

BIOMARKERS (NON-NEUROIMAGING)

Biomarkers and proteomics in amyloid PET negative persons with clinical signs of MCI or mild dementia

Richard Mohs¹ | Douglas W. Bearegard¹ | Allan I. Levey² | Erik C.B. Johnson³ |
Jessie Nicodemus-Johnson⁴ | Robin Wolz⁵ | John Dwyer¹

¹Global Alzheimer's Platform Foundation,
Washington, DC, USA

²Emory University School of Medicine,
Atlanta, GA, USA

³Goizueta Alzheimer's Disease Research
Center, Atlanta, GA, USA

⁴Pentara Corporation, Salt Lake City, UT, USA

⁵IXICO, London, London, United Kingdom

Correspondence

Richard Mohs, Global Alzheimer's Platform
Foundation, Washington, DC, USA.
Email: mohsrichard@yahoo.com

Abstract

Background: Screening for clinical trials identifies persons with clinical symptoms of Mild Cognitive Impairment (MCI) or Alzheimer's disease (AD) but no amyloid on PET. We compared blood biomarkers and proteomics in these screen failures with cognitively normal, amyloid PET negative persons and with amyloid PET positive MCI or mild AD patients.

Method: We analyzed data from 296 persons with clinical symptoms of MCI or mild AD from the Bio-Hermes study who were amyloid PET negative (MCI + AD AB-); we compared them with 313 Bio-Hermes participants who were cognitively normal and amyloid PET negative (CN AB-) and with 258 amyloid PET positive persons with clinical MCI or mild AD (MCI + AD AB+). Measures included regional amyloid PET, plasma A-beta40 and 42, total tau, p-tau 181, p-tau 217, NfL, GFAP, a panel of 69 cytokines (Fireplex) and 7596 proteins from the Somalogic panel.

Result: Relative to the CN AB- group, the MCI + AD AB- group were older, more cognitively and functionally impaired, had slightly less education and were more likely to be non-white; the groups did not differ in gender or APOE4 rates. The groups did not differ on amyloid SUVR, p-tau 217, t-tau or GFAP. NfL was higher in MCI + AD AB- persons compared with CN AB- persons (Table 1 and 2). After using a False Discovery Rate adjustment there were no Somalogic proteins significantly different in MCI + AD AB- participants vs CN AB- participants. Several proteins were different in amyloid PET positive persons compared with amyloid PET negative persons (Figure 1).

Conclusion: NfL data indicate very significant neurodegeneration in symptomatic but amyloid PET negative clinical trial screen failures. Biomarkers reflecting amyloid and tau were not different and the proteomics profile did not find specific abnormalities in amyloid negative, symptomatic persons.

This is an open access article under the terms of the [Creative Commons Attribution](https://creativecommons.org/licenses/by/4.0/) License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2025 The Alzheimer's Association. *Alzheimer's & Dementia* published by Wiley Periodicals LLC on behalf of Alzheimer's Association.

Table 1. Blood-based Biomarkers

Biomarker	Lab	Cognitively Normal		Cognitively Impaired	
		CN Aβ- (N=313)	CN Aβ+ (N=84)	MCI + Mild AD Aβ- (N=296)	MCI + Mild AD Aβ+ (N=258)
		Mean (SD)	Mean (SD)	Mean (SD)	Mean (SD)
P-tau217 (U/mL)	Lilly	0.17 (0.06)	0.28 (0.10)	0.21 (0.14)	0.44 (0.26)
P-tau217 (ng/mL)	Gothenburg	2.11 (1.44)	3.50 (1.52)	2.49 (2.24)	4.81 (2.50)
T-tau (ng/L)	Quanterix	2.19 (2.19)	2.17 (0.98)	2.71 (6.77)	2.04 (1.00)
sNfL (pg/mL)	Merck	23.59 (13.03)	28.97 (14.71)	33.77 (30.89)	40.45 (28.38)
	Quanterix	21.22 (12.17)	25.80 (13.04)	30.44 (31.57)	36.23 (27.03)
	Roche	2.76 (1.48)	3.24 (1.85)	3.57 (3.00)	4.59 (3.55)
GFAP (pg/mL)	Merck	136.92 (68.83)	203.53 (102.95)	161.58 (157.38)	252.70 (118.24)
	Quanterix	122.23 (63.21)	181.38 (97.49)	146.53 (151.54)	230.16 (111.30)
	Roche	87.27 (44.26)	130.24 (72.99)	100.93 (95.06)	157.70 (66.83)

Abbreviations: CN, cognitively normal; MCI, mild cognitive impairment; AD, Alzheimer's disease; SD, standard deviation; P-tau217, phosphorylated tau 217; T-tau, total tau; GFAP, glial fibrillary acetic protein; NfL, neurofilament light

(Data source: file t_2_item_35_biomarker.rtf Jan 21))

Table 2. Blood-based Biomarkers Comparisons – Adjusted P Values for Multiple Comparisons

Populations Compared	Versus	CN Aβ+	MCI + Mild AD Aβ-	MCI + Mild AD Aβ-	MCI + Mild AD Aβ-	MCI + Mild AD Aβ+	MCI + Mild AD Aβ+
		CN Aβ-	CN Aβ-	MCI + Mild AD Aβ+	CN Aβ+	CN Aβ-	CN Aβ+
Biomarker	Lab						
P-tau217 (F=100.105; P<.0001)	Lilly	<.0001	0.1702	<.0001	0.0192	<.0001	<.0001
P-tau217 (F=79.512; P<.0001)	Gothenburg	<.0001	0.3421	<.0001	0.0004	<.0001	<.0001
T-tau F=1.473 (NS)	Quanterix	-	-	-	-	-	-
NfL (F=13.051; P<.0001)	Merck	0.8066	0.0003	0.1354	0.2619	<.0001	0.0059
NfL (F=10.638; P<.0001)	Quanterix	0.9113	0.0011	0.2579	0.2539	<.0001	0.0118
NfL (F=12.873; P<.0001)	Roche	0.9197	0.0259	0.0029	0.5996	<.0001	0.0018
GFAP (F=34.157; P<.0001)	Merck	0.0010	0.3410	<.0001	0.0415	0.0059	<.0001
GFAP (F=31.872; P<.0001)	Quanterix	0.0036	0.2866	<.0001	0.1141	<.0001	0.0106
GFAP (F=36.774; P<.0001)	Roche	0.0002	0.4109	<.0001	0.0093	<.0001	0.0361

Abbreviations: P-tau217, phosphorylated tau 217; T-tau, total tau; NfL, neurofilament light; GFAP, GFAP, glial fibrillary acetic protein
 Note: All other cytokines compared for populations listed were nonsignificant.

((Data source: file t_2_item_36_biomarkerstat.rtf Jan 21))

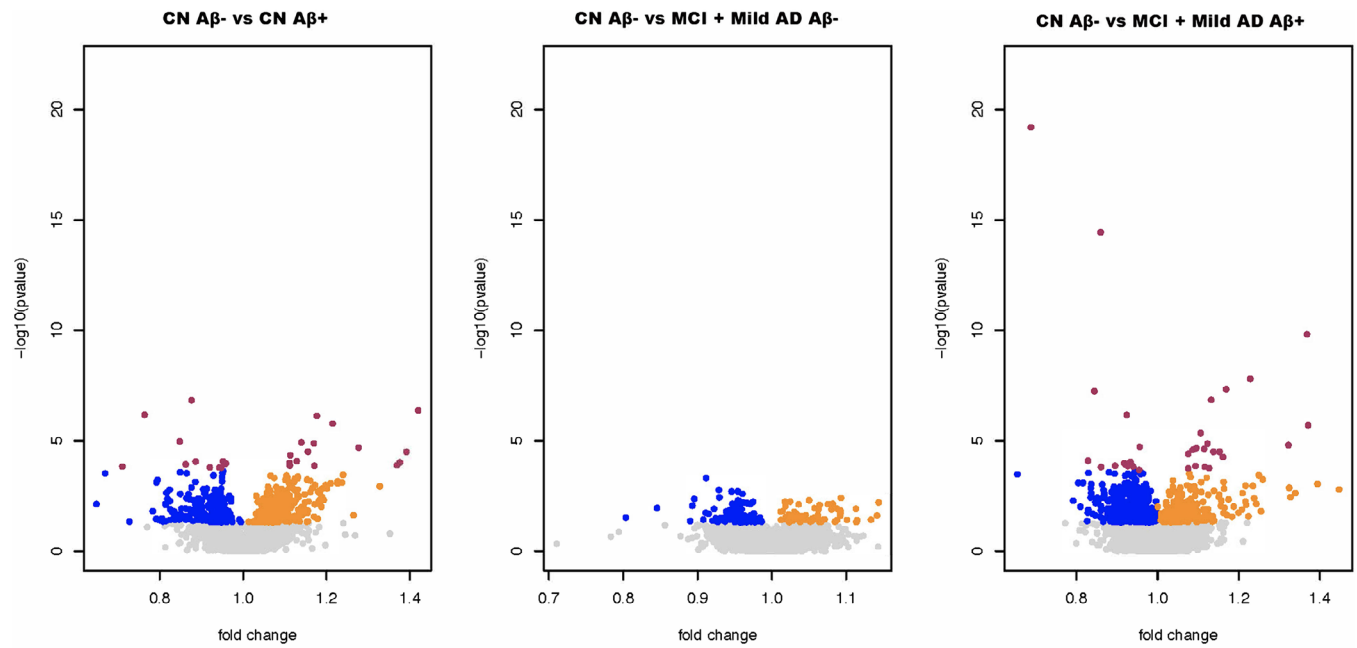


Figure 1: Proteomics Group Comparisons; Beyond FDR in Purple