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High-throughput Screening of POME Metagenomic DNA Libraries for Bioprospecting Novel Cellulose-Degrading Enzymes

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Biotechnology has the potential for biofuel production from plants biomass. However, the number of cellulose-degrading enzymes indispensable in such industry is yet to be effectively commercialized. Metagenomic, “the culture-independent approach” has not only answered many questions about phylogenetic diversity with “sequence-based screening” but it has also permitted the bioprospecting of completely new families of biocatalysts with “function-based screening”. In our study, functional metagenomic approach coupled with high throughput screening are strengthened by an enrichment process for bioprospecting of novel cellulose-degrading enzymes with greater diversity from palm oil mill effluent (POME). Fosmid metagenomic DNA libraries of around 20Mb size were constructed. Fluorogenic substrates were used for high throughput, sensitive screening. The results obtained from metagenomic DNA quantification and titer test of enriched and non-enriched clones showed five to ten times high concentration of enriched metagenomic DNA and high positive clone numbers of enriched cultures. Our study demonstrated the potential of enrichment and high throughput screening as an efficient tool to enhance bioprospecting of novel, efficient and specific cellulose-degrading enzymes.

Keywords: Cellulose-degrading enzyme; Palm oil mill effluent (POME); Enrichment, metagenomic DNA library; High-throughput screening; Fluorogenic substrate