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MRI acquisition parameters

Patients had the T1-weighted magnetization prepared rapid gradient echo (MPRAGE) sequence acquired either on a 3T Siemens Tim Trio or a 3T Siemens Prisma Fit scanner at University of California, San Francisco (UCSF). Both scanners had very similar acquisition parameters (sagittal slice orientation; slice thickness $= 1.0$ mm; slices per slab $= 160$; in-plane resolution = 1.0 x 1.0 mm; matrix = 240 x 256; repetition time = 2,300 ms; inversion time = 900 ms; flip angle = 9°), though echo time differed slightly (Trio= 2.98 ms; Prisma= 2.9ms).

 The fourteen young, non-autopsy, cognitively normal controls had the T1-weighted MPRAGE sequence acquired on a 3T Siemens TIM Trio scanner at University of California, Berkeley (sagittal slice orientation; slice thickness $= 1.0$ mm; slices per slab $= 160$; in-plane resolution = 1.0×1.0 mm; matrix = $240x256$; repetition time = 2300 ms; echo time = 2.98 ms; flip angle $= 9^{\circ}$).

Amyloid-β PET acquisition and preprocessing details

Seventeen patients received an injection of ~15 mCi \lceil ¹¹C] Pittsburgh compound-B (PiB) and images were acquired on the Siemens Biograph PET/CT scanner at Lawrence Berkeley National Laboratory (LBNL). Thirteen patients underwent a full 90-minute acquisition, and four patients underwent a 50-70 minute post-injection acquisition. Distribution volume ratio (DVR) maps were created from 90-minute PET acquisitions. SUVR maps were created from 20-minute PET acquisitions; MRI and Freesurfer-defined cerebellar gray matter was used as the reference region (Villeneuve *et al.*, 2015).

One patient received an injection of ~ 10 mCi $\lceil^{18}F\rceil$ Florbetapir and underwent a 50-70 minute post-injection acquisition on the GE Discovery STE/VCT PET/CT scanner at UCSF. Whole cerebellum was used as the reference region (Landau *et al*., 2013). Regardless of the type of scan, attenuation correction and reconstruction were performed analogously to [18F]Flortaucipir PET.

Amyloid-β PET analyses

The average DVR or SUVR was extracted from a large neocortical region of interest (ROI) encompassing frontal, cingulate, temporal, and parietal areas (Villeneuve *et al.*, 2015) and subsequently converted into Centiloid values using previously validated and published methods (Klunk *et al.*, 2015; La Joie *et al.*, 2019; Lesman-Segev *et al.*, 2019). A threshold of 24.4 Centiloids, which was previously shown to accurately identify intermediate-to-high ADNC, was used to determine amyloid-β PET positivity (La Joie *et al.*, 2019).

[18F]Flortaucipir (FTP) PET acquisition and preprocessing details

For patients undergoing FTP-PET at LBNL, $[{}^{18}F]FTP$ was synthesized and radiolabeled at the Lab's Biomedical Isotope Facility (Harrison *et al.*, 2019). For the patient scanned at UCSF, [¹⁸F]FTP was provided by the Avid Radiopharmaceuticals clinical trials distribution network. LBNL scans have a resolution of $6.5 \times 6.5 \times 7.25$ mm and UCSF scans have a resolution of 6.8 x 6.8 x 7.2 mm (based on Hoffman phantom).

FTP-PET W-score map details

Native-space FTP-PET SUVR images were warped to Montreal Neurological Institute (MNI) template-space using the deformation parameters derived from the MRI-based unified segmentation procedure using SPM12 (Ashburner and Friston, 2005). Warped SUVRs were masked to limit contamination from non-relevant areas (e.g. off-target binding from meninges, eyes, or skull) and smoothed with a 4 mm isotropic Gaussian kernel to be used for voxelwise analyses (La Joie *et al.*, 2018). Voxelwise FTP-PET W-score (i.e. covariate-adjusted Z-score) maps were computed from these SUVR images.

 In the present study, we were interested in controlling for age as a covariate because older age is associated with increased off-target FTP binding in a regionally dependent manner (Choi *et al.*, 2018; Baker *et al.*, 2019). W-scores allow comparison of a patient's SUVR in a given voxel to the SUVR value expected for the patient's age, based on a normative dataset (La Joie *et al.*, 2018). Our normative sample consisted of 88 clinically and cognitively normal individuals from the Berkeley Aging Cohort between the age of 20 and 93 (mean age 66, standard deviation 20 years, 50% female) who underwent FTP-PET on the Biograph scanner. Cognitively normal individuals older than 60-years-old who were included in the normative dataset were amyloid-negative based on a PiB DVR < 10 Centiloids (Villeneuve *et al.*, 2015; Maass *et al.*, 2017).

FTP-PET region of interest (ROI) analysis details

Freesurfer cortical segmentation was used to define the precentral and postcentral gyrus (Desikan *et al.*, 2006), and subcortical segmentation was used to define globus pallidus and putamen ROIs (Fischl *et al.*, 2002). An MNI-space version of the Talairach atlas (Wake Forest University Pickatlas Toolbox) was used to define the subthalamic nucleus and substantia nigra ROIs (Maldjian *et al.*, 2003). Lastly, an MNI-space cerebellar atlas (SUIT template) was used to define the dentate nucleus ROI (Diedrichsen *et al*., 2009, 2011)*.* All ROIs in MNI-space were reverse-normalized to native space for each subject prior to extraction of SUVR values.

Supplementary Tables

Supplementary Table 1: Distribution of neurofibrillary tangles on tau immunohistochemistry

AD = Alzheimer's Disease; AGD = Argyrophilic Grain Disease; CBD = Corticobasal Degeneration; HS = Hippocampal Sclerosis; NFT = Neurofibrillary Tangle; LBD = Lewy Body Disease; PSP = Progressive Supranuclear Palsy; FTLD = Frontotemporal Lobar Degeneration; TDP- $43 =$ TAR DNA-Binding Protein 43; FUS = Fused in Sarcoma

The neuroanatomical structures used for determination of Braak neurofibrillary tangle staging are noted in the first two columns in the top half of the table. Other evaluated neuroanatomical structures are noted in the bottom half of the table. The columns to the right of the double lines show the distribution of neurofibrillary tangle pathology for each patient. Each patient's primary and contributing autopsy diagnoses and Braak staging of neurofibrillary tangle pathology are noted at the top of each column. The orange highlighting indicates locations that were evaluated with tau (CP-13 antibody) immunohistochemistry. Each "X" indicates a location where neurofibrillary tangles were documented by the pathologist.

Supplementary Tables 2-21: Distribution of non-neurofibrillary tangle tau pathology on tau immunohistochemistry

GCI = Glial Cytoplasmic Inclusions; NCI = Neuronal Cytoplasmic Inclusions; NFT = Neurofibrillary Tangle

Each patient's primary and contributing autopsy diagnoses and Braak staging of neurofibrillary tangle pathology are noted at the top of each table. Incidental non-Alzheimer tau pathology and the types of neuronal and glial cytoplasmic inclusions present are noted below the primary and contributing autopsy pathology. The orange highlighting indicates locations that were evaluated with tau (CP-13 antibody) immunohistochemistry. Each "X" indicates a location were non-neurofibrillary tangle tau pathology was documented by the pathologist.

Supplementary Figures

Supplementary Figure 1: FTP-PET SUVR and W-score map images in patients with Alzheimer's disease autopsy diagnosis

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SUVR and W-map images are shown for patients with primary Alzheimer's disease autopsy diagnosis. W-maps highlight areas of increased tracer retention compared to cognitively normal, amyloid-negative controls, adjusting for age as a covariate. Patients with primary Alzheimer's disease pathology had high FTP uptake, and SUVR and W-map thresholds were chosen to highlight the full range of tracer retention in these patients.

Supplementary Figure 2: FTP-PET SUVR and W-score map images in patients with autopsy diagnoses of non-Alzheimer tauopathies, FTLD-TDP, and FTLD-FUS (See next page)

SUVR and W-map images are shown for patients with primary autopsy diagnoses of non-Alzheimer tauopathies, FTLD-TDP, and FTLD-FUS. These patients had lower FTP uptake than patients with primary Alzheimer's disease autopsy diagnosis, and lower SUVR and Wmap thresholds needed to be used to highlight the areas of tracer retention in these patients. The W-map upper threshold ($W > 3.10$) is the same as the lower threshold used in patients with primary Alzheimer's disease pathology. AD = Alzheimer's disease; AGD = Argyrophilic Grain Disease; CBD = Corticobasal Degeneration; HS = Hippocampal Sclerosis; PSP = Progressive Supranuclear Palsy.

Supplementary Figure 3: FTP-PET SUVR quantification at precentral gyrus,

postcentral gyrus, and subcortical regions of interest with partial volume corrected data

(See next page)

SUVR quantification, corrected for partial volume effects, was performed at precentral gyrus, postcentral gyrus, putamen, globus pallidus, subthalamic nucleus, substantia nigra, and dentate nucleus regions of interest. Each patient is represented by a single point and coded by time from PET-to-autopsy (shape) and primary neuropathological diagnosis (X-axis). The dotted line represents the threshold for significance, which is calculated from the mean SUVR plus two standard deviations for the young, cognitively normal (CN), non-autopsy controls. Points crossing the significance threshold are highlighted with a black halo. Please note that the range of SUVR values is different for the partial volume corrected data compared to the uncorrected data.

Supplementary Figure 4: FTP-PET SUVR quantification of Braak stage regions of

interest with partial volume corrected data

SUVR quantification, corrected for partial volume effects, was performed at entorhinal cortex (Braak I), Braak III/IV, and Braak V/VI regions of interest. Each patient is represented by a single point and coded by their primary autopsy diagnosis (color), time from PET-to-autopsy (shape), and Braak neurofibrillary tangle stage (X-axis). The dotted line represents the threshold for significance, which is calculated from the mean SUVR plus two standard deviations for the young, cognitively normal (CN), non-autopsy controls. Points crossing the significance threshold are highlighted with a black halo. Please note that the range of SUVR values is different for the partial volume corrected data compared to the uncorrected data.

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