T.C.
KAHRAMANMARAŞ SÜTÇÜ İMAM ÜNİVERSİTESİ
BİLİMSEL ARAŞTIRMA PROJELERİ KOORDİNASYON BİRİMİ
PROJE YAYIN DİLEKÇESİ

Proje Adı		
Vankomisine Dirençli Enterokok (VRE) Suşlarında Vankomisin Direnç ve Virülans Genlerinin Multiplex PCR Yöntemi Kullanılarak Tesbiti ile Vankomisin Direnç Genlerinin Endojen veya Eksojen Flora ile İlişkisinin Araştırılması		
Proje No	**Başlama Tarihi**	**Bitiş Tarihi**
2017/7-200 M	19-01-2018	19-01-2020
Yayın Türü	**Yayın / Makele Başlığı**	
Makale	*Determination of Glycopeptide Resistance Genes and Virulence Factors in Vancomycin-Resistant Enterococci Isolates and the Relationship Between Glycopeptide Resistance Genes and Endogenous/Exogenous Flora*	
Dergi ISSN	**DOI**	**Cilt / Sayfa / Yıl**
2980-2156	10.14744/cpr.2024.03419	46 / 145-153 / 2024
Yayınlandıgı Dergi Kısa Ad	**Yayınlandıgı Dergi**	
J CLIN PRACT RES	Journal of Clinical Practice and Research	

İLGİLİ MAKAMA

Yukarıda bilgileri verilen ilgili otomasyona girilmiş yayın bilgileri içerisinde ; *"Söz konusu çalışma/yayın/sunum/poster/bildiri/* ***KAHRAMANMARAŞ SÜTÇÜ İMAM ÜNİVERSİTESİ Bilimsel Araştırma Projeleri birimi*** *tarafından 2017/7-200 M proje numaralı "Vankomisine Dirençli Enterokok (VRE) Suşlarında Vankomisin Direnç ve Virülans Genlerinin Multiplex PCR Yöntemi Kullanılarak Tesbiti ile Vankomisin Direnç Genlerinin Endojen veya Eksojen Flora ile İlişkisinin Araştırılması" konusu ile ilgili olup, ilgili birimce desteklenmiştir." ("This work is supported by the* ***Scientific Research Project Fund of KAHRAMANMARAŞ SÜTÇÜ İMAM ÜNİVERSİTESİ*** *under the project number 2017/7-200 M")* ifadesi yer almaktadır.

PROJE YÜRÜTÜCÜSÜNÜN

Ünvanı, Adı-Soyadı : Dr.Öğr.Üyesi Filiz ORAK

Tarih : 18-10-2024

Bu belge, güvenli elektronik imza ile imzalanmıştır.

Belge Doğrulama Kodu :63bddef80b

Belge Takip Adresi : https://bapotomasyon.ksu.edu.tr/belgedogrula

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Official Journal of Erciyes University Faculty of Medicine

DOI: 10.14744/cpr.2024.03419
J Clin Pract Res 2024;46(2):145–153

Determination of Glycopeptide Resistance Genes and Virulence Factors in Vancomycin-Resistant Enterococci Isolates and the Relationship Between Glycopeptide Resistance Genes and Endogenous/Exogenous Flora

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Cite this article as:
Orak F, Yalçınkaya KT, Aydın F, Karakaya E, Doğaner A, Müştak İB, et al. Determination of Glycopeptide Resistance Genes and Virulence Factors in Vancomycin-Resistant Enterococci Isolates and the Relationship Between Glycopeptide Resistance Genes and Endogenous/Exogenous Flora. J Clin Pract Res 2024; 46(2): 145–153.

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Submitted: 17.10.2023
Revised: 28.11.2023
Accepted: 18.03.2024
Available Online: 16.04.2024

Erciyes University Faculty of Medicine Publications - Available online at www.jcpres.com

ABSTRACT

Objective: This study aimed to identify glycopeptide resistance genes and virulence factors in vancomycin-resistant *Enterococcus* species and to investigate the influence of the microbiota and hospital environment on glycopeptide resistance.

Materials and Methods: A total of 107 enterococcal isolates were collected from patients' rectal swab cultures and environmental samples taken for surveillance purposes. Multiplex Polymerase Chain Reaction (PCR) analysis was conducted to investigate specific virulence genes (*esp, hyl, asa1, cyl,* and *galE*) and glycopeptide resistance genes (*vanA, vanB, van C1-C2, van D, vanE,* and *vanG*). Additionally, perirectal swab cultures were obtained from patients without vancomycin-resistant enterococcal colonization to investigate the presence of glycopeptide resistance genes in their microbiota.

Results: Seven isolates (6.5%) were identified as infectious agents. The most common vancomycin resistance genes were *vanA* (23.3%), followed by *vanA* + *vanB* (14%) and *vanB* + *vanD* (14%), respectively. The Random Amplified Polymorphic DNA Polymerase Chain Reaction (RAPD-PCR) method showed that patient surveillance and environmental isolates were clonally related. Moreover, microbiota analysis of patients without vancomycin-resistant enterococcal colonization revealed *Clostridium* spp. in two patients and *Lactobacillus* spp. in one patient, with the *vanG* gene found in the microbiota of only one (2.5%) patient.

Conclusion: The detection of genes responsible for dissemination indicates that colonized isolates also have the potential for infection, and the hospital environment plays a primary role in the acquisition of vancomycin-resistant enterococci.

Keywords: Vancomycin-resistant *Enterococcus*, multiplex PCR, glycopeptide, virulence, gene.