

Molecular characterization of *Pseudomonas aeruginosa* UPM P3 from oil palm rhizosphere

ABSTRACT

Problem statement: *Pseudomonas aeruginosa* has been used in agriculture as biological agents. It has shown substantial control of a variety of soil-borne plant pathogens including *Macrophomina phaseolina*, *Botrytis cinerea*, *Rhizoctonia solani*, *Colletotrichum truncatum*, *Pythium*, *Fusarium* and others. Species aggregate of *Pseudomonas aeruginosa* strain UPM P3 was shown to have potential as a biocontrol agent against *Ganoderma boninense*, the causal agent of Basal Stem Rot (BSR) of oil palm. However, *P. aeruginosa* is also an opportunistic pathogen. It typically infects the pulmonary tract, urinary tract, burns, wounds and also causes other blood infections. The objective of this study was to carry out DNA fingerprinting for strain differentiation to differentiate between pathogenic and non-pathogenic forms of *P. aeruginosa* strain UPM P3. **Approach:** Genotype characterization was carried out by amplification of the *recA* gene using specific primers, purified using QIA Quick PCR purification Kit and sent for sequencing. Multiple sequence alignments were performed on the selected closely related sequence accessions using CLUSTAL W software. The *recA* gene was used for phylogenetic and PCR-RFLP studies. **Results:** From the phylogenetic tree, UPM P3 has more than 90% similarity with *Pseudomonas aeruginosa* strains: PAM7, PAO1, UCBPP-PA14 and PA7. UPM P3 was further digested with restriction enzymes; *PvuII*, *BsrI*, *ZraI*, *FokI* and *SgrAI*. RFLP results showed that strain UPM P3 has close similarity with strain PAO1 of *Pseudomonas aeruginosa*. **Conclusion:** Strain PAO1 is commonly associated with strains of medical, human or plant pathogens and agricultural environment. Common habitats include soil, hosts, aquatic environment and wastewater and also a common contaminant of public places. Thus the use of *Pseudomonas aeruginosa* strain UPMP3 as a biological control candidate in agriculture has to be monitored.

Keyword: Basal Stem Rot (BSR), *Ganoderma boninense*, PAO1, *Pseudomonas aeruginosa*, *recA* gene, RFLP, UPM P3