

TITLE: PHYLOGENETIC RELATIONSHIPS OF ISOLATED ANTAGONISTIC ISOLATES IN COMPOST BARN SYSTEM

AUTORS: FAUSTINO, M. A.1 ; CESAR, D. E.1 ; DEL'DUCA, A.2 ; RODRIGUES, E.M.3.

INSTITUTION: 1. UNIVERSIDADE FEDERAL DE JUIZ DE FORA - BRASIL; 2.INSTITUTO FEDERAL DE CIÊNCIAS TECNOLOGIA DO SUDESTE DE MG - BRASIL; 3.INSTITUTO FEDERAL DO CEARÁ CAMPUS CAMOCIM - BRASIL.

ABSTRACT

The Compost Barn (CB) is an alternative dairy cows confinement system on mattresses mainly composed of sawdust. To environmental conditions contribute the system presents great quantity and complexity of microorganisms. It's known that some species are causing pathogenesis in the animal such as mastitis. Previous studies prove isolated bacterias from this system have shown capability of inhibit the development of potential pathogenic species. To analyse the phylogenetic proximity from bacterial isolates with antagonistic activity obtained in two farms in Minas Gerais, which share the system. From the two farms twenty six isolated were selected presenting halos between 3 mm and 20 mm. DNA extraction was performed by the protocol PCR (DNeasy Blood & Tissue kit, Qiagen) using the primers 27F and 806R from the marker 16S rRNA, afterwards was submitted to the Sanger sequencing. The sequences were aligned at the sequencing with the acquired at GeneBank to make the alignment possible. Athwart the tool from Mr. Bayes applied the interference Baysiana to an estimation of phylogenetic approximation. Analysis of the tree evidenced phylogenetic proximity between the isolated bacteria from the farms. It is noticeable that the environment of the bed, by the conditions imposed that compose the environment select some bacteria. Taxonomic isolates were found of the same species and phylogenetically close taxonomic groups, which can execute similar physiological functions as the case with *Bacillus* sp. and *Bacillus licheniformis*, which presents inhibition halos with close sizes compared to an isolated of *Sthaphylococcus aureus*. The Bayesian inference show that occurs variation in the phylogenetic distance between the isolated. Phylogenetically distant groups presents the formation of inhibition halos, as with the case of *Acinebacter* sp., *Pseudomonas* sp., *Escherichia coli*, *Lysinibacillus* sp., *Exiguobacterium* sp. and *Enterococcus* sp.. In conclusion our work demonstrated that the Compost Barn system selects bacterias from different phylogenetic distances and even isolated with minor phylogenetic proximity are capable of acting as antagonists of potential pathogenic microorganisms.

Keywords: Antagonistic bacteria, Baysian interference, Compost Barn, Pathogenic microorganisms, Phylogenetic analysis.