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SUMMARY OF THESIS*

LEAL, Tereza Cristina Arcanjo - **Análise dos plasmídeos e do loco *pgm* em diferentes cepas de *Yersinia pestis***. Recife, 2001. (Tese de Doutorado – Centro de Ciências Biológicas da Universidade Federal de Pernambuco).

ANALYSIS OF THE PLASMIDS AND LOCUS *pgm* IN DIFFERENT STRAINS OF THE *Yersinia pestis*

The virulence of *Yersinia pestis*, the causative agent of plague, depends on plasmidial and chromosomal genes. It was observed that a region of the *Y. pestis* chromosome (locus *pgm*) is deleted in high frequency. Initially it was supposed that these deletions occurred in block. However, recently it was evidenced independent modifications in the two segments (iron acquisition and pigmentation segments) that compose this locus. Previous studies on Brazilian *Y. pestis* strains stocked at the laboratory showed that some of them displayed an atypical plasmid profile, characterized by the absence of some plasmid or the presence of extra-cryptic DNA bands. In the present study, it was demonstrated that those DNA bands resulted from "in vitro" rearrangement of the typical *Y. pestis* plasmids. Furthermore it was observed that the stability of the strains varies among them: the strain P. CE 882 proved to be stable and no alteration on its plasmid profile neither in the *pgm* locus was produced after two years of storage nor through serial subculturing on the Congo Red Agar medium (CRA). However, for some unexplained reasons, its virulence in mice decreased. The strains P. Exu 340 and P. Peru proved to be unstable and their virulence in mice decreased according to the modifications of their plasmid profiles and phenotypes in the CRA medium. PCR amplifications with specific primers evidenced modifications in the *pgm* locus of the cultures displaying different phenotypes, proving that the events of deletion of that locus involve specific rearrangement besides the homologue recombination among the IS100 that flank the region. A new type of culture that had not been described before (*psn*/*fyuA*+;*irp2*-) was identified in this study.

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