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DETECTION OF SOME PUTATIVE VIRULENCE GENES BY PCR IN LOCAL STRAINS OF *ENTEROCOCCUS FAECALIS*

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ABSTRACT

In this study, 39 strains of *Enterococcus faecalis* were collected and isolated from different sources including (stool, urine samples and vagina swabs), where, 18 (46%) strains were isolated from human intestine (stool), 14 (36%) from urine, and 7 (18%) from vagina.

Some putative virulence genes were detected by using specific PCR primers which include *mefA/E*, *msrC, asa1 and ace genes.* The results of this study showed that four strains of *E. faecalis* possessed the (*mefA/E)* gene, two from urine strains 2:14 (14%), one from vagina 1:7 (14%) and one from stool 1:18 (5.5%). Besides only one strain which was isolated from vagina 1:7(14%) gave positive amplicon for *(msrC)* gene, where as the others did not have this gene. On the other hand only four strains gave positive results for *ace* gene 2 (14%) from urine and 2 (28.5%) from vagina, where as all strains gave positive results for *asa1* gene.

Keywords: *Enterococcus faecalis,* PCR, *asa1* Gene

INTRODUCTION

Enterococcus faecalis is a Gram positive bacterium, facultative anaerobic andnon-spore forming, microscopically appear as short chains, pairs, or in single cells. They inhabit at the intestine of humans as normal commensals **[1]**.

Enterococcus are common inhabitants of the human intestinal micro flora and the genitourinary tract of men and women **[2]**. They are now recognized as important causes of health care-associated infections including urinary tract infections, postsurgical wound infections, bacteremia, endocarditis, meningitis, neonatal sepsis **[3]**.

There are many virulence associated factors which have an essential role in causing disease. The dual genes *mef A/E* and *msr C*