

TITLE: IDENTIFICATION OF BACTERIOPHAGES IN SAMPLES *Enterobacter aerogenes*: POSSIBLE STRATEGY FOR PATHOGEN CONTROL.

AUTHORS: SILVA, J.R.M; BEZERRA, E.C.S; REZENDE, M.A.; GALHARDO, R.S.; LOPES, A.C.S; CABRAL, A.B.; ALVES, I.R.

INSTITUTION: UNIVERSIDADE ESTADUAL DE CIÊNCIAS DA SAÚDE DE ALAGOAS, MACEIÓ, ALAGOAS (R. DR. JORGE DE LIMA, 113 – TRAPICHE DA BARRA, CEP 57010-300, MACEIÓ, AL, BRAZIL)

ABSTRACT:

Bacteriophages are multidrug-resistant viruses that infect prokaryotes, their applicability and recognition as a mechanism of biocontrol against bacterial pathogenic species is increasingly gaining importance in the medical field, recently due to the increase in the onset of infections resistant to traditional Antimicrobials. Thus, the present study aimed to identify the genes related to bacteriophages in colonization samples and isolates of *Enterobacter aerogenes* infection, From the intensive care unit of a public Hospital in Recife-PE, as a possible strategy for controlling pathogens. Its identification was performed by manual and precise analysis of the genes registered in the colonization and infection isolate. In this context, data bases were used and scientific literature with the purpose of highlighting the genes that are related to bacteriophages in the isolates of infection and compares them with the genes found in the colonization isolate thus allowing to discuss the current panorama of virus infection in these bacterial samples. Regarding the results obtained in the genome of the isolate from colonization, 5845 chromosomal genes and 439 plasmid genes were identified, among these 83 genes were related to bacteriophages in chromosome DNA and 10 genes in plasmidial DNA, already referring to the genes of the infection isolates, were totalized 1051 genes, among these quantified 40 genes were related to bacteriophages. In this context it is possible to verify that in the colonization isolate it was possible to identify a higher number of genes related to bacteriophages. Being important, for example, to cite, *Phage integrase* that its function is necessary for the integration of the Phagus into the host genome by specific recombination of the site, the *Lytic enzyme* that are produced during infection by Bacteriophages responsible for the ability of these bacterial cell lyse viroses, and the viral protein *Probable Bacteriophage integrates* that is involved in the entry of the virion in the host cell and other genes related to the lysogenic cycle. It is therefore possible to conclude that although the isolates analyzed have genes related to bacteriophages and some with function in the lysogenic cycle, deeper analyses should be performed to prove that they are exclusively lytic, since some genes also identified have not yet defined function.

KEYWORDS: ENTEROBACTÉRIAS; PHAGES; BIOLOGICAL CONTROL.

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