

Structural brain signature of FTLD driven by granulin mutation

Valentina Battistoni¹, Barbara Borroni², Giovanni Giulietti¹, Antonella Alberici², Enrico Premi², Carlo Cerini², Silvana Archetti³, Roberto Gasparotti⁴, Carlo Caltagirone^{5,6}, Alessandro Padovani², and Marco Bozzali¹

¹Neuroimaging Laboratory, Santa Lucia Foundation IRCCS, Rome, Italy, ²Centre for Ageing Brain and Neurodegenerative Disorder, Neurology Unit, University of Brescia, Brescia, Italy, ³III Laboratory of Biotechnology, Brescia Hospital, Brescia, Italy, ⁴Neuroradiology Unit, University of Brescia, Brescia, Italy,

⁵Department of Clinical and Behavioural Neurology, Santa Lucia Foundation IRCCS, Rome, Italy, ⁶Department of Neuroscience, University of Rome 'Tor Vergata', Rome, Italy

INTRODUCTION. The frontotemporal lobar degeneration (FTLD) spectrum is clinically characterized by behavioural symptoms, language impairment, and deficits of executive functions [1,2]. Over the last few years, a number of causative gene mutations have been identified in FTLD patients, and the *GRN Thr272fs* mutation has been identified as a major cause of FTLD [3]. Nonetheless, the molecular mechanisms that link together gene mutations, neurodegeneration and clinical features of FTLD still remain largely unclear. We have recently shown that, despite similar disease duration, FTLD patients carriers of *GRN Thr272fs* mutation exhibit a more severe pattern of brain abnormalities than those with sporadic FTLD [4]. One of missing elements in this complex picture is the potential role played by the white matter microstructure, which is already known to be altered in FTLD [5,6], and might represents the neuroanatomical substrate that links together GM loss and functional changes in broader networks. Aim of the current study was therefore to extend our previous investigation of FTLD patients (carriers and non carriers of *GRN Thr272fs mutation*) [4], and to assess using diffusion MRI the contribution of microscopic WM damage in accounting for the more severe clinical features observed as driven by *GRN Thr272fs mutation*.

METHODS. This study included the following participants: 6 FTLD patients carriers of *GRN Thr272fs* mutation [GRN+] (F/M=3/3, mean (SD) age= 62.2 (4.3) years); 17 FTLD patients non mutation carriers [GRN-] (F/M=5/12; mean (SD) age= 67.8 (6.9) years); 12 healthy elderly subjects [HS] (F/M=8/4, mean (SD) age=60.7 (9.5) years). All subjects underwent a genetic assessment, a neuropsychological evaluation and an MRI scanning at 1.5 T including: 1) Dual echo turbo spin echo (TSE); 2) 3D magnetization-prepared rapid gradient echo (MPRAGE) T1-weighted scan; 3) Diffusion weighted Spin-Echo Planar imaging (SE-EPI). MPRAGE data were processed using the VBM protocol in SPM8, including normalisation, segmentation and "modulation" to yield maps of GM volume in MNI space. GM maps were analyzed using a full factorial design (ANOVA) modelling the 3 groups. Different contrasts were tested to characterise the GM differences across groups. For every T-contrast, we applied family-wise error (FWE) correction for multiple comparisons, and we accepted as significant *P* values of less than 0.005 at cluster level. DWI data were processed to compute, for each subject, the diffusion tensor (DT), fractional anisotropy (FA) and mean diffusivity (MD) maps (using FSL, www.fmrib.ox.ac.uk/fsl). Probabilistic tractography (PICo, implemented in CAMINO, www.camino.org.uk) was used to reconstruct the frontal projections of the corpus callosum (CC1). Every subject's FA map was then warped to the FA template (JHU-ICBM-FA-2mm, available in FSL), using a nonlinear transformation (FSL-FNIRT) [7], that was also applied to the MD map and the CC1 tract map. These warped CC1 masks were averaged across all subjects to yield a customised template-mask of CC1 which was used to confine the voxel-wise group comparisons of FA and MD values to this anatomical region. Six contrasts, GRN+ vs GRN-, GRN+ vs HS and GRN- vs HS (all in both directions) were estimated. The resultant statistical maps were thresholded at *p* < 0.05, FWE corrected for multiple comparisons.

RESULTS. The VBM analysis revealed a widespread pattern of atrophy in both groups of patients with respect to elderly healthy subjects. In particular patients carriers of *GRN Thr272fs* mutation showed a left medial frontal area of GM atrophy compared to patients non mutation carrier (Figure 1). The voxel-wise group comparisons of FA and MD in the CC1 showed widespread areas of reduced FA and increased MD in CC1 of patients with respect to elderly healthy subjects. But, more interestingly, GRN+ patients compared to GRN- patients showed anterior regions of FA reduction and increased MD in CC1 (Figure1). **Post-hoc Analysis:** Given the anatomical proximity between the medial frontal cluster of reduced GM volume and CC1 (see Fig 1), we performed a post-hoc analysis investigating the association between the mean GM density (m-GM) of this cluster and FA and MD of CC1, voxel-wise.

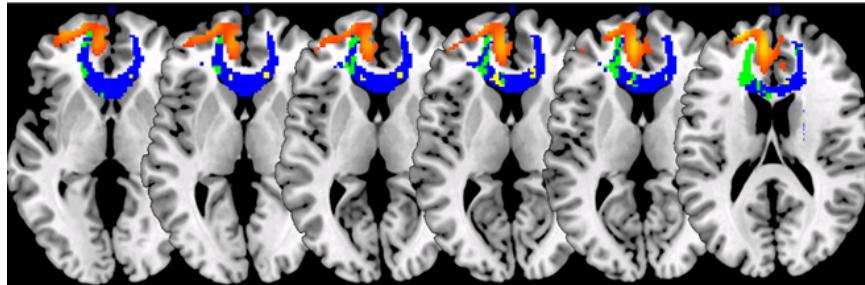


Fig 1. Region of GM atrophy (orange), areas of FA reduction (yellow) and increased MD (green) in CC1 in patients mutation carrier compared to patients non mutation carrier. The CC1 mask is shown in blue.

This analysis showed that m-GM was positively correlated with FA (fig2, in yellow), and negatively with MD, particularly in the left CC1 (fig.2 green regions), only for the group of GRN+ patients.

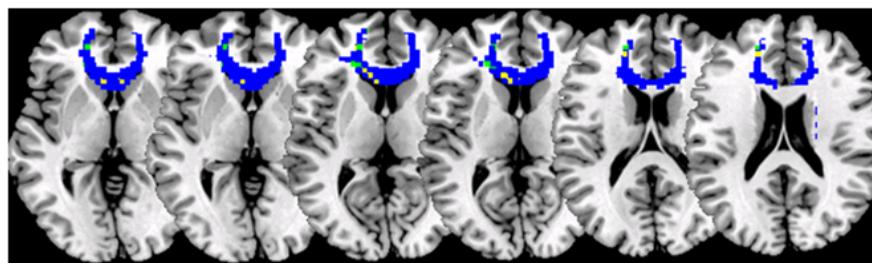


Fig 2. Areas of correlation to FA (yellow) and anticorrelation to MD (green), in correspondence to the cluster of GM, only for the group of GRN+ patients.

DISCUSSION. Our study confirms previous results [4] of more severe GM volume loss in patients with FTLD and the *GRN Thr272fs* mutation. Moreover, it indicates that GRN+ patients have also more severe WM damage in the anterior part of the CC with respect to GRN- patients, as demonstrated by the voxel-wise analysis of FA and MD. Finally, we have shown a correlation between GM atrophy of the medial frontal lobe and FA and MD of the adjacent WM. Although the correlation between WM and GM indices does not imply causality between the two events, it cannot be ruled out. We are in process of investigating the presence of correlations between these changes and clinical and neuropsychological scores.

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