**1. Abstract**

 Bacterial strains capable of degradation of different organophosphorus compounds (OPCs) were isolated from the soil and different aquatic ecosystems (agriculture wastewater, domestic sewage water, and agricultural soil) by an enrichment culture technique. From overall 36 environmental samples 3 bacterial strains show high ability for degradation of various OPCs. They were screened and identified as *Acinetobacter baumannii* (AFA), *Pseudomonas aeruginosa* (PA),and *Pseudomonas mendocina* (PM) based on morphological, biochemical identification and 16S rRNA sequence analysis. Bacterial strains were able to grow in mineral salt medium (MSM) supplemented with malathion (MAL) at a concentration of (100 mg L-1) as a sole carbon and energy source. The degradation profile reveals that *Ps.aeruginosa* strain PA were able to completely remove MAL within day of inoculation, while *A.baumannii* strain AFA degraded 84.4% of MAL within 14 day. On the other hand, *Ps.mendocina* strain PM was the least efficient degrading bacterium, only removed 77.6% of MAL within 14 days. All strains could also degrade other organophosphorus compounds including diazinon, chlorpyrifos and fenitrothion to different degree. The effect of different culture conditions on the degradation of malathion like inoculum density, other carbon or nitrogen sources, temperature and shaking were examined. Degradation of malathion and bacterial cell growth were accelerated when culture media were supplemented with yeast extract, glucose and citrate. The optimum conditions for malathion degradation by the 3 strain were; an inoculum density of 1.5x 1012 cfu ml-1 at 30°C with shaking speed of 150 rpm min-1. From HPLC/MS analysis, malathion monocarboxylic acid (MMC) and malathion dicarboxylic acid (MDC) were the main biodegradation metabolites, so carboxylesterase enzyme may be the responsible enzyme for biodegradation process. A specific polymerase chain reaction primers were designed manually using multiple sequence alignment of the corresponding carboxylesterase enzymes of the 3species. Sequencing result of amplified PCR product and phylogenetic analysis showed low degree of homology with the other carboxylesterase enzymes of different *Pseudomonas* and *Acinetobacter* strains, so we suggested that this enzyme may be a novel esterase enzyme. Isolated bacterial strains may have potential role for use in bioremediation of malathion and OPCs contaminated soil.