Nonlinear Association Between Cerebrospinal Fluid and Florbetapir F-18 β-Amyloid Measures Across the Spectrum of Alzheimer Disease

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IMPORTANCE Cerebrospinal fluid (CSF) and positron emission tomographic (PET) amyloid biomarkers have been proposed for the detection of Alzheimer disease (AD) pathology in living patients and for the tracking of longitudinal changes, but the relation between biomarkers needs further study.

OBJECTIVE To determine the association between CSF and PET amyloid biomarkers (cross-sectional and longitudinal measures) and compare the cutoffs for these measures.

DESIGN, SETTING, AND PARTICIPANTS Longitudinal clinical cohort study from 2005 to 2014 including 820 participants with at least 1 florbetapir F-18 (hereafter referred to as simply florbetapir)-PET scan and at least 1 CSF β-amyloid 1-42 (Aβ1-42) sample obtained within 30 days of each other (501 participants had a second PET scan after 2 years, including 150 participants with CSF Aβ1-42 measurements). Data were obtained from the Alzheimer’s Disease Neuroimaging Initiative database.

MAIN OUTCOMES AND MEASURES Four different PET scans processing pipelines from 2 different laboratories were compared. The PET cutoff values were established using a mixture-modeling approach, and different mathematical models were applied to define the association between CSF and PET amyloid measures.

RESULTS The values of the CSF Aβ1-42 samples and florbetapir-PET scans showed a nonlinear association ($R^2 = 0.48-0.66$), with the strongest association for values in the middle range. The presence of a larger dynamic range of florbetapir-PET scan values in the higher range compared with the CSF Aβ1-42 plateau explained the differences in correlation with cognition ($R^2 = 0.36$ and $R^2 = 0.25$, respectively). The APOE genotype significantly modified the association between both biomarkers. The PET cutoff values derived from an unsupervised classifier converged with previous PET cutoff values and the established CSF Aβ1-42 cutoff levels. There was no association between longitudinal Aβ1-42 levels and standardized uptake value ratios during follow-up.

CONCLUSIONS AND RELEVANCE The association between both biomarkers is limited to a middle range of values, is modified by the APOE genotype, and is absent for longitudinal changes; 4 different approaches in 2 different platforms converge on similar pathological Aβ cutoff levels; and different pipelines to process PET scans showed correlated but not identical results. Our findings suggest that both biomarkers measure different aspects of AD Aβ pathology.

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**Methods**

**Participants**

A total of 820 Alzheimer’s Disease Neuroimaging Initiative (ADNI) participants with CSF Aβ1-42 and florbetapir-PET Aβ measures across the spectrum of AD pathology were included in our study (Table 1). Florbetapir was not available at the baseline ADNI 1 visit, and therefore some of these participants had their first florbetapir-PET scan performed during subsequent visits. The number of visits in which PET scans were performed were 739 at baseline, 23 at 24 months, 3 at 36 months, 25 at 48 months, 25 at 60 months, and 5 at 72 months. For the CSF Aβ1-42 mixture model analysis, 1005 participants with a CSF Aβ1-42 measurement were included (ie, all participants with at least 1 CSF Aβ1-42 measurement to estimate the CSF Aβ1-42 cutoff level). Data were downloaded on September 12, 2014. A total of 501 participants had a second PET amyloid scan performed within 2 years, and a total of 150 participants also had CSF samples obtained within 30 days of the second PET scan. The CSF Aβ1-42 data used in the preparation of this article were obtained from UPENNBIOMK and UPPENNBIO-MK5-7 data generated by the ADNI Biomarker Core.

**CSF and Florbetapir Aβ Measures Across Spectrum of AD**

The CSF samples were obtained in the morning after an overnight fast and processed as previously described (eAppendix in the Supplement). The Aβ1-42 level was measured using the multiplex xMAP Lumienx platform (Lumienx Corp) with Innogenetics (INNO-BIA AlzBio3, for research use–only reagents) immunoassay kit–based reagents. The capture and detection antibodies for Aβ1-42 were 4D7A3 and 3D6, respectively. All longitudinal CSF samples belonging to the same participant were measured in the same plate to avoid assay-to-assay variation.

**Florbetapir-PET Scan Processing**

Florbetapir image data were acquired from a variety of PET scanners at ADNI sites nationwide. Image data were acquired in four 5-minute frames 50 to 70 minutes after injection of approximately 10 mCi, and the 4 frames were coregistered to each other, averaged, interpolated to a uniform image (160 × 106 × 96) and voxel size (1.5 mm³), and smoothed to a

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**Table 1. Characteristics of the ADNI Participants Included in the Study at the Time of the Scan**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Cognitively Normal (n = 259)</th>
<th>Participants With MCI (n = 415)</th>
<th>Participants With AD (n = 146)</th>
<th>P Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age at time of scan, mean (SD), y</td>
<td>72.8 (5.8)</td>
<td>71.3 (7.4)</td>
<td>73.5 (8.5)</td>
<td>.002</td>
</tr>
<tr>
<td>Male sex, %</td>
<td>45.2</td>
<td>56.0</td>
<td>58.3</td>
<td>.009</td>
</tr>
<tr>
<td>ADAS-cog score, mean (SD)</td>
<td>9.0 (4.4)</td>
<td>15.0 (6.8)</td>
<td>30.9 (8.9)</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>SUVR, median (Q1-Q3)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Average CB</td>
<td>1.17 (1.12-1.32)</td>
<td>1.27 (1.13-1.53)</td>
<td>1.54 (1.37-1.68)</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Average WM</td>
<td>0.66 (0.63-0.72)</td>
<td>0.74 (0.66-0.84)</td>
<td>0.87 (0.83-0.90)</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Summary CB</td>
<td>1.06 (1.00-1.17)</td>
<td>1.18 (1.02-1.39)</td>
<td>1.42 (1.27-1.53)</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Summary composite</td>
<td>0.73 (0.70-0.82)</td>
<td>0.83 (0.72-0.99)</td>
<td>1.03 (0.94-1.09)</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Aβ1-42 level, median (Q1-Q3), pg/mL</td>
<td>209.3 (159.2-237.6)</td>
<td>160.9 (131.9-214.4)</td>
<td>131.8 (114.4-150.7)</td>
<td>&lt;.001</td>
</tr>
</tbody>
</table>

Abbreviations: Aβ, β-amyloid; AD, Alzheimer disease; ADAS-cog, Alzheimer Disease Assessment Scale–cognitive subscale; ADNI, Alzheimer’s Disease Neuroimaging Initiative; CB, cerebellum; MCI, mild cognitive impairment; Q, first quarter; Q3, third quarter; SUVR, standardized uptake value ratio; WM, white matter.
uniform resolution (8-mm full width at half-maximum) to account for differences between scanners.77

We included florbetapir SUVRs developed in 2 different laboratories (the University of Utah in Salt Lake City and the University of California, Berkeley), each including 2 different measures obtained using a different reference (eAppendix in the Supplement). Both laboratories used the same scans that were preprocessed as already detailed. From the University of Utah analysis, we included averaged regional values from medial and lateral frontal, temporal, and parietal cortices that were normalized either using the cerebellar region (the average cerebellum) or the white matter (the average white matter) as reference region. Two summary measures were obtained at the University of California, Berkeley using Aβ deposition in frontal, cingulate, lateral parietal, and temporal cortices and either the whole cerebellum as reference (the summary cerebellum) or the whole cerebellum, brainstem/pons, and eroded subcortical white matter (the summary composite) as reference region. There were 450 and 501 participants who had 2 PET scans obtained within 2 years at the University of Utah and University of California, Berkeley laboratories, respectively.

Statistical Analysis
For univariate group comparisons, analysis of variance and χ² tests were applied for quantitative and qualitative variables. Power transformations were applied to normalize distributions in the analyses performed for the demographic variables included in Table 1. We used 5 different models to test which one better explained the association between CSF Aβ1-42 levels and PET SUVRs: lineal, polynomial, exponential, hyperbolic, and multivariate adaptive regression splines (MARSs). An MARS creates piecewise regression models (hinges) for each variable in the model, and these models are separated by knots to capture changes in the association according to different ranges of the measures, using a data-driven approach. To test the models, the sample was divided into a training set and a test set, which included two-thirds and one-third of the participants, respectively. Each participant was only included once in this analysis. The different statistical models were developed in the training set using a 10-fold cross-validation and afterward applied to the test set. The coefficient of determination (R²) is reported to summarize the goodness of fit of each model. Cutoffs for amyloid biomarkers were obtained using a previously reported strategy that uses finite mixture models (eTable 1 and eFigure 1 in the Supplement).28,29

Results
Cross-sectional Association Between Individual CSF and Florbetapir-PET Aβ Measures
The first and second columns in Figure 1 show the CSF and PET Aβ levels for the participants included in the training and test sets, respectively, and the fitted models (the solid gray areas show disagreement in participant classification between both biomarkers). Coefficients of determination (R²) for the different models are summarized in eTable 2 in the Supplement. In all comparisons, the linear model showed the worst performance in the training and test sets, whereas the hyperbolic and MARS models showed overall the best performance.

APOE genotype influenced the relationship; an increasing number of ε4 copies were associated with lower CSF Aβ1-42 levels, as shown by the solid gray areas indicated in the plots for participants with 0, 1, or 2 ε4 allele copies. A model for participants with 2 APOE ε4 copies is not included. The solid gray areas indicate disagreement in the classification based on the pair of Aβ measures. Aβ indicates β-amyloid; AD, Alzheimer disease; CB, cerebellum; CSF, cerebrospinal fluid; MARS, multivariate adaptive regression spline; MCI, mild cognitive impairment; PET, positron emission tomographic; SUVR, standardized uptake value ratio; and WM, white matter.

Figure 1. Association Between CSF Aβ1-42 Levels and Florbetapir F-18 PET SUVRs

Aβ1-42 Level, pg/mL

Average CB, SUVR

Aβ1-42 Level, pg/mL

Average CB, SUVR

Aβ1-42 Level, pg/mL

Average CB, SUVR

Aβ1-42 Level, pg/mL

Average CB, SUVR

Aβ1-42 Level, pg/mL

Average CB, SUVR

Aβ1-42 Level, pg/mL

Average CB, SUVR
levels for the same PET SUVR in all models. In all MARS models, the first hinge was located in a narrow range of Aβ1-42 levels (225−288 pg/mL for participants with 0 copies of the APOE ε4 allele and 208−214 pg/mL for participants with 1 copy of the APOE ε4 allele), and the second hinge showed a slightly higher variability (137−144 pg/mL for participants with 0 copies of the APOE ε4 allele and 119−132 pg/mL for participants with 1 copy of the APOE ε4 allele). The PET SUVRs could not accurately predict CSF Aβ1-42 levels before the first hinge ($R^2 = 0.01-0.10$) and after the second hinge ($R^2 = 0.11-0.26$). We tested whether clinical diagnosis was a significant predictor, but it was not selected in any of the MARS models. Similar results that included 2 hinges in the MARS were obtained when CSF Aβ1-42 level was selected as the predictor and the florbetapir measure were selected as outcomes (data not shown).

Table 2 in the Supplement shows PET SUVRs that corresponded to the CSF Aβ1-42 cutoff level of 192 pg/mL for participants with 0 copies or 1 copy of the APOE ε4 allele. Table 2 summarizes the κ coefficients and overall percentage agreement for each pair of biomarkers. There was a substantial agreement between the CSF Aβ1-42–defined groups and the groups that were defined based on the different florbetapir-derived measures (κ = 0.69-0.76), but it was lower than the excellent agreement observed for the different florbetapir-PET measures (κ = 0.80-0.91). Most of the participants who were classified differently by CSF and PET Aβ measures presented with abnormal CSF Aβ1-42 levels and normal PET SUVRs (8.9%-12.5%) compared with participants with normal CSF Aβ1-42 levels and abnormal PET SUVRs (0.7%-4.5%). We compared clinical characteristics in the groups with mismatched biomarker results (eTables 4 and 5 in the Supplement). Although there were a larger number of participants who were cognitively impaired in the group that had only abnormal CSF Aβ1-42 levels compared with the group that had only abnormal summary cerebellum values, the differences were not significant ($P = .50$). Whereas there were no differences in the Alzheimer’s Disease Assessment Scale-cognitive subscale (ADAS-cog) scores between groups at the 12-month follow-up, the participants who had only abnormal CSF Aβ1-42 levels showed memory decline, and the participants who had only abnormal summary cerebellum values showed executive decline.

The different PET SUVRs obtained with the different references and pipelines were highly correlated (eFigure 2 in the Supplement), with correlation coefficients between 0.81 and 0.95, although the values were not comparable and needed a transformation between pipelines (eTable 6 in the Supplement). When we tested the ability of florbetapir-PET measures and CSF Aβ1-42 levels to predict the ADAS-cog score, the summary composite measure ($R^2 = 0.36$) outperformed the Aβ1-42 level ($R^2 = 0.25$) in a cross-validated MARS model that included age as a covariate (Figure 2A and B). The MARS model fits calculated for each of the clinical diagnostic groups are summarized in eTable 7 in the Supplement. Results were similar for other PET Aβ measures.

### Longitudinal CSF and PET Aβ Measurements

Figure 2C-F shows baseline SUVRs for each of the PET measurements (x-axis) and the corresponding yearly change (y-axis) for participants with 2 PET measurements, and Figure 2G shows the changes in the CSF Aβ1-42 level for the same period. For 304 participants who had 2 PET scans and CSF samples obtained during the baseline visit, only the group with abnormal Aβ1-42 levels and abnormal PET SUVR summary measures showed a greater increase during follow-up (Figure 2H and I).

A total of 150 participants (53 cognitively normal participants, 90 participants with mild cognitive impairment, and 7 participants with AD) had 2 CSF and PET Aβ measurements obtained during the same visits, with the second set of measurements occurring within 2 years (ie, mean [SD], 729.7 [20.8] days) of the first. Figure 3 displays scatterplots with the yearly value changes during follow-up for the CSF Aβ1-42 and florbetapir-PET measurements below the diagonal and their correlation above the diagonal (eFigure 3 in the Supplement also shows associations between the PET SUVRs). There was no correlation between CSF and PET amyloid value changes, while the different PET Aβ amyloid measurements correlated with a higher degree. The correlation between CSF Aβ1-42 level and florbetapir-PET measure did not improve when only participants with Aβ1-42 levels between both MARS hinges (140-215 pg/mL) were included (data not shown).

### Discussion

Cross-sectional CSF Aβ1-42 levels and florbetapir-PET measures were associated for a limited middle range of values that included the cutoffs, and they were consistent with AD. The association was significantly modified by the number of APOE ε4 alleles. Nevertheless, there was a large agreement for the
classification of participants as having an AD-like Aβ burden between the different measures. Different approaches converged on a similar cutoff for pathological Aβ deposition across platforms. However, there was no correlation between longitudinal changes observed after 2 years of follow-up.

Previous studies have mainly analyzed the agreement between CSF and PET Aβ measures in the same cohort using a single florbetapir-PET measure or using Pearson correlation or linear regressions assuming a linear association. Good agreement between CSF Aβ1-42 level and florbetapir-PET SUVR has been previously reported using a single PET measure or using Pearson correlation-classification agreement using 4 separate platforms. However, there was no correlation between longitudinal changes observed after 2 years of follow-up.

Scatterplots showing the association between Alzheimer’s Disease Assessment Scale-cognitive subscale (ADAS-cog) scores on the y-axis and the summary composite standardized uptake value ratios (SUVRs) (A) and the cerebrospinal fluid (CSF) β-amyloid 1-42 (Aβ1-42) levels (B) on the x-axis. The blue continuous line represents the multivariate adaptive regression spline for a 65-year-old participant. The red dashed line represents the cutoff for the biomarker represented in the plot, and the green dashed line represents the value at which the CSF Aβ1-42 level plateaus. Longitudinal SUVR yearly changes (after a 2-year follow-up) for the average cerebellum (CB) (C), the average white matter (WM) (D), the summary CB (E), and the summary composite (F) are shown on the y-axes, with the x-axes representing baseline SUVRs. G, Longitudinal changes in CSF Aβ1-42 level after a 2-year follow-up are shown. The red dashed line represents the value that corresponds to the CSF Aβ1-42 level of 192 pg/mL. Yearly changes in the summary CB (H) and the summary composite (I) values during follow-up (y-axis) are based on the presence of normal or abnormal baseline CSF Aβ1-42 levels and florbetapir F-18–positron emission tomographic (PET) measures. The horizontal line in each box indicates the median, while the top and bottom borders of the box mark the 75th and 25th percentiles, respectively. The whiskers above and below the box mark the 90th and 10th percentiles, respectively. The points beyond the whiskers are outliers beyond the 90th and 10th percentiles.
The validity of the cutoffs has been previously demonstrated in a 3-fold manner: (1) the CSF Aβ1-42 level cutoff was initially demonstrated using autopsy-validated diagnoses to prevent biases due to clinical diagnostic uncertainties, (2) this cutoff was then validated using a “diagnosis-free”-driven mixture model analysis of CSF Aβ1-42 levels, and (3) for florbetapir-PET SUVRs, investigators used young controls and autopsy cases. In the mixture model analysis of summary CB values that we performed, 1.12 was designated as the cutoff that corresponds to an SUVR of 1.11 using the semiautomated quantification applied by Avid and, therefore, overlaps with their validated cutoff (eFigure 4 in the Supplement). Furthermore, the 1.12 summary CB cutoff value is close to the average of the transformation of the CSF Aβ1-42 autopsy-validated cutoff level for participants with 0 or 1 APOE ε4 allele. In addition, using a mixture-modeling approach in a sample of 1005 levels of CSF Aβ1-42, we reached the same level as the one previously described in our autopsy study.

Therefore, we confirmed the previous florbetapir-PET cutoff established based on young controls using an unsupervised classification method, in a sample that included a large number of cognitively normal participants, participants with mild cognitive impairment, and participants with AD, and the CSF Aβ1-42 autopsy-validated cutoff level in a larger sample using the approach applied by De Meyer et al in a larger sample. Most importantly, we demonstrated that the conversion of the values across different platforms and methods converges robustly on the similar burden of Aβ pathology. However, we emphasize that recommended SUVR cutoffs vary according to the pipeline that was used, and therefore any modification in the pipeline must be followed by a validation of new cutoffs. Previous studies have described groups of participants that show disagreement in classification between CSF Aβ1-42 levels and florbetapir-PET measures. The size of these groups varies depending on the reference region, and the disagreement decreases when white matter regions are used as a reference. This might be explained by the fact that the cerebellum is affected in latter stages of AD, and therefore reference regions might be affected differently in later stages of disease.

Recently, a lower cutoff level for CSF Aβ1-42 (ie, 157 pg/mL) and an average cerebellum with a cutoff SUVR of 1.26 that is skewed toward more abnormal values of pathological Aβ biomarkers were suggested. These values were obtained using clinical diagnosis as the gold standard and contradict evidence from previous autopsy-based studies using unsupervised diagnosis-independent methods. This can be explained by our current understanding of the pathological Aβ
biodmarkermodeforAD, which describest bi omarker and neu
ropathological changes that precede cognitive changes and that 
are being used for the staging of preclinical AD in cognite
ily normal participants, and by autopsy studies showing that 
44.2% of cognitively normal participants have Consortium to 
Establish a Registry for Alzheimer’s Disease B and C scores and 
that 22.5% of cognitively normal participants have an inter-
mediat probability of AD neuropathological changes. Hence, 
these and other studies emphasize that optimizing cuttofs 
based on clinical diagnosis to classify all participants with nor-
mal cognition as healthy controls will contradict the neuropa-
thologicalfindings for many participants and prevent an ac-
curate preclinical diagnosis of the underlying Aβ pathology. 
This is of critical importance for the design and conduct of clini-
cal trials of new therapies targeting pathological Aβ biomar-
kers in participants with underlying AD pathology who are cog-
nitively normal.

One previous study pursued efforts to transform CSF 
Aβ1-42 levels to Pittsburgh Compound B-PET SUVRs, and vice 
versa, and used a log2 transformation for both values owing 
to the lack of a linear association. However, the goal of our study 
was to transform the values between the different methods and 
to understand how both are related (in order to interpret dif-
fences in the timing of the biomarker changes for both bio-
markers across the whole clinical spectrum) and the implica-
tions thereof. Based on the MARS models, it can be concluded 
that there is only a strong association between CSF and flor-
betapir-PET Aβ values for the midrange values of both mea-
sures, which include the currently applied CSF Aβ1-42 level 
measured using the multiplex xMAP Luminex platform and 
the florbetapir-PET Aβ amyloid measure normalized to cerebellum 
cutoff values. It is also in this range where most 
of the discrepant classification appears. This could be due, in 
part, to the variability inherent to any clinical measure that can 
have an important effect for cases with values close to a di-
chotomic cutoff.

Another explanation for this disagreement might be the lower affinity of PET amyloid ligands for diffuse plaques and 
the differential effect of the APOE genotype on bio-
marker values. Different amyloid PET ligands share their 
binding site and show a higher affinity for neuritic amyloid 
plaques compared with diffuse amyloid plaques, which can 
lead to false negatives. While it is thought that the 
decrease in CSF Aβ1-42 levels, but not in other Aβ levels, 
reflects brain Aβ deposition, more mature forms might not 
be in equilibrium with CSF and, therefore, might lead to the plateau observed in the CSF Aβ1-42 level, or later stages 
might represent Aβ levels that are not in equilibrium with the 
CSF. Therefore, the wider range of CSF Aβ1-42 levels in the lower range of florbetapir-PET SUVRs might imply a 
stronger association of the CSF Aβ1-42 level with diffuse 
amyloid plaques, which appear in earlier phases without the presence of neuritic plaques.

Another explanation is that different sensitivities or ceil-
ing effects of the assays could account for the strong associa-
tion between CSF Aβ1-42 levels and florbetapir-PET Aβ measures 
only for the midrange values of these 2 most widely used 
measures of pathological Aβ deposition. However, the CSF 
Aβ1-42 level plateau is well above the lower detection limit of 
the Luminox assay. Furthermore, APOE ε4 is associated with 
a higher proportion of fibrillar amyloid and neurotic 
plaques, which show a higher affinity for amyloid PET lig-
ands and, therefore, would explain the higher SUVRs, and this 
would explain why the presence of APOE ε4 had different ef-
fects on both the CSF Aβ1-42 levels and the florbetapir-PET 
measures across all pipelines. For the same CSF Aβ1-42 levels, 
participants with no ε4 alleles had lower florbetapir-PET 
SUVRs. We performed several analyses to assess the clinical 
correlations of participants who showed either abnormal CSF 
Aβ1-42 levels or abnormal florbetapir-PET measures and found 
differences in the cognitive changes, but a longer follow-up (in-
cluding autopsies) will be needed to characterize these small 
groups of participants.

Surprisingly, there was no correlation between the changes 
in CSF Aβ1-42 levels and the changes in florbetapir-PET mea-
sures after a 2-year follow-up. There are several non-
mutually exclusive explanations for this finding: (1) the changes 
are small and might not be detected owing to the inherent vari-
bility of the measurements, (2) a longer follow-up is needed to 
see larger changes, and (3) the different dynamic ranges of 
these 2 biomarkers could lead to different rates of changes in 
them across the biomarker spectrum. This might be due to the 
fact that these 2 biomarkers reflect different aspects of dis-
ease mechanisms, leading to Aβ fibrillation and deposition, as 
well as different floor and ceiling effects as already noted. How-
ever, another factor that might explain these differences is 
the sensitivity of the measures of CSF Aβ1-42 level and florbetapir-
PET SUVR to track small changes during a 2-year follow-up. In 
any case, it is not surprising that the methods used to mea-
sure CSF Aβ1-42 level and brain Aβ amyloid deposits do, in fact, 
measure different aspects of pathological Aβ amyloid as pre-
aviously discussed.

Florbetapir-PET SUVRs showed a stronger association with ADAS-cog scores, which can be explained by the 
absence of the floor effect observed for CSF Aβ1-42 levels, and 
thus can offer a larger dynamic range along disease pro-
gression. Nevertheless, the association with cognition is 
lower than the one observed for neuronal injury neuroimag-
ing biomarkers.

Conclusions

Thus, in conclusion, although CSF Aβ1-42 levels and florbetapir-PET Aβ measures show a high-classification agreement for dementia due to underlying AD pathology, these are clearly dif-
ferent measures of pathological Aβ amyloidosis that con-
verge to similar diagnostic cutoffs across different cohorts, 
methods, and amyloid biomarkers, but they do not closely cor-
correlate in the cross-sectional low and high range of values. 
Notably, this extends to a lack of correlation for the longitudinal 
changes in these 2 biomarkers during a 2-year follow-up. Hence, 
our novel findings are significant for understanding how to in-
terpret CSF Aβ1-42 levels and florbetapir-PET Aβ measures for 
diagnosis and for understanding the mechanisms of Aβ 
amyloidosis.
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Authors Contributions: Dr Trojanowski had full access to all of the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis. Study concept and design: Toledo. Acquisition, analysis, or interpretation of data: All authors. Drafting of the manuscript: Toledo, Trojanowski. Critical revision of the manuscript for important intellectual content: All authors. Statistical analysis: Toledo. Obtaining funding: Foster, Jagust, Jack, Weiner, Trojanowski. Administrative, technical, or material support: Weiner, Shaw. Study supervision: Trojanowski.

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CSF and Flortebatapir Aβ42 Measures Across Spectrum of AD

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REFERENCES
CSF and Florbetapir Aβ Measures Across Spectrum of AD

Original Investigation Research


