

Bioremediation of environment contaminated with organophosphate pesticides using Indonesian indigenous bacteria

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ABSTRACT

Pesticide pollution in soils is one of the most critical environmental issues worldwide. Organophosphate pesticides (OPPs) are commonly used in agricultural field leading to changes in their biological diversity. The indigenous bacterial community contributed important roles in the remediation of OPPs exposed in the soil. This study analyzes the overall bacterial community composition of three agricultural fields exposed to OPPs in Yogyakarta, Java, Indonesia. The agricultural field was segregated into close to beach, residence, and highland zones. The soil bacterial community was examined using 16S rRNA amplicon sequencing. Proteobacteria, Actinobacteria, and Firmicutes were found to be the main composition of the bacterial community. In addition, genera such as *Bacillus*, *Bradyrhizobium*, *Chryseobacterium*, *Cystobacter*, *Microvirga*, and *Burkholderia* have high relative abundance in the samples. The high alpha diversity indexes suggest that the agricultural soil microbiome not only provides important ecological services but also may host a broad range of bacteria and genes of biotechnological interest. Bacterial community structure is also correlated with the physicochemical soil characteristics. The findings can be used to develop bioremediation strategies that use indigenous microbes to clean up and restore agricultural soil that has been contaminated with OPPs.

Kata Kunci: *16S rRNA, agricultural soil, bacterial diversity, organophosphate pesticides (OPPs), Proteobacteria*