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SUMMARY OF THESIS*

SILVA, Marise Sobreira Bezerra da - **A análise das regiões espaçadoras intergênicas do rRNA 16S-23S em diferentes gêneros bacterianos.** Recife, 2002. (Tese de Doutorado – Universidade Federal de Pernambuco).

ANALYSIS OF 16S-23S rRNA INTERGENIC SPACER REGIONS OF DIFFERENT BACTERIAS

Bacterial ribosomes carry three types of rRNA: 23S, 16S and 5S encoded in genes organized in operons separated by intergenic spacer regions (ISRs) containing one or more tRNA genes. The genetic information derived from the rRNA operon provides a valuable taxonomic information, since the ISRs, especially those located between the 16S and 23S regions of the rDNAs, suffer lesser evolutionary pressure, then they present greater genetic variation than the regions encoding for the rRNAs. Ribotyping has being applied successfully to detect genetic polymorphism among bacteria. In this work, we analyzed the amplification profile of the ISRs obtained by PCR using primers drawn to complementary sequences of the conserved regions 16S-23S of the rRNA genes from several bacteria species in samples of *Staphylococcus aureus*, *Providencia alcalifaciens* and the three pathogenic species of *Yersinia*. The amplification patterns of the ISRs obtained revealed to be characteristic for each genus and species. Seven ribotyping profiles had been observed among the *S. aureus* strains studied and more than forty profiles in *P. alcalifaciens* evidencing great genetic polymorphism in these species. The strains of *Y. pseudotuberculosis* and *Y. pestis* analyzed displayed the same amplification profile which was different from the *Y. enterocolitica* profile. Four distinct ribotyping profiles were observed in the *Y. enterocolitica* strains analyzed. The profiles obtained from the three species had been analyzed by sequencing and restriction. The results confirmed the high homology between *Y. pseudotuberculosis* and *Y. pestis,* attributed to the *Y. pestis* evolution, supposed to be a clone derived from *Y. pseudotuberculosis*.

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