

**Occurrence and characterization of different bacterial isolates
from the rhizosphere of *Bactris gasipaes* H.B.K. and
Theobroma grandiflorum (WILLD. EX SPRENG.) SCHUM**

Wolfgang Kruse¹, Jose Perreira da Silva Jr.²,
Reinhard Lieberei¹

¹ Institute of Applied Botany, University of Hamburg

² Agroforestry Research Center for Western Amazonia
(EMBRAPA/CPAA), Manaus, Brazil

Ecosystem functioning is governed largely by soil microbial dynamics. Thus, soil microorganisms play a major role in ecosystems.

Differences in microbial properties and activities in soils have been reported but are limited in their ability to describe the specific plant-microbe interaction. Particularly in the tropics there is a lack of information on distribution, composition and description of physiological groups of microorganisms apart from nitrogen fixers and mycorrhiza.

Plant microbe interactions are particularly pronounced in the rhizosphere which is defined as the narrow zone of soil surrounding the root strongly influenced by the root. On the other hand, the rhizoplane refers to the actual surface of the root.

In this study samples were collected from the rhizosphere (rhizoplane and inner rhizosphere) of *Theobroma grandiflorum* and *Bactris gasipaes* in spring 1997 on the SHIFT area near Manaus, Brazil.

For bacterial counts the soil and rhizoplane samples were plated on four different media. Plate counts were taken and log transformed before statistical analyses. The number of bacteria decreased with increasing distance from the rhizoplane.

To assess the bacterial community structure, we examined 75 bacterial isolates for their substrate utilization potential on BIOLOG microtiter (96 substrates) plates. We found to different substrate utilization patterns (profiles) depending on the plant species they were isolated from. Thus, plant species strongly influence the composition of their rhizosphere microflora.

Additionally, the isolates were tested for their capacity to solubilize poorly soluble phosphates. P-solubilizing bacteria may play an important role in providing the plants with poorly available P in tropical soils. Four isolates were selected because of their high solubilization capacity. These were investigated in a PCR-assay with two primers (Y1 and Y2, Young et al., 1991) of highly conserved sequence regions from the 16S rDNA-gene. The amplification products were purified, sequenced and, if unambiguous, analysed for database homologies (BLAST). The bacteria from the rhizoplane and inner rhizosphere of the above described plant species, exhibited 96 to 98% homology either to the genera of *Bacillus* or *Gordona*.

Mailing adress: wkruse@iangbot.uni-hamburg.de