

P5.07 Detection and Analysis of anammox bacteria in Brazilian Mangrove Sediments

D.M. Luvizotto¹, A.C.F. Dias², A.A. Pizzirani-Kleiner¹, I.S. Melo³, F.D. Andreote⁴

¹ Department of Genetics, Escola Superior de Agricultura 'Luiz de Queiroz' - University of São Paulo, Pádua Dias Avenue, number 11, Piracicaba, São Paulo, Brazil, Postal code: 13400-970

² Center for Nuclear Energy in Agriculture - University of São Paulo, Centenário Avenue, number 303, Piracicaba, São Paulo, Brazil, Postal code: 13416-000

³ Laboratory of Environmental Microbiology, CNPMA - Embrapa Meio Ambiente, Jaguariúna, São Paulo, Brazil - Rodovia SP 340 - Km 127, Postal code: 13820-000

⁴ Department of Soil Science, Escola Superior de Agricultura 'Luiz de Queiroz' - University of São Paulo, Pádua Dias Avenue, number 11, Piracicaba, São Paulo, Brazil, Postal code: 13418-900

Corresponding mail: D.M. Luvizotto, danice@usp.br

The anaerobic ammonium oxidation process is based in the combination of ammonium with nitrite under anoxic conditions, resulting in the generation of dinitrogen gas. The bacteria responsible for this process all belong to the order of *Planctomycetales*, form a monophyletic order branching off deep inside the planctomycete lineage and have a evolutionary distance among the genera described so far: *Candidatus "Brocadia"*, *"Kuenenia"*, *"Scalindua"*, *"Anammoxglobus"* and *"Jettenia"*. Since their identification, anammox bacteria have been detected in almost every type of aquatic habitat that contains oxygen-depleted zones. Here it is presented a survey of anammox bacteria in three mangroves located in the coastline of the São Paulo State (Brazil): i) oil-contaminated mangrove at *Bertioga*, ii) non-contaminated mangrove at *Bertioga*, iii) non-disturbed mangrove at *Ilha do Cardoso*. The goals of this study were to estimate the amount of anammox-related bacteria in samples by quantitative real time PCR (qPCR), and also to infer about the diversity of such group by denaturing gradient gel electrophoresis (DGGE). The detection and amplification system was based on specific primers described for the anammox bacterial groups *16S rRNA* gene Brod541F/Brod1260R. The qPCR results have shown an abundance of anammox bacteria in all mangroves; however, the samples collected closely to oil spill showed to harbor higher abundances of anammox bacteria (log values from 6.53 to 6.76) in comparison to other samples (log values from 4.66 to 5.68), possibly due to the strict anaerobiosis induced by the oil layer and the lower density of vegetation found in this area. The analyses of DGGE band patterns has indicated the presence of distinct anammox-related bacterial communities in each sampled mangrove, with a remark for samples collected near the oil spill. Such samples presented major differences in comparison to others, reinforcing that the oil contamination can directly act on the anammox bacterial community, modulating it is structuring, and possibly it is functioning. In summary, these results initiate a tentative in deciphering the ammonium processing in mangroves, what can add information on the diversity of functioning microbial groups involved in the nitrogen transformations.