

State of Globe: Enterococci: Virulence Factors and Biofilm Formation

Enterococcus causes a variety of infections that most infections associated with burns, wound infections, and urinary tract; and also implicated in endocarditis, pyogenic infections, pelvic infections, blood stream, and intra-abdominal infections.^[1-3] Two species of Enterococci associated with nosocomial infections are *Enterococcus faecalis* and *Enterococcus faecium*.^[4] Enterococci play both as commensals and as pathogens in the human body because of its many virulence factors (VFs) associated with capsule formation including gelatinase, enterococcal surface protein, biofilm formation, and aggregation substance.^[4] Biofilms formation is very important in *in vivo* environment such as the human body and other living systems and also on medical devices favors disease because it reduces the influence of antimicrobials.^[3] In the recent years, *E. faecium* has led to an increase in the prevalence of urinary tract infection in the worldwide and dominant detectable species among *Enterococcus* spp. The impact on the colonization of enterococci in the intestinal tract seems to be mainly based on the presence of different VFs.^[5] In this study, we discuss on the present VFs and biofilm formation in *Enterococcus* spp. Bacterial adherence is a necessary step to establish infection in the host and vital step in initiation of any infection process. For this purpose, different VFs exist in bacteria. Some studies believed that the increased incidence of *E. faecalis* and *E. faecium* infection has been related to present VFs and biofilm formation. Several virulence molecules associated with infection by *E. faecalis* isolates have been described; these molecules include cytolysin encoded by *cylA*, aggregation substance encoded by the gene *asa1*, enterococcal surface protein encoded by *esp* gene, gelatinase encoded by *gelE* and hyaluronidase encoded by *hyl*.^[6,7] Studies have shown that some virulence genes such as cytolysin (*Cyl*), aggregation substance (*asa1*), enterococcal surface protein (*esp*), hyaluronidase (*hyl*), and gelatinase (*gelE*) are related to pathogenicity of enterococci in the human and animal models.^[6,8] Some genes are located on specific regions of the genome, distinctively the area

known as “pathogenicity islands.”^[9] VFs play a key role in bacterial survival in special conditions such as in the human blood and exposure to serum and poor environments that cause diseases. Some studies believed that there is a direct relationship between VFs and biofilm formation, and hence they increase bacterial pathogenicity.^[1,6] In some studies, all enterococci strains were able to grow under limiting conditions because they are able to express several factors adhesion and biofilm formation.^[1,6,10]

Enterococci are intrinsically resistant to multiple antimicrobial agents normally used to treat infections resulting from Gram-positive bacteria. Multiple antibiotic resistances in enterococci have been held responsible for the emergence of *E. faecium* as a dominant species, especially as vancomycin-resistant enterococci (VRE) isolates. Treatment of infections with opportunistic pathogens such as VRE has been a great challenge.^[3,5]

Enterococcus has clearly emerged as an opportunistic pathogen, causing outbreaks of many nosocomial infections,^[1] an organism causing severe surgical wound infections, urinary tract infections, bacterial endocarditis, and bacteremia.^[3] In summary, correlation between the presences of virulence markers and biofilm formation are necessary for tissue invasion, adhesion and causing disease in the human body. Frequent screening for these VFs may contribute to a better understanding of infection, infection control measures and to the investigate new treatment options.

In final, the article entitled, “Molecular Characterization of Virulence genes in Vancomycin Resistant and Vancomycin Sensitive Enterococci” is a good study in which the authors evaluated VFs and vancomycin-resistant genes in clinical isolates of enterococci from various clinical specimens in Tertiary Care Hospital, Eastern Bihar, India. High distribution of virulence gene is important in clinical settings. Thus, additional

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understanding on the co-occurrence of resistance and VFs would be valuable.

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