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ISSN: 2684-1622
Journal of Eye Diseases and Disorders

Short Communication

Proteomics Technique Based on Mass Spectrometry Used In Cataract Research

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DESCRIPTION

A cataract is a clouding of the lens of the eye, which is ordinarily clear. For people with cataracts, gazing through cloudy lenses is rather like peering through a snowy or occluded window. It is the major source of blindness in the world, accounting for over 42% of all cases. Lens fibers contain the largest protein concentration in the body, accounting for more than 35% of their dry weight. Given the eye lens's high concentration of structural proteins crystalline (up to 90%), it appears to be an appropriate proteomic entity to investigate, and it might potentially be used to simulate other protein conformational illnesses. Crystalline have a very long lifespan and almost negligible protein turnover. This opens the door to Post-Translational Changes (PTM), which can predispose the lens to cataract development. Despite recent advances in proteomics, little is known about the human lens proteome. The use of mass spectrometry to detect which crystalline changes cause cataracts has a lot of potential. For lens-tissue samples, quantitative analysis of PTMs at the peptide level using proteomics is a strong bio analytical method that yields more thorough data. The use of new mass spectrometry-based methods in lens research will be emphasized. Finally, the future directions of cataract proteomics research will be discussed.

Crystallins are extraordinarily abundant lens fiber structural proteins that make up around 90% of the lens proteins. Crystallins are divided into three groups: α, β, and ɣ crystalline. The oligomers of α crystalline and β crystalline exist, but the monomer of ɣ crystalline exists. The tiny heat shock protein α crystallin makes up a large amount of the cytoplasm in the eye lens, accounting for up to 50% of the total protein [1]. The monomer of α crystallin has a molecular weight of 20 kDa. The lenticular a-crystallin occurs in humans as a hetero-oligomer with an estimated molecular weight of 800 kDa and two subunits, α A and α B, that occur in a 3:1 stoichiometry [2]. α A-crystallin seems toward being lens-specific, whereas α B-crystallin is identified in a variety of tissues including the heart, skeletal muscle, kidney and brain. Many neurological illnesses, cancers, and diabetes situations have been shown to have elevated amounts of α crystallin, β crystallin [3]. Both of these proteins are renowned for their chaperone function, as seen by their ability to prevent protein aggregation. They are thought to shield other lens proteins from the harmful effects of heat, chemicals, and UV light [4].

The proteins in the eye lens have a very long lifespan and almost negligible protein turnover. This situation allows for a lot of Post-Translational Modifications (PTM), the majority of which lead to aggregation; this process is enhanced even more by the physiological, environmental, and genetic variables that predispose the lens to cataract development. PTMs are chemical changes made to a protein after it has been translated. PTM are thus either the result of pathological alterations or one of the final stages in protein production. PTM that occur throughout the differentiation and ageing processes are shown to generate changes in higher-order structure of lens proteins associated to opacification due to the lens's sluggish turnover rate [5].

The most complete map of PTM in human lens was generated using recently established blind modification search strategies. They compared spectral counts between the Water-Soluble (WS) and Water-Insoluble (WI) fractions of aged lenses, and found that the degree of deamination was considerably higher in the WI fractions, proving the long-held idea that PTM contribute to age-related loss of crystallin solubility. Deamination and methylated cysteine were the most prevalent PTMs identified in old lenses, according to spectral counts, with other PTMs present at lesser levels. The cross-linking characteristics of a gD-crystallin fragment from human lenses were revealed by mass spectrometric analysis as oxidized methionine and tryptophan residues included two oxygen's. Crystallin fragments from human cataract us and age-matched normal lenses were compared and found to have cataract-specific alterations such as truncation, asparagine deamination, and tryptophan residue oxidation. Three PTM (*i.e.* oxidation of methionine and tryptophan, conversion of serine to dehydroalanine, and formulation of histidine) were detected in a A-crystallin fragment identified using MS/MS covalent multimers in the WI proteins of aged human lenses.

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Received: 02-Mar-2022, Manuscript No. JEDD-22-16257; **Editor assigned:** 04-Mar-2022, PreQC No. JEDD-22-16257 (PQ); **Reviewed:** 18-Mar-2022, QC No. JEDD-22-16257; **Revised:** 25-Mar-2022, Manuscript No. JEDD-22-16257 (R); **Published:** 02-Apr-2022. DOI: 10.35248/2684-1622.22.7.169

Citation: Thaddi BN (2022) Proteomics Technique Based on Mass Spectrometry Used In Cataract Research. J Eye Dis Disord. 7:169.

CONCLUSION

In conclusion, proteomics technology is a crucial to achieving sustainable tool that will help us better understand a myriad of molecular pathways in ocular tissues and disorders. Understanding the proteome, each protein's structure and function, and the complexity of protein to protein interactions will be important in the future development of the most effective diagnostic procedures and disease therapies. The use of particular protein biomarkers to treatment will be an intriguing use of proteomics.

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