## Poster (Painel)

## 791-1 THE SULFUR-PROCESSING COMMUNITY OF MANGROVES UNDER DISTINCT HISTORIC OF CONTAMINATION IN BRAZIL

Autores: <u>Ademir Durrer (ESALQ - Escola Superior de Agricultura)</u>; Maryiemy Varon Lopez (ESALQ -Escola Superior de Agricultura); Armando Cavalcante Franco Dias (CENA - Centro de Energia Nuclear na Agricultura); Cristiane Cipola Fasanella (ESALQ - Escola Superior de Agricultura); Rodrigo Gouvea Taketani (EMBRAPA - Embrapa Meio Ambiente); Itamar Soares de Melo (EMBRAPA - Embrapa Meio Ambiente); Fernando Dini Andreote (ESALQ - Escola Superior de Agricultura)

## Resumo

The mangrove is a coastal ecosystem, which represents the transition between terrestrial and marine environments. In Brazil there are about 15% (26,000 Km2) of the global mangrove area. The characteristics of mangrove sediments are the anaerobiosis, the high salinity and the abundance of non-decomposed organic matter, making it optimal for anaerobic microorganisms, such as sulphatereducing bacteria. However, despite the range of methodological approaches available for assessing the major microbial players in the sulphur cycle, it is still poorly described in the mangroves. In this study, two genes related to sulphur transformations were target (dsrB and aprA) in a survey involving three mangroves located in the coastline of the São Paulo State (Brazil): i) oil-contaminated mangrove at Bertioga, ii) anthropogenic-impacted mangrove at Bertioga, iii) non-disturbed mangrove at Ilha do Cardoso. Samples were subjected to the estimative of the diversity and abundace by denaturing gradient gel electrophoresis (DGGE), followed by multivariate analyses (Cluster and one-way analysis of similarity), by clone libraries of target genes with results analyzed by Mothur and the quantification of target genes was made by real time PCR (qPCR). In general, results have indicated that both genes studied in the three mangroves have distinct structures. However, the analysis of dsrB gene has determined that anthropization is the most significant factor modulating the diversity of such gene, while the analysis based on gene aprA has shown the oil contamination as a main modulator for the diversity of such gene. Also, a quantification of these genes has indicated that both genes did not reveal changes among mangroves in absolute numbers, with the log values of the copies per gram of sediment ranging from: 4.88 to 5.32 for dsrB and 5.00 to 5.67 for aprA. However, if a relative quantification (dsrB/aprA) is made a different pattern unfolds; while in anthropogenic-impacted area the dsrB amount is around 20% of the aprA, in non-disturbed is 35% and this value reach 90% in the area with a higher contamination with oil. These results suggest that the oil spill and the anthropization affect the structure of the sulphur-processing microbial communities in mangroves, possibly interfering in the efficiency of the metabolic web present in this ecosystem.