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Thursday

Profiling lipid metabolism alterations in genetic FTD within the GENFI cohort.

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State of the art
Although frontotemporal dementia (FTD) is a heterogeneous disease, lysosomal dysfunction and inflammation appear to be affected across all forms causing alterations on lipid metabolism. With the lack of fluid biomarkers specific for FTD we explored a panel of lipid metabolites in serum samples from the GENFI cohort.
Methodology
A total of 522 serum samples from GENFI were analysed using the Nightingale Blood Biomarker Analysis Service (Nightingale Health Ltd.). In this cross-sectional study we included 113 symptomatic FTD mutation carries (56 *C9orf72*, 40 *GRN*, 17 *MAPT*), 205 presymptomatic mutation carriers (93 *C9orf72*, 70 *GRN*, 42 *MAPT*) and 204 non-carrier family members. In total, 220 metabolites were analysed using a NMR based metabolomics technology. Bootstrapped regression analysis was performed to compare groups adjusting for age, sex, mutation carrier status and family membership.
Results
Total cholesterol levels were significantly increased in both symptomatic *C9orf72* expansion carriers ($p = 0.0499$) and symptomatic *MAPT* mutation carriers ($p = 0.005$) when compared to the control group. Total triglycerides were also increased in symptomatic *MAPT* mutation carriers when compared to controls ($p = 0.022$). In contrast, apolipoprotein A1 levels were decreased in all symptomatic groups (*C9orf72* $p = 0.004$, *GRN* $p = 0.032$, *MAPT* $p = 0.018$) when compared to controls.
Conclusion
Our initial results suggest alterations in lipid metabolism in the genetic forms of FTD. Further studies of lipid metabolites in genetic FTD are needed in order to show whether these could be promising candidates for diagnosis and monitoring within clinical trials.

Conflicts of interest

N/A