BIOTA-FAPESP PROGRAM

PLANT BIODIVERSITY AND SOIL ORGANISMS IN NATURAL AND IMPACTED *ARAUCARIA ANGUSTIFOLIA* ECOSYSTEMS IN THE STATE SÃO PAULO, BRAZIL

Elke Jurandy Bran Nogueira Cardoso

Higher School of Agriculture Luiz de Queiroz / University of São Paulo (USP)

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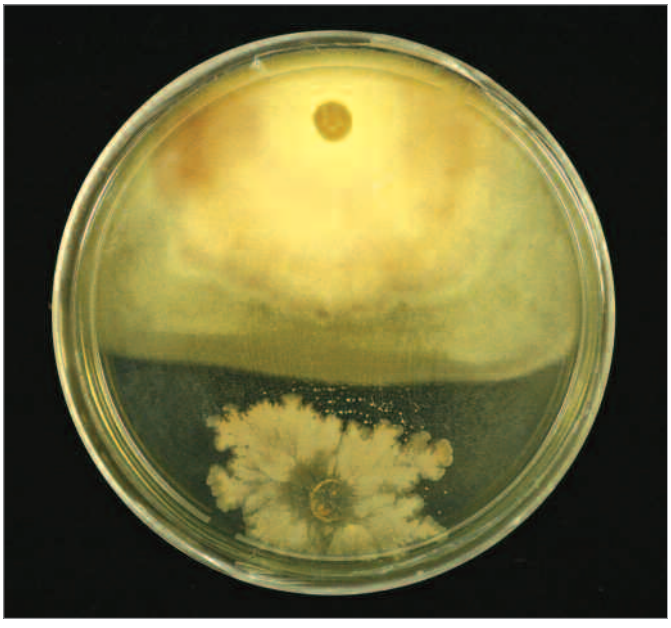
Araucaria angustifolia is a plant species of great social and economic importance, and characteristic of the sub-tropical forest in Brazil. This species has been submitted to predatory exploitation and to-day is considered in danger of extinction. Therefore, new management technologies are urgently needed, with the goal of conservation and recuperation of the small remnant areas. The Araucaria ecosystem presents a high animal and plant diversity with high mutual interactions. The consequences of loosing this tree species would have a negative impact on the whole ecosystem, which would also involve a loss in the microbial diversity below the soil, impairing the functioning and sustainability of the system. The objectives of this project were to study the floristic and microbial diversity of different Araucaria forests, with special consideration of the growth promoting rhizobacteria, mycorrhizal fungi and diazotrophic bacteria, especially those in symbiosis with leguminous plants in the forest understory. A survey of the chemical and microbial attributes of these forests will contribute to select the most promising methodologies to help maintaining and to recuperate these ecosystems in the State São Paulo.



General view of the Araucaria Forest in Campos do Jordão, SP, Brazil. Cardoso EJBN, Vasconcellos RLF, Ribeiro C, Miyauchi MYH. PGPR in Coniferous Trees. In: Dinesh K. Maheshwari. (Org.). Bacteria in Agrobiology: *Crop Ecosystems. 1 ed. Berlin: Springer, 2011.* ***1****:345-360*

Antagonism Bacillus x Fusarium. Ribeiro CM, Cardoso EJBN. 2011. Saving the forest. ESALQ Notícias, *Piracicaba, p. 4, April 1st.*

SUMMARY OF RESULTS TO DATE AND PERSPECTIVES

PCR-DGGE analyses has shown greater similarity between bacteria community structure in the soil of native forest (NF) and in recently burnt area (RQ), than in the soil of degraded areas (RF). A multidimensional scale analysis (NMDS) with Anosim, based on bacteria amplicon profiles, has shown that these 3 Araucaria areas are different. Biolog has shown that NF has greater substrate utilization index than RF and RQ, which do not differ from one another, the same as occurring with PLFA profiles. The genetic diversity of natural populations of *A. angustifolia*, evaluated by intron *matK* SSR (simple sequence repeat, microsatellite) marker has shown high diversity indices, cross breeding rates, and a special genetic structure of up to 25m. The tree and shrub community structures were estimated in different areas of the *A. angustifolia* forests. In Campos do Jordão, the highest stratus contained 1918 individuals, and the lower stratus, 576 individuals. In Barra do Chapéu, the superior stratus contained 1879 individuals, and the inferior stratus, 915 individuals. Actinobacterial isolates were tested to find out their antagonism to the plant pathogenic fungi *Fusarium sp.* and *Armillaria sp.* in Araucaria. Twenty four out of 28 isolates were able to inhibit the production of rhizomorphs in Armillaria, while the isolate A43 was outstanding in the control of both pathogens. The same actinobacterial isolate favored spore germination of the AMF Gigaspora rosea *in vitro*. The isolate A43 stimulated growth of Pinus seedlings in the absence of the ectomycorrizal fungus, with a 100% gain of biomass in comparison to the control. A pot experiment had evaluated the effect of inoculation of the earthworm *Amynthas corticis*, AMF, and a diazotrophic bacterium isolated or growing on Araucaria seedlings. The FMA promoted growth and development of the seedlings which had presented higher contents of N and P than control samples. The fungi producing mycorrhizal associations with the orchid *Coppensia doniana* were identified as two morphotypes of the genus Ceratorhiza and one uninucleate Rhizoctonia. All three clades were successful in germinating the orchid seeds, bringing the seedlings to an advanced stage of development around 30 days. Replanted Araucaria in PETAR, and burned forest in Campos do Jordão were related to arylsulfatase, dehydrogenase, microbial biomass carbon and qMIC. Fatty acids 10Me 18:0 (actinobacteria), saturated to unsaturated fatty acids conversion rate, and metal-D-glycosides and 2-hydrobenzoic acid substract consumptions were also related to the replanted area in Petar and in Campos do Jordão. However, fatty acids 18:19c (fungi) and 16:17c (Gram+ bacteria), glucose-1-phosphate consumption, D-lactose and hydroxibutyric acid were related to the highly impacted areas. Looking for PGPR, eighteen (out of 97) isolates had produced indol-acetic acid, 27 were phosphate solubilizers, 37 produced siderophores and 83 produced phosphatases. Forty five isolates were antagonic to *Fusarium oxysporum*. Using the Fame technology and 16S rRNA sequencing, the most effective isolates belonged to Bacillaceae, Enterobacteriaceae and Pseudomonadaceae.

MAIN PUBLICATIONS

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Elke Jurandy Bran Nogueira Cardoso

Escola Superior de Agricultura Luiz de Queiroz (Esalq)
Universidade de São Paulo (USP)

Departamento de Solos e Nutrição de Plantas
Av. Pádua Dias, 11
CEP 13418-900 – Piracicaba, SP – Brasil

+55-19-3429-4171 ramal 2143
ejbncard@esalq.usp.br