APPLICATION OF MULTILOCUS SEQUENCE ANALYSIS FOR MOLECULAR CHARACTERIZATION OF ENTEROCOCCI WITH VIRULENCE FACTORS RECOVERED FROM A TROPICAL RECREATIONAL BEACH

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Abstract. Partial gene sequences of phenylalanyl-tRNA synthase alpha subunit (pheS) and RNA polymerase alpha subunit (rpoA) were evaluated for species delineation and detection of recombination among enterococci populations recovered from a bathing beach impacted by low tide river flow. At inter-species level, a maximum similarity of 86.5% and 94.8% was observed among the enterococci pheS and rpoA sequence, respectively. A superimposed plot of delimited pair-wise similarity values obtained for 266 pair-wise observations revealed that while there was a harmony between species identity obtained from both genes, pheS was more discriminatory than rpoA. The difference was more pronounced for inter-species comparison. A number of putative recombination events between indigenous and non-indigenous strains was detected based on a library of aligned sequences. Virulence genes cyl, esp, gelE and asa were detected in 7, 22, 100 and 63%, respectively among river isolates but at lower proportion of 0, 20, 67 and 42%, respectively among beach water isolates. Random amplified polymorphic DNA profiling presented evidence suggesting low tide river as a source of fecal enterococci entering the recreation beach water. Multilocus sequence typing analysis of a number of Enterococcus faecalis isolates presented four sequence types, ST59, 117, 181 and 474. The presence of genetically diverse fecal enterococci with associated virulence traits and a background of recombination events in surface recreational water could present a potential public health risk.

Keywords: enterococci, MLST, pheS, RAPD, recombination, rpoA, sequence type