

DIFFERENTIALLY EXPRESSED PROTEINS IN BLOOD PLASMA OF INDIVIDUALS WITH ALZHEIMER'S DISEASE THROUGH MASS SPECTROMETRY

P-1283

Franco Andrei da Cunha Junqueira¹, Maria Luiza Vasconcelos Montenegro², Josivan Barbosa de Farias³, Roberto Afonso da Silva³, Breno José Alencar Pires Barbosa⁴, Fábio Rocha Formiga⁵

1. University of Pernambuco, Garanhuns, Brazil; 2. Faculty of Medical Sciences, University of Pernambuco, Recife, Brazil; 3. Keizo Asami Institute, Federal University of Pernambuco, Recife, Brazil; 4. Federal University of Pernambuco, Recife, Brazil; 5. University of Pernambuco, Recife, Brazil.

Inflammatory processes are present in all phases of the pathophysiology of Alzheimer's Disease, in a more diffuse way at the beginning of the disease and more concentrated at the end of its course.

INTRODUCTION	METHODS	RESULTS	CONCLUSIONS	REFERENCES
It is estimated that by 2030, 75 million people worldwide will be living with dementia; therefore, making an early diagnosis is essential. Proteomic analysis emerges as a promising approach for identifying potential biomarkers to differentiate individuals with and without amyloid pathology. This study aimed to identify differentially expressed proteins (DEPs) in the blood plasma of individuals with Alzheimer's Disease (AD) through mass spectrometry.	37 participants were included, 17 with probable AD according to clinical criteria and 20 controls. 5 ml of peripheral blood was collected from the participants. The samples were centrifuged to obtain blood plasma, followed by albumin and IgG depletion, precipitation, and proteolytic digestion. Proteomic analysis was performed using the hyphenated Mass Spectrometry technique, with ultra-high performance liquid chromatography coupled to tandem mass spectrometry. The PROGENESIS QI Waters software was used for data analysis with the identification of proteins from the Uniprot database.	The sample consisted of 55.3% women, mean age of 75.1 years in the AD group, and 69.6 years in the controls. 47% of the AD group were in the advanced dementia stage, 23.5% were in the moderate stage, and 29.5% were in the mild stage. MILD AD X CONTROL ↑ SAA1, ARFIP1, METTL18, AMBP, SERPINA4, APOH, ITIH3, PRSS3, SERPINA7, ECM1, CHMP4A, APOB, C7, IGHV3-23, APOC4, F9, HBZ, SERPINA5, HPR, PLG, GPX3. ↓ PROS1, MAPKAPK3, IGKV6D-21, SERPINA6, CT62, HABP2, HYI, IGHG2, KIF16B, ACTA2, -, RUNDC3A. MODERATE AD X CONTROL ↑ SAA1, -, IGKV6D-21, HBA1, HBD, APOH, S100A9, S100A8, AMBP, HBB, CFD, PPBP, C1RL. ↓ NONE. ADVANCED AD X CONTROL ↑ S100A8, S100A9, HBD, HBA1. ↓ CLEC3B, SAA1. Figure 1. Pattern of upregulated and downregulated identified DEPs (p ≤ 0.05) between groups.	DEPs involved in inflammatory processes were identified in all AD subgroups, from mild to severe, in agreement with literature. A gradual reduction in the number of DEPs was observed as the disease progressed, resulting in a diffuse inflammatory pattern in the initial phases and a concentrated pattern in the more advanced stages. Our results corroborate the implications of deregulated inflammatory pathophysiology of AD and present data from northeastern Brazil, a population that is commonly underrepresented in the global landscape of research on blood biomarkers for AD.	1. Dong Y, et al. The early diagnosis of Alzheimer's Disease: Blood-based panel biomarker discover by proteomics and metabolomics. CNS Neurosci Ther. 2024; 30(11):e70060. 2. Roveta F, et al. Neuroinflammatory Biomarkers in Alzheimer's Disease: From Pathophysiology to Clinical Implications. Int J Mol Sci. 2024; 25(32). 3. Schindler S.E, et al. Fluid Biomarkers in Dementia Diagnosis. Continuum (Minneapolis, Minn.). 2022; 28(3): 822-833. CONTACT E-mail: franco.junqueira@upe.br 