

1st International INCT Symposium on Biological Nitrogen Fixation

<http://nfn.genopar.org/symposium>

Program and Index

National Institute of Science and Technology of Biological Nitrogen Fixation

Instituto Nacional de Ciência e Tecnologia [INCT] da Fixação Biológica de Nitrogênio

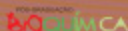
Organizers

Fábio de Oliveira Pedrosa
Emanuel Maltempi de Souza
Maria Reremice Reynaud Steffens

Curitiba, September 2009



Ciência e Tecnologia
Ministério de Ciência e Tecnologia



September, 13th to 15th

Universidade Federal do Paraná (UFPR)
Centro Politécnico
Setor de Ciências Biológicas
Departamento de Bioquímica e Biologia Molecular
Curitiba, Paraná, Brazil

Venue

Auditório da Administração do Centro Politécnico
Centro Politécnico
Universidade Federal do Paraná
Rua Francisco H. dos Santos, s/n
Jardim das Américas

Financial Support

We gratefully acknowledge our sponsors.



Cover design
Carolina C. Huergo



POSTER ABSTRACTS

P33. Diazotrophic Endophytic Bacteria from Fruit and Biofuel Plants: Physiological aspects

Weber¹, O. B., Silva², J. G.

¹Embrapa Tropical Agroindustry, Rua Dra. Sara Mesquita, 2270, Pici, 60511-110, Fortaleza, Ceará, Brazil

²Universidade Federal do Ceará, Av. Mister Hull, 2977, Campus do Pici, Fortaleza

Diazotrophic bacteria have been isolated from tropical fruit crops, especially pineapple (*Ananas comosus* L Merrill) and banana (*Musa* spp.), which have been exploited economically in different regions of Brazil. These plants can obtain benefits from that plant-bacteria association. In crops of castor and jatropha, where the exploitation of bioenergy has recently attracted much scientific and commercial attention, apparently there is no report on the presence of that bacterial group. This paper presents the first results of the occurrence of diazotrophs in castor (*Ricinus communis* L.) and “pinhão-mansão” (*Jatropha curcas* L), both belonging to the family *Euphorbiaceae*, as well as comparative physiological aspects of bacterial growth in different semi-solid and semi-specific media. The population of diazotrophic bacteria in bioenergy plants ranged from 10⁴ cells g⁻¹ in roots to 10² cells g⁻¹ in stems, while the fruit trees support a higher bacterial population, up to 10⁷ bacteria g⁻¹ in fresh root biomass. Strains of isolated bacteria from bioenergy plants exhibited different growth in semi-solid and semi-specific media. Some strains exhibited growth with in a large number of carbon sources similar to that observed for fruit bacteria identified within *Burkholderia* genus. The diversity in terms of growth of bacteria suggests that there are diazotrophic bacteria associated with the bioenergy and fruit plants, and these bacteria can be successfully exploited to promote better plant growth.

determine and compare the biodiversity of diazotrophic and total bacteria in a meat industry lagoon effluent by culture independent methodology. The bacterial identification was based on amplification and sequencing of the *nifH* gene, which codes for a subunit of dinitrogenase reductase of the nitrogenase complex. DNA extraction was performed by indirect method and the *nifH* gene was amplified by PCR with the primers *nifH*-F (AAAGGYGGWATCGGYAARTCCACCAC) and *nifH*-R (TTGTTSGCSGCRTACATSGCCATCAT). PCR fragments, with an average of 459pb, were cloned into the cloning vector pCR2.1 and transformed into *Escherichia coli* strain DH10B. This produced a library with approximately 200 clones. The plasmidial DNA was extract through alkaline lyses and sequenced. The identification of taxonomic groups was made through the search for homology in the GenBank database with the programs BLASTn and BLASTx. So far, 107 sequences of *nifH* gene were analyzed. They have, on average, 89,37% of identity with the fragment aligned to the database. Among the 107 organisms identified, 13,08% belong to the β-Proteobacteria (*Azoarcus* sp. and *Dechloromonas aromatica*); 75,70% belong to the γ-Proteobacteria (*Klebsiella pneumoniae*, *Azotobacter vinelandii*, *Tolomonas auensis*, *Pectobacterium atrosepticum*, *Vibrio diazotrophicus*, *Dickeya dadantii*, *Halorhodospira halophila*); 0,94% belong to the δ-Proteobacteria (*Desulfovibrio magneticus*); 1,87% belong to the firmicutes/clostridia group, *Heliobacterium modescaldum*, *Clostridium beijerinckii*; and 8,41% are uncultured or unidentified organisms. The extracted DNA was also used to construct a 16S rRNA gene library from amplified fragmentes with the primers 27f (AGAGTTTGTATCCTGGCTCAG) and 1492r (AGCGCTACCTTGTTACGACTT). These PCR fragments were cloned into the cloning vector pCR2.1 and transformed into *Escherichia coli*, strain TOP10. The library constructed has, approximately, 300 clones. The preliminary analysis shows the presence of many uncultured organisms.

Supported by: CNPq; Institutos do Milênio; INCT-NBF

P34. Diversity of Diazotrophic Bacteria in a Meat Industry Effluent Lagoon

Cotta¹, M. S., Malinowski¹, A. K., Magnani¹, G. S., Glogauer¹, A., Faoro¹, H., Cruz¹, L. M., Souza¹, E. M., Monteiro¹, R. A., Pedrosa¹, F. O.

¹Department of Biochemistry and Molecular Biology, Universidade Federal do Paraná, D.P. 19046, 81531-990, Curitiba-PR, Brazil
(marincotta@hotmail.com)

Description of a microorganism's community can contribute to the understanding of the role they play in the environment. This study aims to