# 5 Conclusion

In present work, pesticide degrading bacterial species has been successfully and identified through microscopic observation and nucleic acid analysis. The isolated species (*Bacillus* sp. S4) exhibited better potential for Malathion biodegradation than *Bacillus* sp. $S_1$ and *Bacillus* sp. $S_2$. Using *Bacillus* sp. $S_4$ Malathion removal efficiency was studied in packed bed bioreactor as well as continuous bioreactor under optimized process conditions. The performance of continuous packed bed bioreactor was evaluated and removal efficiency was found greater than 90%. The values of growth inhibition kinetics study results also confirmed the superiority of the S4 over other two species of isolated bacteria. The FTIR and GCMS results helped to identify the metabolites in the biodegradation of Malathion and results were finally used to propose a degradation pathway for Malathion. The proteomics study along with molecular docking and active site analysis demonstrated significant change in the protein profile during the biodegradation of Malathion. Best quality model (NP_390682.1) was used for Docking calculation using YASARA, concluded that malathion may have prominent role and strong interaction with selected major active binding site of hypothetical protein. The suitability of *Bacillus* sp. S4 is applicable in bioremediation of malathion contaminated environment. This study would be helpful in the practical application of *Bacillus* sp. $S_4$ for removal of Malathion from the contaminated environment under *in-situ* condition

This study also successfully demonstrated the treatment of synthetic wastewater containing mixture of Atrazine, Malathion and Parathion two-stage IATP. The highly

efficient *Bacillus* species were successfully isolated from contaminated site and more than 90% removal was obtained. The GC-MS analysis results confirmed the presence of Biuret, Succinic acid monomethyl ester and Dithiodiphosphoric acid tetraethyl ester which are common metabolites reported during degradation of Atrazine, Malathion and Parathion. Kinetic parameters such as first order biological rate kinetic constant $K_{obs}$ (0.00425 per hr), cell yield $Y_{X/C}$ (0.696 mg of COD/mg MLSS) and decay coefficients $K_{dp}$ (0.0010 per hr) were evaluated in order to determine the biomass concentration over the period of operation.

The coupled system consisting UV Fenton and bioreactor was effectively used for the treatment of Atrazine up to concentration of 300 mg/L. The bioreactor was packed with Loofa sponge immobilized with consortia and the potential microbes obtained from Atrazine contaminated site. The performance of the coupled system was found superior than stand alone systems. The important process parameters were optimized and under optimum condition the maximum removal efficiency of coupled system was found to be 93 %. The high removal at higher concentration of Atrazine may be due to use of packed system in the batch reactor.

Bioremediation is a promising field to be explored extensively to identify microbial species for efficient treatment of pesticides and other pollutants. In bioremediation the bioinformatics and biostatistics analyses conducted on microbial species will helps to evaluate and justify the need for genetically modified microorganisms. Genetically modified microbes are expected to possess efficient metabolic processes, enzymes, genes and capable of bioremediation of specific pollutant. Further study is required to scaling of technology from lab to industrial level.