

## عنوان مقاله:

Comparative analysis of virulence genes, antibiotic resistance and capsule locus polymorphism of *Enterococcus faecalis* isolated from canals of root-filled teeth with periapical lesions with those from different clinical infections and fecal flora

## محل انتشار:

بیستمین کنگره بین المللی میکروب شناسی ایران (سال: 1398)

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## نویسندگان:

Roya Ahmadrajabi - *Department of Microbiology and Virology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran*

Arash Shahravan - *Endodontology Research Center, Kerman University of Medical Sciences, Kerman, Iran*

Fereshteh Saffari - *Department of Microbiology and Virology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran*

Mohammad Hossein Sobhanipoor - *Department of Microbiology and Virology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran*

## خلاصه مقاله:

**Introduction and Objectives:** *Enterococcus faecalis* (*E. faecalis*) is considered normal flora in human but has been considered a leading cause of hospital-acquired infections. In the oral cavity, it is commonly detected from canals of root-filled teeth with periapical lesions. The aim of this study was to compare antibiotic resistance patterns, the presence of virulence factors and capsule locus polymorphism among *E. faecalis* isolates recovered from different sources. **Materials and Methods:** Eighty-eight *E. faecalis* isolates recovered from canals of root-filled teeth with apical periodontitis (n=22), human blood and CSF as invasive isolates (n=22), urine and wound as non-invasive isolates (n=22) and fecal flora of healthy individuals (n=22) were examined. Resistance to different antibiotic agents was determined by disk diffusion method. Phenotypic method was used to determination of gelatinase production and biofilm formation. Polymerase chain reaction technique was used to detection of *esp*, *ace*, *ebp*, *gelE*, *cyl*, *cps1*, *cps2*, *cps5* and *cbh* genes. **Result:** The antibiotic susceptibility of the isolated dental, invasive, non-invasive and fecal *E. faecalis* showed the presence of multidrug resistant isolates. This property was significantly more common in non-invasive compared with fecal isolates ( $P=0.022$ ). Antimicrobial resistance rates were not significantly different between isolates from root canals and fecal flora ( $p>0.05$ ). There were significantly different among isolates from root canals and fecal flora in gelatinase production ( $p=0.009$ ) and strong biofilm formation ( $p=0.003$ ). *E. faecalis* isolates from root canals carried *cyl* gene at a significantly higher frequency than invasive infections ( $p=0.002$ ) and fecal flora ( $p=0.035$ ). The presence of the *esp* gene was also significantly different between root canals isolates and the other isolates ( $p=0.000$ ). The most common type of capsule locus polymorphism among the root canals isolates was CPS 1 (63%) which suggests the lack of essential genes in *cps* operon for capsule production in these isolates. **Conclusion:** This study demonstrated that there are major genetic differences between the *E. faecalis* isolates from root canal infections and those from clinical and normal flora. Knowledge about the characterizations of *E. faecalis* isolated from different sources may help to find appreciated procedures preventing enterococcal infections

**کلمات کلیدی:**

;Enterococcus faecalis; virulence factors; antibiotic resistance; apical periodontitis; infection; normal flora

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