



Research project of counterparts funded at UNJA

Name	Counterpart	Title
Hesti Riany, Ummi Mardhiah, Zulkarnain	B02	Isolation and amplification of the 16S rRNA gene for metagenomic analysis from the oil palm rhizosphere in different locations (based on soil textures)

Background and Method

Soil microbes, especially bacteria, play key roles in ecosystems and influence a large number of important ecosystem processes, such as nutrient acquisition cycling, plant productivity, soil formation, biocontrol of some diseases, and fertilizer. The rhizosphere (root zone) is an important habitat for bacteria to function as plant growth promoters and protectors of plants from pathogenic infection. The large area of oil palm tree plantations in Jambi Province provide good habitat for soil bacteria. But oil palm tree plantations in Jambi grow on soils of different textures. It is assumed that different soil textures lead to different diversities of soil bacteria in the root zone of the oil palm trees. The OBJECTIVES of this study were to investigate the diversity of soil bacteria in the oil palm rhizosphere from different soil textures.

The bacteria in the collected soil samples were identified by conventional methods and by DNA extraction and amplification of the 16S rRNA gene.

Result

Eight soil textures were recognized in this study: sandy loam, sandy clay, loamy sandy, salty clay, salty clay loam, sandy clay loam, sandy and clay. And we found four genera of bacteria: *Streptomyces*, *Micrococcus*, *Bacillus* and *Azotobacter*. In the attempt to use the metagenomics method we obtained DNA of purity 1.2-1.7. Sequences of more than 3000bp were detected by electrophoretic visualization. Unfortunately, however, 16S rRNA genes were not obtained. A more effective optimization procedure is therefore needed before sequencing and metagenomics analysis can be successfully applied.