

Distribution and genetic characteristics of vancomycin-resistant enterococci in domestic food animals

Hyun Mi Kang, Byeong Yeal Jung, Jin San Moon, Min Su Kang,
Jong Man Kim, Choong Il Chung¹

National Veterinary Research and Quarantine Service, Konkuk University¹

Since vancomycin resistant enterococci have first reported in 1988, occurrence incidence of enterococci has increased rapidly all over the world, problems of these enterococci infections are multi-drug resistance for antimicrobial agents such as cephalosporin and amonoglycosides, and also it is easily transferable van gene to other gram positive bacteria. In VRE infection rate against 5 types food animals, high concentration VRE were not isolated in bovine mastitic milk, just intermediate and low VRE isolated 9, 7 strains, respectively, and detected one *VanC*-2 gene using multiplex-PCR method. In case dairy cow feces, intermediate VRE 4 strains and low VRE 38 strains were isolated, and *E. gallinarum* 6 strains and *E. casseliflavus* 28 strains had *VanC*-2 gene. Just low concentration VRE 22 strains isolated from Hanwoo feces, and *E. casseliflavus* 6 strains showing low resistance had *VanC*-2 gene. All strains isolated from porcine feces showed intermediate · low resistance, and all of *E. casseliflavus* 9 strains had *VanC*-2 gene. Three strains of high concentration VRE(MIC \geq 256 $\mu\text{g/ml}$) *E. faecium* 3 strains were isolated in cecum of chicken, and distribution rate of these high concentration VRE was 2.1%(3/144) in chicken. Also intermediate VRE 9 strains, and low VRE 49 strains in chicken were isolated, this results suggest that VRE contamination of chicken was so extended. High concentration *E. faecium* 3 strains was all *VanA* gene, and all of them showed “a” type at PCR-RFLP, and *E. gallinarum* 7 strains had *VanC*-1 gene. In conclusion, high concentration VRE infections in domestic food animals was so low, but was so extended in chicken.