

## ABSTRACT

Widespread utilization and the inherent toxic nature of chlorpyrifos (CP) enlist it as a major environmental threat. Since current methods to reduce the effect of CP is costly, the focus has been shifted towards bioremediation, an eco-friendly, natural process of degrading CP using microbes. In line with this, the present study focused on isolating indigenous microbes from landfill and paddy field, screening for CP biodegradation, biodegradation assessment using GC analysis and genome annotation of a CP-biodegrader. Twenty one strains were isolated from the study. Among the isolated strains, *Sphingomonas paucimobilis* AIMST S2 (Sph) exhibited the most rapid growth on M9 medium supplemented with CP as sole carbon source. Subsequently, *Sphingomonas paucimobilis* was subjected to degradation for 7 days. With the aid of GC, presence of 3,5,6-trichloro-2-pyridinol (TCP), the by-product from CP breakdown had been detected and the increase in TCP corresponds to the reduction of CP, further suggesting *Sphingomonas paucimobilis* ability to degrade CP. The percentage of reduction for CP in the *Sphingomonas paucimobilis* cultured medium (experimental group) was 88.27 %. Following this, the genomic DNA of *Sphingomonas paucimobilis* was subjected to sequencing via Illumina's HiSeq 2500 and Oxford Nanopore's MinION, resulting in good quality short reads (~150 bp) and long reads (~ 10,000 bp), respectively. Hybrid genome assembly using Unicycler has provided a single contig consisting of 4,005,505 bp with 65.7 % GC content. A total of 3746 genes including 3648 CDS and 61 tRNAs were annotated in the genome. KEGG had functionally annotated 1810 genes including 32 genes related to xenobiotic degradation and *gst*, glutathione S-transferase, which has been previously indicated to be responsible for CP biodegradation in *Acinetobacter baumannii* DS002. Apart from that, an array of genes encoding plant growth promoters were also identified, suggesting its' potential role as an effective microorganism (EM) in agriculture. In conclusion, outcome of this study marked the successful characterization and annotation of a complete genome sequence of *Sphingomonas paucimobilis*, the first available in the public domain. Insights obtained from this study could serve as a stepping stone to an efficient CP bioremediation in the future.