vancomycin-resistant Enterococcus Outbreak in a Tertiary-care Hospital in Bangkok, Thailand

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Background: Outbreaks and endemic of vancomycin-resistant enterococci (VRE) have been reported in many countries. However, there is little experience and limited data regarding VRE outbreak and intervention strategies in resource-limited settings. We report a first VRE outbreak and molecular epidemiology, as well as the control measurement at our hospital.

Methods: After the first index case of VRE colonization was detected in an 18-bed medical intermediate care unit, a bundle of interventions was simultaneously implemented, including active surveillance cultures for VRE, strict contact precautions, enhanced standard precautions, cohorting positive VRE cases in the dedicated units, extensive cleaning of environmental surfaces, and encourage the restricted use of antibiotics, from June 10 to July 31, 2013. Microbiology and molecular analysis were performed using polymerase chain reaction and random amplified polymorphic DNA.

Results: Among 1498 culture samples from 757 patients screened, 44 (5.8%) patients were found to be colonized with VRE. Of all cases, 39 (88.6%) cases were positive during the first 3 weeks of the study period. All VRE isolates were Enterococcus faecium and all carried the vanA gene. Molecular analysis showed a single predominant clone. During July 2-18, 2013 (17 days), new VRE cases were detected in 2 outpatients who were recently discharged from the positive VRE units, while there was no new case in inpatients.

Conclusions: VRE can easily spread and result in outbreak, particularly in multiple-bed units. Active surveillance, early infection control intervention, and effective patient cohorting play important roles in rapid control of the outbreak.