found EXII in these conditions. We used gemini surfactants alkanediyl-α,ω-bis(Hydroxyethylmethylhexadecyl ammonium bromide) in this study. 1D NMR experiments showed gemini surfactants bind to DSS. 2D 1H-NMR and Circular Dichroism (CD) spectroscopies show that the conformation of RNase A is unaffected at acidic pH where this protein is positively charged, although hydrogen exchange results shows that the conformational stability of RNase A is slightly lowered at high molar ratios. The denaturation curve of RNase A in the presence of gemini surfactant was analyzed on basis of a two-transition model. These gemini surfactants slightly activate and stabilize RNase A at low molar ratios and acidic pH (Table 1). The gemini surfactant with the shorter spacer interacts more efficiently with RNase A than those with longer spacers. These gemini surfactants neither interact strongly with nor severely destabilize this well folded protein in physiological conditions and we advance that can serve as useful membrane mimetics for studying interactions between membrane components and positively charged proteins.

Keywords: Gemini Surfactant, Ribonuclease A, Hydrogen Exchange, Fluorescence Spectroscopy, Circular Dichroism Spectroscopy.

Abstract No.31

Enzymetic Activity of RNase A in the Presence of Sodium N-dodecyl Sulphate

Shadi Salehpour[1], Razieh Amiri*[2], Abdol-khalegh Bordbar*[2], Sayyed Hossein Rasa*[2]

1. Department of Chemistry, Kashan University, IR
2. Department of Chemistry, University of Isfahan, IR
(E-mail: salehpourshadi@gmail.com)

Protein-surfactant systems may serve as models for the study of the interactions between membrane proteins and lipids, additionally, the widespread use of the anionic surfactant sodium n-dodecyl sulphate for the solubilization of membrane proteins and in polyacrylamide-gel electrophoresis has stimulated interest in the nature of the interaction between this surfactant and globular proteins. Bovine pancreatic ribonuclease A is an enzyme that catalyses the depolymerization of RNA. In this study the enzymatic activity of RNAase A in the absence and presence of SDS is measured with cytidine 2': 3'-cyclic monophosphate as substrate. The enzyme reaction carried out with UV-VIS spectroscopy and was measured by following the changes in absorption spectra of cytidine 2':3'-phosphate toward time at 284 nm. We obtained initial rate of reaction enzyme from several kinetic spectra and extract Michealis Menten parameters (V_{max} and K_m). We investigated effect of sodium n-dodecyl sulphate on structure of ribonuclease A with fluorescence spectroscopy and observed changes in quantum yiled of ribonuclease A. fluorescence properties of ribonuclease A is due to tyrosin, and this experiment show that SDS has effect on ribonuclease structure specially in tyrosin region.

Keywords: RNase A, Cytidine 2': 3'-cyclic Monophosphate, SDS, Enzymatic Activity, Michealis Menten Parameters.

Abstract No.32

Investigation on the Effect of salt Concentration on the Binding Modes of Doxorubicin to DNA with the Use of McGhee-von Hippel Equation

Havva Mehralitabar, Olena Krouglova, Saeed Emadi*

Department of Biological Sciences, Institute for Advanced Studies in Basic Sciences, Zanjan, IR
(E-mail: hmehralitabar@gmail.com)

For many years the study on the therapeutic properties of doxorubicin (DOX), like determination of its effective dosage and side effects, were the subject of study in basic and medical sciences. Since these studies are related to the DOX interactions with double stranded DNA, it is interesting to know that intercalation is just one mode of interaction between DOX and DNA at different DOX concentrations. The new method of fitting spectroscopic (spectrophotometric or spectrofluorometric) titration data obtained for DOX-DNA mixtures to different binding models (e.g., McGhee-von Hippel equation describing formation of one or two kinds of complexes, classical chemical equilibrium systems) was used. We investigated the interactions between DOX and salmon testes DNA (%G-C = 41.2) in solutions with various NaCl concentrations at neutral pH. For the fitting we used a set of computer optimization programs worked out by us to estimate the optimal spectra of complexes and thermodynamical binding parameters (binding constants, site sizes and cooperativity factor values). Using these programs we could also take into account the formation of dimeric species in the free DOX and DOX-DNA mixtures with log Kd = 4.3 ± 0.2. We observed that the model in which not only monomeric but also the dimeric DOX species were simultaneously bound to DNA through different mechanisms. We also found that apart from intercalation (with the site size of 3.7-4.0 bp), considerable amounts of aggregated outside bound DOX (with the site size of about 2 bp per one dimeric molecule) were formed with binding constants dependent at different ways on ionic strength. By comparing the Hamilton's Q and Qlim factors, calculated at the end of every iterative process of fitting

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-Tehrani*[2]

1. Cellularand 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 chloresis 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 Km and Vmax had been changed in treated samples. The Km of enzyme was 1.13 and 1.5 mM and Vmax 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 Safaie*[2], *Babak Bakhshinejad*[3], *Majid Sadeghzadeh*[3]

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 effecter 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 examinating 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.
