

Neurofilaments in ALS: Sporadic vs. Familial- A Meta-Analysis

Gina Tatiabela*

Department of Neurodegenerative Diseases, University of Naples, 80131 Naples, Italy

Introduction

Amyotrophic Lateral Sclerosis (ALS), a devastating neurodegenerative disorder, manifests as progressive degeneration of upper and lower motor neurons, leading to muscle weakness, atrophy and ultimately, paralysis. While the underlying etiology of ALS remains incompletely understood, emerging evidence suggests a multifactorial interplay of genetic, environmental and biochemical factors. Neurofilaments, structural proteins crucial for maintaining neuronal integrity and function, have garnered increasing attention as potential biomarkers and pathogenic contributors in ALS. Discrepancies in neurofilament levels between sporadic and familial ALS cases have been reported, prompting the need for a comprehensive meta-analysis to elucidate the differential roles of neurofilaments in these distinct disease subtypes. ALS presents a complex clinical phenotype characterized by considerable heterogeneity in disease progression, age of onset and genetic background. Approximately 90-95% of ALS cases are sporadic, lacking a clear family history, while the remaining 5-10% is familial, with an identified genetic component. The discovery of causative mutations in genes such as SOD1, C9orf72, TARDBP and FUS has shed light on the genetic underpinnings of familial ALS, yet the pathogenic mechanisms underlying sporadic cases remain elusive. Neurofilaments, as integral components of neuronal cytoskeletons, have emerged as potential biomarkers reflecting axonal damage and neurodegeneration in ALS. Sporadic ALS is thought to result from a complex interplay of genetic susceptibility, environmental exposures and stochastic processes, whereas familial ALS is predominantly driven by inherited genetic mutations. Understanding the differential impact of these factors on neurofilament dynamics may offer valuable insights into the pathophysiological mechanisms underlying ALS subtypes. Moreover, elucidating the relationship between neurofilament levels and disease severity, progression and response to therapy holds promise for refining prognostic biomarkers and developing targeted therapeutic interventions [1,2].

Description

Neurofilaments, comprising subunits of varying molecular weights (NF-L, NF-M, NF-H), form the structural framework of neuronal axons, providing mechanical support and facilitating axonal transport. In ALS, pathological processes such as axonal degeneration, protein aggregation and neuroinflammation contribute to neurofilament release into the Cerebrospinal Fluid (CSF) and bloodstream, where they serve as potential biomarkers of disease activity and progression. While studies have implicated elevated neurofilament levels in ALS patients compared to healthy controls, variations in neurofilament profiles between sporadic and familial cases remain poorly characterized. Given the growing interest in neurofilaments as biomarkers of neurodegeneration, numerous studies have explored their utility in

**Address for Correspondence: Gina Tatiabela, Department of Neurodegenerative Diseases, University of Naples, 80131 Naples, Italy, E-mail: ginabela@yahoo.com*

Copyright: © 2024 Tatiabela G. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Received: 02 March, 2024, Manuscript No. jppr-24-132686; **Editor Assigned:** 04 March, 2024, PreQC No. P-132686; **Reviewed:** 16 March, 2024, QC No. Q-132686; **Revised:** 21 March, 2024, Manuscript No. R-132686; **Published:** 28 March, 2024, DOI: 10.37421/2573-0312.2024.9.377

ALS diagnosis, prognosis and monitoring disease progression. However, inconsistencies in findings across studies, particularly regarding differences between sporadic and familial ALS cohorts, necessitate a comprehensive meta-analysis to synthesize existing evidence and provide a more cohesive understanding of neurofilament alterations in ALS subtypes. By pooling data from diverse cohorts and applying rigorous analytical approaches, this meta-analysis aims to address existing gaps in knowledge regarding the differential roles of neurofilaments in sporadic versus familial ALS. The findings of this study have the potential to inform clinical practice by identifying novel biomarkers for disease monitoring and guiding the development of targeted therapeutic strategies aimed at modulating neurofilament dynamics and preserving neuronal integrity in ALS. Through collaborative efforts and interdisciplinary research, we can advance our understanding of ALS pathophysiology and ultimately improve outcomes for individuals affected by this devastating neurodegenerative disorder [3].

This meta-analysis aims to synthesize existing literature and quantify differences in neurofilament concentrations between sporadic and familial ALS cohorts. A comprehensive search of electronic databases will be conducted to identify relevant studies reporting neurofilament levels in ALS patients, stratified by familial or sporadic disease status. Eligible studies will undergo rigorous quality assessment and data extraction, including sample size, demographic characteristics, neurofilament measurement techniques and outcome measures. Pooled effect estimates will be calculated using appropriate statistical methods, such as weighted mean differences or standardized mean differences, to compare neurofilament levels between sporadic and familial ALS groups. Subgroup analyses will be performed to explore sources of heterogeneity, including variations in study design, patient populations and assay methodologies. Sensitivity analyses will assess the robustness of findings by examining the impact of individual studies on overall effect estimates. Furthermore, meta-regression analyses will be employed to explore potential moderators of the observed associations, including age, disease duration, clinical phenotype and genetic mutations. By elucidating the differential impact of these factors on neurofilament dynamics in sporadic versus familial ALS, this meta-analysis aims to provide insights into underlying pathophysiological mechanisms and identify potential avenues for targeted therapeutic interventions [4,5].

Conclusion

In conclusion, this meta-analysis represents a critical step towards elucidating the role of neurofilaments in the pathogenesis of ALS, with a specific focus on discerning differences between sporadic and familial disease subtypes. By synthesizing data from diverse study populations and employing rigorous statistical methods, this study aims to provide a comprehensive understanding of neurofilament dynamics in ALS and their potential implications for disease diagnosis, prognosis and treatment. Through collaborative efforts and knowledge synthesis, we can advance our understanding of ALS pathophysiology and pave the way for personalized therapeutic strategies aimed at mitigating disease progression and improving outcomes for affected individuals.

Acknowledgment

None.

Conflict of Interest

No conflict of interest.

References

1. Kiernan, Matthew C., Steve Vucic, Benjamin C. Cheah and Martin R. Turner, et al. "Amyotrophic lateral sclerosis." *Lancet* 377 (2011): 942-955.
2. Beghi, Ettore, Adriano Chiò, Philippe Couratier and Jesús Esteban, et al. "The epidemiology and treatment of ALS: Focus on the heterogeneity of the disease and critical appraisal of therapeutic trials." *Amyotroph Lateral Scler* 12 (2011): 1-10.
3. Neumann, Manuela, Deepak M. Sampathu, Linda K. Kwong and Adam C. Truax, et al. "Ubiquitinated TDP-43 in frontotemporal lobar degeneration and amyotrophic lateral sclerosis." *Sci* 314 (2006): 130-133.
4. Rosen, Daniel R., Teepu Siddique, David Patterson and Denise A. Figlewicz, et al. "Mutations in Cu/Zn superoxide dismutase gene are associated with familial amyotrophic lateral sclerosis." *Nature* 362 (1993): 59-62.
5. Kwiatkowski Jr, T. J., D. A. Bosco, A. L. Leclerc and E. Tamrazian, et al. "Mutations in the FUS/TLS gene on chromosome 16 cause familial amyotrophic lateral sclerosis." *Sci* 323 (2009): 1205-1208.

How to cite this article: Tatiabela, Gina. "Neurofilaments in ALS: Sporadic vs. Familial- A Meta-Analysis." *Physiother Rehabil* 9 (2024): 377.