Intranuclear inclusions in neural cells with premutation alleles in fragile X associated tremor/ataxia syndrome

F. Tassone, R. J. Hagerman, D. Garcia-Arocena, E. W. Khandjian, C. M. Greco, P. J. Hagerman

MATERIALS AND METHODS

Clinical history
The individual studied was a carrier of an FMR1 premutation allele of 113 CGG repeats, and died of pneumonia at 70 years of age. Clinical involvements of this case have been already reported (case 1).

Tissue preparation
The samples from specific brain regions of this carrier that were used for the histological analysis were taken from the left cerebral hemisphere fixed in formalin. The postmortem intervals for the brains derived from the premutation carrier (aged 70 years) and from normal male control (aged 69 years) were 10 and 12 hours, respectively.

The presence of a large premutation allele, of the same size in all brain tissue regions analysed as well as in peripheral blood leucocytes, demonstrated both somatic stability in this size range and the association between FMR1 premutation and fragile X associated tremor/ataxia syndrome (FXTAS).

In the premutation carrier FMR1, mRNA levels were elevated in both peripheral blood leucocytes and in several brain regions, relative to normal controls.

Frequent intranuclear inclusions were present in ependymal and subependymal cells, and in the epithelial lining cells of the choroids plexus from a premutation carrier brain.

Intranuclear inclusions and clinical involvement in FXTAS were associated with the presence of an FMR1 premutation allele.

Neuropathology studies
Standard techniques, including haematoxylin and eosin staining and immunohistochemistry, were used for the neurohistological analysis. Details of the methodology were as described by Greco et al (2002).5

DNA analysis
Genomic DNA was isolated from peripheral blood leucocytes (5 ml of whole blood) before death, and from postmortem sections of about 500 mg of brain tissue using standard methods (Puregene Kit, Gentra, Minneapolis, USA). For Southern blot analysis, 5–10 µg of isolated DNA was digested with EcoRI and NruI and transferred to a charged nylon membrane using a vacuum transfer apparatus. Membranes were hybridised with the FMR1 genomic probe StB12.3 labelled with Dig-11-dUTP by PCR (PCR Dig Synthesis Kit, Roche Diagnostics, www.roche-diagnostics.us). Filters were exposed to x ray film for two hours. For PCR analysis, DNA was amplified using primers c and f.1 PCR products, separated on 6% denaturing polyacrylamide gels, were washed before detection of the FMR1 PCR products. Filters were exposed to x ray film for one hour.

FMR1 mRNA expression levels
Total RNA was isolated from peripheral blood leucocytes (approximately 3 ml) before death and from postmortem brain tissue using standard methods (Purescript, Gentra,
Minneapolis, USA). Reverse transcriptase reactions and QRT-PCR were carried out as described by Tassone et al (2000).12

**FMRP expression levels**

FMRP expression from peripheral blood leucocytes was determined by immunocytochemistry as the percentage of FMRP positive lymphocytes.13 14 FMRP expression levels in brain samples were determined by Western blot analysis according to standard methods. After immunoblot analysis, the films were scanned, and densitometric analysis was carried out by measuring and quantifying the band intensity using the NIH Image 1.62f program.

**RESULTS**

**Neuropathological studies**

As previously reported, extensive neurohistological studies revealed the presence of ubiquitin positive, intranuclear inclusions in both neuronal and astrocytic cells, with highest frequencies (~38% of neuronal nuclei) in the hippocampus.5 A pronounced dropout of Purkinje cells, and occasional axonal torpedoes, were also observed.3 We have since found intranuclear inclusions in ependymal and subependymal cells (fig 1), and in the epithelial lining cells of the choroids plexus.

**Molecular studies**

Sizing of the CGG repeat within the FMR1 gene, by both Southern blot and PCR analysis, demonstrated the presence of a premutation allele of 113 CGG repeats in peripheral blood leucocytes and in 13 different brain samples, thus demonstrating a lack of any interregion allelic size heterogeneity. Southern blot analysis revealed the presence of a single premutation allele and the absence of detectable full mutation alleles.

FMR1 mRNA levels showed an almost fourfold increase (3.8, SD 0.13) in peripheral blood leucocytes relative to normal controls, consistent with previous findings in premutation carriers.12 The relative brain FMR1 mRNA levels were substantially higher than in peripheral blood leucocytes, relative to the reference gene (glucuronidase, GUS), in the brains of both carrier and control (table 1). However, the net increase in the carrier cerebral levels relative to the control (1.5, SD 0.12; p = 0.02) was much less pronounced than in blood leucocytes, and no difference was observed for cerebellar cortex. This last observation is intriguing in view of the fact that cerebellar cortex is the only brain region devoid of inclusions; the significance of this observation is not known at present.

Immunocytochemical analysis showed a moderate FMRP deficit in peripheral blood leucocytes, with 62% of FMRP-positive lymphocytes. Western blot analysis revealed a more pronounced FMRP deficit in three brain regions. Specifically, FMRP expression levels were found to be 0.34, 0.45, and 0.92 relative to normal in hippocampus, temporal cortex, and frontal cortex, respectively. The observed FMRP deficit was consistent with a defect in the translation efficiency of FMR1 premutation alleles as recently reported.11

**DISCUSSION**

The presence of intranuclear inclusions in all brains derived from individuals with FXTAS examined to date is strongly supportive of an association with the premutation alleles of the FMR1 gene, since the clinical manifestations of the tremor/ataxia syndrome have not been observed in males with a full mutation. From Southern blot analysis, we can now reject the hypothesis that inclusions, and presumably disease formation, are a consequence of allelic mosaicism. However, before the current report, the presence of cryptic full mutation alleles that might be responsible for inclusion formation could not be ruled out. The presence of a large

Table 1

<table>
<thead>
<tr>
<th>Tissue</th>
<th>Carrier Relative FMR1 mRNA levels</th>
<th>Normal Relative FMR1 mRNA levels</th>
<th>Ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>Peripheral blood leucocytes</td>
<td>3.8 ± 0.13</td>
<td>1.0</td>
<td>3.8</td>
</tr>
<tr>
<td>Amygdala*</td>
<td>10.4 ± 0.58</td>
<td>6.95 ± 0.16</td>
<td>1.5</td>
</tr>
<tr>
<td>Frontal cortex*</td>
<td>9.04 ± 0.57</td>
<td>6.8 ± 0.74</td>
<td>1.32</td>
</tr>
<tr>
<td>Hippocampus*</td>
<td>7.1 ± 0.41</td>
<td>5.2 ± 0.48</td>
<td>1.4</td>
</tr>
<tr>
<td>Temporal cortex*</td>
<td>15.3 ± 0.85</td>
<td>9.3 ± 0.72</td>
<td>1.6</td>
</tr>
<tr>
<td>Occipital cortex*</td>
<td>5.18 ± 0.27</td>
<td>3.62 ± 0.26</td>
<td>1.4</td>
</tr>
<tr>
<td>Cerebellum</td>
<td>6.1 ± 0.36</td>
<td>7.11 ± 0.35</td>
<td>0.9</td>
</tr>
</tbody>
</table>

*Mean of the five tissues = 1.45 ± 0.12.
premutation allele of the same size in all brain tissue regions analyzed, as well as in peripheral blood leukocytes, in one premutation carrier, demonstrates both somatic stability in this size range and the association between FMR1 premutation and FXTAS.

Further support for the association of premutation alleles and inclusions comes from the recent observation that ubiquitin positive intranuclear inclusions have been observed in brains of mice with premutation (CGG) repeat expansions. Both the mice with expanded CGG repeat numbers, and all FXTAS patients so far analyzed, have shown elevated levels of FMR1 transcripts relative to normal, suggesting that elevated FMR1 message might contribute to the neuropathologies. In premutation carrier, demonstrates both somatic stability in this size range and the association between FMR1 premutation and FXTAS.

Finally, we have observed intranuclear inclusions in ependymal cells, subependymal cells, and the epithelial lining cells of the choroids plexus. Subependymal cells include multipotent stem cells which can give rise to astrocytes, oligodendrocytes, and neurons, as well as fully differentiated astrocytes, which participate in reactive processes in the subventricular zone. Epithelial lining cells of the choroids plexus, which are responsible for cerebrospinal fluid production and secretion, are derived from ependymal cells early in fetal development. The presence of inclusions in these three cell populations is not yet understood, but may be related to a shared lineage with astrocytes, perhaps in a common basic cellular function.

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REFERENCES