ORIGINAL RESEARCH

Plasma glial fibrillary acidic protein is raised in progranulin-associated frontotemporal dementia

Carolin Heller 1, Martha S Foiani 1, Katrina Moore 2, Rhian Convery 2, Martina Bocchetta 2, Mollie Neason 2, David M Cash 2, David Thomas 4, Caroline V Greaves 2, Ione OC Woollacott 2, Rachelle Shafei 2, John C Van Swieten 5, Raquel Sanchez-Valle 7, Barbara Borroni 8, Robert Laforce Jr 9, Mario Masellis 10, Maria Carmela Tartaglia 11, Caroline Graff 12, Daniela Galimberti 13, James B Rowe 15, Elizabeth Finger 16, Matthys Synofzik 17, Rik Vandenberge 19, Alexandre de Mendonca 20, Fabrizio Tagliavini 21, Isabel Santana 22, Simon Ducharme 23, Christopher R Butler 24, Alex Gerhard 25, Johannes Levin 26, Adrian Danek 27, Giovanni Frisoni 29, Sandro Sorbi 30, Markus Otto 31, Amanda J Heslegrave 1, Henrik Zetterberg 1, Jonathan D Rohrer 2, on behalf of GENFI

ABSTRACT

Background There are few validated fluid biomarkers in frontotemporal dementia (FTD). Glial fibrillary acidic protein (GFAP) is a measure of astrogliosis, a known pathological process of FTD, but has yet to be explored as potential biomarker.

Methods Plasma GFAP and neurofilament light chain (NFL) concentration were measured in 469 individuals enrolled in the Genetic FTD Initiative: 114 C9orf72 expansion carriers (74 presymptomatic, 40 symptomatic), 119 GRN mutation carriers (88 presymptomatic, 31 symptomatic), 53 MAPT mutation carriers (34 presymptomatic, 19 symptomatic) and 183 non-carrier controls. Biomarker measures were compared between groups using linear regression models adjusted for age and sex with family membership included as random effect. Participants underwent standardised clinical assessments including the Mini-Mental State Examination (MMSE), Frontotemporal Lobar Degeneration-Clinical Dementia Rating scale and MRI. Spearman’s correlation coefficient was used to investigate the relationship of plasma GFAP to clinical and imaging measures.

Results Plasma GFAP concentration was significantly increased in symptomatic GRN mutation carriers (adjusted mean difference from controls 192.3 pg/mL, 95% CI 126.5 to 445.6), but not in those with C9orf72 expansions (9.0, –61.3 to 54.6), MAPT mutations (12.7, –33.3 to 90.4) or the presymptomatic groups. GFAP concentration was significantly positively correlated with age in both controls and the majority of the disease groups, as well as with NFL concentration. In the presymptomatic period, higher GFAP concentrations were correlated with a lower cognitive score (MMSE) and lower brain volume, while in the symptomatic period, higher concentrations were associated with faster rates of atrophy in the temporal lobe.

Conclusions Raised GFAP concentrations appear to be unique to GRN-related FTD, with levels potentially increasing just prior to symptom onset, suggesting that GFAP may be an important marker of proximity to onset, and helpful for forthcoming therapeutic prevention trials.

INTRODUCTION

Frontotemporal dementia (FTD) is a progressive neurodegenerative condition with around a third of cases caused by an autosomal dominant gene mutation in progranulin (GRN), chromosome 9 open reading frame 72 (C9orf72) or microtubule-associated protein tau (MAPT).1 As clinical trials in genetic FTD are fast approaching, robust biomarkers that allow accurate measurement of disease onset and progression are becoming increasingly important. In particular, many trials will focus on the presymptomatic stage of disease where neuropathological alterations are already present2–5 and yet few biomarkers have been shown to be abnormal in this phase.3–5

Cerebrospinal fluid (CSF) or plasma/serum progranulin levels in GRN mutation carriers6–6 and CSF (poly)GP dipeptide repeat concentrations in C9orf72 expansion carriers,7,8 are markers of specific protein abnormalities in genetic FTD, but both are abnormal from early in the presymptomatic period (and potentially from birth). In contrast, neurofilament light chain (NFL) is a marker of neuronal death and axonal degeneration (measurable in CSF9,10 as well as both plasma11 and serum12,13) that is not specific to FTD14 and has only been shown to be abnormal in the very late presymptomatic period prior to conversion to the symptomatic phase.5 Glial fibrillary acidic protein (GFAP) is a marker of astrogliosis, the abnormal proliferation of astrocytes due to neuronal damage15 and has previously been shown to be increased in frontal cortical tissue in FTD,16 and raised in both the CSF and serum of patients with symptomatic FTD.17–19 However, it has yet to be
Table 1: Demographic, cognitive and biomarker data from study participants

<table>
<thead>
<tr>
<th></th>
<th>Controls</th>
<th>Presymptomatic mutation carriers</th>
<th>Symptomatic mutation carriers</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>C9orf72</td>
<td>GRN</td>
</tr>
<tr>
<td>Number of participants</td>
<td>183</td>
<td>74</td>
<td>88</td>
</tr>
<tr>
<td>Sex: number male (%)</td>
<td>81 (44.3)</td>
<td>29 (39.2)</td>
<td>34</td>
</tr>
<tr>
<td>Median (IQR) age (years)</td>
<td>43.8</td>
<td>44.1</td>
<td>42.4</td>
</tr>
<tr>
<td>Mean (range) age at onset (years)</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>Median (IQR) disease duration (years)</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>Diagnosis</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>Median (range) MMSE</td>
<td>30 (26–30)</td>
<td>30 (25–30)</td>
<td>30 (26–30)</td>
</tr>
<tr>
<td>Median (range) FTLD-CDR-SOB</td>
<td>0.0 (0–3.0)</td>
<td>0.0 (0.0–3.0)</td>
<td>0.0 (0.0–2.5)</td>
</tr>
<tr>
<td>Median (IQR) plasma NfL (pg/mL)</td>
<td>9.3 (6.8–13.0)</td>
<td>11.3 (8.3–17.0)</td>
<td>9.2 (7.0–12.8)</td>
</tr>
<tr>
<td>Median (IQR) plasma GFAP (pg/mL)</td>
<td>105.8 (80.4–146.1)</td>
<td>116.1 (88.3–180.0)</td>
<td>113.4 (80.5–168.1)</td>
</tr>
</tbody>
</table>

For sex, age, MMSE and FTLD-CDR-SOB, significant differences are shown at p<0.05:
* Compared with controls.
† In C9orf72 group between symptomatic and presymptomatic carriers.
‡ In GRN group between symptomatic and presymptomatic carriers.
§ In MAPT group between symptomatic and presymptomatic carriers.

T1-weighted MRI of the brain: 432 scans were available for cross-sectional analysis, of which a subgroup of 243 participants had a follow-up scan (on the same scanner) for analysis (mean (SD) interval 1.12 (0.29) years between baseline and follow-up). Volumetric measures of whole brain and cortical regions were calculated using a previously described method that uses the geodesic information flow (GIF) algorithm, which is based on atlas propagation and label fusion (online supplementary table 1). An annualised longitudinal rate of atrophy was found by calculating the difference in each specific measure between the baseline and longitudinal scan and expressing it as a percentage of the baseline volume over 1 year (online supplementary table 2).

METHODS

Participants

Participants were recruited from GENFI, a natural history study of genetic FTD involving 23 research centres across Europe and Canada (www.genfi.org.uk) involving symptomatic carriers of mutations in GRN, MAPT or C9orf72, and those at risk of carrying a mutation because a first-degree relative was a known symptomatic carrier. Four hundred sixty-nine consecutively recruited individuals from the GENFI study were included: 114 C9orf72 expansion carriers (74 presymptomatic, 40 symptomatic), 119 GRN mutation carriers (88 presymptomatic, 31 symptomatic), 53 MAPT mutation carriers (34 presymptomatic, 19 symptomatic) and 183 non-carriers who acted as a control group. Demographic information is shown in table 1: age and sex differed significantly between groups. All people in the study underwent a clinical assessment consisting of a medical history with the participant and informant, and physical examination, with symptomatic status diagnosed by a clinician who was an expert in the FTD field (specific diagnoses are shown in table 1). All participants underwent a standardised examination including the Mini-Mental State Examination (MMSE) and the Frontotemporal Lobar Degeneration—Clinical Dementia Rating scale (FTLD-CDR). Participants also performed three-dimensional exploration using ultrasonic blood-based assays in genetic FTD mutation carriers.

In this study, we aimed to investigate within the Genetic FTD Initiative (GENFI) cohort whether plasma GFAP was abnormal in each of the different genetic FTD groups during the symptomatic period, and whether we could detect any presymptomatic changes. We also aimed to explore the relationship of GFAP with plasma NfL, cognitive, and neuroimaging measures.

Measurement of plasma markers

Plasma was collected, processed and stored in aliquots at −80°C according to standardised procedures. Samples were measured using the multiplex Neurology 4-Plex A kit (102153, Quanterix, Lexington, USA) on the SIMOA HD-1 Analyzer following manufacturer’s instructions. The lower limit of detection of the assay for GFAP and NfL were 0.221 and 0.104 pg/mL, respectively. Measurements were carried out at the same study site on consecutive days and the operator was blinded to all clinical information, including genetic status. To keep sample processing and plating consistent, plasma samples were thawed at room temperature for 2 hours and subsequently centrifuged at 10,000g for 5 min; 150 µL samples were aliquoted in a 96-well plate (Quanterix) and frozen at −80°C until analysis. Quality control samples had a mean intra- and interassay coefficient of variation of <10%.

Statistical analysis

Fisher’s exact test was used to compare sex frequencies between groups. Distributions for demographic and biomarker data
were investigated graphically using histograms and quantile-quantile plots and tested for normality using the Shapiro-Wilk test. As demographic data did not follow a normal distribution, group differences for age at sample collection and FTLD-CDR-Sum Of Boxes were compared using the Kruskal-Wallis test. A linear regression adjusting for age was used to compare MMSE scores between groups. The primary analysis in the study was to investigate whether there were any differences in plasma GFAP concentration from controls in the different genetic mutation groups both symptomatically and presymptomatically, as well as between genetic groups. As biomarker values were not normally distributed, group means were compared by performing a linear mixed regression model with 95% bias-corrected bootstrapped CIs with 2000 repetitions in STATA (V.14; StataCorp, College Station, Texas, USA), adjusting for age and sex with family membership included as a random effect. Diagnostic performance of GFAP was assessed by areas under the curve (AUC) obtained by receiver operating characteristic (ROC) analyses, with optimal cut-off levels at the highest Youden’s index (sensitivity + specificity -1) using GraphPad Prism (V6; GraphPad Software, San Diego, California, USA). In order to investigate the relationship of GFAP concentration to demographic, cognitive and imaging measures as well as NfL concentrations, Spearman’s correlation coefficient was used.

RESULTS
Plasma GFAP concentration
Plasma GFAP concentration was significantly higher in the symptomatic GRN mutation carriers compared with controls (adjusted mean difference 192.3 pg/mL, 95% CI 126.3 to 445.6), but not in either the symptomatic C9orf72 (9.0, −61.3 to 54.6) or MAPT (12.7, −33.3 to 90.4) groups (figure 1, tables 1 and 2). Within the symptomatic groups, concentrations in GRN were significantly higher than both C9orf72 (183.3, 106.1 to 427.2) and MAPT (179.6, 99.8 to 348.1) mutation carriers. A ROC curve analysis measuring the ability of GFAP to distinguish symptomatic GRN mutation carriers from controls showed a sensitivity of 90.3% and specificity of 82.0% with a cut-off point of 163.2 pg/mL and an AUC of 0.90. For distinguishing symptomatic GRN mutation carriers from C9orf72 mutation carriers there was a sensitivity of 71.0% and specificity of 70.0% with a cut-off point of 226.2 pg/mL and an AUC of 0.74, while for distinguishing symptomatic GRN mutation carriers from MAPT mutation carriers there was a sensitivity of 79.0% and specificity of 77.4% with a cut-off point of 209.1 pg/mL and an AUC of 0.80 (online supplementary figure 1).

In the presymptomatic groups, concentrations were not significantly increased in any of the groups compared with controls: GRN (14.2, −2.4 to 38.3), C9orf72 (21.1, −18.8 to 66.5), MAPT (−7.0, −61.8 to 7.8) (figure 1, tables 1 and 2). There were also no differences across the presymptomatic groups.

Comparing symptomatic and presymptomatic carriers, a significantly higher concentration was also seen in the symptomatic versus the presymptomatic GRN mutation carriers (178.1, 114.3 to 365.2), but not in the other groups (figure 1, tables 1 and 2).

Correlation with age
GFAP concentration was significantly correlated with age at sample collection in controls (r=0.53, p<0.001), presymptomatic mutation carriers (all groups combined: r=0.53, p<0.001; GRN: r=0.58, p<0.001; C9orf72: r=0.50, p<0.001; MAPT: r=0.36, p=0.036) and symptomatic mutation carriers for all genetic groups together (r=0.38, p<0.001) and the GRN group alone (r=0.65, p<0.001) (figure 2). No significant correlation was seen for the symptomatic C9orf72 (r=0.27, p=0.088) or MAPT mutation carriers (r=0.00, p=0.989).

Correlation with plasma NfL
Plasma NfL was increased in all three symptomatic groups compared with controls (figure 1, tables 1 and 3): GRN mutation carriers (adjusted mean difference 70.5 pg/mL, 95% CI 51.6 to 92.6), C9orf72 mutation carriers (29.7, 18.7 to 47.5) and MAPT mutation carriers (12.6, 3.3 to 26.1). Within the symptomatic groups, concentrations in GRN were significantly higher than both C9orf72 (40.7, 16.5 to 62.2) and MAPT (57.9, 36.8 to 265.2) mutation carriers from controls showed a sensitivity of 90.3% and specificity of 82.0% with a cut-off point of 163.2 pg/mL and an AUC of 0.90. For distinguishing symptomatic GRN mutation carriers from C9orf72 mutation carriers there was a sensitivity of 71.0% and specificity of 70.0% with a cut-off point of 226.2 pg/mL and an AUC of 0.74, while for distinguishing symptomatic GRN mutation carriers from MAPT mutation carriers there was a sensitivity of 79.0% and specificity of 77.4% with a cut-off point of 209.1 pg/mL and an AUC of 0.80 (online supplementary figure 1).

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Comparing symptomatic and presymptomatic carriers, a significantly higher concentration was also seen in the symptomatic versus the presymptomatic GRN mutation carriers (178.1, 114.3 to 365.2), but not in the other groups (figure 1, tables 1 and 2).
to 81.5) mutation carriers, and C9orf72 mutation carriers were higher than MAPT mutation carriers (17.2, 2.9 to 35.7). Concentration was also increased in presymptomatic C9orf72 mutation carriers compared with controls (9.0, 1.3 to 26.8), but not in the GRN or MAPT presymptomatic groups (figure 1, tables 1 and 3). Comparing symptomatic and presymptomatic carriers, a significantly higher concentration was also seen in the symptomatic versus the presymptomatic mutation carriers in each of the groups (figure 1, tables 1 and 3): GRN mutation carriers (70.5, 52.5 to 92.2), C9orf72 mutation carriers (20.7, 3.2 to 36.1) and MAPT mutation carriers (11.7, 0.8 to 23.4).

Plasma GFAP and NfL concentrations were significantly correlated in controls ($r=0.66$, $p<0.001$), presymptomatic mutation carriers (GRN: $r=0.66$, $p<0.001$; C9orf72: $r=0.75$, $p<0.001$; MAPT: $r=0.41$, $p=0.017$) and symptomatic mutation carriers (GRN: $r=0.38$, $p=0.036$; C9orf72: $r=0.57$, $p<0.001$; MAPT: $r=0.76$, $p<0.001$).

**Correlation with cognitive measures**

A significant negative correlation between GFAP concentrations and MMSE was seen in the presymptomatic GRN ($r=−0.24$, $p=0.033$) and C9orf72 ($r=−0.40$, $p<0.001$) but not MAPT ($r=0.05$, $p=0.801$) mutation carriers. No significant correlation was seen during the symptomatic period in any of the genetic groups (GRN: $r=−0.29$, $p=0.153$; C9orf72: $r=−0.24$, $p=0.146$; MAPT: $r=−0.48$, $p=0.080$).

No significant correlations were seen between GFAP concentration and FTLD-CDR sum of boxes score in either the presymptomatic or symptomatic period in any group: GRN: $r=−0.04$, $p=0.768$ presymptomatic, $r=0.18$, $p=0.409$ symptomatic; C9orf72: $r=−0.17$, $p=0.234$ presymptomatic, $r=0.21$, $p=0.321$ symptomatic; MAPT: $r=−0.17$, $p=0.446$ presymptomatic, $r=0.14$, $p=0.736$ symptomatic.

**Correlation with cross-sectional imaging data**

A significant negative correlation was seen between GFAP concentrations and both GRN and C9orf72 presymptomatic carrier brain volumes for frontal cortex ($r=−0.23$, $p=0.039$; $r=−0.35$, $p=0.002$), temporal cortex ($r=−0.35$, $p=0.001$; $r=−0.27$, $p=0.024$), cingulate cortex ($r=−0.24$, $p=0.027$; $r=−0.44$, $p<0.001$) and insular cortex ($r=−0.27$, $p=0.016$; $r=−0.26$, $p=0.029$) as well as whole brain ($r=−0.45$, $p<0.001$) and parietal cortex ($r=−0.33$, $p=0.005$) for the C9orf72 group (online supplementary table 3). No significant correlations were seen in the presymptomatic MAPT mutation carrier group or any of the symptomatic genetic groups.

**Correlation with longitudinal imaging data**

No significant positive correlation of GFAP concentration with longitudinal rates of atrophy were seen in any of the groups except for in the temporal cortex of symptomatic GRN mutation carriers ($r=0.66$, $p=0.010$) (online supplementary table 4). However, within the same symptomatic GRN group there was also a trend in relationship between GFAP concentration and atrophy rates in the cingulate cortex ($r=0.55$, $p=0.052$).

**DISCUSSION**

In this study, we found that plasma GFAP concentration was significantly increased in genetic FTD but only in GRN mutation carriers, and not in those with C9orf72 expansions or mutations.

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**Table 2** Adjusted mean differences in plasma GFAP concentrations between groups with 95% bias-corrected bootstrap CIs

<table>
<thead>
<tr>
<th>GFAP</th>
<th>C9orf72 PS</th>
<th>C9orf72 S</th>
<th>GRN PS</th>
<th>GRN S</th>
<th>MAPT PS</th>
<th>MAPT S</th>
</tr>
</thead>
<tbody>
<tr>
<td>Controls</td>
<td>21.1 (−18.8 to 66.5)</td>
<td>9.0 (−61.3 to 54.6)</td>
<td>14.2 (−2.4 to 38.3)</td>
<td>192.3** (126.5 to 445.6)</td>
<td>−7.0 (−61.8 to 7.8)</td>
<td>12.7 (−33.3 to 90.4)</td>
</tr>
<tr>
<td>C9orf72 PS</td>
<td>12.1 (−61.4 to 85.1)</td>
<td>−6.9 (−51.0 to 43.0)</td>
<td>171.2** (88.5 to 433.7)</td>
<td>−28.1 (−83.3 to 8.0)</td>
<td>8.4 (−87.5 to 74.5)</td>
<td></td>
</tr>
<tr>
<td>C9orf72 S</td>
<td>−5.2 (−79.4 to 39.4)</td>
<td>183.3** (106.1 to 427.2)</td>
<td>178.1** (114.3 to 365.2)</td>
<td>−12.1 (−78.3 to 1.5)</td>
<td>1.5 (−75.4 to 49.1)</td>
<td></td>
</tr>
<tr>
<td>GRN PS</td>
<td>−199.3** (−439.2 to −124.9)</td>
<td>−179.6** (−348.1 to −99.8)</td>
<td>19.6 (−30.8 to 114.4)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GRN S</td>
<td>MAPT PS</td>
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</tbody>
</table>

Significant differences in bold: **$p<0.01$. GFAP, glial fibrillary acidic protein; PS, presymptomatic; S, symptomatic.
in the MAPT gene. In the presymptomatic period, higher concentrations were correlated with a lower cognitive score (MMSE) and lower brain volumes (in regions characteristically affected in FTD), potentially suggesting GFAP is increased in the late presymptomatic period. In the symptomatic period, higher concentrations were associated with faster rates of atrophy, suggesting GFAP levels are associated with disease intensity, and therefore progression and survival.

GFAP is a major constituent of the astrocytic cytoskeleton and its expression pattern is highly brain-enriched. Its levels increase following acute damage to astrocytes such as after a stroke or traumatic brain injury, but also in relation to more chronic insults, such as in neurodegeneration, when astrocytes become reactive, increasing in size and proliferating, a process called astrogliosis. In neurodegeneration, increased GFAP concentrations in biofluid have been reported in Alzheimer’s disease (in both CSF and serum) and amyotrophic lateral sclerosis. Previous studies in FTD have found increased CSF concentrations in symptomatic patients within combined clinical and genetic cohorts but have not previously found changes in blood, nor investigated individual genetic groups previously. Our results suggest that there are differential increases in FTD, with concentrations being higher in people with GRN mutations than in other groups. GRN encodes the progranulin protein, which is a secreted growth factor and known to be deficient in GRN-deficient mice. However, progranulin is also taken up by astrocytes for storage or transportation to the is also taken up by astrocytes for storage or transportation to the inflammatory phenotype of astrocytes. This suggests that deficiency of progranulin in astrocytes. This suggests that deficiency of progranulin in astrocytes may be less. Future work will be required to investigate this further.

It is well established that multiple biomarkers of neurodegeneration increase in concentration with age, attributed to the reduction of neural integrity in the ageing brain. CSF GFAP concentrations have previously been shown to increase as one gets older, with multiple studies showing proliferation of astrocytes, increased GFAP immunoreactivity and elevated levels of GFAP mRNA with age. Consistent with this, we also found a significant positive correlation of plasma GFAP concentration with age in the majority of the groups. This highlights the importance of adjusting plasma GFAP concentrations for age in statistical analyses: symptomatic mutation carriers in the C9orf72 and MAPT groups (as well as the GRN group) in this study showed increased levels of plasma GFAP compared with controls and their presymptomatic counterparts, but significance was lost once adjusting for age.

NFL, part of the axonal cytoskeleton, is released following cellular damage. A previous study has shown that NFL concentrations are increased in both the CSF and blood of symptomatic genetic FTD in all three mutation groups, C9orf72, GRN and MAPT. The results in this study replicate these findings in plasma, although we also found elevated levels in presymptomatic C9orf72 mutation carriers. In this latter group, NFL concentrations correlated negatively with MMSE (r = −0.33, p = 0.004; online supplementary table S) and with brain volumes (whole brain, r = −0.53, p < 0.001 and cortical regions: frontal, −0.51, < 0.001; temporal, −0.37, 0.001; parietal, −0.51, < 0.001; occipital, −0.33, 0.005; cingulate, −0.49, < 0.001; insula, −0.47, < 0.001: online supplementary tables 6 and 7), suggesting that NFL increases particularly towards the end of the presymptomatic period with increasing neurodegeneration. Although GRN NFL concentration was not significantly increased presymptomatically, a similar pattern of negative correlation with brain volumes was seen in this group (in whole brain and all cortical regions except the occipital lobe, r = −0.30 to −0.48, p ≤ 0.006). NFL and GFAP concentrations were significantly correlated in all groups including controls, although the correlation coefficient varied from 0.38 to 0.76. A similar correlation has been shown in CSF previously. As both increase with age (online supplementary table 8 for NFL correlations with age), the correlation is not unexpected, but other unexplained factors are likely to affect the different patterns within genetic FTD; interestingly,

### Table 3: Adjusted mean differences in plasma NfL concentrations between groups with 95% bias-corrected bootstrap CI

<table>
<thead>
<tr>
<th></th>
<th>C9orf72 PS</th>
<th>C9orf72 S</th>
<th>GRN PS</th>
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<th>MAPT PS</th>
<th>MAPT S</th>
</tr>
</thead>
<tbody>
<tr>
<td>Controls</td>
<td>9.0* (1.3 to 26.8)</td>
<td>29.7** (18.7 to 47.5)</td>
<td>0.0 (−3.1 to 3.3)</td>
<td>70.5** (51.6 to 92.6)</td>
<td>0.9 (−2.2 to 6.4)</td>
<td>12.6* (3.3 to 26.1)</td>
</tr>
<tr>
<td>C9orf72 PS</td>
<td>20.7* (3.2 to 36.1)</td>
<td>−9.0* (−27.5 to −1.4)</td>
<td>61.4** (37.7 to 82.7)</td>
<td>−8.1* (−27.0 to −0.6)</td>
<td>3.6 (−15.6 to 17.0)</td>
<td></td>
</tr>
<tr>
<td>C9orf72 S</td>
<td>−29.8** (−47.7 to −18.7)</td>
<td>40.7** (16.5 to 62.2)</td>
<td>−28.9** (−46.2 to −16.9)</td>
<td>−17.2* (−35.7 to −2.9)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>GRN PS</td>
<td>70.5** (52.5 to 92.2)</td>
<td>0.9 (−5.9 to 2.9)</td>
<td>12.6* (2.9 to 25.2)</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>GRN S</td>
<td>−69.6** (−91.7 to −50.6)</td>
<td>−57.9** (−81.5 to −36.8)</td>
<td>11.7* (0.8 to 23.4)</td>
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</tr>
</tbody>
</table>

Significant differences in bold: *p<0.05; **p<0.01.

NfL, neurofilament light chain; PS, presymptomatic; S, symptomatic.
the lowest correlation ($r=0.38$) was in the symptomatic GRN mutation carriers, suggesting that in this group astrogliosis and neurodegeneration are not so closely related.

Correlation of GFAP concentration with cognitive and imaging measures revealed a negative correlation, that is, higher concentration with a lower cognitive score and lower cross-sectional brain volumes in FTD-related regions in presymptomatic GRN mutation carriers. This suggests that GFAP levels start to increase as the brain starts to decrease in volume, and as cognition starts to become affected thus in the later stages of the presymptomatic period in proximity to symptom onset. This would be an important biomarker for GRN-related FTD, as an increase in concentration from baseline during the presymptomatic period would identify a time around the onset of neurodegeneration, and potentially a time when therapeutic intervention may be optimal. Despite the lack of a significant increase in concentration in C9orf72 mutation carriers, a similar pattern of negative correlation with cognition and brain imaging was seen in the presymptomatic period—it would be useful in future studies to investigate the subset of C9orf72 expansion carriers that have increased GFAP concentrations, and how they differ from those with a lower concentration. In particular, it would be helpful to compare carriers with and without concomitant ALS. We also assessed whether GFAP correlated with the rate of brain atrophy measured with longitudinal brain imaging and found a significant positive correlation only in the symptomatic mutation carriers measured with longitudinal brain imaging and ALS. We also assessed whether GFAP correlated with the rate of brain atrophy measured with longitudinal brain imaging and found a significant positive correlation only in the symptomatic GRN mutation carriers (the temporal lobe), implicating an association of GFAP levels with the intensity of the disease process, that is, how fast the disease is progressing. With longitudinal follow-up of participants, it would therefore be hypothesised that higher GFAP concentration would be associated with shorter survival in GRN-related FTD.

While the multicentre nature of the GENFI study allows collection of samples from a large genetic cohort of FTD worldwide, there remains a relatively small number of cases in each group (leading to low statistical power to detect differences), particularly in the symptomatic carriers, and replication in a larger dataset would be helpful. Due to the nature of the disease process, the mean age of the controls overall is lower compared with the symptomatic mutation carriers, but nonetheless the same results are found whether performing an age-adjusted comparison (as presented above in Plasma GFAP concentration) or when symptomatic mutation carriers are compared with an age-matched and gender-matched subset of older controls (see online supplementary figure 2). The advantage of studying levels in plasma is that blood is more easily accessible and a relatively cost-efficient way to access bodily fluids in comparison to performing a lumbar puncture; in this study, the use of the ultra-sensitive SMOA assay allowed detection at a level in blood that other assays do not. However, it will be important to study CSF levels in more detail in this group, as concentrations can differ between blood and CSF. Lastly, despite significant differences between the groups, there is a substantial overlap in concentrations between carriers and controls: longitudinal study of GFAP concentration over time, particularly in participants that convert from presymptomatic to symptomatic status, will therefore be important to truly evaluate whether changes do occur towards the end of the presymptomatic period and how levels change with progression of disease.

In summary, plasma GFAP levels appear to be uniquely increased in GRN mutation carriers in the current study, and importantly, concentrations may well be abnormal during the late presymptomatic period, suggesting that GFAP might act as marker of proximity to symptom onset.

Author affiliations
1UK Dementia Research Institute, Department of Neurodegenerative Disease, University College London, London, UK
2Dementia Research Centre, UCL Queen Square Institute of Neurology, London, UK
3Centre for Medical Image Computing, University College London, London, UK
4Neurological Academic Unit, UCL Queen Square Institute of Neurology, London, UK
5Department of Neurology, Erasmus Medical Centre, Rotterdam, The Netherlands
6Cognitive Disorders Unit, Department of Neurology, Donostia University Hospital, San Sebastian, País Vasco, Spain
7Alzheimer’s Disease and Other Cognitive Disorders Unit, Neurology Service, Hospital Clinic, Barcelona, Spain
8Centre for Neurodegenerative Disorders, Neurology Unit, Department of Clinical and Experimental Sciences, University of Brescia, Brescia, Italy
9Clinique Interdisciplinaire de Mémoire du CHU de Québec, Département des Sciences Neurologiques, Université Laval, Québec, Québec, Canada
10Sunnybrook Health Sciences Centre, Sunnybrook Research Institute, University of Toronto, Toronto, Ontario, Canada
11Tan Centre for Research in Neurodegenerative Disease, University of Toronto, Toronto, Ontario, Canada
12Department of Geriatric Medicine, Karolinska University Hospital-Huddinge, Stockholm, Sweden
13Department of Biomedical, Surgical and Dental Sciences, University of Milan, Centro Dino Ferrari, Milan, Italy
14Fondazione IRCCS Ca’ Granda, Ospedale Maggiore Policlinico, Milan, Italy
15Department of Clinical Neurosciences, University of Cambridge, Cambridge, UK
16Department of Clinical Neurological Sciences, University of Western Ontario, London, Ontario, Canada
17Department of Neurodegenerative Diseases, Hertie Institute for Clinical Brain Research, Tübingen, Germany
18German Center for Neurodegenerative Diseases (DZNE), University of Tübingen, Tübingen, Germany
19Laboratory for Cognitive Neurology, Department of Neurosciences, KU Leuven, Leuven, Belgium
20Faculty of Medicine, University of Lisbon, Lisbon, Portugal
21Fondazione Istituto di Ricoaro e Cura a Carattere Scientifico, Istituto Neurologico Carlo Besta, Milan, Italy
22Faculty of Medicine, University of Coimbra, Coimbra, Portugal
23Department of Neurology and Neurosurgery, McGill University, Montreal, Québec, Canada
24Department of Clinical Neurology, University of Oxford, Oxford, UK
25Faculty of Medical and Human Sciences, Institute of Brain, Behaviour and Mental Health, University of Manchester, Manchester, UK
26German Center for Neurodegenerative Diseases (DZNE), Munich, Germany
27Department of Neurology, Ludwig-Maximilians-University, Munich, Germany
28Munich Cluster for Systems Neurology (SysNeuro), Munich, Germany
29IRCCS San Giovanni di Dio Fatebenefratelli, Brescia, Italy
30Department of Neuroscience, Psychology, Drug Research, and Child Health, University of Florence, Florence, Italy
31Department of Neurology, University of Ulm, Ulm, Germany
32Department of Psychiatry and Neurochemistry, Sahlgrenska Academy at the University of Gothenburg, Mölndal, Sweden

Twitter Martha S Foiani @marthafoiani; David Thomas @dave_mri and Simon Ducharme @sducharme66

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Collaborators Martin N Rossor, Jason D Warren (Dementia Research Centre, Department of Neurodegenerative Disease, UCL Queen Square Institute of Neurology, London, UK); Nick C Fox (Dementia Research Centre, Department of Neurodegenerative Disease, UCL Queen Square Institute of Neurology, London, UK); Rita Guerreiro, Jose Bras (Center for Neurodegenerative Science, Van Andel Research Institute, Grand Rapids, Michigan, USA); Jennifer Nicholas (Department of Medical Statistics, London School of Hygiene and Tropical Medicine, London, UK); Simon Mead (MRC Prion Unit, Department of Neurodegenerative Disease, UCL Institute of Neurology, Queen Square, London, UK); Lize Jiskoot, Lieke Meeter, Jessica Panman, Janne Pempa (Department of Neurology, Erasmus Medical Centre, Rotterdam, Netherlands); Rick van Minkelen (Department of Clinical Genetics, Erasmus Medical Centre, Rotterdam, Netherlands); Yolanda Pijnepen (Amsterdam University Medical Centre, Amsterdam, The Netherlands); Myriam Barandiaran, Begoña Ingandio (Cognitive Disorders Unit, Department of Neurology, Donostia University Hospital, San Sebastian, Gipuzkoa, Spain; Neuroscience Area, Biodonostia Health Research Institute, San Sebastian, Gipuzkoa, Spain); Alazne Gablondo, Mikel Tainta, Maria de Arriba, Ana Gorosti, Miren Zulaica (Neuroscience Area, Biodonostia Health Research Institute, San Sebastian, Gipuzkoa, Spain); Begoña Ingandio, Mikel Tainta, Maria de Arriba, Ana Gorosti, Miren Zulaica (Neuroscience Area, Biodonostia Health Research Institute, San Sebastian, Gipuzkoa, Spain);
Neurodegeneration

Research Institute, San Sebastian, Gipuzkoa, Spain); Jorge Villanueva (OSATEK, University of Donostia, San Sebastian, Gipuzkoa, Spain); Zigor Diaz (1CITA Alzheimer, San Sebastian, Gipuzkoa, Spain); Sergi Borrego-Ecija, Jaume Olives, Albert Lladó, Mircea Balasa, Anna Antonell (Alzheimer’s disease and Other Cognitive Disorders Unit, Neurology Service, Hospital Clinic, Barcelona, Spain); Nuria Bargallo (Imaging Diagnostic Center, Hospital Clinic, Barcelona, Spain); Enric Premi, Laura Corredor, Stefano Gazzina, Alessandro Padovani (Center for Neurodegenerative Disorders, Neurology Unit, Department of Clinical and Experimental Sciences, University of Brescia, Brescia, Italy); Roberto Gasparotti (Neuroradiology Unit, University of Brescia, Brescia, Italy); Silvana Archetti (Biotechnology Laboratory, Department of Diagnostics, Spedali Civili Hospital, Brescia, Italy); Sandra Black, Sarah Mitchell (Sunnybrook Health Sciences Centre, Sunnybrook Research Institute, University of Toronto, Toronto, Canada); Katerina Rogovaya (Tan Centre for Excellence in Neurodegenerative Diseases, University of Toronto, Toronto, Canada); Morris Freedman (Baylor Research Institute, University of Texas, Houston, Texas); Ron Kerin (The University Health Network, Toronto Rehabilitation Institute, Toronto, Canada); David Tang-Wai (The University Health Network, Krembil Research Institute, Toronto, Canada); Linn Oj Jentoft (Department of Geriatric Medicine, University Hospital, Bergen, Norway); Camino Garcia (Department of Clinical Neurological Sciences, University of Western Ontario, London, Ontario, Canada); Robert Bartha (Department of Medical Biophysics, The University of Western Ontario, London, Ontario, Canada); Centre for Functional and Metabolic Mapping, Rotbers Research Institute, The University of Western Ontario, London, Ontario, Canada); Rosa Rademakers (Department of Neuroscience, Mayo Clinic, Jacksonville, Florida, USA); Carlo Wille (Department of Neurodegenerative Diseases, Hertie Institute for Clinical Brain Research, University of Tübingen, Tübingen, Germany); Hans-Otto Karmath (Division of Neurophysiology, Hertie-Institute for Clinical Brain Research and Center of Neurology, University of Tübingen, Tübingen, Germany); Benjamin Bender (Department of Diagnostic and Interventional Neuroradiology, University of Tübingen, Tübingen, Germany); Rose Bruyfts (Laboratory for Cognitive Neurology, Department of Neurosciences, KU Leuven, Leuven, Belgium); Philip Vandamme (Neurology Service, University Hospitals Leuven, Belgium); Laboratorium for Neurobiologiy, VIB-KU Leuven Centre for Brain Research, Leuven, Belgium); Mathieu Vandenbulcke (Geriatric Psychiatry Service, University Hospitals Leuven, Belgium); Neurophysiay, Department of Neurosciences, KU Leuven, Leuven, Belgium); Catarina B Ferreira (Laboratory of Neurosciences, Instituto de Medicina Molecular, University of Lisbon, Lisbon, Portugal); Gabriel Miltenberger (45Faculty of Medicine, University of Lisbon, Lisbon, Portugal); Carolina Maruta (Labaro of Language Research, Centro de Estudos Evas Moniz, Faculty of Medicine, University of Lisbon, Lisbon, Portugal); Ana Verde! (Department of Neurosciences and Mental Health, Centro Hospitalar Lisboa Norte - Hospital da Santa Maria & Faculty of Medicine, University of Lisbon, Portugal); José António da Silva (Centro de Neurociencias Nuclearas de Sao Caetano, Sao Caetano de Oeiras, Portugal); Ana Taipa (Neuropathology Unit and Department of Neurology, Centro Hospitalar do Porto - Hospital do Santo António, Oporto, Portugal); Paola Carropio, Giuseppe Di Fede, Giorgio Giaccone, Sara Prinzi, Veronica Redaeli, Giaccomia Rossi, Pietro Tiralbosi (Fondazione IRCCS Istituto Neurologico Carlo Besta, Milano, Italy); Diane Dunn, Maria Rosa Almeida, Maria Estela Casale, Faculty of Medicine, University of Coimbra, Coimbra, Portugal); Maria João Leitão (Centre of Neurosciences and Cell biology, Universidade de Coimbra, Coimbra, Portugal); Miguel Tabuas-Pereira, Beatriz Santiago (Neurology Department, Centro Hospitalar e Universitário de Coimbra, Coimbra, Portugal); Serge Gauthier (Alzheimer Disease Research Unit, McGill Centre for Studies in Aging, Department of Neurology & Neurosurgery, McGill University, Montreal, Quebec, Canada); Pedro Rosa-Neto (Translational Neuroimaging Laboratory, McGill Centre for Studies in Aging, Centre for Clinical Brain Research and Centre of Neorology, University of Ulm, Ulm); Luisa Benussi, Giuliano Bini, Roberta Ghidoni, Michaela Pivian (Instituto de Recouvo e Cura a Carattere Scientifico Istituto CenS Giovanni di Dio Fatebenefratelli, Brescia, Italy); Gemma Lombardi, Benedetta Naciunas, Camilla Ferrari, Valentina Besi (Department of Neuroscience, Psychology, Drug Research, and Child Health, University of Florence, Florence, Italy).

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ORCID iDs

Carolin Heller http://orcid.org/0000-0002-1934-6162

Martha S Fontai http://orcid.org/0000-0003-4157-2606

Katrina Moore https://orcid.org/0000-0002-4458-8390

Rhiannon Convey http://orcid.org/0000-0002-9477-1812

Martina Bocchetta http://orcid.org/0000-0003-1814-5024

Mollie Neason http://orcid.org/0000-0001-9419-7171

David Thomas https://orcid.org/0000-0003-4561-7427

Caroline V Greaves https://orcid.org/0000-0002-6646-1960

Ione OC Woolacott https://orcid.org/0000-0003-1166-6417

Rachelle Shafei https://orcid.org/0000-0002-4760-8684

John C Van Swieten http://orcid.org/0000-0001-6278-6844

Barbara Borroni http://orcid.org/0000-0001-9340-9814

James B Rowe http://orcid.org/0000-0001-7216-6879

Elizabeth Finger http://orcid.org/0000-0003-4864-7427

Markus Otto http://orcid.org/0000-0002-6647-5944

Jonathan D Rohrer https://orcid.org/0000-0002-6155-8417

REFERENCES


Neurodegeneration


