Opinion
Volume 17:06, 2023

Journal of Molecular and Genetic Medicine

ISSN: 1747-0862 Open Access

Human-induced Pluripotent Stem Cell-derived Excitatory Neurons Display Differentiations in Transcriptomes Between Alzheimer's Patients and Controls

Ava Kensington*

Department of Genetic Research, University of Washington, Seattle, WA 98195, USA

Introduction

Alzheimer's Disease (AD) remains a significant challenge in the field of neuroscience, with its complex etiology and elusive mechanisms. Recent advancements in stem cell technology have opened new avenues for exploring the intricacies of AD pathology. A groundbreaking area of research involves the generation of human-induced Pluripotent Stem Cells (hiPSCs) and their subsequent differentiation into excitatory neurons. This innovative approach provides a unique platform to study AD at the cellular level, offering insights into transcriptomic differentiations between individuals with Alzheimer's and healthy controls [1]. Alzheimer's disease, a progressive neurodegenerative disorder, is characterized by the accumulation of beta-amyloid plaques and tau tangles in the brain. The hallmark features of AD include cognitive decline, memory loss, and impaired neuronal function.

The exact mechanisms underlying these pathological changes remain elusive, making the development of effective treatments a daunting task. Excitatory neurons, which release the neurotransmitter glutamate, play a pivotal role in cognitive functions such as learning and memory. Dysfunction in these neurons is a key aspect of AD pathology. By employing hiPSC technology to generate excitatory neurons from both AD patients and unaffected individuals, researchers have unlocked a powerful tool to study the molecular nuances associated with the disease [2].

Description

In the context of Alzheimer's research, skin cells from both patients with AD and healthy controls are reprogrammed into hiPSCs. These hiPSCs serve as a versatile cellular source, allowing researchers to recapitulate the early stages of neuronal development and investigate how these cells differentiate into excitatory neurons. The next crucial step involves directing hiPSCs to differentiate into excitatory neurons. This process mimics the natural development of neurons in the human brain, enabling the creation of a controlled and reproducible cellular model for studying AD. The resulting excitatory neurons share key characteristics with those found in the brains of AD patients, offering a unique opportunity to investigate disease-specific molecular alterations [3].

Researchers have successfully optimized protocols for differentiating hiPSCs into excitatory neurons, ensuring that the generated cells closely resemble their in vivo counterparts. This standardized approach enhances the reliability and reproducibility of experiments, facilitating meaningful comparisons between cells derived from AD patients and those from healthy controls. Once the hiPSCs have been differentiated into excitatory neurons, researchers employ advanced transcriptomic profiling techniques to analyze the gene expression patterns within these cells. Transcriptomics, a branch of molecular biology, focuses on the study of RNA molecules, providing insights into which genes are active and to what extent. By comparing the transcriptomes of excitatory neurons from AD patients and controls, researchers can identify differentially expressed genes and unravel the molecular signatures associated with Alzheimer's disease [4].

The transcriptomic analyses have unveiled striking differences in gene expression between excitatory neurons derived from AD patients and those from healthy controls. Genes involved in various cellular processes, including synaptic function, inflammation, and neuronal communication, exhibit altered expression levels in AD-derived neurons. Notably, genes associated with the regulation of amyloid-beta metabolism and tau phosphorylation, central players in AD pathology, display dysregulation. The transcriptomic signatures provide valuable insights into the molecular mechanisms underlying the aberrant accumulation of amyloid-beta plaques and tau tangles observed in the brains of individuals with Alzheimer's disease. Preliminary findings suggest that the dysregulated genes contribute to disruptions in synaptic transmission, impairments in neuronal connectivity, and increased susceptibility to excitotoxicity – a process wherein excessive activation of excitatory neurotransmission leads to neuronal damage. Unraveling these functional consequences is crucial for developing targeted interventions that address the specific molecular pathways implicated in AD [5].

Conclusion

Despite the groundbreaking discoveries facilitated by hiPSC-derived excitatory neurons, several challenges remain. The complexity of AD and the multitude of factors contributing to its pathogenesis necessitate comprehensive and multidimensional analyses. Integrating data from transcriptomics with other omics technologies, such as proteomics and metabolomics, will provide a more holistic understanding of the molecular landscape of Alzheimer's disease. The exploration of transcriptomic differentiations in hiPSC-derived excitatory neurons also prompts further questions about the temporal dynamics of gene expression changes. Longitudinal studies tracking these alterations throughout different stages of AD progression will offer insights into the evolving molecular landscape of the disease. In conclusion, the use of hiPSC-derived excitatory neurons has revolutionized our approach to studying Alzheimer's disease at the cellular and molecular levels. Transcriptomic analyses of these neurons have provided a wealth of information, unraveling differentiations in gene expression between AD patients and controls. This research not only enhances our understanding of the molecular mechanisms underlying AD but also opens new avenues for the development of targeted therapeutics.

Acknowledgement

None.

Conflict of Interest

None.

***Address for Correspondence:** Ava Kensington, Department of Genetic Research, University of Washington, Seattle, WA 98195, USA, E-mail: Avakeng7@gmail.com*

Received: 07 October, 2023, Manuscript No. jmgm-24-125758; **Editor assigned:** 09 October, 2023, PreQC No. P-125758; **Reviewed:** 21 October, 2023, QC No. Q-125758; **Revised:** 27 October, 2023, Manuscript No. R-125758; **Published:** 06 November, 2023, DOI: 10.37421/1747-0862.2023.17.637

References

1. Chou, Bin-Kuan, Prashant Mali, Xiaosong Huang and Zhaohui Ye, et al. "Efficient human iPS cell derivation by a non-integrating plasmid from blood cells with unique epigenetic and gene expression signatures." *Cell Res* 21 (2011): 518-529.
2. Takahashi, Kazutoshi and Shinya Yamanaka. "Induction of pluripotent stem cells from mouse embryonic and adult fibroblast cultures by defined factors." *Cell* 126 (2006): 663-676.
3. Das, Debamitra, Kyra Feuer, Marah Wahbeh and Dimitrios Avramopoulos. "Modeling psychiatric disorder biology with stem cells." *Currt Psych Rep* 22 (2020): 1-23.
4. Yu, Junying, Kejin Hu, Kim Smuga-Otto and Shulan Tian, et al. "Human induced pluripotent stem cells free of vector and transgene sequences." *Sci* 324 (2009): 797-801.
5. Love, Michael I., Wolfgang Huber and Simon Anders. "Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2." *Genome Biol* 15 (2014): 1-21.

How to cite this article: Kensington, Ava. "Human-induced Pluripotent Stem Cell-derived Excitatory Neurons Display Differentiations in Transcriptomes Between Alzheimer's Patients and Controls." *J Mol Genet Med* 17 (2023): 637.