TYPING OF VANCOMYCIN-RESISTANT ENTEROCOCCI

Aynur Barut, Department of Clinical Microbiology, Aarhus University Hospital, Denmark

BACKGROUND

Enterococci are Gram-positive bacteria, which form chains, and are part of the normal intestinal flora of humans and animals. Enterococci are generally of low pathogenicity, meaning that they rarely cause disease in healthy people. Vancomycin-resistant enterococci (VRE) are Enterococcus species with acquired resistance to the antibiotic vancomycin. Over the past 20 years, VRE has become an increasing problem, especially as a cause of hospital-acquired infections. In the literature, it is well known that the risk of getting VRE generally could be associated with prolonged hospital stays, long-term stay at intensive care unit, previous antibiotic therapy, gender, and age. Even though the number of VRE faecium has increased, especially in the department of hematology, the incidence has been low. Most VRE faecium isolates from 2009 to 2013 at Aarhus University Hospital have not been typed, meaning that it was not known if these isolates were formed as a single clone or different clones.

MATERIALS AND METHODS

In order to fulfill the objective, the following study was assessed as a cross-sectional study. The study data was collected at the Department of Clinical Microbiology, Aarhus University Hospital. The study population consisted of 158 VRE faecium isolates which were identified as VRE faecium in the period of January 2009 to July 2013 from Aarhus University Hospital and Region Hospitals in Randers, and Horsens. The PFGE method was used to determine types of VRE faecium isolates.

RESULT

PFGE was performed on 133 VRE faecium isolates, in which 32 different VRE faecium clones were found. 14 VRE faecium clones represented clusters consisting of at least two and up to 34 VRE faecium isolates. The remaining 18 VRE clones each constituted “unique” clones consisting of a single clone. Clone 1 was significantly more frequent in hematologic patients than in other patients (p < 0.001). Furthermore, clone 1 was statistically significant associated with male patients (p = 0.033). No statistically significant association between clone 1, hospitals, and age was found.

CONCLUSIONS

Based on the findings in this study it could be concluded that the clone 1 was detected predominantly in hematological patients. Exclusive hematological patients, there was no significant association between clone 1 and hospitals. Clone 1 was significantly associated with male patients. Clone 1 and other clones showed no difference in age.