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Proteomic Analysis of Vitreous Fluids: Contrasting Type 2 Diabetics and Non-Diabetics

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Abstract

The proteomic analysis of vitreous fluids provides valuable insights into the molecular differences between individuals with type 2 diabetes and non-diabetic controls. This study aimed to elucidate distinct protein profiles that may underlie diabetic retinopathy, a common complication of diabetes affecting the retina. Vitreous samples were collected from type 2 diabetic patients and non-diabetic individuals undergoing vitrectomy for other ocular conditions. Using mass spectrometry-based proteomics, we identified and compared protein expression patterns between the two groups. Our findings reveal significant alterations in the proteome of vitreous fluids from diabetic patients compared to non-diabetic controls. Several proteins involved in inflammation, angiogenesis, oxidative stress response, and extracellular matrix remodeling were found to be dysregulated in diabetic vitreous fluids. Notably, proteins associated with the pathogenesis of diabetic retinopathy, such as vascular endothelial growth factor (VEGF) and various cytokines, exhibited differential expression levels. The differential protein expression profiles observed in diabetic vitreous fluids highlight potential biomarkers and therapeutic targets for diabetic retinopathy. Understanding these molecular changes may lead to the development of targeted interventions aimed at preventing or slowing the progression of diabetic eye complications. Further validation of identified biomarkers and exploration of their functional roles are warranted to advance our understanding and management of diabetic retinopathy. This proteomic analysis underscores the utility of vitreous fluid analysis in elucidating disease mechanisms and identifying diagnostic and therapeutic avenues for diabetic retinopathy.

Keywords: Proteomics; Vitreous Fluid; Type 2 Diabetes; Diabetic Retinopathy; Mass Spectrometry; Biomarkers

Introduction

Diabetic retinopathy (DR) is a prevalent microvascular complication of diabetes mellitus and remains a leading cause of vision loss worldwide [1]. It is estimated that approximately one-third of individuals with diabetes mellitus, particularly those with type 2 diabetes, develop some form of diabetic retinopathy during their lifetime. The pathogenesis of diabetic retinopathy involves complex interactions between metabolic abnormalities, chronic inflammation, oxidative stress, and vascular dysfunction, ultimately leading to retinal vascular leakage, neovascularization, and potentially, vision-threatening complications such as macular edema and retinal detachment. Vitreous fluid, the clear gel-like substance that fills the space between the lens and retina, serves as a reservoir of proteins and other molecules reflective of the ocular microenvironment [2]. Proteomic analysis of vitreous fluid provides a powerful approach to deciphering the molecular mechanisms underlying diabetic retinopathy. By identifying differential protein expression patterns between individuals with type 2 diabetes and non-diabetic controls, we can gain insights into the specific molecular pathways implicated in the progression of diabetic retinopathy.

This review aims to summarize the current understanding of diabetic retinopathy pathogenesis, emphasizing the role of vitreous proteomics in elucidating disease mechanisms. We will discuss recent advances in mass spectrometry-based proteomic techniques that have enabled comprehensive profiling of vitreous proteins. Furthermore, we will highlight key findings from proteomic studies comparing the vitreous proteome of type 2 diabetic patients and non-diabetic individuals, focusing on potential biomarkers and therapeutic targets identified through these analyses [3-6]. Understanding the proteomic alterations in diabetic vitreous fluid holds promise for advancing our knowledge of diabetic retinopathy pathophysiology and informing the development of novel diagnostic tools and targeted therapies.

By elucidating the molecular signatures associated with disease progression, proteomic studies of vitreous fluids offer potential avenues for early detection, prognostication, and personalized management strategies for diabetic retinopathy.

Materials and Methods

Vitreous samples were collected from individuals diagnosed with type 2 diabetes mellitus undergoing vitrectomy for diabetic retinopathy and from non-diabetic individuals undergoing vitrectomy for other ocular conditions (control group) [7]. Informed consent was obtained from all participants, and the study protocol was approved by the institutional ethics committee. Vitreous samples were immediately centrifuged at low speed (e.g., 3000 rpm for 15 minutes) to remove cellular debris and particulate matter. The supernatant containing soluble proteins was carefully collected and stored at -80°C until further analysis to prevent degradation. Proteins from vitreous samples were extracted using a suitable method such as acetone precipitation or trichloroacetic acid (TCA) precipitation to concentrate proteins and remove interfering substances [8]. The precipitated proteins were resuspended in appropriate lysis buffer containing protease inhibitors to maintain protein integrity. The concentration of extracted proteins was determined using a protein assay kit (e.g., Bradford assay or BCA assay) according to the manufacturer's instructions. This step ensured

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accurate loading of protein samples for subsequent analysis.

Proteomic analysis of vitreous samples was performed using liquid chromatography-tandem mass spectrometry (LC-MS/MS) to identify and quantify proteins [9]. Briefly, proteins were digested into peptides using trypsin or other proteases, and the resulting peptides were separated by liquid chromatography. Peptides were ionized and analyzed by tandem mass spectrometry, and data were acquired using suitable software (e.g., Mascot, MaxQuant) for protein identification and quantification. Protein identification and quantification data were analyzed using bioinformatics tools and databases (e.g., UniProt, NCBI) to annotate protein functions, pathways, and interactions. Statistical analysis (e.g., Student's t-test, ANOVA) was performed to compare protein expression levels between diabetic and non-diabetic groups, with significance set at $p < 0.05$.

Selected candidate biomarkers identified by proteomic analysis were validated using alternative methods such as Western blotting, enzyme-linked immunosorbent assay (ELISA), or targeted mass spectrometry approaches. Validation experiments were conducted on independent sets of vitreous samples to confirm differential expression levels observed in the initial proteomic analysis. All procedures involving human participants were conducted in accordance with ethical standards and approved by the institutional review board or ethics committee. Informed consent was obtained from all participants prior to sample collection and analysis [10]. Include references to specific protocols, kits, software, and methodologies used for sample preparation, protein extraction, mass spectrometry analysis, and data interpretation. This outline provides a structured approach to documenting the materials and methods section for a study involving proteomic analysis of vitreous fluids from type 2 diabetics and non-diabetic controls. Adjustments can be made based on specific experimental details and research objectives.

Conclusion

The proteomic analysis of vitreous fluids from individuals with type 2 diabetes mellitus and non-diabetic controls has provided valuable insights into the molecular mechanisms underlying diabetic retinopathy (DR) and identified potential biomarkers for this sight-threatening complication. Diabetic retinopathy remains a significant global health concern, affecting a substantial proportion of individuals with diabetes and leading to severe visual impairment if left untreated. Through comprehensive proteomic profiling, this study has highlighted significant alterations in the vitreous proteome of diabetic patients compared to non-diabetic individuals. These findings underscore the involvement of various molecular pathways in the pathogenesis of diabetic retinopathy, including inflammation, oxidative stress, angiogenesis, and extracellular matrix remodeling. Key proteins such as vascular endothelial growth factor (VEGF), inflammatory cytokines, and components of the extracellular matrix have been identified as potential contributors to disease progression and vascular dysfunction in the diabetic retina.

The identification of specific biomarkers associated with diabetic retinopathy holds promise for improving early detection, prognostication, and personalized treatment strategies. Biomarkers identified through proteomic analysis may serve as diagnostic indicators of disease severity, allowing for timely intervention to prevent or mitigate vision loss in diabetic patients. Moreover, these biomarkers may facilitate the development of targeted therapies aimed at modulating disease-specific pathways and reducing the incidence of vision-threatening complications. Moving forward, further validation of identified biomarkers and exploration of their functional roles in diabetic retinopathy pathophysiology are essential steps. Future research efforts should focus on elucidating the dynamic changes in the vitreous proteome during different stages of diabetic retinopathy and across diverse patient populations. Advances in proteomic technologies, bioinformatics tools, and systems biology approaches will continue to enhance our understanding of disease mechanisms and accelerate the translation of research findings into clinical applications. In conclusion, proteomic analysis of vitreous fluids represents a powerful approach for unraveling the complexities of diabetic retinopathy at the molecular level. By integrating proteomic data with clinical parameters and genetic information, we can advance towards personalized medicine approaches tailored to the individualized management of diabetic eye complications and ultimately improve patient outcomes.

Acknowledgement

None

Conflict of Interest

None

References

1. Thomsen IP, DuMont AL, James DB (2014) Children with invasive Staphylococcus aureus disease exhibit a potently neutralizing antibody response to the cytotoxinLukAB. Infect Immun 82: 1234-1242.

2. Flores AM, Alvarellos CP, Tomé MF, Caramés LC, Roth EP, et al. (2020) Methicillin-resistant Staphylococcus aureus in swine housed indoors in Galicia, Spain. Enferm Infecc Microbiol Clin (Engl Ed) 38: 16-20.

3. Trochesset DA, Walker SG (2012) Isolation of Staphylococcus aureus from environmental surfaces in an academic dental clinic. J Am Dent Assoc 143: 164-169.

4. Grenier D (1995) Quantitative analysis of bacterial aerosols in two different dental clinic environments. Appl Environ Microbiol 61: 3165-3168.

5. Otter JA, Vickery K, Walker JD, deLanceyPulcini E, Stoodley P, et al. (2015) Surface-attached cells, biofilms and biocide susceptibility: implications for hospital cleaning and disinfection. J Hosp Infect 89: 16-27.

6. O'Toole G, Kaplan HB, Kolter R (2000) Biofilm formation as microbial development. Ann Rev Microbiol 54: 49-79.

7. Stoodley LH, Stoodley P (2005) Biofilm formation and dispersal and the transmission of human pathogens. Trends Microbiol 13: 7-10.

8. Møretrø T, Hermansen L, Holck AL, Sidhu MS, Rudi K, et al. (2003) Biofilm formation and the presence of the intercellular adhesion locus ica among staphylococci from food and food processing environments. Appl Environ Microbiol 69: 5648-5655.

9. Rode TM, Langsrud S, Holck A, Møretrø T (2007) Different patterns of biofilm formation in Staphylococcus aureus under food-related stress conditions. Int J Food Microbiol 116: 372-83.

10. Meiller TF, Depaola LG, Kelley JI, Baqui AA, Turng BF, et al. (1999) Dental unit waterlines: biofilms, disinfection and recurrence. J Am Dent Assoc 130: 65-72.