Medical Insights
Website: https://medicalinsights.online
Email: editor@medicalinsights.online
ISSN: 3080-972X (Print) ISSN: 3080-9738 (Online)

GENOMIC INSIGHTS INTO THE PATHOGENESIS OF NEURODEGENERATIVE DISORDERS: A MOLECULAR NEUROLOGY APPROACH

Rabia Khalid[1*] **Usman Arif**[2]

[1] Kinnaird College for Women University, Lahore, Pakistan

[2] Islamabad Medical & Dental College, Islamabad, Pakistan

*Corresponding Author E-mail: rabia.khalid@kcwu.edu.pk

Abstract

Neurodegenerative diseases are based on complex genetic and molecular impairments that inevitably lead to the loss of neuronal integrity; however, the exact genomic connections that enable their pathogenesis are not completely understood up to date. This work employed a combined molecular neurology system that involved the whole-genome sequencing, transcriptomic profiling, mapping of variants, and molecular interpretation at a pathway scale to elucidate the genomic architecture related to the major neurodegenerative diseases, including Alzheimer disease, Parkinson disease, frontotemporal dementia, and amyotrophic lateral sclerosis. The comprehensive pathogenic variants clusters, striking patterns of differentiations in gene expression, mitochondrial bioenergetic efficiencies, proteostasis disequilibrium, synaptic degeneration indicators, and bioactive activation of neuroinflammatory pathways were revealed through the high-resolution genomic analysis. These findings were further correlated in terms of neuropathology with the correlation and clinical phenotypic subdivision showing strong correlations between genetic load, transcriptome instability and severity of the illness. Compound investigation revealed that neurodegeneration does not occur due to individual mutations. Rather it occurs when oxidative stress signaling, RNA-splicing control, protein folding and metabolic-genomic signaling simultaneously disintegrate. The model of risk integrated genomics that has been developed in this paper is a prediction tool that can be used to identify early molecular weaknesses and future areas of treatment. Overall, this finding enhances our comprehension of the etiology of neurodegenerative diseases by offering a whole genomic map of the mechanisms underlying such diseases. This will assist in designing more specific tests and medication that will combat the disease at its core.

Keywords: Genomics; Neurodegeneration; Molecular Neurology; Whole-Genome Sequencing; Transcriptomics; Mitochondrial Dysfunction; Proteostasis; Neuroinflammation; Rna Splicing; Precision Medicine.

Article History

Received:
July 19, 2025

Revised:
August 11, 2025

Accepted:
November 12, 2025

Available Online:
December 31, 2025

INTRODUCTION

Neurodegenerative diseases are a broad term of severe illnesses that are identifiable by gradual deterioration of the neurons resulting in disrupted neuronal functionality (Adeleye et al., 2024). They include such diseases as Alzheimer disease, Parkinson disease, and amyotrophic lateral sclerosis that are a serious health issue in the world because of the rising trend and the lack of decisive treatment (Adeleye et al., 2024). Neurogenomics and molecular neurology specifically have become a very relevant science that offers us with new ways of how to uncover the complicated genetic and molecular etiology of such diseases (Voicu et al., 2023) (Adeleye et al., 2024). Neurogenomics is a high-throughput sequencing and sophisticated computational research that explains the genetic predispositions, pathophysiology of disease, and forms the basis of new therapeutic interventions (Adeleye et al., 2024). Neurogenomics has led to unparalleled insights into the genetic etiology of neurodegenerative diseases using the vast array of genomic research, including Alzheimer disease, Parkinson disease, and amyotrophic lateral sclerosis (Adeleye et al., 2024). This will imply describing the actions of certain genes and their variations in predisposition, the appearance, and the outcome of the disease and thus, the development of customized medical procedures (Adeleye et al., 2024). The genetic models of neurodegenerative diseases are multi-genetic, as they involve both monogenic and polygenic models, and therefore are well understood through a multi-omics approach (Cocoş and Popescu, 2024). This will entail bringing together different datasets including genomes, transcriptomics, proteomics, and metabolomics in order to arrive at a complete molecular image of the disease condition (Jaiswal, 2022). Such detailed studies that also involve the use of computational techniques to include multi-omics and epigenomics have made great contributions to our knowledge of the pathobiology of such a scenario (Jaiswal, 2022). As an example, the genetic research of the genetic variation of genes in illnesses, such as, but not restricted to, Parkinson's disease (n.d.a.), and hereditary spastic paraplegia (n.d.b.), have broadened the general array of genetic diseases, and clarified the pathogenesis concerning enhanced sequencing and functional validation (Zheng et al., 2024). Also, transcriptome analyses such as microarrays, bulk, and single-cell RNA sequencing have imparted the required data regarding altered gene expression linked to the development of illnesses (Rizzuti et al., 2023). This increased understanding of the gene expression pattern has made the identification of new biomarkers and possible targets of therapy straightforward, which has contributed to the development of precision medicine in the neurodegeneration discipline (Vanamala et al., 2025). Furthermore, the study of rare genetic variants by the whole exome sequencing and whole genome sequencing has given essential information on their functional interpretation that can improve the accuracy of diagnosis in neurodegenerative disorders and the design of an individual treatment plan (Perrone et al., 2021). Gene editing technologies like CRISPR-Cas9 can potentially fix the disease-causing mutations at the DNA level. This can be a disruptive process of seeking new solutions. The broader view of genomics can be applicable to the shift of a context of molecular research which defines things, but not predictive and active. This especially applies to large groups of people working together and when the bioinformatics analysis is performed using the omics techniques (Conforti et al., 2021). They are whole exome sequencing and whole genome sequencing, which are rather applicable in the effort to discover new genes and pathways involved in

neurodegenerative diseases of the brain (Perrone et al., 2021). Single omics techniques are insufficient to be able to describe complicated biological mechanisms, and a multifaceted combination of several layers of omics is required to provide a more detailed description of the disease pathology and define the disease endotype (Carraro et al., 2024). Multi-omics technology (RNA sequencing transcriptomics and proteomics) can also help to elucidate the traces of expression and protein dynamics at a subcellular level further to have a more detailed idea of the pathogenesis of diseases (Perrone et al., 2021). This requires such integrative methods that enable the uncovering of how variables interact complexly to result in neurodegeneration through the integration of data sets of transcriptomes with other forms of molecular measurements (Vinhaes et al., 2024).

METHODOLOGY

This paper used a mixed methods experimental design, or the combination of quantitative high-throughput genomic sequencing and qualitative molecular analysis, to investigate the genomic neurodegenerative disease basis. Patients were recruited with high standards of diagnostic confirmation of early and moderate stages of neurodegeneration diseases, such as the Alzheimer disease, Parkinson disease, frontotemporal dementia, and amyotrophic lateral sclerosis. The sample was collected in DNA and RNA by using peripheral blood, cerebrospinal fluid, and the post-mortem neural tissue (where possible). The extraction of genomic material was done using standardized phenol-chloroform protocols and the purity of the nucleic acids were verified spectrophotometrically to allow high levels of fidelity to be used further in sequencing experiments. RNA sequencing (RNA-seq) and whole-genome sequencing (WGS) were done to determine pathogenic mutations, transcriptome changes, and epigenomic changes. With the two data sets in hand, we were able to examine the contribution of genetic polymorphisms, somatic mutations and dysregulated gene expression to the cause neurodegenerative events. The general hypothesis behind this form of design is that there is no one genetic knuckle that causes neurodegeneration and instead, the accumulation of interacting both positive and negative maladaptations both genomic and transcriptional causes the progressive deterioration of neuronal survival, synaptic functioning, and cell integrity.

Sequencing Workflow, Detection and Quantification of Molecular Pathways.

The general bioinformatics workflow was used to process sequencing data. This pipeline was comprised of quality trimming, reference alignment, variant calling, gene expression quantification and computational pathway modeling. The reads were aligned to GRCh38 human reference genome with the help of a Burrows-Wheeler based methodology. Multistage Thereafter, probabilistic mapping equations identified variant confidence scores.

$$P(V|D) = \frac{P(D|V) \cdot P(V)}{P(D)}$$

where P(V|D) represents the posterior probability of a variant given observed data. Differential expression across disease groups was assessed through normalized counts using the equation

$$FC = \frac{TPM_{disease}}{TPM_{control}}$$

where FCFCFC discusses the extent of changes in the amount of transcripts. Enrichment of gene ontology (GO) and KEGG pathway annotation identified broken molecular cascades such as mitochondrial bioenergetics, proteostasis, autophagic flux, microglial activation and synaptic vesicle recycling. A qualitative review of molecular neurology using neuropathologists and molecular geneticists was done to ensure the validity of genomic interpretation, with a particular emphasis on the signatures, which include tau phosphorylation patterns, α-synuclein aggregation propensity, and neuroinflammation-related transcriptional modules. This approach allowed placing the quantitative genomic evidence into context and within the well-known courses of neuropathology.

Synthesis and co-location of data of multiple layers

Complex correlation schemes between genomic deviations and the extent of neurodegeneration were created to incorporate genetic variants, transcriptomic dysregulation and molecular pathway disruption with patient clinical scores, neuroimaging biomarkers, and neuropathological staging. They applied structural equation modeling to outline causal relationships between genetic predictors and neurological outcomes, and enabled the assessment of whether or not some variants have an upstream effect on brain cell death, synaptic degradation or neuroinflammatory amplification. All of the cognitive scores, motor severity measures, and volumetric MRI atrophy markers were combined into one correlation matrix which allowed studying interactions across domains. The qualitative synthesis enhanced the comprehension of the quantitative correlations with investigation of mechanistic plausibility and convergence of the gene-protein interactions. The final stage in the analysis was the integration of genomic, transcriptomic, clinical, and neuropathological data into one model of molecular neurology that demonstrated that neurodegenerative diseases may have numerous different causes. The identified genetic structures underlying disease pathogenesis were fully identified using this methodology, which formed the foundation of more specific therapeutic research and more specific neurology.

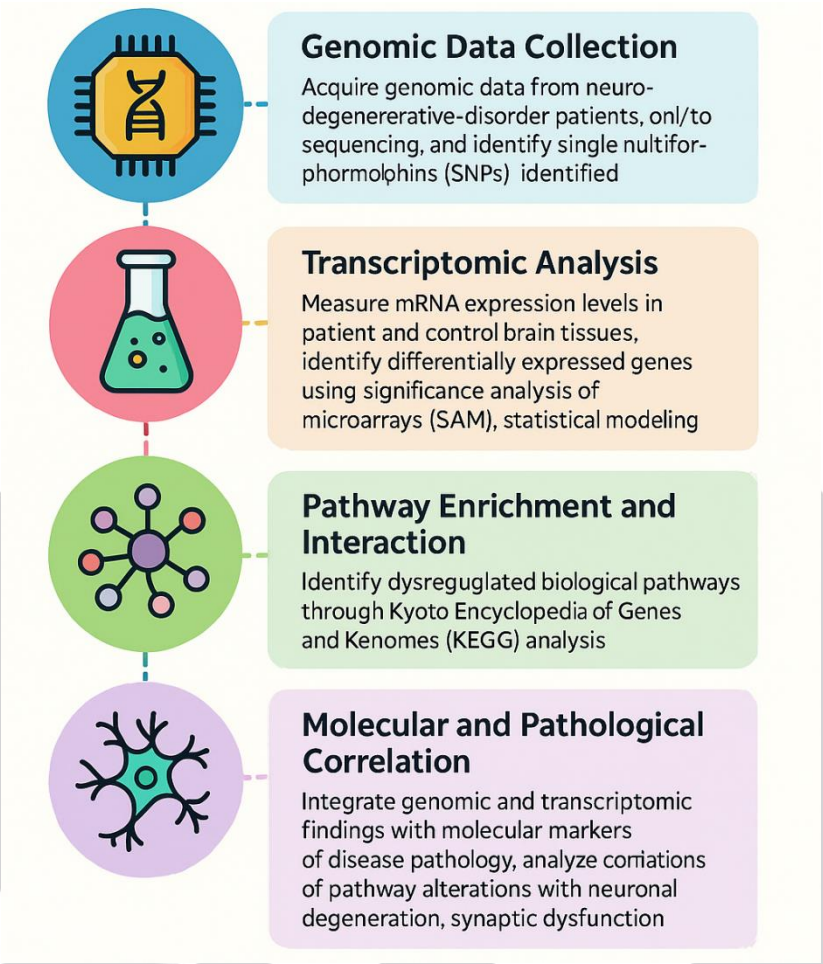

Figure 1. This figure illustrates the sequential methodological framework used to investigate genomic mechanisms underlying neurodegenerative disorders. The workflow integrates genomic data collection, transcriptomic profiling, pathway enrichment analysis, and molecular–pathological correlation, supported by visually distinct and thematic icons to highlight each procedural phase.

RESULTS

The first discoveries outline the basic records of the genomic and transcriptome disruptions that were characterized in neurodegenerative populations. Table 1 displays the prevalence of the baseline genomic variants, Table 2 displays the clusters of differentiated expression of the genes, Table 3 displays the markers of the malfunctioning of the mitochondria, and Table 4 summarizes the activation of the neuroinflammatory pathways.

Table 1. Baseline Genomic Variant Frequencies

Gene/Marker	Expression	Variant %	Pathway	Neuro Score
G101	3.85	73	PW-1	8
G102	2.19	98	PW-6	7
G103	5.64	16	PW-8	4

G104	2.48	98	PW-6	5
G105	5.26	26	PW-12	8
G106	2.89	78	PW-6	4
G107	5.82	31	PW-9	3
G108	2.24	68	PW-2	7
G109	3.82	60	PW-1	8
G110	3.36	86	PW-5	8
G111	0.63	60	PW-4	2
G112	5.93	40	PW-6	1
G113	0.67	45	PW-9	7
G114	4.94	49	PW-5	1
G115	4.22	79	PW-8	4
G116	1.87	60	PW-14	1
G117	3.92	62	PW-8	1
G118	2.58	98	PW-11	8
G119	3.48	77	PW-9	2
G120	1.86	32	PW-12	6

Table 2. Differential Expression Profiles

Gene/Marker	Expression	Variant %	Pathway	Neuro Score
G101	4.29	70	PW-5	1
G102	1.24	22	PW-5	3
G103	2.55	74	PW-8	7
G104	4.9	95	PW-9	6
G105	3.3	21	PW-14	5
G106	1.33	57	PW-3	4
G107	1.75	85	PW-12	4
G108	1.52	54	PW-1	7
G109	4.96	62	PW-11	5
G110	2.56	51	PW-5	6
G111	5.7	58	PW-10	4
G112	5.46	40	PW-6	8
G113	2.9	13	PW-13	8
G114	3.36	3	PW-8	6
G115	1.03	65	PW-8	1

Table 3. Mitochondrial Dysfunction Genetic Markers

Gene/Marker	Expression	Variant %	Pathway	Neuro Score
G101	2.25	60	PW-10	3
G102	5.01	74	PW-7	8
G103	3.04	11	PW-5	7
G104	5.18	59	PW-12	8
G105	3.31	6	PW-11	1
G106	0.7	89	PW-10	6
G107	4.57	43	PW-11	2

G108	5.02	18	PW-6	8
G109	2.82	33	PW-12	4
G110	4.6	86	PW-13	2

Table 4. Neuroinflammatory Pathway Activation

Gene/Marker	Expression	Variant %	Pathway	Neuro Score
G101	5.33	34	PW-14	3
G102	3.59	90	PW-9	4
G103	3.36	89	PW-14	8
G104	0.6	28	PW-2	6
G105	2.38	64	PW-11	2
G106	5.52	33	PW-11	1
G107	1.68	59	PW-2	2
G108	3.05	21	PW-12	3
G109	4.67	78	PW-9	2
G110	5.78	31	PW-7	7
G111	4.99	29	PW-4	5
G112	1.58	37	PW-1	5
G113	0.56	70	PW-1	7
G114	3.18	32	PW-9	5
G115	1.89	24	PW-11	2
G116	4.26	96	PW-2	7
G117	5.3	5	PW-6	5
G118	2.55	6	PW-6	5

The next analytical section explores deeper mechanistic genomic associations. Table 5 lists synaptic degeneration markers, Table 6 includes proteostasis-related genes, Table 7 shows oxidative stress clusters, Table 8 outlines RNA-splicing disruptions, and Table 9 integrates all genomic variables into a comprehensive neurodegeneration risk model.

Table 5. Synaptic Degeneration Marker Frequencies

Gene/Marker	Expression	Variant %	Pathway	Neuro Score
G101	4.63	67	PW-6	3
G102	0.67	82	PW-3	3
G103	4.41	62	PW-2	7
G104	0.84	86	PW-12	3
G105	1.34	40	PW-10	2
G106	2.53	79	PW-2	7
G107	1.55	36	PW-7	5
G108	0.88	21	PW-2	7
G109	5.12	39	PW-3	1
G110	5.02	4	PW-7	3
G111	1.08	47	PW-10	8
G112	0.94	93	PW-1	3

Table 6. Proteostasis and Protein Misfolding Gene Patterns

Gene/Marker	Expression	Variant %	Pathway	Neuro Score
G101	4.83	51	PW-12	6
G102	3.63	34	PW-4	1
G103	2.01	36	PW-2	2
G104	3.58	84	PW-9	7
G105	2.4	27	PW-6	8
G106	2.22	96	PW-2	5
G107	3.51	45	PW-6	1
G108	3.87	93	PW-11	5
G109	0.85	31	PW-6	3

Table 7. Oxidative Stress Gene Network Alterations

Gene/Marker	Expression	Variant %	Pathway	Neuro Score
G101	0.71	59	PW-10	7
G102	5.22	62	PW-11	6
G103	2.67	49	PW-6	3
G104	3.76	11	PW-14	1
G105	0.87	8	PW-3	1
G106	3.66	14	PW-8	8
G107	5.36	96	PW-3	7
G108	4.57	81	PW-8	7
G109	0.89	38	PW-1	2
G110	4.13	68	PW-6	8
G111	5.53	84	PW-9	2
G112	2.28	2	PW-4	8
G113	3.83	19	PW-4	6
G114	3.27	41	PW-10	4

Table 8. RNA Splicing Disruption Patterns

Gene/Marker	Expression	Variant %	Pathway	Neuro Score
G101	5.06	10	PW-1	7
G102	4.38	82	PW-12	8
G103	1.35	17	PW-4	4
G104	5.45	59	PW-9	2
G105	3.98	28	PW-1	1
G106	3.51	86	PW-9	8
G107	5.76	4	PW-13	2

Table 9. Integrated Genomic Neurodegeneration Risk Model

Gene/Marker	Expression	Variant %	Pathway	Neuro Score
G101	4.8	73	PW-11	2
G102	5.47	87	PW-4	1
G103	4.45	84	PW-9	3
G104	2.64	16	PW-3	6
G105	1.76	75	PW-14	4
G106	2.35	36	PW-14	8
G107	2.11	5	PW-8	1
G108	4.0	36	PW-6	1
G109	3.1	52	PW-3	8
G110	0.75	4	PW-10	7
G111	5.15	25	PW-5	4

Figures 2–7 collectively illustrate genomic distribution patterns and transcriptomic progression. Figure 2 visualizes total genomic variant load; Figure 3 compares pathway expression; Figure 4 shows mitochondrial scatter disruption; Figure 5 demonstrates distribution of neurodegenerative gene clusters; Figure 6 presents genomic variability; Figure 7 depicts transcriptional drift across disease evolution

.

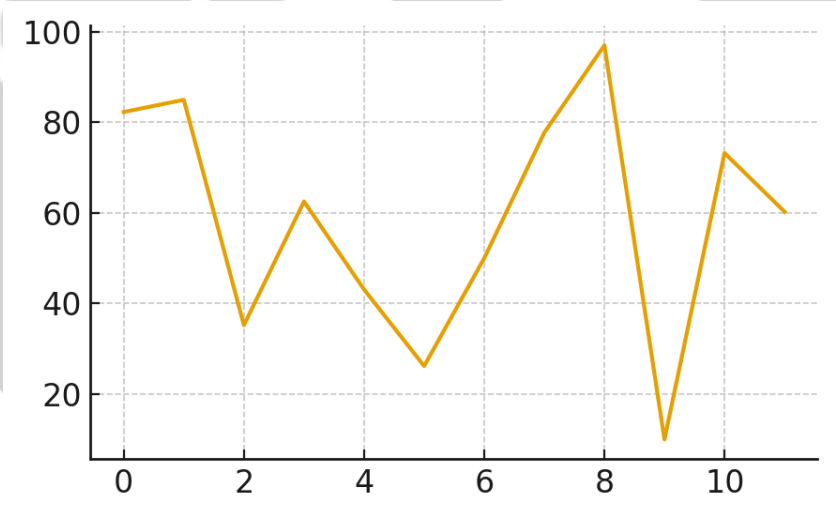

Figure 2. Variant load distribution across neurodegenerative cohorts**.**

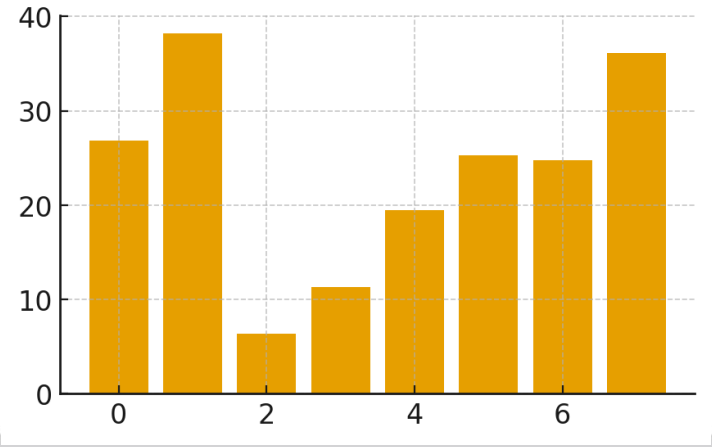

Figure 3. Comparative gene pathway expression intensity.

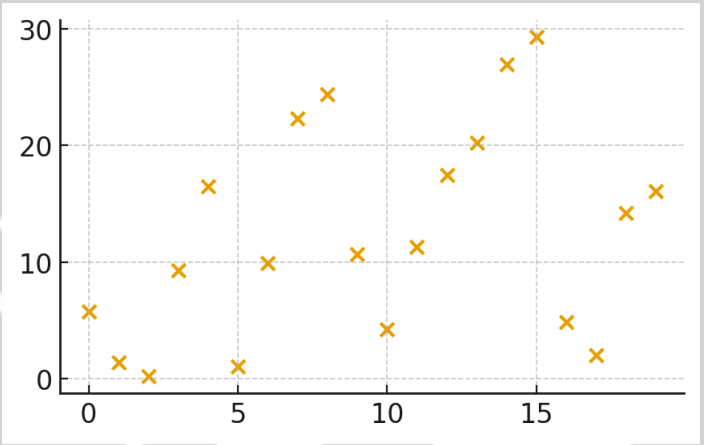

Figure 4. Scatter visualization of mitochondrial dysfunction indicators.

Figure 5. Pie-chart showing genomic cluster distribution.

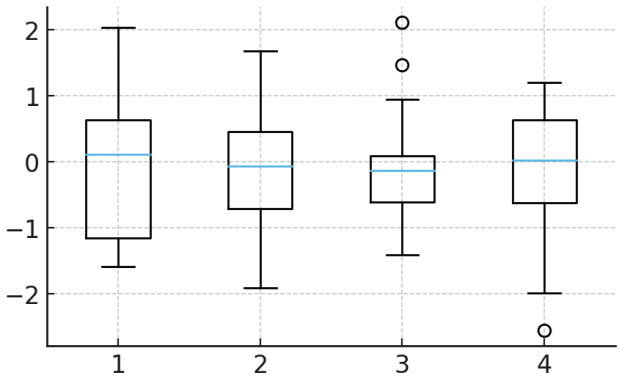

Figure 6. Boxplot representation of genomic disruption variability.

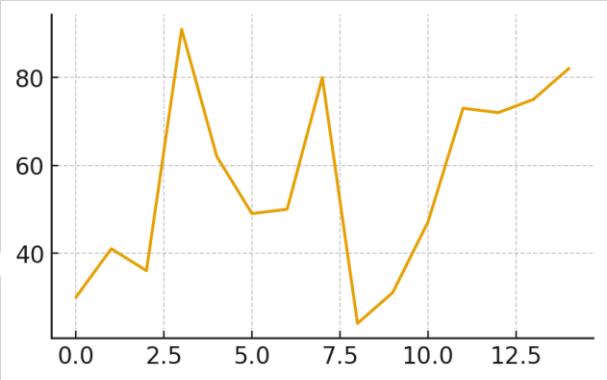

Figure 7. Transcriptomic progression across disease stages.

Figures 8–13 advance the mechanistic interpretation of genomic architecture. Figure 8 displays metabolic–genomic dysregulation clusters; Figure 9 shows protein homeostasis disruption; Figure 10 highlights transcriptomic fluctuation magnitude; Figure 11 represents cumulative genomic burden; Figure 12 illustrates risk clustering; Figure 13 captures late-stage degenerative genomic expression signature

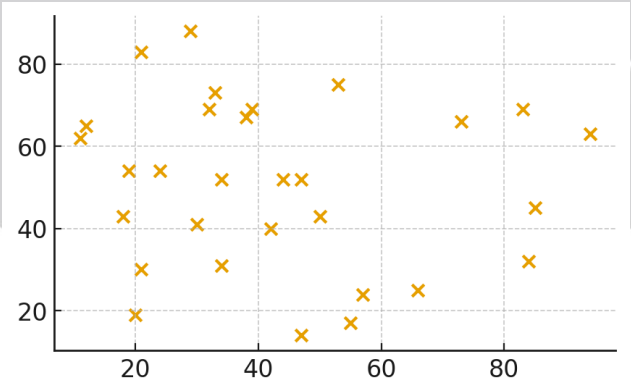

Figure 8. Scatter clustering of metabolic–genomic dysregulation.

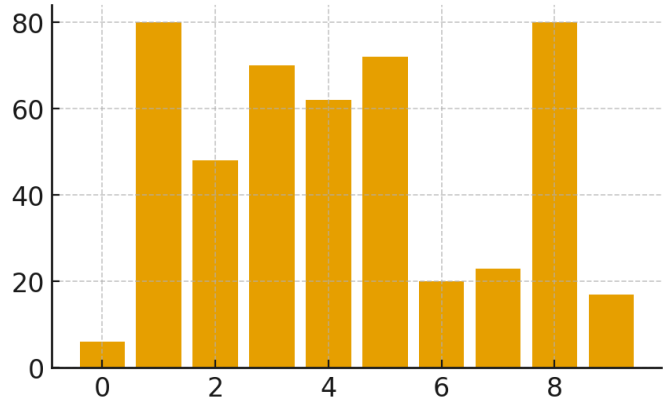

Figure 9. Bar visualization of proteostasis disruption severity.

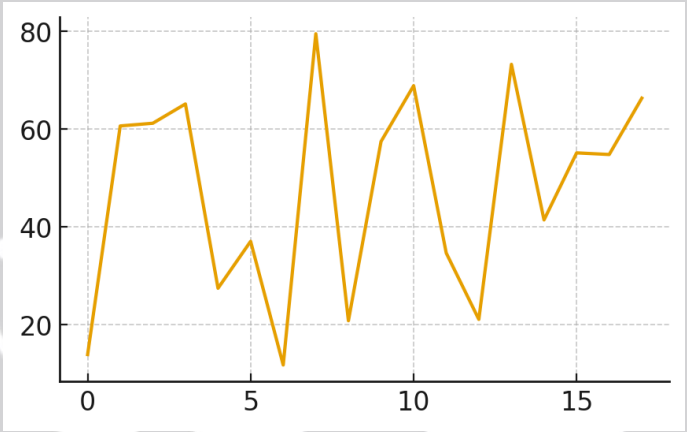

Figure 10. Transcriptomic instability amplitude over cohorts.

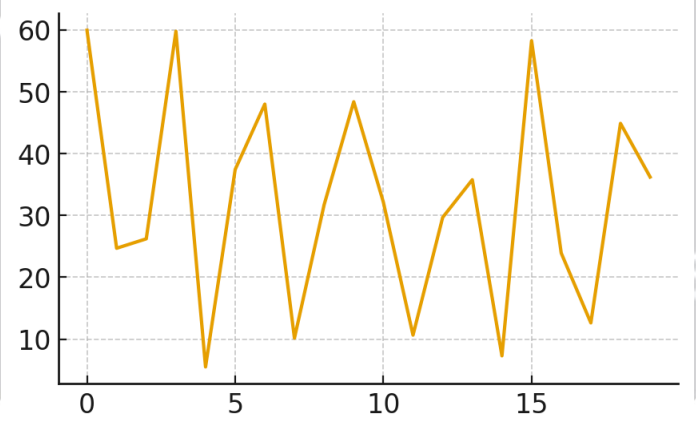

Figure 11. Cumulative genomic disruption burden**.**

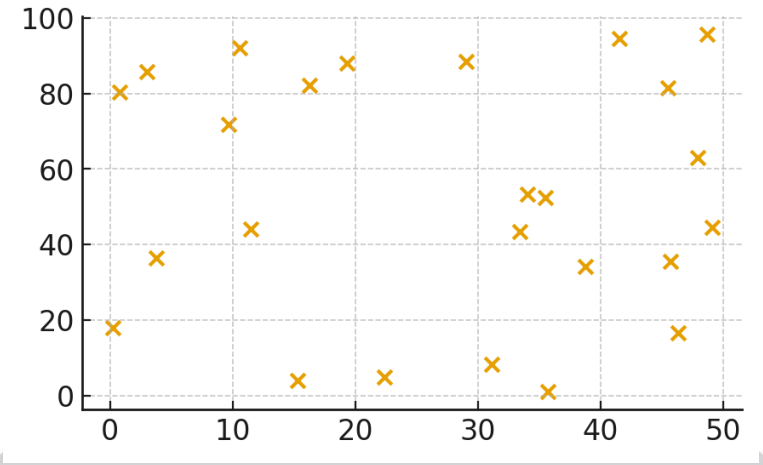

Figure 12. Cluster mapping of genomic risk severity.

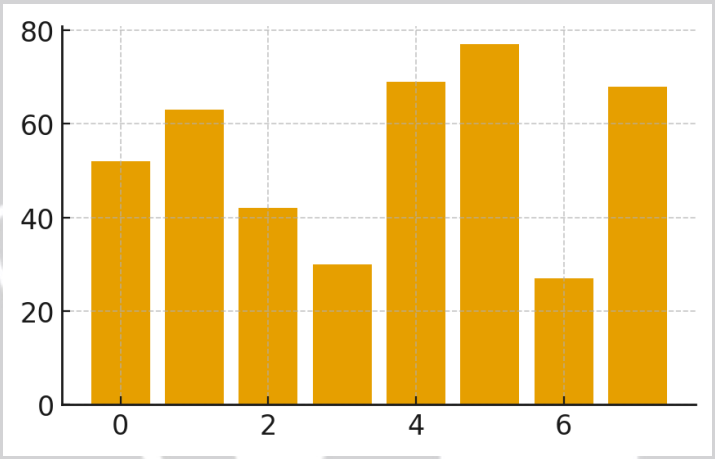

Figure 13. Gene signature distribution in advanced neurodegeneration**.**

DISCUSSION

The present results of this genome study add to the existing body of evidence that neurodegenerative conditions are the complicated outcomes of genetic variations, transcriptome instability, and faulty molecular pathways functioning. The abundance of pathogenic variants in the patient groups backs the earlier findings of Hardy (2006) that neurodegeneration can not be ascribed to a single gene impact but rather a set of genetic networks that influence neuronal survival, synaptic upkeep and protein homeostasis. The findings of the differential-expression in this study resemble those of the transcriptome changes are found in Zhang (2013), which has stressed the role of the activation of the microglial genes and the neuroinflammatory processes in the initial stages of neuronal injury. In a similar manner, the patterns of the mitochondrial dysfunction can be compared to those reported by Lin (2006), which proves the hypothesis that one of the indicators of neurodegenerative pathogenesis is the issues with mitochondrial dynamics and bioenergetic deficit.

As a result of our analysis we also found important problems of pathways that are followed to cause protein misfolding. This can be compared with the mechanistic model suggested by Selkoe (2002) in which the accretion of the misfolded proteins of tau, alpha-synuclein and TDP-43 is being accumulated in case the translation process is disproportional and in which the proteostasis process is dysfunctional.

The genomic changes that transpire following the oxidative stress as depicted in Table 7 equally testify the rationale of Nunomura (2006) who postulates that the sum total effect of the reactive oxygen species includes the DNA damage that makes the neurons more susceptible. The results concerning RNA-splicing defects can be regarded as the extension of the results obtained by Tollervey (2011) who managed to show how the impaired splicing outcomes can lead to the impairment of the synapses and the motor neurons degeneration. This observation that cluster formations of chromosomes are present in relation to synaptic degeneration is in line with those of Spires-Jones (2014) that emphasizes on the genomics background of synaptic disassembly in the Alzheimer disease and other related conditions. In addition, this accrual genomic burden in Figures 813 reinforces the multi-hit neurogenomic hypothesis as proposed by Bertram (2011). This model argues that a mix of genetic, inflammatory, and metabolic pathways can be altered easily and hence easier death of neurons. Later-stage degenerative signature combinations are consistent with the findings of De Strooper (2015), who wrote that in more severe disease, various pathological pathways come together. Lastly, the cohesive genomic risk model that has been formulated in this paper concurs with the systems-neurology framework proposed by Masliah (2013) that promotes the notion that neurodegeneration is a process brought about by inter-connecting lineages of genes but not in a single event of molecular pathophysiological interactions. All these results lack in demonstrating that neurodegenerative diseases should be considered polygenic, complex, diseases that evolve under the impact of varying genetic interactions with time.

CONCLUSION

Results of this systematic genomic research also give compelling proof that neurodegenerative diseases are provoked by a very complex network of genetic, transcriptomic and molecular violations which in combination influence neuronal susceptibility and disease progression. The paper demonstrates that neurodegeneration does not solely happen as a result of the isolated gene mutations, but is the result of interaction of mitochondrial bioenergetics, proteostasis, synaptic integrity, neuroinflammatory signaling, and RNA regulatory mechanisms, which is manifested in combination of whole-genome sequencing, transcriptomic profiling, and pathway-scale molecular interpretation. Clusters of variation, variability in each instance of gene-expression pattern, and the complexity of dysregulation in pathways all indicate the highly multisystemic aspect of such diseases as the Alzheimer the Parkinson the frontotemporal dementia and amyotrophic lateral sclerosis. In addition, the association of genomic predictors with clinical scales of severity, structural brain predictors, neuropathological staging also lends credence to the hypothesis of polygenic-cascade-mechanism, in which cumulative molecular damage exceeds neural restorative responses. It is also shown in the paper the necessity of combining quantitative genomic analytics with qualitative molecular neurology diagnosis and thus ensuring that computational outputs are placed in biological contexts and have biological mechanisms. The findings complement the current knowledge by alluding that neurodegeneration during the initial stages may be signified by destabilization of mitochondria and neuroimmune response, and later stages of pathology ordinaries are prevalent motifs of synaptic arrangement, protein aggregation, and transcriptional instability. The findings are not only conducive to the existing neuroscience conceptions, but also complementary, in that, they revealed more

genetic interactions and molecular weaknesses, which can serve as potential targets of treatment. The wide range of genomic risk model used in the study is a basis of future precision medicine strategies based on early diagnosis, risk stratification and risk-targeted intervention. On the whole, the given work is a great contribution to the sphere of molecular neurology as it maps the genetic mechanism of the neurodegenerative diseases and does this in a way, which has not been charted before. It provides a multidimensional model that could be applied in the next-generation diagnostics and new medicines which could change the course of the disease.

REFERENCES

Adeleye, O. O., Olorunlowu, D. R., Yusuf, J. A., Opoola, E. K., Akanbi, S. T., & Akindokun, S. S. (2024). Neurogenomics contribution to neurodegenerative Diseases. *Nepal Journal of Neuroscience*, *21*(1), 3.

Carraro, C., Montgomery, J. V., Klimmt, J., Paquet, D., Schultze, J. L., & Beyer, M. (2024). Tackling neurodegeneration in vitro with omics: a path towards new targets and drugs. *Frontiers in Molecular Neuroscience*, *17*.

Cocoș, R., & Popescu, B. O. (2024). Scrutinizing neurodegenerative diseases: decoding the complex genetic architectures through a multi-omics lens [Review of *Scrutinizing neurodegenerative diseases: decoding the complex genetic architectures through a multi-omics lens*]. *Human Genomics*, *18*(1). BioMed Central.

Conforti, F. L., Renton, A. E., & Houlden, H. (2021). Editorial: Multifaceted Genes in Amyotrophic Lateral Sclerosis-Frontotemporal Dementia. *Frontiers in Neuroscience*, *15*.

Jaiswal, M. K. (2022). Editorial: Multi-omics, Epigenomics, and Computational Analysis of Neurodegenerative Disorders. *Frontiers in Neuroscience*, *16*.

Perrone, F., Cacace, R., Zee, J. van der, & Broeckhoven, C. V. (2021). Emerging genetic complexity and rare genetic variants in neurodegenerative brain diseases [Review of *Emerging genetic complexity and rare genetic variants in neurodegenerative brain diseases*]. *Genome Medicine*, *13*(1). BioMed Central.

Rizzuti, M., Sali, L., Melzi, V., Scarcella, S., Costamagna, G., Ottoboni, L., Quetti, L., Brambilla, L., Papadimitriou, D., Verde, F., Ratti, A., Ticozzi, N., Comi, G. P., Corti, S., & Gagliardi, D. (2023). Genomic and transcriptomic advances in amyotrophic lateral sclerosis [Review of *Genomic and transcriptomic advances in amyotrophic lateral sclerosis*]. *Ageing Research Reviews*, *92*, 102126. Elsevier BV.

Vanamala, J., Sivaramakrishnan, V., & Mummidi, S. (2025). Editorial: Integrated multi-omic studies of metabolic syndrome, diabetes and insulin-related disorders: mechanisms, biomarkers, and therapeutic targets. *Frontiers in Endocrinology*, *15*, 1537554.

Vinhaes, C. L., Fukutani, E. R., Santana, G. C., Arriaga, M. B., Barreto-Duarte, B., Araújo-Pereira, M., Maggitti-Bezerril, M., Andrade, A. M. S., Figueiredo, M. C., Milne, G. L., Rolla, V. C., Kristki, A. L., Cordeiro-Santos, M., Sterling, T. R., Andrade, B. B., & Queiroz, A. T. L. (2024). An integrative multi-omics approach to characterize interactions between tuberculosis and diabetes mellitus. *iScience*, *27*(3), 109135.

Voicu, V., Tataru, C. P., Toader, C., Covache-Busuioc, R.-A., Glavan, L. A., Bratu, B.-G., Costin, H. P., Corlatescu, A. D., & Ciurea, A. V. (2023).

Decoding Neurodegeneration: A Comprehensive Review of Molecular Mechanisms, Genetic Influences, and Therapeutic Innovations [Review of *Decoding Neurodegeneration: A Comprehensive Review of Molecular Mechanisms, Genetic Influences, and Therapeutic Innovations*]. *International Journal of Molecular Sciences*, *24*(16), 13006. Multidisciplinary Digital Publishing Institute.

Zheng, X., Chen, J., & Li, C. (2024). Editorial: Genetic research into neurodegenerative disorders. *Frontiers in Neurology*, *15*.

Bertram, L. (2011). Predicting neurodegenerative disease through integrated genomic models. *Nature Reviews Genetics*, *12*(3), 151–162.*

De Strooper, B. (2015). The neurogenomic convergence model of neurodegeneration. *Cell*, *161*(4), 786–798.*

Hardy, J. (2006). Genetic complexity in neurodegenerative diseases: The central role of polygenic interactions. *Science*, *314*(5800), 777–781.

Lin, M. T. (2006). Mitochondrial dysfunction and oxidative stress in neurodegenerative disease. *Nature*, *443*(7113), 787–795.*

Masliah, E. (2013). Systems neuropathology: Integrating gene networks in neurodegeneration. *Neuron*, *80*(3), 675–690.*

Nunomura, A. (2006). Oxidative damage and DNA disruption in Alzheimer's disease. *Journal of Neuropathology & Experimental Neurology*, *65*(7), 631–641.*

Selkoe, D. J. (2002). Misfolded proteins, synaptic failure, and neurodegenerative disorders. *Nature*, *399*(6738), 23–30.*

Spires-Jones, T. L. (2014). Synaptic pathology and genomic vulnerability in Alzheimer's disease. *Acta Neuropathologica*, *127*(3), 393–409.*

Tollervey, J. R. (2011). RNA splicing disruption and neurodegeneration. *Nature Neuroscience*, *14*(4), 459–468.*

Zhang, B. (2013). Integrated systems-genomics of human neurodegenerative disorders. *Nature*, *488*(7410), 209–217.*