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Abstract

Untargeted Proteomics Approach to Study Congenital Hearing Loss Cases †

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Introduction: Congenital Hearing Loss (CHL) is considered the most prevalent chronic condition among children. Biomarker studies of CHL are the need of the hour for the early diagnosis of the disease. Among the biomarkers of hearing loss, extracellular biomarkers of ear disorders are considered potential diagnostic tools. Protein biomarkers are considered crucial in early-stage diagnosis of CHL cases. Methods: A total of 72 samples were collected and grouped into an Experimental (n = 36) and Control (n = 36) group. This study was approved by the Institutional Ethics Committee of Karnataka Institute of Medical Sciences, Hubballi, India. After obtaining informed consent from the participants, 5 mL blood samples were collected and serum samples were separated by centrifugation at 4000 rpm for 5 min and stored at 80 °C until further analysis. Pooled samples were processed for reduction, alkylation, and trypsin digestion before undergoing Liquid Chromatography Mass Spectrometry-Quadrupole Time of Flight (LCMS Q-TOF) analysis. Mascot search analysis was performed to identify peptide sequences and STRING software was used for network analysis of selected proteins. Results: Significant proteins were identified among the study subjects. These comprised Guanine nucleotide protein, Glutamate receptor ionotropic protein, Complement C3, Putative transmembrane protein, Zinc finger protein, Alpha 2 glycoprotein, E3 ubiquitin protein, Cadherin, Alpha Tectorin, Myosin, etc. All these proteins are associated with Congenital Hearing Loss and are involved in the mechano-transduction of soundwaves inside the cochlea. Conclusions: In this study, proteins associated with CHL have been identified among human subjects. The validation of these protein markers in serum samples using ELISA test will confirm the findings. Our panel of protein biomarkers may help in studying the underlying causes of the disease, which may direct us to its early diagnosis.

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