p-014

Thursday

MiRNA expression profile in genetic FTD

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State of The Art
MicroRNAs (miRNA) are regulatory non-coding RNA involved in several cellular processes; recently they gained interest since they appear to be altered in neurodegenerative diseases and therefore have great potential as biomarkers. The aim of this project was to evaluate the expression profile of miRNAs in FTD genetic cases.

Methodology
Patients from Genetic FTD Initiative (GENFI) were retrospectively included in the study. They comprised 10 *C9ORF72* expansion carriers, 10 *MAPT* and 9 *GRN* mutation carriers, and 9 non-carrier subjects.
RNA was extracted from peripheral blood mononuclear cells (PBMC). Real-Time PCR analysis was performed using TaqMan OpenArray technology, which enabled to detect 754 miRNAs simultaneously.

Results
Several miRNAs were altered in patients compared to controls. Two miRNA, hsa-miR-223# and hsa-miR-20b, were overexpressed in *C9ORF72* expansion carriers ($p<0.05$). A signature of six miRNA was found for *GRN* mutation carriers: hsa-miR-28-3p, hsa-miR-342-3p, hsa-miR-365, hsa-miR-576-5p and hsa-miR-642 were overexpressed, while hsa-miR-590-5p was downregulated ($p<0.04$). In MAPT group, nine miRNA were differentially expressed: hsa-miR-146a, hsa-miR-192, hsa-miR-25, hsa-miR-28, hsa-miR-28-3p, hsa-miR-30c, hsa-miR-339-5p, hsa-miR-576-3p were upregulated, while hsa-miR-532-3p was downregulated ($p<0.05$).

Conclusions
We showed that several miRNAs are upregulated in genetic FTD. These miRNAs have been previously involved in neuroinflammatory processes, suggesting a role of inflammation in FTD.
Expression profile of miRNA could be helpful in further elucidating neuropathological changes that take place in FTD brain. In this scenario, miRNAs have great potential as biomarkers and therapeutic targets.

Conflicts of interest

N/A