Differential synaptic marker involvement in the different genetic forms of frontotemporal dementia

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INTRODUCTION

A third of frontotemporal dementia (FTD) is genetic with mutations in three genes accounting for most of the inheritance: C9orf72, GRN and MAPT.

Synaptic dysfunction is a common mechanism in all of them and the use of fluid biomarkers could be helpful to improve the diagnostic accuracy and useful as a readout of cellular dysfunction within therapeutic trials.

METHODS

In this study were included 193 CSF samples from the GENetic FTD Initiative (GENFI): 77 presymptomatic (31 C9orf72(PS C9), 23 GRN (PS GRN), 23 MAPT (PS MAPT)), 55 symptomatic mutation carriers (26 C9orf72 (symp C9), 17 GRN (symp GRN), 12 MAPT (symp MAPT)) and 61 mutation-negative controls (non-carriers). The methodology used was a microflow LC PRM-MS set-up targeting 15 synaptic proteins: 14-3-3 proteins (eta, zeta/delta and epsilon), AP-2 complex subunit beta, beta-synuclein, gamma-synuclein, complexin-2, neurogranin, neuronal pentraxin receptor (NPTXR), neuronal (NPTXI), neuronal pentraxin 2 pentraxin phosphatidylethanolamine-binding protein I (PEBP-I), rab GDP dissociation inhibitor α (rab GDI α), syntaxin-IB and syntaxin-7. Mutation carrier groups were compared to each other and to controls using a bootstrapped linear regression model, adjusting for age and sex.

CONCLUSION

Here we show a differential involvement of synaptic markers in the genetic forms of FTD. The impairment is seen particularly in those with MAPT mutations, with only the neuronal pentraxins affected in GRN and C9orf72 mutation carriers.





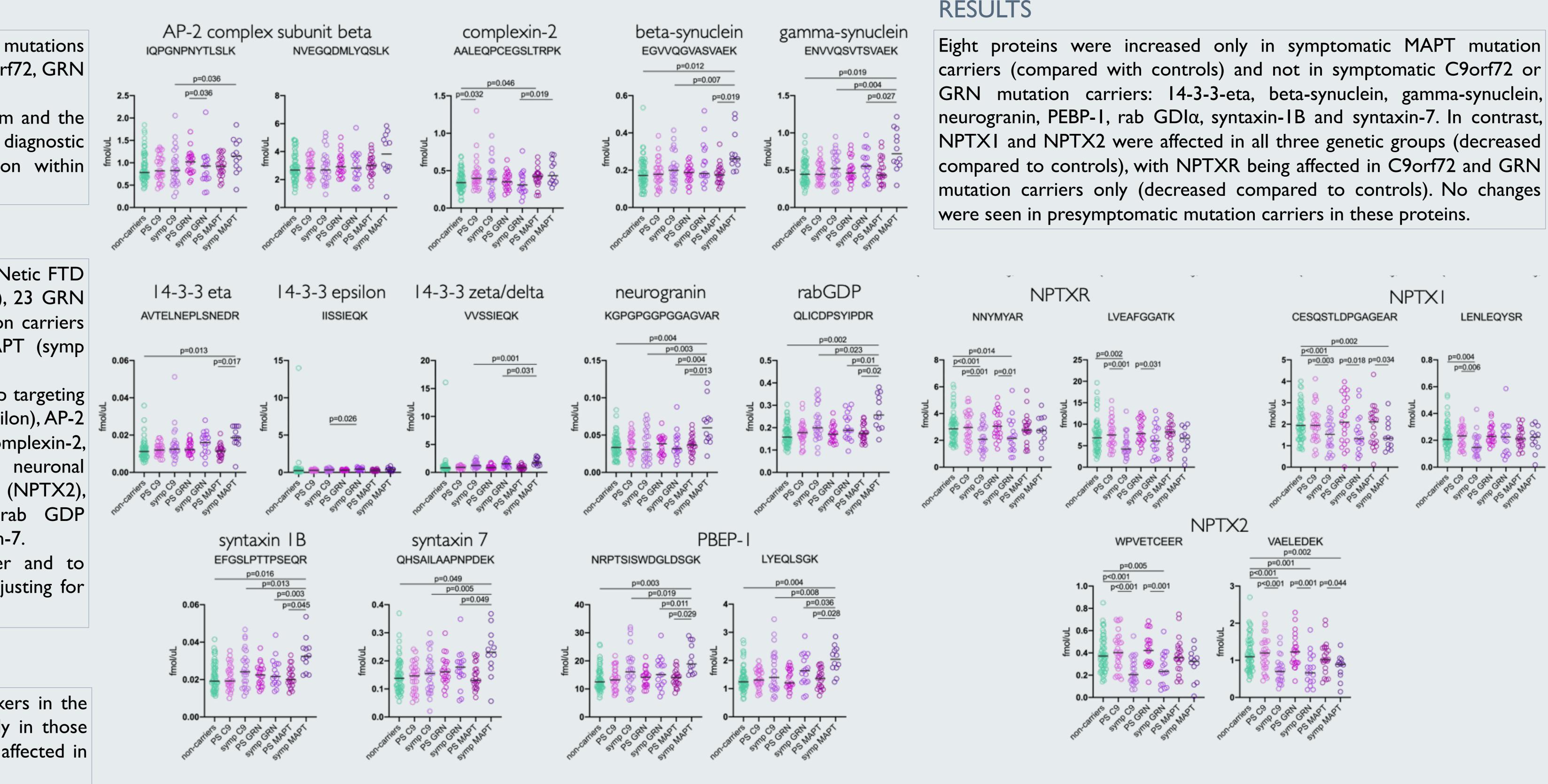


FIGURE. Levels of synaptic markers in CSF from the different genetic groups included in the study. Levels expressed in fmol/mL and p-value of each significant change indicated in each graph.

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