15±1°C, 97 kDa yolk protein was highly available during recovery period at NT, but not in case of 4°C as this protein probably undergoes aggregation thus non-available for cell plate movement.

Keywords: Zebrafish, Embryonic Development, Temperature, Diapause.

Abstract No.156

Role of Low Molecular Weight Biomolecules in Antioxidant Profile of Camel and Bovine Milk

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As reported previously, the antioxidant activity of milk comes from both low- and high molecular weight biomolecules. In this study antioxidant activity of whole milk and milk protein fractions (WF: Whey Fraction, and CF: Casein Fraction) were examined, using an ABTS radical cation assay. To explore the effect of thermal stress on antioxidant activity of either whole milk or milk protein fractions (WF and CF), their antioxidant activities were measured before and after heat treatment for 5 min at 100 °C. The results of heat treatment experiments, suggest that antioxidant activities of both whole milk and WF of camel were more temperature labile than those from bovine source. Also, a slight reduction in antioxidant activity of CF of both animal sources was observed after the heat treatments. Moreover, prior to performing antioxidant measurements, whole milk and WF were extensively dialyzed. The objective was to explore role of low molecular weight (LMW) biomolecules in their antioxidant profile. The results showed that LMW biomolecules participate to the higher extent in shaping antioxidant profile of milk and WF of camel compared to those from bovine source. The antioxidant activity of LMW biomolecules was more heat labile than that of high molecular weight (HMW) biomolecules such as proteins. Overall, this study suggests a significant role for the heat labile LMW biomolecules in shaping the antioxidant profile of camel milk.

Keywords: Antioxidant Activity, Camel Milk, Bovine Milk, Low Molecular Weight Biomolecules, Heat Treatment.

Abstract No.157

Thermal Inactivation and Conformational Lock Study on Horse Liver Alcohol Dehydrogenase

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Horse Liver Alcohol Dehydrogenase (HLADH) is a two subunits metal enzyme that has two catalytic and coenzyme domains for each subunit. The catalytic domain contains two zinc atoms that one of them has a catalytic role and another one has a structural role. The coenzyme domain connects to NAD+ coenzyme for oxidoreductase reactions. These subunits were connected to each other by coenzyme domains. In this report, we are wondering to obtain the precise residues that participate in subunits via interface locks. For this purpose, the kinetics of thermal inactivation of HLADH were studied in a 50 mM pyrophosphate buffer, pH 8.8, using ethanol as substrate and NAD+ as a cofactor. The temperature range was between 46-55°C and the conformational lock was developed based on the Poltrak theory and analysis of the curves was done by the conformational lock method for oligomeric enzymes. We obtained the number of the locks between subunits equal to two by this method and then confirmed it by the Ligplot program computations. This computation give us more detailed information that there are two patches binding sites in the interface that they spread over two regions of each chain. The small region embraces the sequence of 110 to 118 residues and the large region contains residues of 270 to 320 on each chain. The first small and second large patches may be split to two smaller sub-patches.

Keywords: Horse Liver Alcohol Dehydrogenase, Conformational lock, Poltrak theory, Ligplot program.

Abstract No.158

Autolysis Comparison on Isoenzymes of Ficin Extracted from the Fig (Ficus carica cv. Sabz) Latex

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