



IN-SILICO MUTATION ANALYSIS OF PATHOGENIC NON-SYNONYMOUS SINGLE NUCLEOTIDE POLYMORPHISMS (nsSNPs) IN PSEN1 GENE.



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*¹Gershom A. Olajire,² Olaitan I. Awe

*¹ Department of Biochemistry, Faculty of Basic Medical Sciences, University of Ibadan

² African Society for Bioinformatics and Computational Biology (ASBCB)

- nsSNPs in PSEN1 have structural and functional impact on its function and influences AD pathogenesis.
- 14 most damaging nsSNPs occurred in PSEN1 highly conserved region significantly impacting its function.
- G209R, P117R, Y115D, P117D, P264R, L226R SNPs caused decrease in PSEN1 hydrophobicity.
- 8 of these 14 most deleterious SNPs occurred in PSEN1's transmembrane domain involved in its γ -secretase activity.
- PSEN1 was shown to be in interaction with GSK3 β and β -catenin involved in Wnt-signalling which would be distorted by these SNPs.

INTRODUCTION

Presenilin 1 (PSEN1) belongs to the family of transmembrane proteins found in cell organelles, the nuclear envelope, mitochondria, etc.

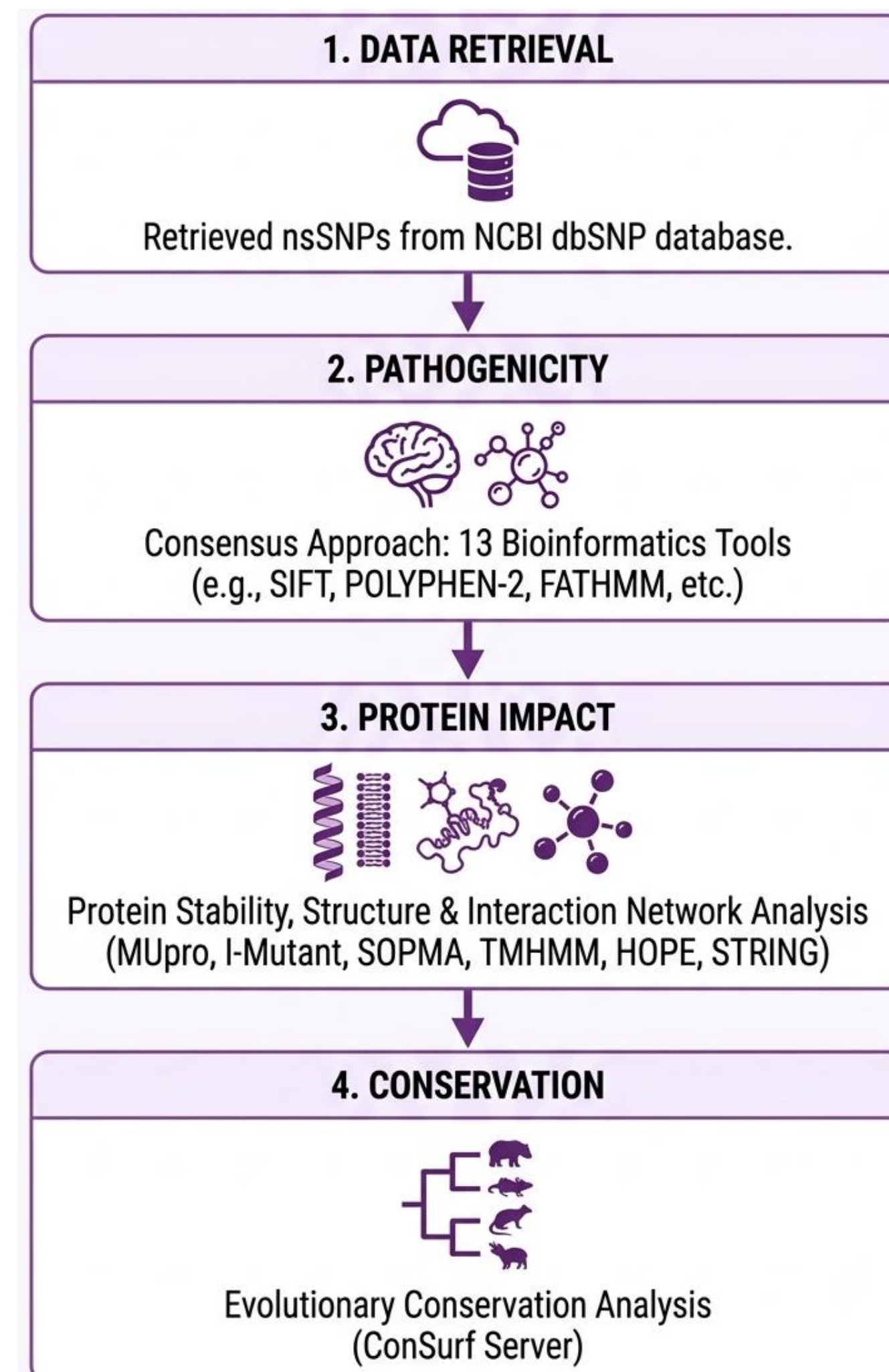
It is linked to the pathogenesis of Alzheimer's disease (AD).

Non-synonymous single-nucleotide polymorphisms (nsSNPs) in PSEN1 distort its protein structure and function, resulting in the formation and accumulation of beta-amyloid plaques in the brain.

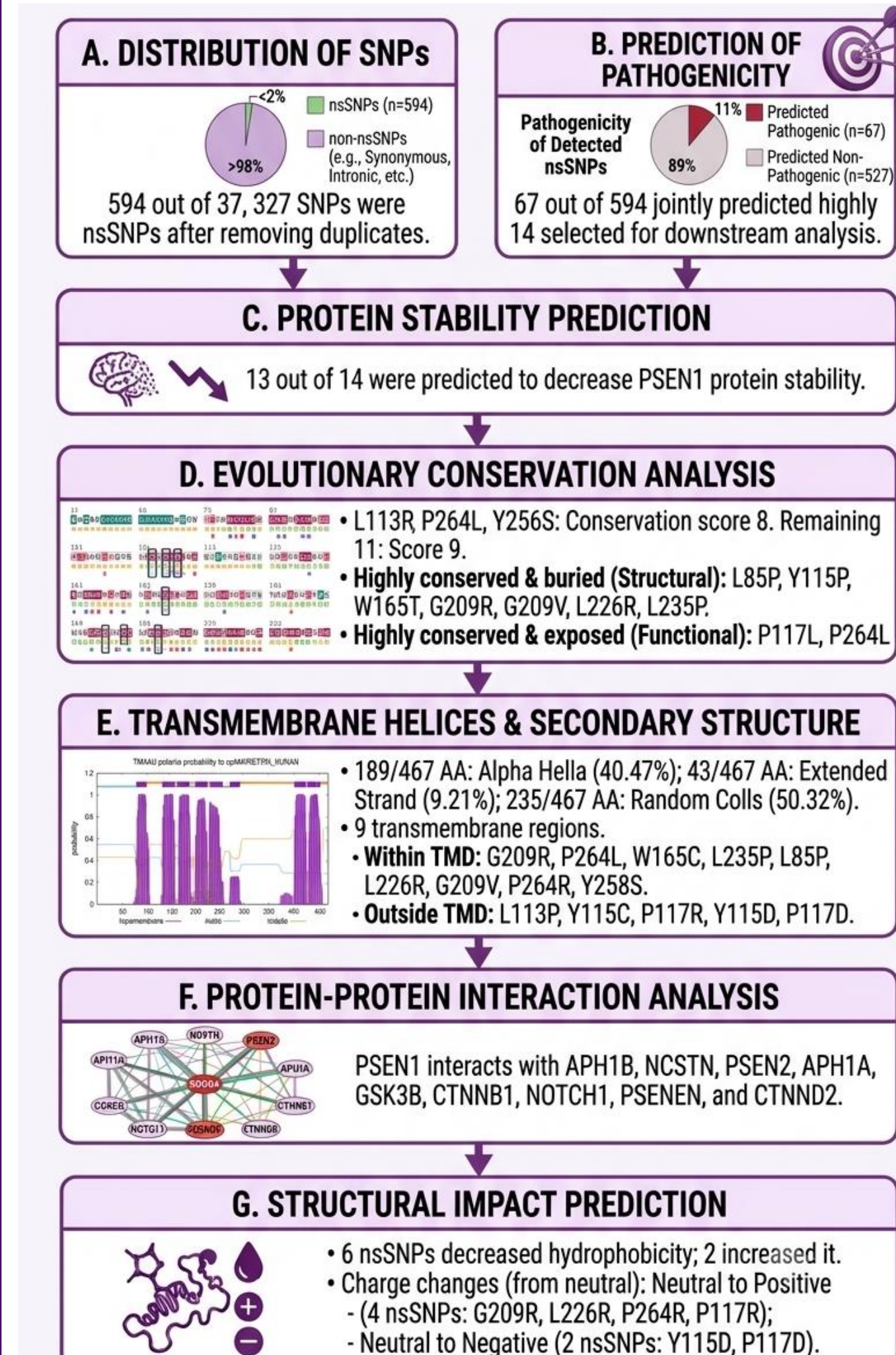
There is a dearth in the comprehensive study of the functional impact of these nsSNPs in AD pathogenesis.

Therefore, this study was conducted to identify deleterious nsSNPs in the PSEN1 gene and their functional consequences using bioinformatics tools.

METHODS



RESULTS



CONCLUSION

Description and prediction of functional impacts of mutations provided by high throughput computational methods and complementary protocols, provides a quick and affordable screening technique to help direct experimental and diagnostic approaches or population studies of disease-causing mutations in AD pathogenesis.

This study provides a comprehensive insight into the impact of high-risk nsSNPs implicated in AD manifestation and can help in the creation of models for therapeutic development and/or personalized medicine in AD treatment and care.

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GeminiAI was used as an assistant in generating images and flow charts.

CONTACT

Email
g.olajire@ui.edu.ng
gershomolajire@gmail.com