

experimental spectra to the calculated ones, the best model and optimal thermodynamic and spectral parameters were estimated.

Keywords: Doxorubicin, DNA, Salt Effects, Binding Parameters.

Abstract No.33

Effect of Crude Oil Contaminated Soil on Catalase Activity of Lentil Root

*Mina Kolahduz Mohammadi*¹, Dariush Minai-Tehrani²*

1. Cellular and Molecular Department, International Kish Campus, Tehran University, IR
2. Faculty of Biological Sciences, Shahid Beheshti University, IR (E-mail: mkolahduz@yahoo.com)

Catalase is a potent enzyme that decomposes hydrogen peroxide with high velocity. In environmental stress, catalase plays an important role to dispose of hydrogen peroxide. Spillage of crude oil into the soil can damage the soil plants and microorganisms. Oil contamination in soil may act as a stressful element for the plants and causes germination delay, reduction of biomass, reduction of the length of shoots and early chlorosis in the plants. In this experiment the effect of crude oil contaminated soil on root catalase activity of lentil was studied. Lentil seeds were planted in crude oil-contaminated soil (5% w/w). After 30 days the plants were removed from the soil and the roots were separated from the shoots. The roots were homogenized to break the cells. The supernatant was used as cell free extract for enzyme assay. The activity of catalase was measured in different temperature and pH and compared with control. Our results showed that in both the control and treated samples, there were two peaks of activity. In the control the peaks were observed at pH 7 and 10, while in treated samples the peaks were at 8 and 10. The optimum pH was 10 in both samples. Maximum activity was observed at 30°C in both samples. Increasing the temperature decreased the activity. No activity was seen at 90°C in the control while in the treated samples, the enzyme showed minor activity at 90°C. Measurement of kinetics parameters revealed that both K_m and V_{max} had been changed in treated samples. The K_m of enzyme was 1.13 and 1.5 mM and V_{max} was determined to be 1.16 and 2 mM/ min/ mg protein in treated and the control sample respectively. These observed results suggested that an isoenzyme of catalase has been induced in treated sample in comparison to the control catalase.

Keywords: Lentil, Catalase, Pollution, Isoenzyme.

Abstract No.34

Bioinformatic Analysis of Type III Secretion System (T3SS) Proteins for Investigating Vertical and Horizontal Gene Transfer of Pathogenicity Islands in Pseudomonas Species

*Akbar Vaseghi*¹, Naser Safaie²,
Babak Bakhshinejad³, Majid Sadeghzadeh³*

1. Department of Biotechnology, Faculty of Agriculture, Tarbiat Modares University, Tehran, IR
2. Department of Plant Pathology, Faculty of Agriculture, Tarbiat Modares University, Tehran, IR
3. Department of Genetics, Faculty of Biological Sciences, Tarbiat Modares University, Tehran, IR (E-mail: vaseghi.akbar@gmail.com)

Pathogenicity islands are genomic regions containing genes which encode the components of type III secretion system (TTSS). These islands have been acquired by one or more horizontal gene transfer events. *hrp* (hypersensitive reaction and pathogenicity), *hra* (hr-associated) and *hrc* (hr and conserved) genes are main constituents of TTSS. The *Hrc* proteins which make it feasible for effector molecules transport across the bacterial envelope, are broadly conserved in the TTSSs of plant and animal pathogens. Herein, we took advantage of a number of databases including ACLAME, Mobil Genetic Elements (MGEs), Multi Locus Sequence Analysis (MLSA) and Pathogenicity Islands DataBase (PAIDB) for bioinformatic analysis for investigating type III secretion system (T3SS) proteins. Our results indicated that PAIDB provides comprehensive information on PAIs, as a reservoir of virulence genes in prokaryotic genomes which could be useful in developing new antibiotics and designing clinical biosensors for disease diagnosis. MLSA encompasses discriminative multigenic sequence for examining the evolution of *Pseudomonas* species. MGEs is a database comprising of protein/ DNA sequences of different transposons, conjugative transposons, transposable phages, genomic islands (GEIs) which reflects their functional roles and evolutionary history.

Keywords: Bioinformatics, (T3SS) Proteins, Pathogenicity Islands and *Pseudomonas*.
