

Mass Spectrometry Based Proteomic Profiling of Three Feeding Categories of Bats in Tirunelveli, Tamilnadu, South India

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Abstract

A comparative protein profile of bat wing-tissue samples for three feeding categories of bats such as Insectivorous, Hipposiderous speoris; Carnivorous Megaderma lyra - and Frugivorous Cynopterus sphinx was studied. All the samples were analyzed using two-dimensional electrophoresis coupled with mass spectrometry. Totally, 38 protein spots were paired across all the three categories of samples and 5 differentially expressed proteins were identified. In the present study, it is reported that proteomics-based analysis for three feeding categories reveal the presence of five candidate proteins namely 1) Hemoglobin subunit beta; 2) V(D)J Recombination activating protein 1; 3) Olfactory receptor; 4) Lysozyme and 5) Brain-derived neurotrophic factor were identified. Among them, 3 proteins such as Olfactory receptor; Lysozyme and Brain-derived neurotrophic factor were up-regulated in M. lyra and C. sphinx compared to H. speoris. Gene ontology analysis reveals three different functional properties of the identified protein such as biological process, cellular component, and molecular function. The present study will shed more light on the importance of chiropteran fauna in proteomics and long-term conservation planning of bat populations of the study area. KEYWORDS : protein profile, three feeding categories, mass spectrometry, Gene ontology

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