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Analysis of ABCA7 in Alzheimer

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Analysis of ABCA7 in Alzheimer Johnathan Daly and Elaine Vanterpool, PhD Oakwood University **Department of Biological Sciences** Huntsville AL, 35896

ABSTRACT

Alzheimer's disease (AD) is a progressive neurological condition that presents a significant global health concern, impacting millions of people worldwide. The causes of AD are intricate and involve a mix of genetic and environmental factors. One noteworthy genetic factor is the ATP-binding cassette transporter A7 (ABCA7) gene, which plays a crucial role in the disease's onset and advancement. This analysis offers a thorough review of the ABCA7 gene's involvement in AD, focusing on its influence on lipid metabolism, immune response modulation, and amyloid-beta processing. Furthermore, it delves into the effects of specific mutations in the ABCA7 gene and their potential role in disease progression. The study also examines the expression patterns of the ABCA7 gene in various tissues, highlighting its diverse functions in human health. While our understanding grows, further research is necessary to fully grasp how the ABCA7 gene contributes to Alzheimer's disease at the molecular level, with the aim of developing innovative treatments targeting this gene and its pathways. Results indicate that the ABCA7 protein features conserved domains, including two nucleotide-binding domains (NBDs) and two transmembrane domains (TMDs), which are vital for its function.

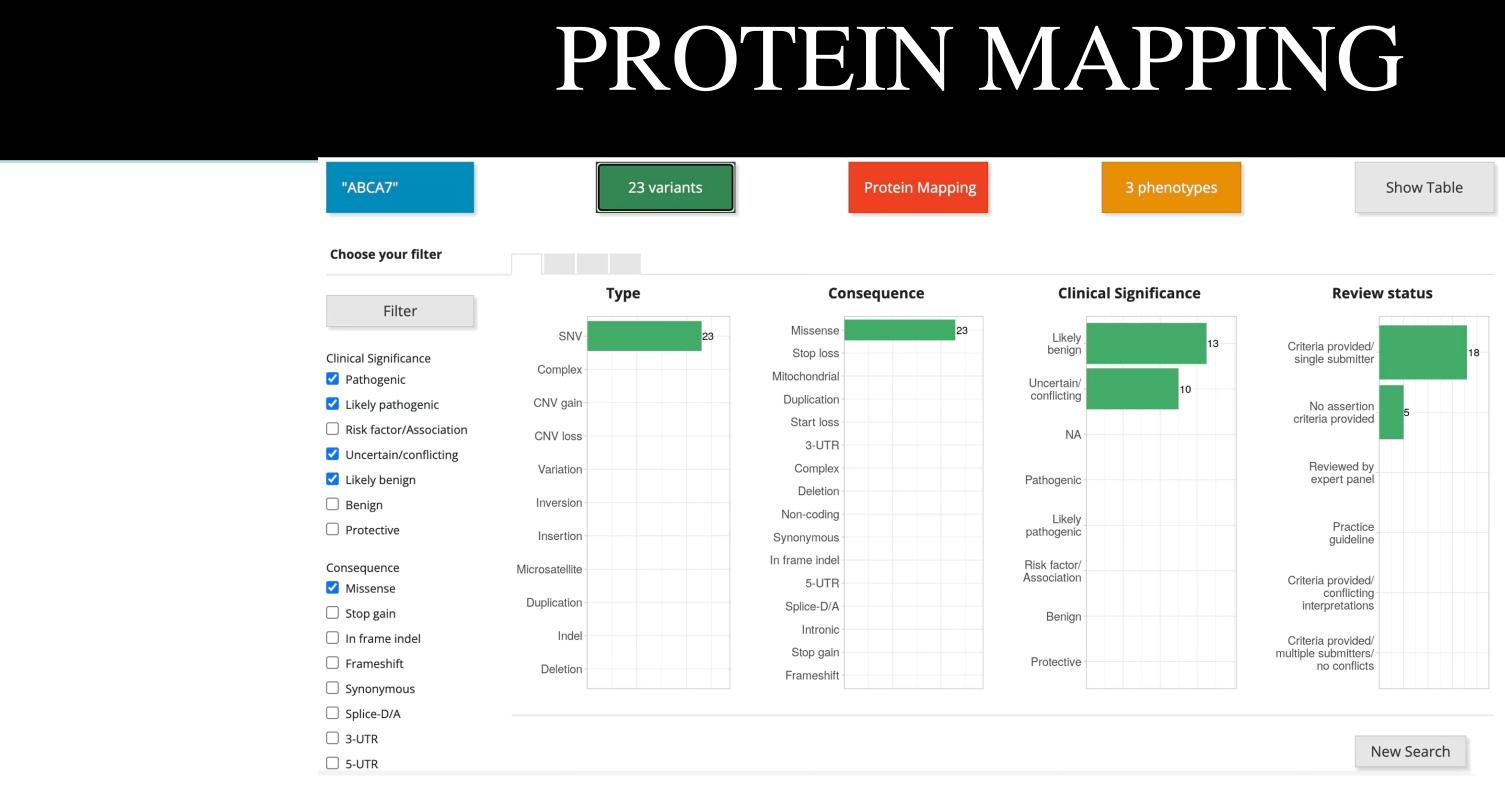
INTRODUCTION

Alzheimer's disease (AD) is a complex neurodegenerative disorder influenced by genetic a environmental factors, leading to cognitive decline affecting millions globally. While progress has been in understanding AD's molecular pathways, effectiv therapies are still lacking. Genetic risk factors like A ε4, PSEN1, PSEN2, APP, and ABCA7 offer insights AD's mechanisms. This review examines AD's gene molecular, and cellular processes and potential therapeutic strategies, emphasizing the need for a comprehensive approach to treatment.

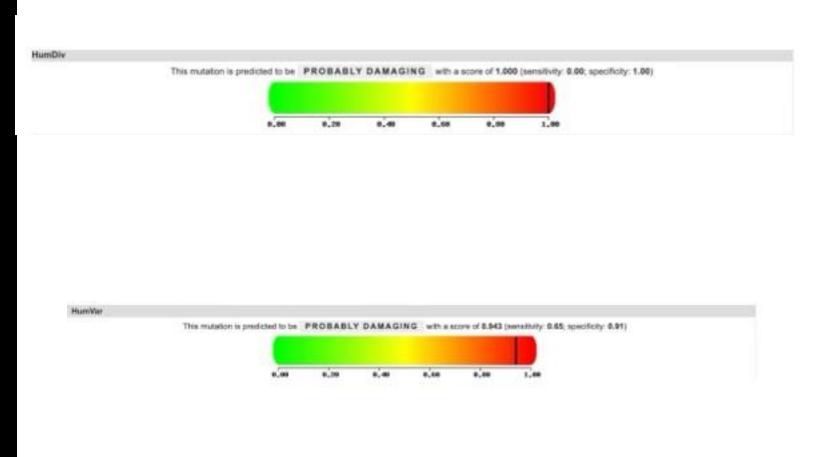
METHODS

Simple ClinVar Identifed genes SIFT and PolyPhen 2 were utilized to analyze variants Swiss Moswl was used to illustrate the protein striuctures

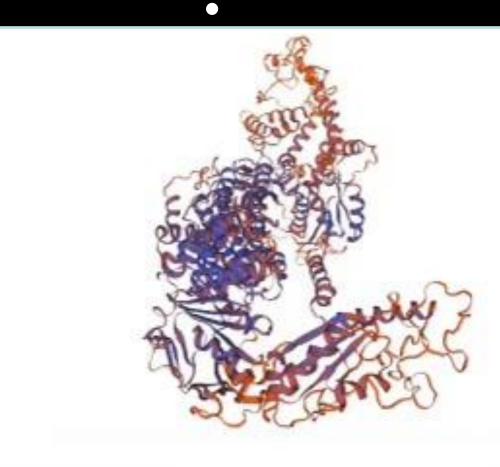
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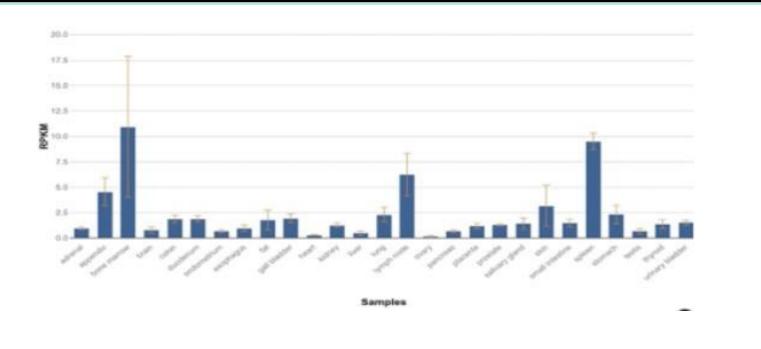


SWISS Pro Model Conserved Domain



RESULTS

Gene Expression





DISCUSSION AND CONCLUSION

Conclusion The study's results indicate that the ABCA7 gene plays a pivotal role in the progression of Alzheimer's disease by affecting lipid metabolism and regulating immune responses. Mutations in the ABCA7 gene, particularly missense mutations, have the potential to disrupt its function and contribute to disease development. The gene's expression patterns across different organs suggest that it may have diverse functions, necessitating urther exploration. Moreover, the ABCA7 gene's involvement in other diseases like age-related macular degeneration and cardiovascular diseases suggests broader implications for human nealth. More research is required to uncover the precise molecular mechanisms by which the ABCA7 gene influences Alzheimer's disease and related conditions, which could lead to the development of innovative treatment approaches. Despite advances in understanding the molecular underpinnings of AD and identifying genetic risk factors, its exact causes remain elusive, and effective disease-modifying therapies are still lacking. A comprehensive approach targeting various aspects of AD, including Aβ production, neuro - inflammation, oxidative stress, and impaired energy metabolism, is necessary. Developing novel therapeutic strategies, combined with personalized medicine approaches, is essential for revolutionizing AD management and enhancing the quality of life for patients and their families.

REFERENCES

https://www.ncbi.nlm.nih.gov/clinvar/variation/4012/ <u> ttps://pubmed.ncbi.nlm.nih.gov/38255788/</u>

ACKNOWLEDGEMENTS

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