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Virulence Genes and Antibiotic Susceptibility of *Enterococcus* spp. in Bandar Abbas City, Iran

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ABSTRACT

Backgrounds: In recent years, *Enterococcus* species have emerged as a leading cause of nosocomial infections worldwide. The aim of this study was to determine the virulence biomarkers and antibiotic resistance profiles of *Enterococcus* spp. collected from a main tertiary teaching hospital in Bandar Abbas, Iran.

Materials & Methods: A total of 71 *Enterococcus* were isolated from clinical specimens of patients in different wards of a hospital. *Enterococcus* spp. were verified by detecting *ddl* gene using PCR-based method. Virulence-encoding genes including *gelE* and *cylA* were detected using PCR. Antibiotic resistance was assessed using the disk diffusion assay, and vancomycin resistance was identified using the E-test method.

Findings: Among *Enterococcus* isolates, 50 and 21 isolates were identified as *E. faecalis* and *E. faecium,* respectively. Most of the *Enterococcus* species were isolated from urine, followed by wound samples. The most prevalent virulence genes among *E. faecalis* isolates were *cylA* (60%) and *gelE* (30%); also, 19 and 14% of *E. faecium* isolates were positive for *cylA* and *gelE* genes, respectively. Many isolates of *E. faecalis* (84%) and *E. faecium* (76%) were resistant to one or more antibiotics and showed high resistance to gentamicin and ciprofloxacin.

Conclusion: This study revealed a high prevalence of ciprofloxacin and gentamicin resistance and a high frequency of virulence genes among *E. faecalis* isolates. Due to the high prevalence of MDR *Enterococcus* strains, control measures are necessary to prevent the emergence and transmission of these strains in different hospital wards.

Keywords: *Enterococcus faecalis*, *Enterococcus faecium*, Antibiotic resistance, Virulence factors

CITATION LINKS

[1] Masoumi Zavaryani S, Mirnejad R, Piranfar V, Moosazadeh Moghaddam M, Sajjadi N, Saeedi S. Assessment ... [2] Benamrouche N, Guettou, B, Henniche FZ, Assaous F, Laouar H, Ziane H, et al. ... [3] Arbabi L, Boustanshenas M, Rahbar M, Owlia P, Adabi M, Rasouli Koohi S, et al. Antibiotic susceptibility ... [4] Sumpradit N, Wongkongkathep S, Malathum K, Janejai N, Paveenkittiporn W, Yingyong T, et al. Thailand's national strategic plan on ... [5] Chen X, Ma K, Yi X, Xiao Z, Xiong L, Wang Y, et al. A novel detection of Enterococcus faecalis using multiple cross ... [6] Ferguson DM, Talavera GN, ... [7] Kiruthiga A, Padmavathy K, Shabana P, Naveenkumar V, Gnanadesikan S, Malaiyan J. Improved detection of *esp, hyl, asa1, gelE,* and... [8] Vankerckhoven V, Autgaerden TV, Vael C, Lammens C, Chapelle S, Rossi R, et al. Development of... [9] Hemalatha G, Bhaskaran K, Sowmiya M, Anusheela A, Sethumadhavan K. A study on ... [10] Abedini P, Soleimani N. A review of designing new vaccines to prevent ... [11] Kafil HS, Asgharzadeh M. Vancomycin-resistant ... [12] Golob M, Pate M, Kušar D, Dermota U, Avberšek J, Papic B, et al. Antimicrobial resistance and virulence ... [13] Church DL. Aerobic bacteria. In: Leber AL, editor. Clinical ... [14] Haghi F, Lohrasbi V, Zeighami H. High incidence of virulence determinants, aminoglycoside and ... [15] Clinical and Laboratory Standards Institute. M100S: Performance standards for antimicrobial susceptibility testing. 26th Edition. Wayne: Clinical and Laboratory ... [16] Sattari-Maraji A, Jabalameli F, Node Farahani N, Beigverdi R, Emaneini M. Antimicrobial resistance pattern, virulence determinants and molecular ... [17] Gawryszewska I, Zabicka D, ... [18] Niu H, Yu H, Hu T, Tian G, Zhang L, Guo X, et al. The prevalence of ... [19] Jia W, Li G, Wang W. Prevalence and... [20] Somily AM, Al-Mohizea MM, Absar MM, Fatani AJ, Ridha AM, Al-Ahdal MN, et al. Molecular epidemiology of ... [21] Heidari H, Emaneini M, Dabiri H, Jabalameli F. Virulence factors ... [22] Çopur SS, Şahin F, Göçmen JS. Determination of virulence and multidrug resistance... [23] Alotaibi FE, Bukhari EE. Emergence of... [24] Rostamzadeha S, Mirnejadb R, Masjedian Jazic F, Masoumi Zavaryanid S, Saeidia S, Zahedi Bialvaeie A. Molecular... [25] Banerjee T, Anupurba S. Prevalence of virulence factors and drug resistance in clinical isolates of enterococci: A study from North India. J Pathog. 2015;2015. ... [26] Soares RO, Fedi AC, Reiter KC, Caierao J, d'Azevedo PA. Correlation... [27] Chajecka-Wierzchowska W, Zadernowska A, ... [28] Arshadi M, Mahmoudi M, Motahar MS, Soltani S, Pourmand MR. Virulence ... [29] Medeiros AW, Pereira RI, Oliveira DV, Martins PD, d'Azevedo PA, Van der Sand S, et al. Molecular detection of...

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Introduction

Enterococcus species are considered as a major part of the gastrointestinal tract normal flora, the third leading cause of bacterial infections, the fourth leading cause of nosocomial infections, and the second leading cause of urinary tract infections worldwide [1]. *Enterococcus* spp. are important causes of nosocomial infections, especially in patients with prolonged hospital stays, immunocompromised patients, or those previously treated with broad-spectrum antibiotics. These isolates are the causative agents of multiple infections such as bacteremia, surgical site infections, urinary tract infections, and endocarditis [2]. *Enterococcus faecium* (*E. faecium*) and *Enterococcus faecalis* (*E. faecalis*) species are the most common causes of healthcare-associated and nosocomial infections. *E. faecalis* is responsible for 80% of all *Enterococcus* infections. However, a recent study reported that the prevalence of *E. faecium* increased during 2012 to 2019, while the prevalence of *E. faecalis* remained stable for 10 years [3, 4]. The traditional method used to detect *Enterococcus* spp. is bacterial growth on a culture medium, while this method takes more than 24-48 hrs. Moreover, after antimicrobial therapy, the number of bacteria is significantly reduced. Polymerase chain reaction (PCR)-based techniques are applied to detect microorganisms because these methods are sensitive and specific [5]. The pathogenesis of *E. faecalis* and *E. faecium* species isolated from hospitalized patients is attributed to an array of genes encoding virulence biomarkers, including hyaluronidase (*hyl*), gelatinase (*gelE*), aggregation substance (*asa1*), enterococcal surface protein (*esp*), cytolysin (*cylA*), and collagen-binding-protein (*ace*) [6]. Gelatinase hydrolyzes gelatin and collagen, causing damages to host tissues and facilitating bacterial spread, colonization, and biofilm formation. Cytolysin production by hemolytic strains significantly contributes to the exacerbation of enterococcal infections. Cytolysin-encoding genes (cyl) are integrated into a chromosome or carried on a plasmid [7, 8].

Enterococcus spp. are increasingly resistant to two or three groups of antimicrobial agents, known as multiple-drug resistant (MDR) strains. These strains show resistance to aminoglycosides, fluoroquinolones, penicillin, and glycopeptides [9, 10]. Also, the emergence of vancomycin-resistant enterococci (VRE) with high levels of resistance to aminoglycoside and vancomycin poses great challenges for controlling enterococci infections [11]. Teicoplanin and vancomycin-resistant strains are of great concern due to the extensive therapeutic use of these antibiotics against MDR enterococci infections. *Enterococcus* spp. are intrinsically resistant to many antibiotics. Intrinsic resistance of *E. faecium* to many antimicrobial agents, especially glycopeptides, as well as *E. faecalis* to quinupristin/dalfopristin and clindamycin has been reported [12].

Objectives: This study was designed to determine the prevalence, virulence genes, and antibiotic resistance profiles of *E. faecalis* and *E. faecium* isolates collected from a main tertiary teaching hospital in Bandar Abbas, southern Iran.

Methods and materials

Clinical samples: In this study, 71 *Enterococcus* isolates were collected from different wards of a main tertiary teaching hospital in Bandar Abbas located in the south of Iran (Payambar-e-Azam therapeutic center) during 2017-2018, including outpatient department (OPD), internal, neurology, cardiac care unit (CCU), intensive care unit (ICU), ear-nose and throat (ENT), gastroenterology, burn, urology, and surgery rooms. *Enterococcus* isolates were

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retrieved from various clinical samples, including urine (n=51), wound (n=9), blood (n=3), abdominal drainage aspirate (n=3), bronchoalveolar lavage (n=2), abscess (n= 2), and central venous catheter (n=1). Clinical samples were collected from 41 females and 30 males. They belonged to different age groups, including ≤15 years (n=4), 15 to 30 years (n=14), 30 to 45 years (n=24), and 45 to 85 years (n=29). All specimens were cultured on blood agar (Merck, Germany). Then in order to confirm *Enterococcus* isolates, standard biochemical and bacteriological tests were used according to the standard protocols [13].

DNA extraction*: Enterococcus* isolates genomic DNA was extracted by CinnapureTM DNA extraction kit (Cinnagen, Iran).

***Enterococcus* spp. isolation**: To verify *E. faecium* and *E. faecalis* isolates, the *ddl* gene was detected by PCR-based method as described previously [11] (Table 1). Confirmed *E. faecium* and *E. faecalis* isolates were stored at -70 °C for further study.

Virulence genes: Multiplex PCR was performed to determine the presence of enterococcal virulence genes (*cylA*, and *gelE*) as described previously [14] (Table 1).

Antimicrobial susceptibility testing: Antibiotic susceptibility testing of *Enterococcus* isolates was performed by disk diffusion method following the Clinical Laboratory Standards Institute guidelines using commercial antimicrobial disks (Mast. Co., UK), including ciprofloxacin (5 µg), ampicillin (10 µg), vancomycin (30 µg), gentamicin (10 µg), teicoplanin (30 µg), linezolid (30 µg), and tigecycline (15 µg). The minimum inhibitory concentration (MICs) of vancomycin was determined using the E-test method based on the CLSI guidelines (2016). MIC breakpoints to determine vancomycin susceptibility were as follows: MIC values ≤4 were considered as sensitive, between 4-32 as intermediate resistant, and ≥32 as resistant [15].

Findings

Bacteria: A total of 71 *Enterococcus* isolates, comprising 50 (70%) *E. faecalis* and 21 (30%) *E. faecium,* were isolated. Most *Enterococcus* species were isolated from patients in the age range of 30-45 and 45-85 years. *E. faecalis* strains were mostly isolated from urine (n=35; 70%), followed by wound (n=6; 12%), blood (n=3; 6%), abdominal drainage aspirate, broncoalveolar lavage, and abscess (n=2; 4% for each of them) samples; also, 21 *E. faecium* strains were isolated from urine (n=16; 76%), wound (n=3; 14%), abdominal drainage aspirate, and central venous catheter (n=1; 4% for each of them) samples (Table 2). The clinical departments from which *Enterococcus* spp. were isolated (Table 2) included: OPD (n=26), internal (n=18), surgery (n=9), ICU (n=6), burn (n=4), urology (n=3), CCU (n=2), neurology (n=1), ENT (n=1), and gastroenterology (n=1).

Table 1) Primers used for identification of *Enterococcus* species and virulence genes in this study

Target	Sequence (5′ to 3′)	Ref
ddl (*E. faecalis*)	ATCAAGTACAGT TAGTCTTTATTAG ACGATTCAAAGCTAACTGAATCAGT	8
ddl (*E. faecium*)	TTGAGGCAGACCAGATTGACG TATGACAGCGACTCCGATTCC	8
gelE	CGAAGTTGGAAAAGGAGGC GGTGAAGAAGTTACTCTGA	11
cylA	ACTCGGGGATTGATAGGC GCTGCTAAAGCTGCGCTT	11

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Table 2) Characteristics of *E. faecium* and *E. faecalis* isolates

Ward*	Species	Sample**	Resistance Pattern***	MIC (µg/mL)	Virulence Genes
OPD	*faecium*	Urine	VA, CIP, GM, TEC	-	-
	faecium	Urine	VA, CIP, GM, TEC	0.75	-
	faecium	Urine	VA, CIP, AP, TEC	1.5	-
	faecalis	Urine	VA, CIP, GM, TEC	0.5	-
	faecium	Urine	CIP, AP, GM	-	-
	faecalis	Urine	CIP, GM	-	*gelE*
	faecalis	Urine	CIP, AP	-	-
	faecalis	BAL	CIP, GM	-	*cylA*
	faecalis	Urine	CIP, GM	-	*cylA*
	faecalis	Urine	CIP, GM	-	*cylA*
	faecalis	Urine	CIP, GM	-	*cylA*, *gelE*
	faecalis	Urine	GM	-	-
	faecalis	Urine	GM	-	*cylA*, *gelE*
	faecalis	Urine	GM	-	*cylA*, *gelE*
	faecalis	Urine	GM	-	*cylA*
	faecalis	Urine	GM	-	*cylA*
	faecalis	Urine	GM	-	*cylA*
	faecalis	Urine	-	-	*cylA*, *gelE*
	faecalis	Urine	-	-	*gelE*
	faecium	Urine	-	-	-
	faecalis	Urine	-	-	*cylA*
	faecalis	Urine	-	-	*cylA*
	faecalis	Urine	-	-	*cylA*
	faecalis	Urine	-	-	*cylA*
	faecium	Urine	-	-	*cylA*, *gelE*
	faecium	Urine	-	-	-
Internal	*faecium*	Abdominal	VA, CIP, AP, GM, TEC	0.5	-
	faecalis	Urine	VA, CIP, AP, GM, TEC	2	-
	faecalis	Urine	VA, CIP, AP, GM, TEC	-	*gelE*
	faecium	Urine	VA, CIP, AP, GM, TEC	1.5	-
	faecium	Urine	VA, CIP, AP, GM	1.5	-
	faecium	Urine	VA, CIP, AP, GM	0.75	*cylA*
	faecalis	Blood	CIP, GM, LZD	-	-
	faecium	Urine	GM, TGC	-	*gelE*
	faecalis	Abscess	CIP, GM	-	-
	faecalis	Urine	CIP, GM	-	*cylA*
	faecalis	Urine	GM	-	*gelE*
	faecium	Urine	GM	-	-
	faecalis	Wound	CIP	-	*cylA*, *gelE*
	faecalis	Urine	GM	-	*gelE*
	faecium	Wound	GM	-	*cylA*
	faecalis	Urine	GM	-	*cylA*
	faecium	Urine	-	-	*gelE*
	faecalis	Urine	-	-	*cylA*

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Table 2) Characteristics of *E. faecium* and *E. faecalis* isolates

Ward*	Species	Sample**	Resistance Pattern***	MIC (µg/mL)	Virulence Genes
Surgery	*faecalis*	Urine	VA, CIP, AP, GM, TEC	0.75	*cylA*
	faecalis	Wound	VA, CIP, GM, TEC	0.5	-
	faecium	Wound	VA, GM, TEC	0.75	-
	faecalis	Wound	VA, CIP, GM	1.5	*cylA*
	faecalis	Abdominal	CIP, AP	-	*cylA*
	faecalis	Abdominal	GM	-	*gelE*
	faecalis	Abscess	GM	-	*gelE*
	faecium	Urine	GM	-	-
	faecium	Urine	GM	-	-
ICU	*faecalis*	Urine	GM, LZD	-	-
	faecium	Catheter	VA, TEC	-	-
	faecalis	Blood	GM, TGC	-	*cylA*
	faecalis	Urine	CIP, GM	-	-
	faecalis	Urine	CIP, GM	-	-
	faecalis	Urine	CIP, GM	-	*cylA*
Burn	*faecalis*	BAL	AP, GM	-	*cylA*
	faecalis	Wound	GM	-	*cylA*
	faecium	Wound	GM	-	*cylA*
	faecalis	Wound	-	-	*cylA*
Urology	*faecalis*	Urine	CIP, GM	-	*cylA*
	faecalis	Wound	GM	-	*cylA*
	faecalis	Urine	GM	-	*cylA*, *gelE*
CCU	*faecalis*	Urine	CIP, GM	-	-
	faecium	Urine	-	-	-
Digestive	*faecalis*	Blood	CIP, GM	-	*gelE*
Neurology	*faecalis*	Urine	GM	-	*cylA*
ENT	*faecalis*	Urine	GM	-	*cylA*, *gelE*

*OPD: outpatient department
**BAL: broncoalveolar lavage, abdominal: abdominal drainage aspirate, catheter: central venous catheter
***CIP: ciprofloxacin, AP: ampicillin, VA: vancomycin, GM: gentamicin, TEC: teicoplanin, LZD: linezolid, TGC: tigecycline

PCR detection of virulence genes among *Enterococcus* isolates: Among *E. faecalis* isolates, *cylA* was the most prevalent gene (n=30; 60%), followed by *gelE* (n=15; 30%). Seven *E. faecalis* isolates were positive for both *gelE* and *cylA* genes. Among *E. faecium* isolates, four (19%) isolates possessed *cylA* gene, whereas three (14%) isolates showed the genetic marker *gelE*. Only one *E. faecium* isolate possessed both *gelE* and *cylA* genes (Table 2).

Antibiotic resistance profiles: In the disk diffusion assay, 42 (84%) *E. faecalis* isolates were resistant to one or more antibiotics, and the highest resistance was shown against gentamicin (n=39; 78%), ciprofloxacin (n=23; 46%), vancomycin and ampicillin (n=6; 12% for each of them), teicoplanin (n=5; 10%), linezolid (n=2; 4%), and tigecycline (n=1; 2%). Out of 21 *E. faecium* strains isolated, 16 isolates (76%) showed resistance to at least one antibiotic. The highest resistance was observed against gentamicin (n=14; 67%), followed by vancomycin (n=9; 43%),

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ciprofloxacin (n=8; 38%), teicoplanin (n=7; 33%), ampicillin (n=6; 28%), and tigecycline (n=1; 5%). In addition, eight *E. faecalis* and five *E. faecium* isolates were sensitive to all of the antibiotics surveyed in this study. The antimicrobial resistance profile of *Enterococcus* isolates is presented in Table 2. Designation of MIC levels showed that 11 *Enterococcus* isolates were susceptible to vancomycin with MIC values in the range of 0.5 to 2 µg/mL (Table 2).

Discussion

In the current study, virulence genes and antibiotic susceptibility profiles of *Enterococcus* spp. isolated from clinical samples were investigated. The isolation rate of *E. faecalis* (70%) was higher than that of *E. faecium* (30%). This finding contradicts the findings of other studies in which the prevalence of *Enterococcus* species isolated from clinical specimens has been reported in favor of *E. faecium* [16-18]. Haghi et al. (2019) in northwestern Iran reported that *E. faecalis* isolates were the predominant enterococci isolated from urine samples, which is similar to the results of the current study [14]. Another study in Iran indicated that *E. faecalis* isolates were more prevalent among enterococci derived from various clinical samples [3]. These results show that the prevalence of *Enterococcus* species varies in different clinical samples and geographical regions.

MDR enterococci as the main pathogens have become a serious problem in nosocomial infections [14]. In this study, 82% of *Enterococcus* isolates were resistant to one or more antibiotics. The prevalence of antibiotic resistance among *E. faecalis* isolates was more than in *E. faecium* isolates; also, the results showed a high prevalence of MDR *Enterococcus* isolates in urine specimens. Most *Enterococcus* isolates were sensitive to linezolid and tigecyclin (97% for each). Previous studies in Iran have shown a high frequency of antibiotic resistance among *Enterococcus* spp., except linezolid, tigecycline, and fosfomycin [11, 14]. A study in China reported a high prevalence of resistance to rifampicin, penicillin, ampicillin, fosfomycin, ciprofloxacin, chloramphenicol, levofloxacin, erythromycin, quinupristin/dalfopristin, minocycline, and tetracycline among *Enterococcus* spp., while the prevalence of resistance to vancomycin, teicoplanin, and linezolid was low in *E. faecium* and *E. faecalis* isolates [19]. Screening of antimicrobial resistance indicated that 75% of the isolates were resistant to gentamycin, which is similar to the results of recent studies indicating that the prevalence of gentamycin resistance ranges from 50 to 65% [20, 21]. In the current study, resistance to vancomycin in *E. faecium* and *E. faecalis* isolates was 43 and 12%, respectively. Another study in Iran showed that the prevalence of vancomycin resistance in *E. faecium* isolates was more than in *E. faecalis* isolates [3]. In a study in Turkey, Çopur et al. (2016) reported a high frequency of vancomycin resistance among *E. faecium* isolates (95.6%) compared to *E. faecalis* isolates (4.3%), and most VRE strains were isolated from specimens of surgery clinics and intensive care units [22]. A higher prevalence rate of VR among *E. faecium* isolates was also reported in a study in Saudi Arabia (62.3%) [23]. In this study, 8% of VRE isolates were isolated from clinical samples of the internal ward, and 6% were isolated from samples of OPD and surgery rooms. A previous study reported that the high prevalence of antibiotic resistance detected in ICU and burn hospital wards may be attributed to immunodeficiency, long-term antibiotic use, and patients' critical illness [19].

In this study, the *gelE* gene was detected in 30% of *E. faecalis* and 14% of *E. faecium*

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isolates, this finding is consistent with the finding of a previous Indian study documenting a high frequency of *gelE* among *E. faecalis* compared to *E. faecium* [7]. In another study in Iran, most *Enterococcus* spp. (79.7%) isolated from clinical samples carried the *gelE* gene; also, 82% out of 128 *E. faecalis* isolates and 60% out of 15 *E. faecium* isolates harbored *gelE* [24]. Banerjee and Anupurba (2015) reported that among enterococci strains isolated from clinical samples, the *gelE* gene was detected in 9.6 and 8.3% of *E. faecalis* and *E. faecium* isolates, respectively; also, most virulence factors were associated with biofilm formation [25]. For invasive *Enterococcus* isolates (infective endocarditis), virulence biomarkers may be more relevant to other traits than adherence, such as collagen and gelatin degradation (by *gelE* gene) which may be relevant to dissemination and invasion [26].

Cytolysin, encoded by *cylA,* is a bacteriocin-type exotoxin with hemolytic activity towards eukaryotic cells. This exotoxin exhibits toxic properties against erythrocytes, leukocytes, and macrophages and bactericidal properties towards Gram-negative bacteria. Cytolysin-encoding sequences (*cyl*) have been detected in *Enterococcus* strains isolated from both invasive and non-invasive infections [27]. Arshadi et al. (2018) in Iran reported that 7.1, 6.2, and 0% of *E. faecium* intestinal isolates, clinical isolates, and environmental isolates possessed hemolysin gene, respectively [28]. In the present study, the frequency of *cylA* gene among *Enterococcus* strains isolated from clinical specimens was 48% (60 and 19% among *E. faecalis* and *E. faecium* strains, respectively). A study in Brazil reported the presence of *cyl* genes in 54.4% of clinical enterococcal strains [29].

Conclusion

This study data indicate that *E. faecalis* isolates carry more virulence genes than *E. faecium*. Thus, we are faced with MDR *E. faecalis* strains with virulence and antimicrobial resistance genes which enable them to adapt and survive in hospital settings and cause severe infections. Infections caused by VRE and MDR isolates could be associated with high mortality in patients. Given that most of the isolates were sensitive to linezolid and tigecycline, it is suggested that therapeutic strategies be reviewed according to new antimicrobial resistance patterns.

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Conflict of Interest: There is no conflict of interest between the authors.

Authors' Contribution: Conceptualization: KA, AH, DT; data curation: KA, DT; formal analysis: KA, DT; funding Acquisition: DT; investigation: KA, AH, DT; methodology: KA, AH, DT; project administration: KA; resources: DT; software: DT; supervision: KA, AH; writing of the original draft: KA, AH; writing-review and editing: KA, AH, DT.

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Consent to participate: Written informed consents were obtained from participants.

References

1. Masoumi Zavaryani S, Mirnejad R, Piranfar V, Moosazadeh Moghaddam M, Sajjadi N, Saeedi S. Assessment of susceptibility to five common antibiotics and their resistance pattern in clinical Enterococcus isolates. Iran J Pathol. 2020;15(2):96-105.
2. Benamrouche N, Guettou, B, Henniche FZ, Assaous F, Laouar H, Ziane H, et al. Vancomycin-resistant Enterococcus faecium in Algeria: Phenotypic and

[DOI: 10.52547/iem.8.2.129]

genotypic characterization of clinical isolates. J Infect Dev Ctries. 2021;15(1):95-101.
3. Arbabi L, Boustanshenas M, Rahbar M, Owlia P, Adabi M, Rasouli Koohi S, et al. Antibiotic susceptibility pattern and virulence genes in *Enterococcus* spp. isolated from clinical samples of Milad hospital of Tehran, Iran. Arch Clin Infect Dis. 2016;11(3):e36260.
4. Sumpradit N, Wongkongkathep S, Malathum K, Janejai N, Paveenkittiporn W, Yingyong T, et al. Thailand's national strategic plan on antimicrobial resistance: progress and challenges. Bull World Health Organ. 2021;1;99(9):661-73.
5. Chen X, Ma K, Yi X, Xiao Z, Xiong L, Wang Y, et al. A novel detection of Enterococcus faecalis using multiple cross displacement amplification linked with gold nanoparticle lateral flow biosensor.Infect Drug Resist. 2019;12:3771-81
6. Ferguson DM, Talavera GN, Hernández LAR, Weisberg SB, Ambrose RF, Jay JA. Virulence genes among *Enterococcus faecalis* and *Enterococcus faecium* isolated from coastal beaches and human and nonhuman sources in southern California and Puerto Rico. J Pathog. 2016;2016.
7. Kiruthiga A, Padmavathy K, Shabana P, Naveenkumar V, Gnanadesikan S, Malaiyan J. Improved detection of *esp, hyl, asa1, gelE,* and *cylA* virulence genes among clinical isolates of enterococci. BMC Res Notes. 2020;13(1):1-7.
8. Vankerckhoven V, Autgaerden TV, Vael C, Lammens C, Chapelle S, Rossi R, et al. Development of a multiplex PCR for the detection of *asa1*, *gelE*, *cylA*, *esp*, and *hyl* genes in enterococci and survey for virulence determinants among European hospital isolates of Enterococcus faecium. J Clin Microbiol. 2004;42(10):4473-9.
9. Hemalatha G, Bhaskaran K, Sowmiya M, Anusheela A, Sethumadhavan K. A study on virulence factors and antimicrobial resistance pattern among enterococci isolated from various clinical specimens from a tertiary care hospital. Int J Res Med Sci. 2017;5(7):2969-74.
10. Abedini P, Soleimani N. A review of designing new vaccines to prevent hospital-acquired antibiotic-resistant infections. Int Electron J Med. 2018;7(2):21-9
11. Kafil HS, Asgharzadeh M. Vancomycin-resistant Enteroccus faecium and Enterococcus faecalis isolated from education hospital of Iran. Mædica. 2014;9(4):323-7.
12. Golob M, Pate M, Kušar D, Dermota U, Avberšek J, Papic B, et al. Antimicrobial resistance and virulence genes in Enterococcus faecium and Enterococcus faecalis from humans and retail red meat. Biomed Res Int. 2019;2019.
13. Church DL. Aerobic bacteria. In: Leber AL, editor. Clinical microbiology procedures handbook. 4th ed. USA, Washington DC: ASM Press; 2016.
14. Haghi F, Lohrasbi V, Zeighami H. High incidence of virulence determinants, aminoglycoside and vancomycin resistance in enterococci isolated from hospitalized patients in Northwest Iran. BMC Infect Dis. 2019;19(1):1-10.
15. Clinical and Laboratory Standards Institute. M100S: Performance standards for antimicrobial susceptibility testing. 26th Edition. Wayne: Clinical and Laboratory Standards Institute; 2016.
16. Sattari-Maraji A, Jabalameli F, Node Farahani N, Beigverdi R, Emaneini M. Antimicrobial resistance pattern, virulence determinants and molecular analysis of Enterococcus faecium isolated from children infections in Iran. BMC Microbiol. 2019;19(1):1-8.
17. Gawryszewska I, Zabicka D, Bojarska K, Malinowska K, Hryniewicz W, Sadowy E. Invasive enterococcal infections in Poland: The current epidemiological situation. Eur J Clin Microbiol Infect Dis. 2016;35(5):847-56.
18. Niu H, Yu H, Hu T, Tian G, Zhang L, Guo X, et al. The prevalence of aminoglycoside-modifying enzyme and virulence genes among enterococci with high-level aminoglycoside resistance in Inner Mongolia, China. Braz J Microbiol. 2016;47(3):691-6.
19. Jia W, Li G, Wang W. Prevalence and antimicrobial resistance of Enterococcus species: A hospital-based study in China. Int J Environ Res Public Health. 2014;11(3):3424-42.
20. Somily AM, Al-Mohizea MM, Absar MM, Fatani AJ, Ridha AM, Al-Ahdal MN, et al. Molecular epidemiology of vancomycin resistant enterococci in a tertiary care hospital in Saudi Arabia. Microb Pathog. 2016;97:79-83.
21. Heidari H, Emaneini M, Dabiri H, Jabalameli F. Virulence factors, antimicrobial resistance pattern and molecular analysis of enterococcal strains isolated from burn patients. Microb Pathog. 2016;90:937-.
22. Çopur SS, Şahin F, Göçmen JS. Determination of virulence and multidrug resistance genes with polymerase chain reaction method in vancomycin-sensitive and resistant enterococci isolated from clinical samples. Turk J Med Sci. 2016;46(3):877-91.
23. Alotaibi FE, Bukhari EE. Emergence of vancomycin-resistant enterococci at a teaching hospital, Saudi Arabia. Chin Med J. 2017;130(3):340-6.
24. Rostamzadeha S, Mirnejadb R, Masjedian Jazic F, Masoumi Zavaryanid S, Saeidia S, Zahedi Bialvaeie A. Molecular characterization of the virulence genes *gelE* and *cylA* in the Enterococcus species isolated from clinical samples. Meta Gene.

[DOI: 10.52547/iem.8.2.129]

2020;24:100695.
25. Banerjee T, Anupurba S. Prevalence of virulence factors and drug resistance in clinical isolates of enterococci: A study from North India. J Pathog. 2015;2015.
26. Soares RO, Fedi AC, Reiter KC, Caierao J, d'Azevedo PA. Correlation between biofilm formation and *gelE*, *esp,* and *agg* genes in Enterococcus spp. clinical isolates. Virulence. 2014;5(5):634-7.
27. Chajecka-Wierzchowska W, Zadernowska A, Laniewska-Trokenheim L. Virulence factors of Enterococcus spp. presented in food. LWT. 2017;75:670-6.
28. Arshadi M, Mahmoudi M, Motahar MS, Soltani S, Pourmand MR. Virulence determinants and antimicrobial resistance patterns of vancomycin-resistant Enterococcus faecium isolated from different sources in Southwest Iran. Iran J Public Health. 2018;47(2):264-72.
29. Medeiros AW, Pereira RI, Oliveira DV, Martins PD, d'Azevedo PA, Van der Sand S, et al. Molecular detection of virulence factors among food and clinical Enterococcus faecalis strains in South Brazil. Braz J Microbiol. 2014;45(1):327-32.

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