Abstract No.265

The Physicochemical and Biochemical Survey of the Honey Types from Iran: Protein and Enzyme Profiling

Elahe Mahmoodi Khaledi[*1], *Mehran Habibi-Rezaei* [1], *Nasim Kashef* [2], *Iisa Sadeghian* [1]

1. Protein Biotechnology Research Lab (PBRL), School of Biology, College of Science, University of Tehran, Tehran, IR
2. Medical Bacteriology Lab ,School of Biology, College of Science, University of Tehran,Tehran, IR

(E-mail: mhabibi@khayam.ut.ac.ir)

Honey has been used since ancient time as both a sweet feed and a traditional medical treatment of many diseases. The greatest biochemical fraction of the honey weight is pertains to the sugars and their sugar profile are applied to characterize the honey quality the origin of honey. Moreover, the acidity of honey is one of the most important factors in quality control of honey. Over time, simple sugars and acids present in honey provides condition to produce the hydroxyl methyl furfural (HMF), therefore its quantity is an important but small percentage of the honey weight. factor in controlling of honey freshness. Proteins are the most important constitute however, at 0.1-0.5% of the honey weight. This amount differs according to the plant origin, and also diverse species of bees. Determination of protein content of honey is considered a new method for evaluating honey quality. In this study, the physicochemical properties and protein contents and enzyme profiling of 20 honey samples collected from different region of Iran were investigated. In this survey physicochemical parameters such as pH, acidity, ash, HMF and sugar content of samples were determined and compared. Upon extraction and concentration by dialysis, centrifuge and ammonium sulfate precipitation methods, the protein content were detected by Bradford assay. The result of this study showed that the physicochemical parameters and protein contents of honey types were different. These data can be used in determination of honey quality and its therapeutic features and provide beneficial information for future studies in this field.

Keywords: Honey, Quality Control, Physicochemical Properties, Protein Content.

Abstract No.266

40 Years of Protein Biochemistry with Escapades

*Bernhard Erni**

Department for Chemistry and Biochemistry, Universität Bern, CH

(E-mail: bernhard.erni@ibc.unibe.ch)

Biochemistry covers a vast area, and I was fortunate to visit a number of spots in it. Membranes caught my attention already when I was a student. In my first encounter during my diploma thesis I calculated the vibrational modes of different triglyceride esterbackbone conformations. The purpose was to characterize the "real" backbone conformation from the infrared spectra of lipid multilayers. I then switched the topic for my PhD, where I helped to establish an in vitro system of mammalian protein synthesis with purified components. At that time such a system was deemed necessary to elucidate the possible role of protein synthesis in the generation of antibody diversity. As a postdoctoral fellow - back on the main track - I synthesized a photoaffinity label for the analysis of apolar membrane lipid-protein interactions. Unfortunately, the label in the apolar environment reacted by intramolecular rearrangement instead of crosslinking and thus was useless. Benefitting from my experience in protein purification I then started to purify the glucose transporter of the Escherichia coli phosphotransferase system (PTS), the protein that became the golden thread of all subsequent research. One reason to choose this protein and no other was the fact, that it also has phosphotransferase (kinase) activity that is much easier to assay in vitro than transport. Along the way of cloning the permease gene a second PTS transporter was picked up, which appeared even more interesting because it also serves as membrane gate for the penetration of bacteriophage DNA and of pore-forming bacteriocins (toxic peptides). Gene sequencing took almost two years, an effort that payed off because it allowed us to overexpress the proteins, to purify them by metal chelate chromatography and to study their function by site-directed as well as random mutagenesis. Because PTS occur and play an important role only in bacteria, it appeared that it could be a target of antibacterial agents. This perspective motivated us to develop in vivo and in vitro assays for high throughput inhibitor screening, to characterize the attenuated virulence of a PTS knock-out strain, and to solve the X-ray structures of several soluble PTS protein subunits. Some of the projects were done in collaboration with a start-up company. Proteome analysis of the knock-out strain then draw our attention to a new family of dihydroxyacetone kinases. They are homologous to the eucaryotic Dha kinases but are supplied with high energy phosphate by the PTS rather than by ATP. The elucidation of their structure, catalytic mechanism and gene expression were the