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Analysis of Bacterial Communities in Rhizosphere Soil of Symptomless and Basal Stem Rot (BSR)-Infected Oil Palm Using Terminal Restriction Fragment Length Polymorphism (T-RFLP)

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Abstract. Basal Stem Rot (BSR) disease caused by pathogenic fungi known as *Ganoderma boninense* has been identified as a major threat in oil palm plantation. Previously used methods to control this disease have been ineffective while method using chemical treatment is not environmentally friendly. An inadequate knowledge on the core microbiome of oil palm rhizosphere and the relationship between BSR disease incidences hinders effective controls against this pathogenic disease. Hence, the objectives of this project are to determine the bacterial communities of symptomless and BSR-infected oil palm using T-RFLP analysis, to perform cluster analysis of the samples based on the T-RFLP data and to analyze the relationship between soil bacterial communities and soil pH. The rhizosphere samples of symptomless and BSR-infected oil palm were collected at different microsites (bulk soil from harvesting path and rhizosphere soil from weeded circle and frond pile) and at different depths (10 cm and 30 cm from upper soil surface) from Oil Palm Plantation, Seberang Perak. In T-RFLP analysis, 16s rRNA region of the bacterial DNA were amplified by using 8F forward primer labelled with 6-FAM fluorescent dye and unlabelled 1492R reverse primer. The PCR products were then digested either with restriction enzyme AluI or HhaI or double digestion using AluI and HhaI. The raw fragments data were aligned and analyzed in T-REX (T-RFLP Analysis Expedited Software). The ordination analysis of Additive Main Effects and Multiplicative Interaction Model (AMMI) analysis from T-REX software revealed higher percentages of signal compared to noise interaction effects for frond pile at depth 30 cm with interaction difference of 21.28% (analysis based on relative abundance). The higher difference between signal and noise indicates that there are larger differences in microbial community between symptomless and BSR-infected oil palm. Meanwhile, cluster analysis showed that the sample obtained from harvesting path (bulk soil) at 10 cm and 30 cm depth clustered closely together indicating that there are small differences in microbial community at these microsites. Clustering analysis based on relative abundance shows that there is larger difference in microbial abundance between symptomless and BSR-infected sample at Frond Pile (30 cm depth). These results will provide preliminary knowledge in selecting representative samples of symptomless and BSR-infected oil palm for further microbial interaction analysis using Next Generation Sequencing.

Keywords: Basal Stem Rot, *Ganoderma boninense*, rhizosphere, T-RFLP, 16S rRNA