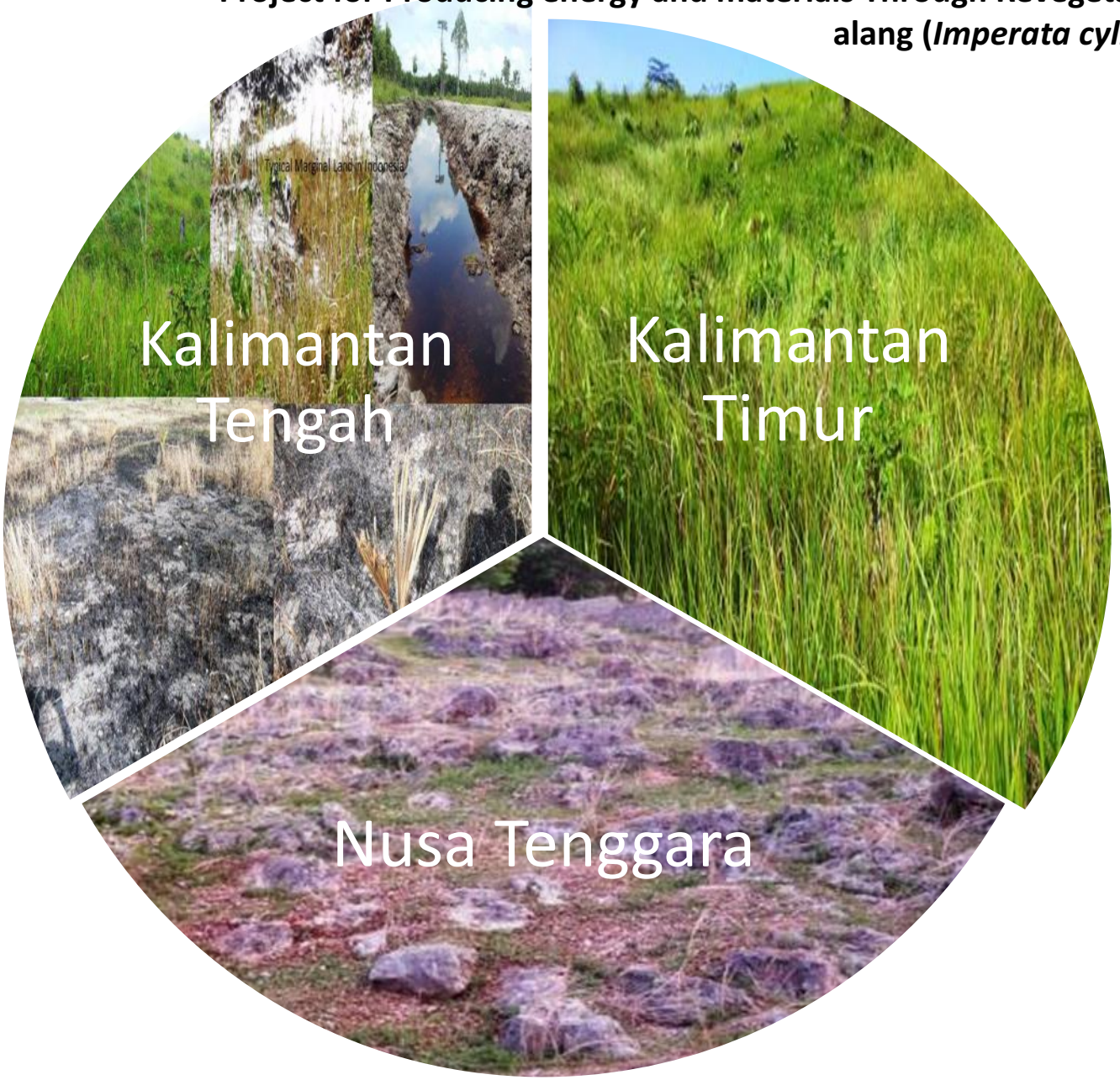
SATREPS PROJECT (2016-2021)

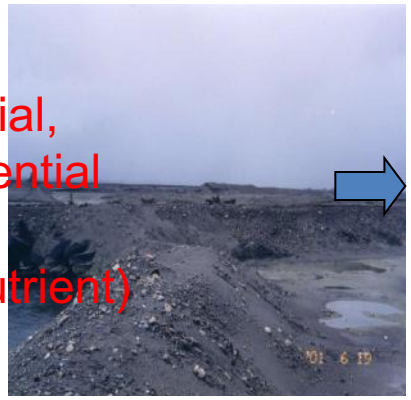
Project for Producing energy and materials Through Revegetation of Alang-alang (*Imperata cylindrica*) Fields

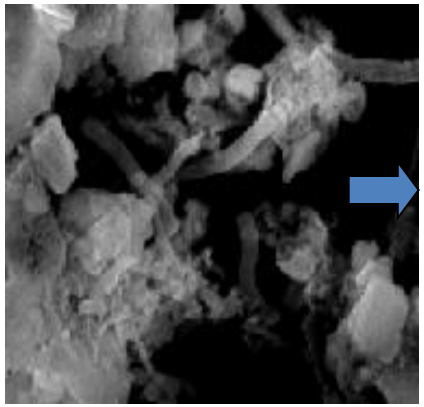


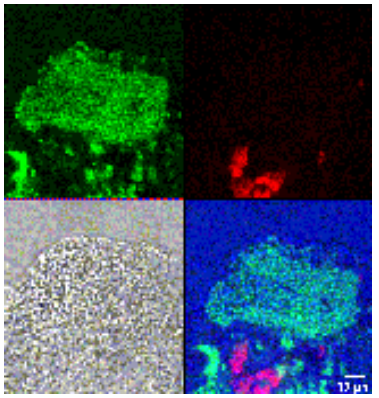
Strategy design for Revegetation

Improvement of Biological and chemical properties of tailing?

Redox potential, CEC, EC potential profile, soil properties (nutrient)







To enhance the capability of plant to grow in critical condition

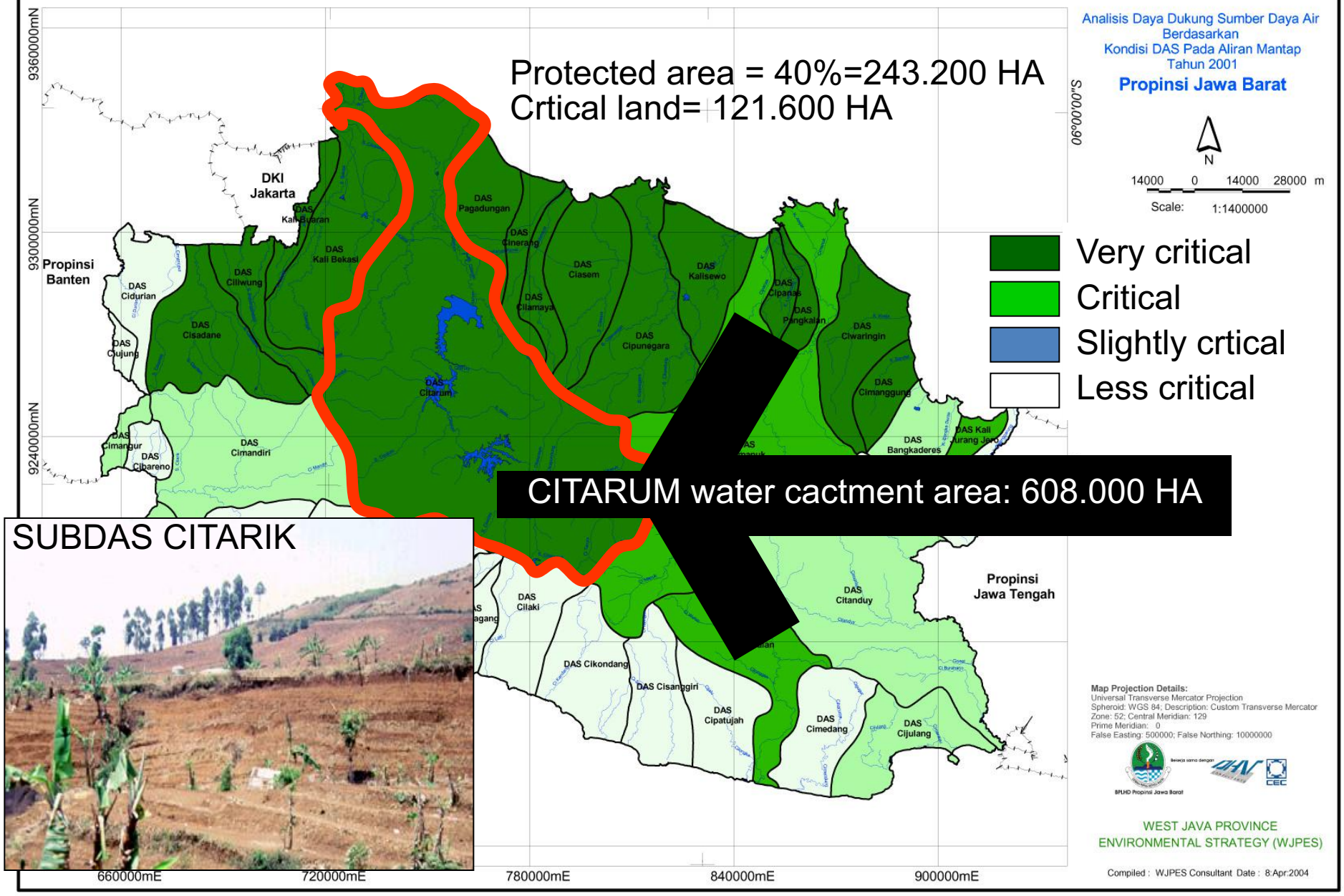
Plant microbes association

SATREPS PROJECT (2016-2021)
Project for Producing energy and materials Through Revegetation of Alang-alang (*Imperata cylindrica*) Fields

Katingan Soil



Revegetation of Water Catchment area

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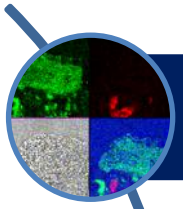
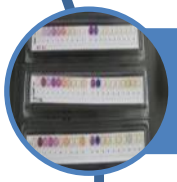
MICROBIAL ECOLOGY

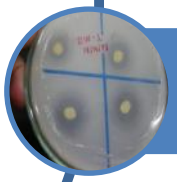
Estimated value of Global 'Ecosystem Processes' $654b a year. (UNEP, 1998)



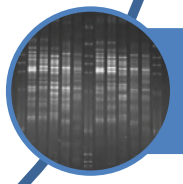
WHO ARE THERE? -----→ Species diversity---Culture dependent and non culture dependent technique



WHAT IS THEIR ROLE?---→ Functional diversity



WHEN AND UNDER WHICH CONDITION? --→ in-situ microbial diversity activity studies



WHAT IS THEIR UNIQUE GENETIC PROPERTIES? Genetic characterization

NIES-University of Tokyo-LIPI

THE ROLE OF SOIL MICROORGANISM IN ECOSYSTEM RECOVERY AFTER AFFECTED BY INTENS FIRE

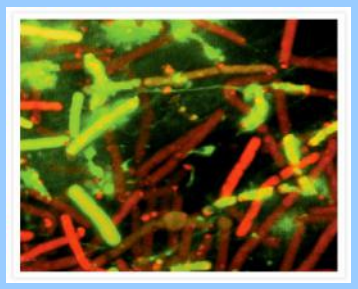
Otsuka S, IM Sudiana, A Komori, K Isobe, S Deguchi, M Nishiyama, H Shimizu and K Senoo. 2008. Community Structure of Soil Bacteria in a Tropical Rainforest Several Years After Fire. Microbes Environ. Vol. 23. No.1: 48-56.

Izobe K, Otsuka S, Sudiana IM, Nurkanto A, and K Senoo. 2009. Community Composition of Soil Bacteria nearly a decade after a fire in a tropical rain forest in East Kalimantan, Indonesia. J. Gen. Appl. Microbiol. 55, 329-337

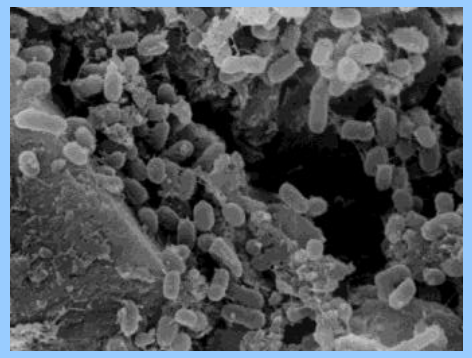


Molecular phylogenetic framework

Soil microbial Communiy



Fluorescence in situ hybridization(FISH)



Extraction

Mixed DNA (or RNA) Metagenome

PCR

Mixture of 16S rRNA gene fragments

Analysis methods

- Cloning/sequencing
- Denaturing gradient gel electrophoresis (DGGE)
- Terminal restriction fragment length polymorphism (TRFLP)

Database search

Phylogenetic identification

Probe design

CULTURE NON DEPENDENT

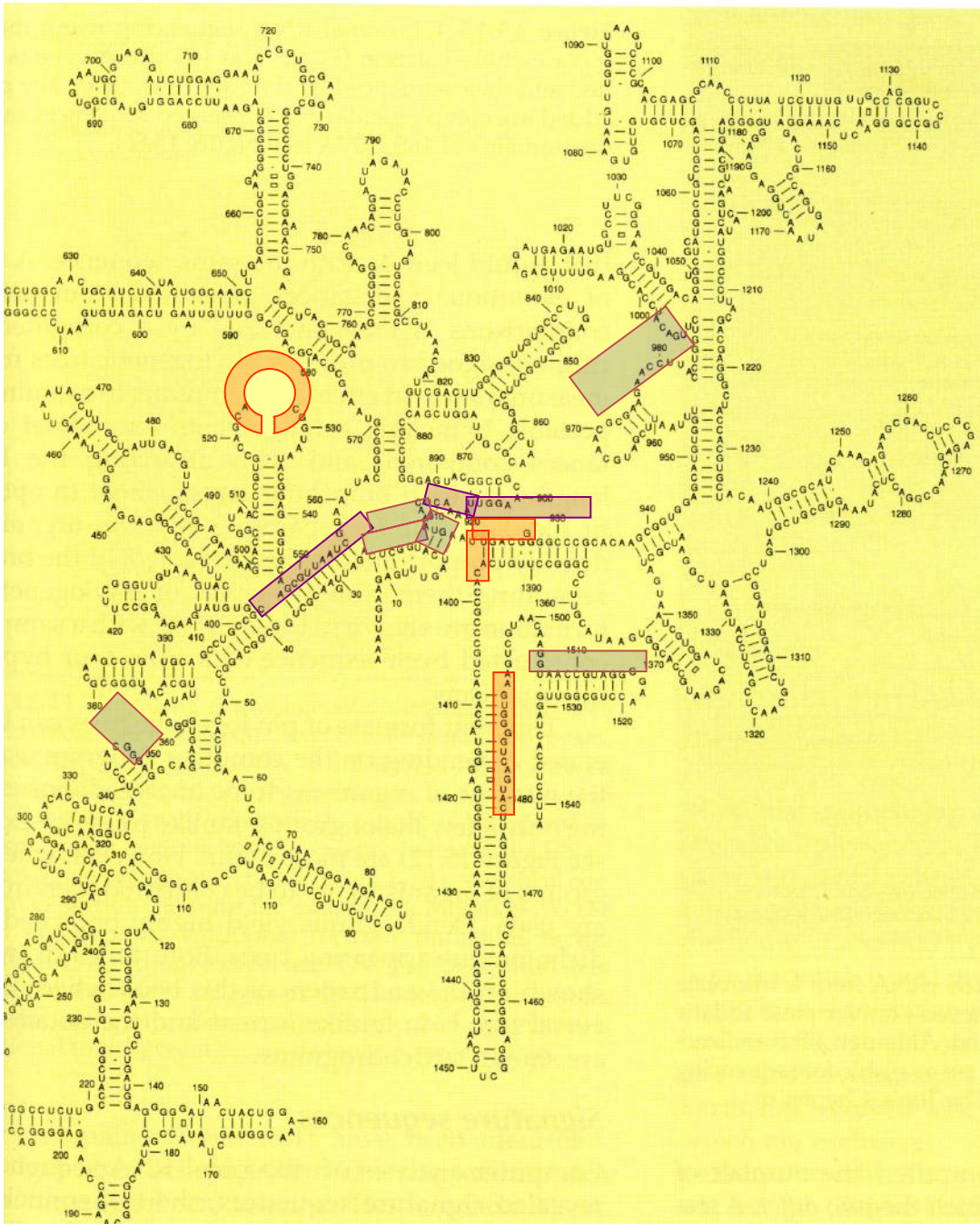
16S rRNA structure

E. coli: 1541 nucleotides

Conserved regions:
used for designing
uviversal primers

Universal
Bacteria specific
Archaea specific

Variable regions:
specific sequence for
each species
used for designing
specific primers



Denaturing gradient gel electrophoresis (DGGE)

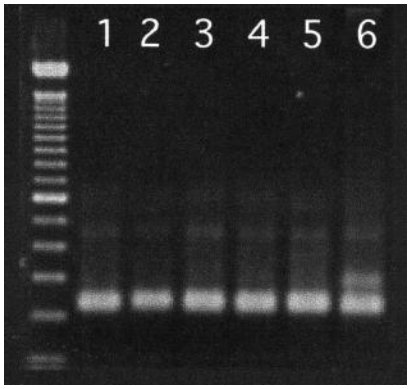
PCR-amplified 16S rRNA genes fragments of multiple organisms

GC-clump attached

341f-GC : CGCCCGCCGCGCGCGGCGGGCGGGGCGGGGGCACGGGGGGCCTACGGGAGGCAGCAG

534r : ATTACCGCGGCTGCTGG

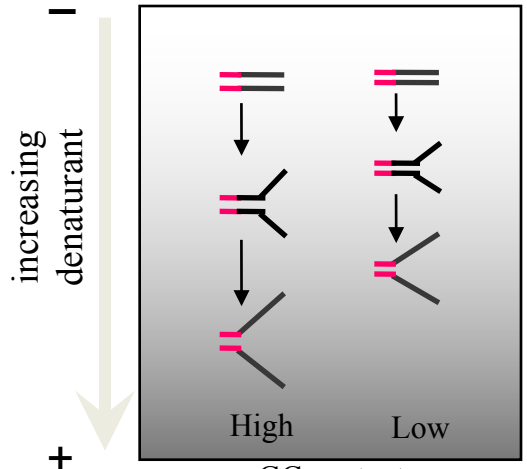
Agarose gel

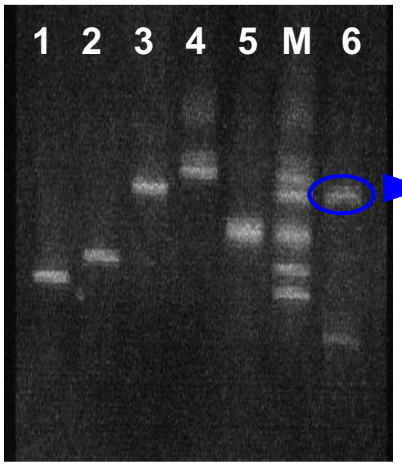


1. Comamonas testosteroni R5
2. Cmamonas sp. E6
3. Acinetobacter calcoaceticus AH
4. Pseudomonas putida BH
5. Escherichia coli K12
6. Activated sludge mixed populations

M, Mixture of 1 to 5

DGGE





Cut out a band and determine its sequence