Background: Dissemination of the vancomycin-resistant Enterococcus faecium (VR-EFM) carrying vanA is one of the major global concerns in clinical settings. Clonal spreads of VR-EFM have been reported worldwide repeatedly, and a multilocus sequence typing (MLST) non-typeable EFM due to absence of pstS was described as the major clone for the dissemination of the vanA gene in Australia. This is the first one-year report for traits of EFM during May 2016 and April 2017 from Kor-GLASS consisted with six sentinel hospitals.

Materials/methods: A total of 218 non-duplicated blood isolates of EFM were collected. The isolates were identified with MALDI-TOF mass spectrometry using Bruker Biotyper. Antimicrobial susceptibilities were tested by the disk diffusion method for ampicillin, ciprofloxacin, tetracycline, and quinupristin-dalfopristin and by Etest for vancomycin, teicoplanin, tigecycline, and linezolid on Muller Hinton agar. High-level resistances (HLR) for gentamicin and streptomycin were screened by the disk diffusion test and the inconclusive isolates were tested by the broth microdilution method. PCR was performed for vanA, vanB, and vanM gene. MLST was also performed as described previously.

Results: The most (90.4%) of the isolates were resistant to ampicillin, and the resistance rate to vancomycin (28.9%) was higher than that to teicoplanin (19.3%). HLR to gentamicin (19.7%) was more prevalent than that to streptomycin (2.8%). The isolates of hospital origin exhibited higher resistance rates to glycopeptides than those of community origin (vancomycin, 34.1% vs 10.4%; and teicoplanin 24.1% vs 2.1%). All the isolates of VR-EFM (n=66) possessed the vanA gene, while vanB and vanM were not detected. Some (9/66, 13.6%) of the vanA (+) isolates exhibited the VanB phenotype. The most frequent strain type was ST17 (n=60), of which 25 isolates were vanA (+). A clone of 51 isolates, sharing 6/7 alleles with ST17, were MLST non-typeable with absence of pstS and nine of them were vanA (+).

Conclusions: ST17 and a MLST non-typeable clone with absence of pstS were the major clones responsible for the vanA gene dissemination. Intercontinental dissemination of the MLST non-typeable clone carrying the vanA gene between Australia and South Korea is suspected.
Figure. Distribution of VR-EFM according to the strain type