SCOPE

AND PLAN
CHAPTER III

SCOPE AND PLAN OF THE STUDY

Enterococci are considered as an important nosocomial pathogen, due to their potential virulence characteristics and increased resistance to antibiotics. Knowledge of antibiotic resistance and its mechanism are important for treatment and control of infections.

Enterococci are intrinsically resistant to β-lactam antibiotics, aminoglycosides, sulphonamides, cephalosporins and streptogramin A types. Species of enterococci are capable of adapting to certain antibiotics due to intrinsic traits present on their chromosome.

Some species in enterococci such as *E. gallinarum, E. flavescence* and *E. casseliflavus* are intrinsically resistant to low levels of vancomycin, *E. faecalis* is intrinsically resistant to quinupristin-dalfopristin, clindamycin and streptogramin A and *E. faecium* strains carrying *aph(6′)-II* gene are intrinsically resistant to aminoglycosides. Thus speciation of enterococci plays a vital role in determining the appropriate antibiotic for treatment.

These organisms acquire resistance genes by enzyme encoded mechanisms and by acquiring plasmids or transposons especially to mediate resistance to high levels of aminoglycoside, macrolide and glycopeptide antibiotics. Thus, the multiple drug resistance in enterococci had reduced the treatment options to treat severe enterococcal infections.

Recent reports have shown higher frequency of high level aminoglycoside (HLARE), macrolide (MLS<sub>B</sub>) and glycopeptide resistance
(VRE) in enterococci. However, the patterns of infections and incidence of resistance are highly variable among countries. Local statistics are of crucial value for selection of empirical therapy. In depth studies are limited in molecular epidemiology of HLARE and VRE in our country.

The knowledge of virulence factors in Enterococcus species helps to understand the pathogenic nature and its complex pathogenic mechanisms isolated from various clinical samples.

The classification of plasmid replicons in enterococci and other gram positive bacteria has emerged as a new area of research and this had raised the knowledge of the repA classes (replication initiation gene type) distributed among pathogenic species of enterococci.

Around 19 rep families had been reported in enterococci and they are grouped into super families such as primases (rep1 pIP501, rep2 pRE25, rep3 pXO02 and rep12 pBMB67), topoisomerases I (rep4 pMBB1, rep5 pN315, rep6 pS86, rep11 pEF1071 and rep18 pEF418), RepL (rep10 and rep10b), Rep_1 (rep13 pC194 and rep16pSAS) and RepA_N rep8 pAM373, rep9, rep17 pRUM, rep15 pSK41 and rep19 pUB101). The study on plasmid replicon types may bring out basic knowledge on the characteristic of plasmids and their significance among isolates of enterococci.

Hence the present study has focused on the prevalence of different mechanisms of resistance and virulence factors along with the distribution of plasmid replicon types among enterococci.
3.1. Objectives

The objectives of this study were

1. To analyze the species distribution of enterococci obtained from different clinical sources.

2. To detect the antibiotic resistance profile of enterococci and to screen for HLAR, VRE and macrolide resistance by phenotypic methods and to characterize their mechanism of resistance by PCR.

3. To detect the prevalence of virulence determinants among all the isolates of enterococci by both phenotypic and molecular methods.

4. To detect the prevalence of plasmid replicon types and their distribution in resistant and virulent enterococcal isolates.