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XylE gene is the gene encoding Catechol 2,3-dioxygenase which responsible to degrading of aromatic compounds. The objective of this paper to observe the relationship of the *Pseudomonas sp.* based on amino acid sequence with the potency of degrading crude oil. The method used were collecting amino acid sequence of xylE gen of *Pseudomonas sp.* which obtained from GeneBank (www.ncbi.nlm.nih.gov), analysis of polimorfism obtained by using BioEdit after alignment, The phylogenetic trees were constructed based on protein sequences of xylE gene MEGA5.05 software, The conserved domains of amino acid relationship from 10 kinds of *Pseudomonas* were identified by using BioEdit software. The phylogenetic tree showed that *Pseudomonas putida* is similar to *Pseudomonas stutzeri* and has a close similarity with *Pseudomonas pseudoalcaligenes* based on amino acid relationship. The data indicated that *Pseudomonas putida* shares genetic similarities with *Pseudomonas stutzeri*, and the both of them probably belong to the same potency of degrading crude oil. Based on the polimorfism site, *Pseudomonas mendocina* and *Pseudomonas veronii* have less potency than other *Pseudomonas species* in degrading crude oil.