cross linking in the network of chitosan in the film and microsphere forms, it seems that the macromolecules probably become more rigid and thus decrease the release of drug. Therefore increase on degree of cross linking affected the release rate. Although fast release of drug from chitosan film, as explained above, was attributed to low degree of cross linking in its network than that of chitosan microsphere (Figure). Figure.In vitro release from chitosan carriers in film and microsphere forms as a function of time at pH 7.4The films and microspheres prepared at 12% w/w degree of cross-linking have shown better features in comparison to those prepared with low and high degree of cross-linking (6 and 18% w/w, respectively). The films and microspheres prepared with all degree of cross-linking (6, 12 and 18% w/w) showed burst-release of mezalazine within a first step of drug release. Then mezalazine was released in a controlled manner in second stage of drug release during 9 h.

Keywords: Release Kinetics, Enzyme Delivery, Bioactive Model.

Abstract No.147

Evaluating of Tyrosinase Mechanism by it's Inhibition and Activation

Mahdi Alijanianzadeh[1], Ali Akbar Saboury*[1], *Mohammad Reza Ganjali*[2], *Ali Akbar Moosavi-Movahedi*[1]

1. Institute of Biochemistry and Biophysics, University of Tehran, Tehran, IR
2. Center of Excellence in Electrochemistry, Faculty of Chemistry, University of Tehran, Tehran, IR
(E-mail: Alijanianzadeh_m@yahoo.com)

The mechanism of mushroom tyrosinase (MT) is complicated because of occurrence of two different enzyme forms (Em and Eo) simultaneously. In this study the inhibition kinetics of a new synthesized ligand (derivative of aniline) in two different forms of the enzyme (Em & Eo) were investigated separately by using Double reciprocal Lineweaver-Burk plots. In both forms the ligand inhibits the enzyme competitively but the results revealed that the oxidation of diphenol by Eo is about 1.3 times faster than oxidation by Em and the tendency of the ligand to bind Em is about 1.57 times more than binding to Eo. These results describe why the low concentration of ligand (2.5 × 10-5 M) activates creolase activity and decreases lag phase and also activates and inhibits the catecholase activity at below and at saturated concentration of substrate, respectively. Also circular dichroism (CD) and fluorescence experiments confirm the binding of ligand to the enzyme. Docking results show that ligand makes 3 hydrogen bonds, 2 with one histidine residue in the active site and one with proline residue.

Keywords: Mushroom Tyrosinase, Inhibition, Activation, Mechanism.

Abstract No.148

Site-directed Mutagenesis of Mnemiopsin: Implication of one of Conserved Residues in Bioluminescence

Reza H. Sajedi[1], *Atiyeh Mahdavi**[2], *Saman Hosseinkhani*[1]

1. Department of Biochemistry, Faculty of Biological Sciences, Tarbiat Modares University, Tehran, IR
2. Department of Biology, Faculty of Science, University of Guilan, Rasht, IR
(E-mail: sajedi_r@modares.ac.ir)

Bioluminescence helps for communication, attraction, repulsion, or camouflage in marine life. Photoproteins are the primary reactants of the light-emitting reactions of various bioluminescent organisms and mostly found in marine organisms including coelenterates and ctenophores. Although many photoproteins in nature were discovered but have been very few studied in detail, except for coelenterate photoproteins. In this group, biochemical aspects of photoproteins aequorin and obelin have been well investigated and their crystal structures have been solved. With the help of protein engineering, they have found variety of analytical and biological applications. In contrast, little efforts have been made on cetenophore photoproteins such as mnemiopsin. Recently, cDNA encoding mnemiopsin photoprotein of mnemiopsis leidyiwas cloned in our lab. In this study, site directed mutagenesis using the quick change method was used to make variants of mnemiopsin displaying different functional and structural properties. Since our goal was determination of the role of one conserved residue in coelenterazine binding cavity in mnemiopsin bioluminescence, mutations were introduced at this position (position 39). This residue is among highly conserved residues in coelenterazine binding cavity in each type of photoproteins. For investigation of side chain size and charge effect on luminescence activity, we replaced Arg 39 by Lys and neutral and negatively charged residues, Met and Glu, respectively. The results indicate that except for R39K mutant, that increases luminescence intensity more than eight fold, compared to wild type, R39M and R39E mutants lost luminescence activity completely. The most notable properties of mutant R39K was its higher activity, slow rate of luminescence decay and broad pH activity profile compared to wild type. These properties make it highly attractive for both basic studies and applications. The results of structural studies

including CD, intrinsic and extrinsic fluorescence and dynamic quenching showed that mutations resulted in different structural features in mutants.

Keywords: Photoprotein, Mnemiopsin, Luminescence, Mutant.

Abstract No.149

Evaluation of the Effects of Glucomannan-Containing Yeast Product (Mycosorb) and Sodium Bentonite on Serum Biochemical Parameters in Broiler Chickens During Aflatoxicosis

Aidin Azizpour[*1], *Yashar Azizpour*[2], *Navid Mogadam*[3]

1. Young Researchers Club, Ardabil Branch, Islamic Azad University, Ardabil, IR
2. Faculty of Nursing and Midwifery, Tehran University of Medical Sciences, Tehran, IR
3. Department of Poultry Diseases, Science and Research Branch, Islamic Azad University, Tehran, IR

(E-mail: aidin_azizpour@yahoo.com)

The aim of this study was to determine the impact of aflatoxin (AF),yeast glucomannan (YG) and sodium bentonite (SB) on serum biochemical parameters in broiler feed with naturally contaminated diet with aflatoxin.Three hundred,7-day-old Ross 308-strain broiler chickens were chosen and randomly assigned to10 dietary treatmentsin 3 replicates of 10 chicks. Treatments were 1) Diet free from afatoxin(control group), 2) naturally contaminated diet with aflatoxin(negative control group), 3, 4, 5, 6,8,9 and 10) naturally contaminated diet with aflatoxin supplemented with1.5% SB, 3% SB, 0.05% YG, 0.1% YG, 1.5% SB+ 0.05% YG, 1.5% SB+ 0.1 % YG, 3% SB + 0.05% YG and 3% SB+ 0.1% YG, respectively. Serum biochemical parameters were investigated on 42 days of age.The measured aflatoxin in contaminated diet, confirmed by thin layer chromatography (TLC), was 250 ppb. Data was evaluated with SPSS.The results showed that cholesterol, uric acid and triglyceride in chickens fed with diet containing aflatoxin alone were lesser than that of those fed with control diet. Their Aspartate Amin transferase enzyme (AST) and Alanin amin transferase enzyme (ALT), however, were greater compared with those fed with control diet. Chickens were received additives with various levels in their diets showed that an decrease in AST and ALT and increase in cholesterol, uric acid and triglyceride, and an improvement in biochemical parameters when compared with the negative control group.The addition of YG and SB, individually and combination to the AF-containing diet ameliorated the adverse effects of aflatoxin, but 0.1%Yeast glucomannan supplementation to the contaminated diet with aflatoxin proved to be much more effective in the amelioration of the adverse effect of AF on serum biochemical parameters.

Keywords: Aflatoxin, Broiler chickens , 0.1%YG, AST, ALT.

Abstract No.150

Parsprot, a New Algorithm for Processing and Analyzing of Protein and Nucleic Acid Codes in Bioinformatics

Khosrow Khalifeh[* 1], *Kamal Naderlu*[2], *Seyedeh Akram Shirdel*[3], *Sakineh Tofighi*[2]

1. Department of Biology, Faculty of Sciences, University of Zanjan, IR
2. Department of Electrical and,Computer Engineering, Faculty of Engineering, University of Zanjan, IR
3. Department of Biophysics and, Biochemistry, Faculty of Biological Sciences, Tarbiat Modares University, Tehran, IR

(E-mail: khalifeh@znu.ac.ir)

We have developed a new algorithm named as "Parsprot", appropriate for the processing and analyzing of protein and nucleic acid sequences and their related structures using raw sequence and pdb file as an entry. Considering amino acid or nucleotide codes as letters, it is possible to make two, three or k-Letter words with every defined sequence, in which we take into account degeneracy of sequential residues in raw sequences of proteins as well as Nucleic Acids. In this manner the number of k-Letter words will be 20k in protein sequences and 4k for Nucleic acid sequences, where k is the number of letters in each word. The output of this algorithm can be used in extracting sequence-based information of related proteins and genes, appropriate for using in different aspects of bioinformatics and neural network computations. It is also possible to determine the number of each residue position and that of k-Letter word incorporated into different secondary structural elements as well as their interactions with neighboring residues in 3D structure of protein. Further refinement of the method and its broader applications is currently in progress. It is also noticeable that we used Java web Application as a good and user friendly interface for developing above mentioned program.

Keywords: Algorithm, Parsprot, Amino Acid codes, K-Letter word, Computation, Java Web Interface, Program.
