INNOVATION IN MOLECULAR BIOTECHNOLOGY
2023, VOL. 1, ISSUE 1
https://doi.org/10.61577/imb.2023.100002

RESEAPRO JOURNALS

SHORT COMMUNICATION

OPEN ACCESS

Advancing ophthalmology research through spatial transcriptomics: a concise overview

Moksha Laxmi[1] and Deepti M Sati[2]

[1]Department of Ophthalmology, Scheie Eye Institute, University of Pennsylvania, Philadelphia, USA
[2]School of Pharmacy, Graphic Era Hill University, Dehradun, India

KEYWORDS

Transcriptome; Retinal diseases; Glaucoma; Drug development; Genetic therapy; Gene expression profiling

ARTICLE HISTORY

Received 11 August 2023; Revised 31 August 2023; Accepted 8 September 2023

In recent years, recent developments in molecular biology and spatial analysis methods have produced a ground-breaking method for comprehending gene expression in the context of tissue architecture. With the aid of the state-of-the-art molecular biology method known as spatial transcriptomics, it is now possible to examine gene expression patterns in relation to tissue architecture and spatial organization. Combining conventional gene expression analysis with geographical data provides a more thorough understanding of how genes are expressed and controlled tissues. Nature Methods dubbed it the "Method of the Year" because of its key impact in 2020 [1].

Spatial transcriptomics, a method that sheds fresh information on the molecular complexities of numerous eye disorders and ailments, has emerged as a potential study area in ophthalmology. A careful examination of the patterns of gene expression across the numerous tissue layers of the eye's complex anatomy is necessary. Spatial transcriptomics in ophthalmology research can be very helpful for comprehending the genetic and cellular mechanisms behind diverse eye disorders and ailments.

By bridging the gap between conventional gene expression analysis and geographical data, spatial transcriptomics enables researchers to unravel the complex network of interactions between various cell types inside the ocular tissue.

The underlying molecular mechanisms of eye disorders are now better understood as a result. Researchers can learn more about the relationships between various cell types, find important genes implicated in disease progression, and perhaps even find new therapeutic targets by examining gene expression patterns in particular parts of the eye. Spatial transcriptomics may also be useful for understanding corneal disorders, which are frequently characterized by complex tissue organization. Researchers can glean insights into corneal dystrophies and devise targeted interventions by dissecting gene expression patterns within different corneal layers. Moreover, the technique's potential in gene therapy and drug development cannot be overlooked. The ability to identify genes enriched in specific ocular tissues holds great potential for the design of precision therapies, addressing the root causes of eye diseases [2].

In the landscape of retinal diseases, spatial transcriptomics offers a multidimensional lens to study conditions such as age-related macular degeneration, retinitis pigmentosa, and diabetic retinopathy. By pinpointing gene expression changes within specific retinal layers or cell types, researchers gain insights into the cascade of events leading to disease progression. The technique holds particular promise in unraveling the complex interactions that contribute to the degeneration of retinal ganglion cells in glaucoma, ultimately guiding the development of novel therapeutic strategies [3,4]. Spatial transcriptomic leads to the identification of the real culprit and the treatment of Macular Neovascularization (MNV) which is the major visual devastating consequence of AMD. It also proved to be the novel approach for the molecular investigation of retinal and vitreous detachment [5,6].

LGACC (Lacrimal Gland Adenoid Cystic Carcinoma) is one of the most common and lethal tumor of the lacrimal gland. Treatment involves the removal of the eye and surrounding socket contents, followed by chemoradiation. Even with this radical treatment, the 10-year survival rate for LGACC is 20%, given the propensity for recurrence and metastasis. Spatial transcriptomics gives the opportunities to develop targeted drug delivery and improve patient outcomes [7]. However, while spatial transcriptomics shows tremendous promise, it is important to acknowledge the challenges that lie ahead. The relatively nascent technology requires refinement and standardization to ensure consistent and meaningful results. Sample preparation, data analysis, and integrating spatial data with existing knowledge pose significant hurdles. As the field of ophthalmology research advances, spatial transcriptomics guides researchers toward personalized medicine approaches. By characterizing unique gene expression patterns in individual patients, tailored treatments can be developed, leading to more effective and efficient care. Additionally, the potential for tissue regeneration and healing following injury or surgery comes to the forefront, with spatial transcriptomics offering insights into the molecular dynamics of these processes.

***Correspondence:** Moksha Laxmi, Department of Ophthalmology, Scheie Eye Institute, University of Pennsylvania, Philadelphia, PA 19104, USA, email: mokshakoul47@gmail.com

In conclusion, integrating spatial transcriptomics within the realm of ophthalmology research can potentially revolutionize our understanding of eye diseases. From dissecting complex interactions to guiding personalized therapeutic approaches, this technique opens a new chapter in ocular health investigation. As the technology matures, collaborative efforts between molecular biologists, clinicians, and bioinformaticians will be crucial to fully harness its capabilities and translate insights into tangible clinical advancements. Through interdisciplinary collaboration and continuous refinement, spatial transcriptomics could pave the way for innovative approaches to tackling some of the most challenging eye diseases of our time. It's important to note that while spatial transcriptomics holds great promise, it's still a relatively new technology, and its application in ophthalmology research is an evolving area. Researchers are continuously working to optimize and refine the techniques to extract meaningful insights from complex tissue samples. As technology advances and more studies are conducted, spatial transcriptomics could significantly enhance our understanding of the molecular basis of eye diseases and pave the way for innovative therapeutic approaches like gene therapy and personalized medicine.

Disclosure statement

No potential conflict of interest was reported by the authors.

References

1. Williams CG, Lee HJ, Asatsuma T, Vento-Tormo R, Haque A. An introduction to spatial transcriptomics for biomedical research. Genome Med. 2022;14(1):1-8.
2. Ligocki AJ, Fury W, Gutierrez C, Adler C, Yang T, Ni M, et al. Molecular characteristics and spatial distribution of adult human corneal cell subtypes. Sci Rep. 2021;11(1):16323.
3. Enz TJ, Tribble JR, Williams PA. Comparison of glaucoma-relevant transcriptomic datasets identifies novel drug targets for retinal ganglion cell neuroprotection. J Clin Med. 2021;10(17):3938.
4. Jakobs TC. Differential gene expression in glaucoma. Cold Spring Harb Perspect Med. 2014;4(7):a020636.
5. Voigt AP, Mullin NK, Navratil EM, Flamme-Wiese MJ, Lin LC, Scheetz TE, et al. Gene expression within a human choroidal neovascular membrane using spatial transcriptomics. bioRxiv. 2023:2023-2006.
6. Maranian M, Snead M. A Novel Transcriptome Approach to the Investigation of the Molecular Pathology of Vitreous and Retinal Detachment. Genes. 2022;13(10):1885.
7. Moeyersoms AH, Gallo RA, Zhang MG, Stathias V, Maeng MM, Owens D, et al. Spatial Transcriptomics Identifies Expression Signatures Specific to Lacrimal Gland Adenoid Cystic Carcinoma Cells. Cancers. 2023;15(12):3211.

https://doi.org/10.61577/imb.2023.100002