IDENTIFICATION OF SUF MACHINERY IN *ENTEROCOCCUS FAECALIS* V583 AND PRESENCE OF POSSIBLE FE/S PROTEINS RELATED TO CYTOLISIN THROUGH *IN SILICO* ANALYSIS

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Iron-sulfur [Fe-S] clusters are ubiquitous and evolutionary ancient inorganic prosthetic groups and its biosynthesis and insertion into various protein partners, coordinated by cysteine ligands, depends on complex protein machineries. Three distinct assembly systems involving the maturation of cellular Fe/S proteins (Nif, Isc and Suf systems) have been described in several organisms, but in Gram positive bacteria these machineries are poorly determined and some studies have linked Fe/S proteins to virulence factors in other microorganisms. The enterococcal cytolysin is a toxin and bacteriocin secreted by pathogenic and nonpathogenic Gram-positive bacteria and proteins are coded in an operon containing six genes. The aim of the present study was to identify [Fe-S] cluster protein machineries in *Enterococcus faecalis* V583 genome sequence through *in silico* analysis and search for cysteine residues in the primary protein sequences of cytolisin operon. Bioinformatic approaches using genomic BLAST program reveals the presence of a genes locus encoding six putative Suf proteins; SufBCDS and NifU-like, which are highly conserved in Gram positive bacteria such as *Streptococcus*, *Staphilococcus* and *Bacillus spp*. The primary protein sequence analysis of the cytolisin operon showed four Fe/S proteins candidates (CylM, CylB, CylI,$CylL_{LS}$) with numerous cys residues, which could anchor [Fe-S] clusters and evidence either the Fe/S protein presence and its feasible involving in an *E. faecalis* pathogenesis process.