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**Paper Poster Session**  
**The MDR enterococcus**

**Antimicrobial resistance and molecular epidemiology of *Enterococcus faecium* isolated from blood in 25 university hospitals in Korea**

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**Background:** *Enterococcus faecium* is known as one of the most prevalent pathogens in healthcare-associated infections and is associated with high mortality rate in bacteremia patients because it shows natural or acquired resistance to many antibiotics. Currently, vancomycin resistance already became the most notorious problem, but emergence of resistance against recently developed antibiotics may be another disaster in future if we do not manage. In this study, we intended to determine the antimicrobial resistance and molecular epidemiology of *E. faecium* isolated from blood in 25 university hospitals in Korea.

**Material/methods:** A total of 179 *E. faecium* non-duplicated isolates were collected from 25 university hospitals in Korea as a result of Korean Antimicrobial Resistance Monitoring System in 2013. All of them were isolated from blood and transferred to central laboratory in order to determine antimicrobial susceptibility by CLSI disk diffusion and Etest. Multilocus sequence typing (MLST) were performed in all isolates to investigate epidemiologic relatedness.

**Results:** The rates of resistance by CLSI disk diffusion method were 86% to ampicillin, 94% to penicillin, 86% to erythromycin, 55% to high-level gentamicin, 11% to high-level streptomycin, 33% to vancomycin, 28% to teicoplanin, 6% to linezolid, and 3% to quinupristin-dalfopristin. According to Etest interpreted by EUCAST breakpoint, MIC<sub>50</sub>, MIC<sub>90</sub> and resistance rates were 1 mg/L, >256 mg/L and 34% in vancomycin, 0.75 mg/L, >256 mg/L and 33% in teicoplanin, 6 mg/L, 8 mg/L, and 58% in linezolid, 1 mg/L, 2 mg/L and 1% (2 isolates) in quinupristin-dalfopristin, and 0.047 mg/dL, 0.094 mg/dL, and 0.6% (1 isolate) in tigecycline. All of VRE confirmed by disk diffusion and Etest were positive for *vanA* gene. In MLST analysis, 33 sequence types were found. ST17 was the most common ST (27%) and ST1021 which was closely related with ST17 was the next common type (16%). Among 58 isolates of VRE, 13 ST were noted, and ST17 (26%) and ST1021 (22%) were the most common STs like among all isolates.

**Conclusions:** The *E. faecium* isolates isolated from blood were frequently resistant to ampicillin, penicillin and erythromycin. The rate of VRE was 33% and all of them had *vanA* gene. Surprisingly, the resistance rate of linezolid was 58% by EUCAST breakpoint and 23% by CLSI breakpoint. The susceptibility of quinupristin-dalfopristin and tigecycline were well maintained until 2013.