C9ORF72 gene expansion in a case of intellectual disability and late-onset neurodegeneration

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Background

The expansion of the hexanucleotide *GGGGCC* in the first intron of chromosome 9 open reading frame 72 (*C9ORF72*) is related to different clinical phenotypes including frontotemporal dementia (FTD), motor neuron disease (MND), and rarely psychiatric symptoms or movement disorders.

Case report



A 67 year-old woman with a history of mild mental retardation until adolescence presented a nine-month history of rapid motor and cognitive impairment. Her mother had the same phenotype, characterized by mental retardation and rapidly progressive dementia at age 60; an uncle had been treated for psychiatric disease and the grandfather had mental retardation.

•Neurological examination: emotional lability, anartria and spasticity of the four limbs.

•At brain CT-scan: diffuse cortical-subcortical atrophy.

•Cerebrospinal fluid examination showed low levels of Amyloid- β_1 -42 (284 pg/ml, n.v. >600) with normal Total Tau (160 pg/ml, n.v. <275) and Phosforylated-Tau (18 pg/ml n.v. <50).

•Molecular analysis of C9ORF72 revealed a pathogenetic expansion (> 45 GGGGCC repeats, cut-off 30 repeats).

Conclusion

Figure legend: Brain TC scan: atrophy and ventricles enlargement

Repeat-primed PCR results of the patient with hexanucleotide expansion showing the typical saw-tooth pattern.



Patients with *C9ORF72* expansion can present with variable clinical phenotypes. Intellectual disability in C9ORF72-mutated patients has been previously described only in two members of a single family subsequently presenting FTD. Our case further suggests a possible link between intellectual disability and *C9ORF72* gene mutation.

It could be useful to perform C9ORF72 analysis in patients affected by intellectual disability with familiar history of psychiatric disorders and/or FTD

The presence of the expanded hexanucleotide repeat and the number of repeat units in the longest allele was determined using previously reported methods for repeat-primed PCR and fluorescence-based fragment size analysis (Renton, 2011). Briefly, repeat-primed PCR was performed in a total reaction volume of 28 µl containing 150 ng genomic DNA, 1× FastStart PCR Master Mix (Roche Applied Science, Indianapolis, IN, USA), 3.5% DMSO, 1× Q solution (Quiagen, Valencia, CA) and 0.18 mM of deazaGTP (NEB, Ipswich, MA). Primer concentrations and sequences (chr9:27563580F and chr9:27563465R) were the same as previously reported (Renton, 2011). PCR products were run on an ABI® 3130 XL Genetic Analyzer (Applied Biosystems) and analyzed using GeneMapper®. Consistent with standards used in prior studies, a sample was considered to have a repeat expansion when assay replicates demonstrated >30 peaks and a decrementing saw-tooth pattern.

References

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