Genetic Distribution of *fsr* and *srt* Virulence Genes in *Enterococcus faecalis* Clinical Isolates

Dear Editor,

Enterococcus faecalis is found in most healthy individuals but can cause urinary tract infections (UTIs), meningitis, and other infections in humans. The fecal streptococci regulator (*fsr*) quorum-sensing system controls biofilm development by regulating the production of gelatinase.[1] Sortase (*srt*) is a transmembrane protein responsible for adhesion to the cell wall of gram-positive bacteria, such as *E. faecalis*.[2]

This study aimed to detect some virulence genes among *E. faecalis* isolates from May to August 2023. A total of 100 clinical specimens were taken from patients suffering from different infections, such as UTI, bacteremia, wound infections,and gastroenteritis , who were admitted to Hilla Surgical Teaching Hospital. The specimens were inoculated and incubated on chromogenic agar. The Geneaid Kit was utilized to isolate the genomic DNA of *E. faecalis*. Polymerase chain reaction conditions and primer sequences were employed.[3,4] The results of this study indicated that 20 isolates related to *E. faecalis* were collected from the following sites: eight isolates (40%) obtained from urine samples, four isolates (20%) from stool, six isolates (30%) from wound for each, six isolates (30%) from the vagina, while two (10%) were isolated from blood samples, as shown in Table 1.

There are several reasons for variations in *Enterococcus* isolation, such as hygienic hospital and staff practices, geographic locations, environmental factors, patients' social and cultural status, the use of multidrug medications that can cause bacterial resistance, and variations in specimen size. These factors can all work together to either prevent or promote the development of bacterial resistance.[5]

Recent years have witnessed increased interest in enterococci not only because of their ability to cause serious infections but also because of their increasing resistance to many antimicrobial agents.[6,7]

In this study, it was shown that *E. faecalis* isolates from urine express more virulence factors or harbor attenuated virulence genes than isolates from other clinical samples, as shown in Table 2.

The existence of several genes and virulence factors in bacteria that are both opportunistic and harmful does not, however, identify which of them might be most crucial for the pathomechanism of infections, because it is a multi-stage, intricate process that depends on a number of variables, such as bacterial virulence, host and habitat conditions, and the presence of additional microbiota components.[7]

However, these virulence determinants play an important role in mediating disease severity and pathogenicity through colonization and invasion of host tissue. The pathogen possesses more than one virulence factor to

Table 1: Distribution of *Enterococcus faecalis* isolates and statistical analysis from different infection sites

infection site	Total specimens	*E. faecalis* isolates (*n*)	Percentage (%)	Odds ratio (vs. blood)	Interpretation
Urine	43	8	18.6	2.67	Higher likelihood in urine samples
Wound	21	6	28.6	2.50	Higher likelihood in wound samples
Blood	16	2	12.5	1.00 (reference)	–
Stool	20	4	20.0	–	–
Total	100	20	100	–	–

Table 2: Prevalence and statistical analysis of *fsr* and *srt* virulence genes in *Enterococcus faecalis* isolates

Sample type	Number of isolates	*srt* gene detected (*n*)	*fsr* gene detected (*n*)	Chi-square (χ^2)	*P* value	Interpretation
Urine	8	8	4	0.86	0.836	No significant association
Wound	6	5	2	–	–	–
Blood	2	1	0	–	–	–
Stool	4	4	3	–	–	–

facilitate its attachment and establishment and then competes with other pathogens in the same environment to cause disease.[8]

The results of our study indicated that numerous genes that encode potential virulence factors are shared by isolates of *E. faecalis* from UTIs, and strains isolated from various sources exhibit unique patterns of possible virulence factors. However, as virulence factors may manifest *in vivo* under ideal circumstances, their presence in the clinical isolates may contribute to the severity.

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Conflicts of interest

There are no conflicts of interest.

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