Hippocampal Subfield Volumetry: Differential Pattern of Atrophy in Different Forms of Genetic Frontotemporal Dementia

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Abstract.

\textbf{Background:} Frontotemporal dementia (FTD) is a heterogeneous neurodegenerative disorder, with a strong genetic component. Previous research has shown that medial temporal lobe atrophy is a common feature of FTD. However, no study has so far investigated the differential vulnerability of the hippocampal subfields in FTD.

\textbf{Objectives:} We aimed to investigate hippocampal subfield volumes in genetic FTD.

\textbf{Methods:} We investigated hippocampal subfield volumes in a cohort of 75 patients with genetic FTD (age: mean (standard deviation) 59.3 (7.7) years; disease duration: 5.1 (3.4) years; 29 with MAPT, 28 with C9orf72, and 18 with GRN mutations) compared with 97 age-matched controls (age: 62.1 (11.1) years). We performed a segmentation of their volumetric T1-weighted MRI scans to extract hippocampal subfields volumes. Left and right volumes were summed and corrected for total intracranial volumes.

\textbf{Results:} All three groups had smaller hippocampi than controls. The MAPT group had the most atrophic hippocampi, with the subfields showing the largest difference from controls being CA1-4 (24–27%, p < 0.0005). For C9orf72, the CA4, CA1, and dentate gyrus regions (8–11%, p < 0.0005), and for GRN the presubiculum and subiculum (10–14%, p < 0.0005) showed the largest differences from controls.

\textbf{Conclusions:} The hippocampus was affected in all mutation types but a different pattern of subfield involvement was found in the three genetic groups, consistent with differential cortical-subcortical network vulnerability.

Keywords: Genetic frontotemporal dementia, hippocampal subfields, magnetic resonance imaging, volumetry

INTRODUCTION

Frontotemporal dementia (FTD) is a clinically, pathologically, and genetically heterogeneous neurodegenerative disorder. Around a third of patients with FTD have an autosomal dominant mutation in one of three genes: microtubule-associated protein tau (MAPT), progranulin (GRN), and chromosome 9 open reading frame 72 (C9orf72) [1]. Although traditionally described as characteristic of Alzheimer’s disease, medial temporal lobe atrophy is commonly seen in FTD [2] with the hippocampus...
often strikingly affected, particularly in carriers of mutations in the MAPT gene [3, 4], where volume loss occurs 15 years before expected onset [5], and there is a faster rate of atrophy compared with other genetic forms of FTD [6, 7].

The hippocampus is composed of different cytoarchitectonic subfields, which have specialized functions and distinctive connections [8, 9]. Recently, advanced parcellation methods based on atlases built from ultra-high resolution scans of histology sections have led to the development of post-processing techniques of high-resolution magnetic resonance (MR) scans that allow visualization and measurement of the hippocampal subfields in vivo [10]. Given the recent availability of this method, the differential vulnerability of the hippocampal subfields across the genetic forms of FTD has so far not been investigated. This study aimed to look into this further with the hypothesis that the three genetic groups would have different patterns of subfield involvement.

### METHODS

We reviewed the UCL Dementia Research Centre FTD database to identify all patients who were symptomatic carriers of a mutation in the MAPT, GRN, or C9orf72 genes and who had also undergone a volumetric T1-weighted MR scan. 75 patients were identified: 29 MAPT (28 with behavioral variant FTD, bvFTD [11], and one with progressive nonfluent aphasia, PNFA [12]), 28 C9orf72 (24 bvFTD, 2 PNFA, 2 FTD with associated motor neuron disease, FTD-MND), and 18 GRN (11 bvFTD, 5 PNFA, and 2 primary progressive aphasia not otherwise specified, PPA-NOS [13]). 97 cognitively normal subjects, with a similar age to the patients and with a usable volumetric T1-weighted MRI, were identified as controls.

The study was approved by the local ethics committee and written informed consent was obtained from all participants. The study was conducted in accordance with the Helsinki Declaration of 1975.

MRIs were acquired from 1993 to 2017 with scanners from three different manufacturers: 69 on 1.5T Signa MRI scanner (GE Medical systems, Milwau-kee, WI, TR = 12 ms, TI = 650 ms, TE = 5 ms, acquisition matrix = 256 × 256, spatial resolution = 1.5 mm), 85 on 3T Trio MRI scanner (Siemens, Erlangen, Germany, TR = 2000 ms, TI = 850 ms, TE = 2.93 ms, acquisition matrix = 256 × 256, spatial resolution = 1.1 mm), and 18 on 3T Prisma MRI scanner (Siemens, Erlangen, Germany, TR = 2200 ms, TI = 900 ms, TE = 2.9 ms, acquisition matrix = 256 × 256, spatial resolution = 1.1 mm). We reviewed the MRIs to make sure we excluded individuals with moderate to severe vascular disease or space occupying lesions.

T1-weighted volumetric MRI scans were first bias field corrected and whole-brain parcellated using the geodesic information flow (GIF) algorithm [14], which is based on atlas propagation and label fusion. Volumes of the whole hippocampus and of 12 hippocampal subfields were subsequently segmented using a customised version of the module available in FreeSurfer 6.0 [10], to adapt the output of GIF to the FreeSurfer format. We focused on the following subregions: hippocampal tail, cornu ammonis 1 (CA1), CA2/3, CA4, subiculum, presubiculum, and the granule cell layer of the dentate gyrus (DG). We decided to exclude from the analysis the hippocampus–amygdala transition area, the parasebulum, the molecular layer of the hippocampus, the fimbria and the hippocampal fissure, as they were too small, not reliably delineated on T1-weighted images, or white matter tissue.

Left and right volumes were summed and corrected for total intracranial volumes (TIV). Volumes are expressed as a percentage of TIV, computed with SPM12 v6470 (Statistical Parametric Mapping, Wellcome Trust Centre for Neuroimaging, London, UK) running under Matlab R2014b (Math Works, Natick, MA, USA) [15]. All segmentations were visually checked for quality by an expert in hippocampal segmentation and none was excluded. We also investigated asymmetry by calculating an Asymmetry Index (AI), defined as the absolute difference between the left and right total hippocampal volumes in relation to the total bilateral volume: |(Left – Right)|(Left + Right). The volumetric differences between groups were computed as follow: (Mean of Controls – Mean of Genetic Group)/Mean of Controls*100.

Statistical analyses were performed on subfield volumes (as percentage of TIV) and AI in SPSS software (SPSS Inc., Chicago, IL, USA) v22.0, between control and patient groups, using the ANCOVA test adjusting for scanner type, gender and age. When comparing each volume and AI between different patient subgroups (in pairs), we also adjusted for disease duration. For the subfield analysis, results were corrected for multiple comparisons (Bonferroni’s correction), and we considered them significant at \( p < 0.007 \).
RESULTS

Demographic and clinical data are reported in Table 1. The mean disease duration for the whole FTD group at the time of the scan was 5.1 years (standard deviation 3.4) with an average age at onset at 54.2 (7.7). There was no significant difference in age between FTD and controls \((p = 0.052, \text{ t-test})\), or for scanner type \((p = 0.297, \text{ Chi square test})\), but there were more males in the FTD group than in the control group \((61\% \text{ versus } 44\%, p = 0.027, \text{ Chi square test})\). Across the different genetic FTD groups, there was no difference for scanner type nor gender \((p = 0.281 \text{ and } 0.322, \text{ Chi square test})\). There was also no difference across the different genetic FTD groups and controls \((p = 0.247 \text{ and } 0.070, \text{ Chi square test})\). However, there was a significant difference in disease duration \((p = 0.010, \text{ ANOVA})\), with C9orf72 having the longest and GRN the shortest duration, and in age \((p = 0.001, \text{ ANOVA})\), with MAPT being the youngest group.

The whole hippocampus was significantly smaller in all three genetic groups when compared to controls \((p < 0.0005, \text{ ANCOVA})\), with the MAPT group showing the highest difference in volume \((19\%; \text{ GRN: } 8\%; \text{ C9orf72: } 5\%)\) (Table 2). For all the subfields, MAPT showed a strong and highly significant difference from controls. In MAPT carriers, the most affected subfields were the CA regions \((27\%–24\%, p < 0.0005)\), followed by the dentate gyrus \((23\%, p < 0.0005)\), while the hippocampal tail was the least affected \((9\%, p < 0.0005)\). The subiculum and presubiculum were the most affected subfields in GRN carriers \((10\%\text{ and } 8\%, p < 0.0005)\), when for C9orf72 CA4 \((11\%)\), the dentate gyrus and CA1 \((8\%\text{ and } 0.0005)\) were the most affected (Figs. 1 and 2 and Table 2).

When directly comparing the three genetic subgroups, the MAPT group showed significantly lower volumes in the whole hippocampus than GRN \((13\%, p < 0.0005, \text{ ANCOVA})\) and C9orf72 \((16\%, p = 0.008)\) (Table 3). For the subfields, the MAPT group showed significantly smaller CA1, CA2/3, CA4, dentate gyrus \((20\%–29\% \text{ difference})\) and subiculum \((11\%)\) than GRN, and significantly smaller CA1, CA2/3, CA4 \((22\%–23\%)\) and dentate gyrus \((18\%)\) than C9orf72. No differences were found between the C9orf72 and GRN groups. Supplementary Table 2: overall volumes tend to be slightly smaller on 1.5T scanner than on 3T ones with the range of difference from 3–9%.

DISCUSSION

We used an advanced automated segmentation method based on atlases built from ultra-high resolution scans of histological sections to extract volumes of hippocampal subfields in a large cohort of patients with genetic FTD. Those with MAPT mutations were the most affected group overall, a finding in line with the literature \([3, 5, 7]\). However, we also showed a pattern of differential involvement: the MAPT group showed an impairment in the hippocampus proper (formed by the CA subfields), C9orf72 in the dentate gyrus and CA1/4, and GRN in the subiculum and presubiculum.

Anatomical and imaging studies of hippocampal subfield connectivity to other cortical and subcortical regions provide insight into the differential involvement of the FTD genetic disorders \([8, 9, 16]\). The MAPT group showed greater involvement of the anterior and central regions of the hippocampus compared with the hippocampal tail. These regions are

| Groups | n   | Gender, male | Age at scan (y) | Disease Duration (y) | Clinical Diagnosis   |
|--------|-----|--------------|-----------------|----------------------|---------------------|
| controls | 97  | 43 (44%)     | 62.1 (11.1)    | –                    | 28 bvFTD, 1 PNFA    |
| MAPT    | 29  | 17 (59%)     | 55.3 (7.9)     | 5.5 (3.3)            | 11 bvFTD, 5 PNFA, 2 PPA-NOS |
| GRN     | 18  | 9 (50%)      | 62.2 (6.4)     | 3.0 (2.6)            |                     |
| C9orf72 | 28  | 20 (71%)     | 61.5 (6.7)     | 6.0 (3.6)            | 24 bvFTD, 2 PNFA, 2 FTD-MND |
Fig. 1. Volume of the hippocampal subfields as a percentage of total intracranial volume in 97 controls and 75 patients with genetic FTD (29 MAPT, 18 GRN, and 28 C9orf72).

Fig. 2. Differential volumetric patterns for the three main genetic FTD forms when compared to controls. The most affected subfields for each gene are shown in color on a coronal representation of the hippocampus at the level of the body. CA, cornu ammonis; DG, granule cell layer of the dentate gyrus.

connected to the amygdala, nucleus accumbens, cingulate, and the medial prefrontal and orbitofrontal cortex [9, 16–18], a network linked to the regulation of emotions and goal-directed behaviour as part of the limbic system, previously described to be affected in MAPT mutations [6]. The GRN group showed the greatest involvement of the subiculum and presubiculum. A recent intrinsic connectivity study of the hippocampal subfields [19] showed that the subiculum connects to the lateral and medial parietal lobes and striatum as well as frontal regions, which have been described as key atrophic areas in GRN mutations [5, 20].

In the same study, CA4 and dentate gyrus (most affected in C9orf72) were connected with temporal and posterior cortical areas [19], similar to the early regions of involvement seen in this mutation group [5, 20]. This hypothesis of differential network involvement and our results are in line with pathological studies: tau deposition is extensively found in the hippocampus and other limbic structures in the early phases of FTD due to MAPT mutations [21]; dipeptide repeat proteins (DPRs), together or without TDP-43 deposition, are found in the CA subregions in C9orf72, and DPRs are also found in the cerebellum and the thalamus; while TDP-43 accumulates in the hippocampus and the cortex in GRN [22].

The GRN carriers were the most asymmetric group, consistent with previous literature highlighting the striking asymmetry in many cases with such mutations [6]. However, we also found that the MAPT and C9orf72 groups were significantly more asymmetric than controls albeit to a lesser extent than the GRN
Table 2

Volumetry of hippocampal subfields in 97 healthy non-carrier controls and 75 genetic FTD patients

| Structure          | Controls (97) | MAPT (29) | GRN (18) | C9orf72 (28) | MAPT vs Controls | GRN vs Controls | C9orf72 vs Controls |
|--------------------|---------------|-----------|----------|--------------|------------------|----------------|------------------|
|                    | Mean SD       | Mean SD   | Mean SD  | Mean SD      | p-value difference| p-value difference| p-value difference |
| Whole hippocampus  | 0.480 0.047   | 0.459 0.079| 0.443 0.068| 0.455 0.073 | <0.0005 19%      | <0.0005 8%       | <0.0005 5%        |
| CA1                | 0.089 0.010   | 0.067 0.017| 0.063 0.012| 0.061 0.012 | <0.0005 24%      | <0.0005 9%       | <0.0005 8%        |
| CA2/CA3            | 0.032 0.004   | 0.024 0.006| 0.030 0.012| 0.033 0.008 | <0.0005 29%      | 0.003 3%         | 0.042 5%          |
| CA4                | 0.036 0.004   | 0.026 0.005| 0.032 0.012| 0.033 0.008 | <0.0005 29%      | 0.003 3%         | 0.042 5%          |
| Dentate gyrus      | 0.035 0.005   | 0.026 0.006| 0.031 0.010| 0.028 0.010 | <0.0005 23%      | 0.003 3%         | 0.042 5%          |
| Subiculum          | 0.038 0.004   | 0.029 0.007| 0.035 0.012| 0.033 0.008 | <0.0005 23%      | 0.003 3%         | 0.042 5%          |
| Presubiculum       | 0.034 0.004   | 0.025 0.006| 0.030 0.010| 0.027 0.009 | <0.0005 23%      | 0.003 3%         | 0.042 5%          |
| Hippocampal tail   | 0.044 0.006   | 0.038 0.011| 0.038 0.010| 0.038 0.010 | <0.0005 23%      | 0.003 3%         | 0.042 5%          |

Values denote mean and standard deviation (SD) volumes as % of total intracranial volume (TIV) or difference (%). p-values denote significance on ANCOVA test. Bold represents a significant difference between groups after correcting for multiple comparisons.

While the majority of studies of MAPT and C9orf72 have shown no difference in symmetry at the level of individual hemispheres, there is commonly subtle asymmetry in individual lobes or subcortical structures which is lost at a hemispheric level—the extent of such differences or their biological basis has yet to be studied in depth. As previously reported in the literature [23], the asymmetry index in the control group is non-zero with the right hippocampus being bigger than the left. Larger studies will be required to understand the asymmetrical involvement of the individual subfields.

This study has a number of limitations. It includes different scanners (three manufacturers, two different magnetic fields: 1.5T and 3T) with slightly different MRI sequence types, and age and disease duration differences between the genetic groups. We took into account these variables and corrected for them in the statistical model, but this cannot completely remove some of the heterogeneity in this genetic dataset. Moreover, we used an automated method to extract the subfield volumes, which is not as accurate as their segmentation on brain tissue postmortem, nor as their manual segmentation on MR images. After reviewing the segmentations, we decided to exclude from the analysis the smallest subfields which were not reliably delineated on T1 MR imaging, particularly in this cohort who had atrophic hippocampi. However, nonetheless, the larger subfields are consistently and accurately defined using this methodology providing in vivo volumetry of hippocampal subfields, with the automated nature allowing analysis of large cohorts. Manual segmentation on these large datasets would be very time-consuming and labor-intensive, as it would require extensive anatomical knowledge and may take several hours per MR scan for even an expert manual rater.

The whole hippocampus is affected in all genetic forms of FTD [2, 5], as we have also shown here. The advantage of subfield delineation as we have done here (rather than focusing on the whole hippocampal volume) is the ability to better understand group differences and therefore distinguish between the different genetic forms and their intrinsic networks: limbic system in MAPT, temporal and posterior areas in C9orf72 and fronto-parietal-striatum in GRN. Being able to investigate the hippocampal subfields with their clearly different projections will be helpful in providing further insights in disentangling the differences among the genetic forms of FTD.

Future studies, using functional and diffusion MR imaging, will be needed to investigate the different...
Table 3
Comparisons of volumetry of the hippocampal subfields in 75 genetic FTD patients

| Structure              | MAPT versus GRN | MAPT versus C9orf72 | GRN versus C9orf72 |
|------------------------|-----------------|---------------------|-------------------|
| Whole hippocampus      | 0.001           | -13%                | 0.008             | -16%               | 0.764             | -3%               |
| CA1                    | <0.0005         | -20%                | <0.0005           | -22%               | 0.968             | -1%               |
| CA2/CA3                | <0.0005         | -27%                | <0.0005           | -23%               | 0.445             | 3%                |
| CA4                    | <0.0005         | -29%                | <0.0005           | -22%               | 0.131             | 6%                |
| Dentate gyrus          | <0.0005         | -24%                | 0.001             | -18%               | 0.394             | 5%                |
| Subiculum              | 0.005           | -11%                | 0.013             | -16%               | 0.669             | -4%               |
| Presubiculum           | 0.146           | 1%                  | 0.309             | -10%               | 0.193             | -11%              |
| Hippocampal tail       | 0.089           | -5%                 | 0.144             | -13%               | 0.807             | -8%               |

p-values denote significance on ANCOVA test. Bold represents a significant difference between groups after correcting for multiple comparisons.

connections of these hippocampal subfields in each genetic form of FTD in more detail. Moreover, it will be important to investigate subfield volumetry both at the presymptomatic stage (through cohorts such as the Genetic FTD Initiative [5]) and longitudinally, to understand the differential involvement of the hippocampus over the course of the disease.

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SUPPLEMENTARY MATERIAL

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