Spread of vancomycin-resistant Enterococcus faecium in two haematological centres in Russia.

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This paper describes the clonal diversity of vancomycin-resistant Enterococcus faecium isolated from patients with haematological malignancies in Russia. Pulsed-field gel electrophoresis (PFGE) typing of 129 vanA-positive E. faecium strains revealed 23 independent restriction profiles with two predominant clonal types. Multilocus sequence typing (MLST) of 16 strains selected from two predominant PFGE types showed that they belong to the epidemic clonal complex (CC) 17. Tn1546-like elements of isolates were compared with the prototype element from E. faecium BM4147 by polymerase chain reaction (PCR). Four different Tn1546 types were distinguished according to structural alternations. Polymorphism in the orf1 and vanSH genes was detected. However, a significant prevalence of the prototype Tn1546 was revealed. Tn1546-like elements with the same structures were observed in strains of different PFGE types. The virulence genes esp, gelE and hyl were detected by PCR in 118 isolates (91%), 87 isolates (67%) and 35 isolates (27%) respectively. In contrast, agg and cylA genes were not found. The detection frequency of esp was higher in epidemic strains than in sporadic ones (100% vs. 56%; P<0.05). This study describes a genetically variable population of vancomycin-resistant E. faecium in two Russian haematological centres. The spread of vancomycin resistance was mostly due to the distribution of the two subclones of E. faecium CC17, enriched with the virulence marker esp. At the same time, dissemination of an altered Tn1546 also occurred. Copyright 2009 Elsevier B.V. and the International Society of Chemotherapy. All rights reserved.

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