Cerebrospinal fluid biomarkers in human genetic transmissible spongiform encephalopathies

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Abstract The 14-3-3 protein test has been shown to support the clinical diagnosis of sporadic Creutzfeldt-Jakob disease (CJD) when associated with an adequate clinical context, and a high differential potential for the diagnosis of sporadic CJD has been attributed to other cerebrospinal fluid (CSF) proteins such as tau protein, S100b and neuron specific enolase (NSE). So far there has been only limited information available about biochemical markers in genetic transmissible spongiform encephalopathies (gTSE), although they represent 10–15% of human TSEs. In this study, we analyzed CSF of 174 patients with gTSEs for 14-3-3 (n = 166), tau protein (n = 78), S100b (n = 46) and NSE (n = 50). Levels of brain-derived proteins in CSF varied in different forms of gTSE. Biomarkers were found positive in the majority of gCJD (81%) and insert gTSE (69%), while they were negative in most cases...
of fatal familial insomnia (13%) and Gerstmann–Sträussler–
Scheinker syndrome (10%). Disease duration and codon 129 genotype influence the findings in a different way than
in sporadic CJD.

**Keywords** Creutzfeldt-Jakob disease · CSF proteins ·
14-3-3 protein · Tau

**Introduction**

The analysis of cerebrospinal fluid (CSF) in patients with suspected Creutzfeldt-Jakob disease (CJD) is an important
investigation for the differential diagnosis of CJD from among other forms of rapid progressive dementia. The 14-3-3 protein
levels are often increased in the CSF of sporadic CJD patients, and this test has therefore been included in the diagnostic
criteria for sporadic CJD when associated with an appropriate
clinical profile [6, 31]. Increased levels of other brain-derived
proteins, such as tau protein, S100b or neuron-specific enolase
(NSE) have also been reported, but information on these
markers is limited [20, 27]. However, in most gTSE, studies of
CSF proteins report 14-3-3 test results only in gCJD with
E200K and V210I point mutations. Levels of brain-derived
proteins are low in Gerstmann–Sträussler–Scheinker syndrome
(GSS) and almost all fatal familial insomnia (FFI) patients
reported to date are negative for 14-3-3 [11, 15, 20, 30].

A very few data are available on the levels of the other
marker proteins in the CSF of patients with gTSEs, and no
analyses on factors influencing the percentage of elevated
levels have been done. In this paper, we perform such an
analysis on brain-derived proteins in patients having gTSE
with various mutations.

**Methods**

**Patients and database**

The study was performed in the framework of the EC-
supported multinational study on biomarkers in prion dis-
esases (CJD markers) [20].

A database was set up which included detailed data on
180 patients with genetic TSE, 61 (34%) gTSE patients
from Germany, 58 (32%) from Italy, 36 (20%) from Spain,
13 (7%) from the UK, 10 (5%) from Slovakia and 2 (1%)
from Switzerland.

The diagnoses of gTSE were carried out according to
recent surveillance criteria after PRNP analysis [11, 12].
For the estimation of the disease stage when the LP was
performed we divided the individual disease duration in
thirds and calculated the time of lumbar puncture according
to the first third of the total duration of the disease (early
stage), the second (middle) or the third (advanced stage) of
the disease.

**CSF tests**

14-3-3 and other tests were performed according to pre-
viously described methods [20].

**Statistical analyses**

Differences in CSF levels of tau, S100b and NSE proteins
across the four genetic groups of gTSE were separately
assessed by the Kruskal–Wallis test, followed, when sta-
tistically significant, by the Mann–Whitney test. Since
different techniques were employed for the determination
of S100b and NSE, we included in the quantitative
assessment levels only the results of the most frequently
used kits (Byk Sangtec for S100b and -Hofman LaRoche
for NSE).

We then calculated the percentage of positive results out
of the total for each CSF marker in the four genetic groups.
All samples were included in the analysis, since a positive
result was calculated according to the cut-off of the dif-
ferent techniques. The $\chi^2$ test was used to assess differ-
ences between categorical variables.

A multiple logistic regression model was used to
assess the effect of a set of clinically relevant variables
on the percentage of elevated levels of the different
biomarkers in gTSE patients. These were: type of disease
causing mutation, disease duration (in months), age at
onset (in years), disease stage when the lumbar puncture
was performed (during the first, second or third period of
disease duration), and PRNP codon 129 genotype.

Country of patient and gender were entered as covariates.
Age at onset was categorized in four clinically mean-
ingsful groups, with younger than 40 years as the refer-
ence group. Disease duration was categorized in two
groups (short and long duration), according to the median
survival time. Due to the small numbers of patients,
some of the statistical analyses were restricted to gCJD
groups or to the 14-3-3 test.
Results

General description

Demographic and clinical information on gTSE cases is given in Table 1. A definite neuropathological diagnosis was available in 52% of the cases, ranging from more than 87% of FFI to 22% of GSS patients, while in 47% of gCJD autopsy was not performed. Data on the polymorphic codon 129 of PRNP were available in 86% of all cases. For some patients the only available information was about PRNP with no information on codon 129 genotype. The majority of gTSE patients were either homozygous for methionine (MM, 58%) or heterozygous (MV, 36%), only a few were homozygous for valine (6%). In a few cases, where the PrPSc typing was available, it was invariable PrPSc type I pattern.

Quantitative levels of brain-derived proteins

The CSF concentrations of tau protein ranged from 70.0 to 35,440.0 pg/ml (median 6,255.5 pg/ml) in the gCJD group, from 75.0 to 20,370.0 pg/ml (median 2,354.0 pg/ml) in the insert gTSE group, from 296.0 to 1,698.0 pg/ml (median 675.0 pg/ml) in the GSS group, and from 97.0 to 4,126.0 pg/ml (median 464.5 pg/ml) in the FFI group (Fig. 1a). CSF levels of tau protein significantly differ in the four groups of gTSEs ($p < 0.001$, Kruskal–Wallis test), but did not vary within the gCJD group of patients ($p = 0.13$).

The median CSF concentrations of S100b protein were above the cut-off level in all groups but one (FFI), ranging from 1.0 to 16.0 ng/ml in gCJD (median 9.0 ng/ml), from 3.0 to 17.0 ng/ml in insert gTSE (median 11.0 ng/ml), and from 1.0 to 6.0 ng/ml in FFI (median 3.0 ng/ml), Fig. 1b. The only GSS patient tested for S100b protein had a CSF concentration of 23.0 ng/ml. Statistical analysis showed a significant difference among the three groups ($p = 0.002$, Kruskal–Wallis test).

Table 1 Summary of clinical features of patients in the study

<table>
<thead>
<tr>
<th>Forms of gTSE</th>
<th>Number of cases total (female gender)</th>
<th>Percentage of neuropathologically confirmed cases (n)</th>
<th>Age at onset, years, median (range)</th>
<th>Clinical duration, months, median (range)</th>
<th>Codon 129 polymorphism</th>
<th>PrP type I</th>
</tr>
</thead>
<tbody>
<tr>
<td>gCJD</td>
<td>124 (68)</td>
<td>54.7 (35)</td>
<td>59 (29–86)</td>
<td>6 (0.43–34)</td>
<td>63.5 (33)</td>
<td>4/4</td>
</tr>
<tr>
<td>E200K</td>
<td>64 (37)</td>
<td>47.5 (19)</td>
<td>56.5 (43–87)</td>
<td>4 (1–31)</td>
<td>67.5 (27)</td>
<td>5/5</td>
</tr>
<tr>
<td>V210I</td>
<td>40 (19)</td>
<td>28.6 (6)</td>
<td>65 (32–77)</td>
<td>6.5 (2–12)</td>
<td>37.5 (6)</td>
<td>3/3</td>
</tr>
<tr>
<td>Other</td>
<td>20 (12)</td>
<td>87 (20)</td>
<td>56 (24–83)</td>
<td>12.5 (1–97)</td>
<td>60.9 (14)</td>
<td>0.0 (0)</td>
</tr>
<tr>
<td>FFI</td>
<td>23 (5)</td>
<td>22 (2)</td>
<td>50 (25–70)</td>
<td>80.5 (54–87)</td>
<td>30.0 (3)</td>
<td>1/1</td>
</tr>
<tr>
<td>GSS</td>
<td>10 (4)</td>
<td>52.9 (9)</td>
<td>63 (36–77)</td>
<td>11 (3–19)</td>
<td>46.7 (7)</td>
<td>3/3</td>
</tr>
<tr>
<td>A117V</td>
<td>1</td>
<td>1</td>
<td></td>
<td></td>
<td>0.0 (0)</td>
<td></td>
</tr>
<tr>
<td>P102L</td>
<td>8</td>
<td></td>
<td></td>
<td></td>
<td>0.0 (0)</td>
<td></td>
</tr>
<tr>
<td>P105L</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td>0.0 (0)</td>
<td></td>
</tr>
<tr>
<td>Insert gTSE</td>
<td>17 (11)</td>
<td></td>
<td></td>
<td></td>
<td>1.0 (1)</td>
<td></td>
</tr>
</tbody>
</table>

Abnormal cerebrospinal fluid findings in gTSEs

14-3-3

There was a statistically significant difference in the rate of elevated 14-3-3 levels among the four groups of gTSEs, ($p < 0.001$), see Table 2. A 14-3-3 positive test was present in the majority of gCJD patients, irrespective of the mutation they carried (R208H, V203I, E211Q, T188K, and R148H). Thus, no significant difference in percentage of abnormal tests for 14-3-3 was found between E200K (81%) andV210I (85%) or versus other forms of gCJD (72%). Insert gTSE patients had also a high proportion of positive tests (69%), while the 14-3-3 test was positive in only 10% of GSS and in 13% of FFI cases.

Tau

A high rate of tau levels was found in gCJD and insert gTSE groups, while in GSS only 40% of cases had tau levels above the cut-off level of 1,300 pg. Only a single FFI patient had abnormal tau levels in CSF (Table 2). The levels of tau protein in the CSF were statistically different in the four groups ($p < 0.001$).
A similar distribution was observed for S100b values. Elevated S100b levels were found in 87% of gCJD and 77.8% of insert gTSE patients. These values were lower in GSS and FFI patients. The differences in the gTSE groups were statistically significant, \((p = 0.002)\).

**NSE**

Only 64.3% of gCJD patients and 50% of insert gTSE patients had NSE values above the cut-off level, while NSE values were normal in GSS and FFI patients.

**Effect of octapeptide repeats**

The number of octapeptide repeats was inversely correlated with the values of tau (Spearman \( \rho = -0.51 \) \((p = 0.036)\)); patients with high number of repeats (5 \( \times \) 24) had low tau levels. A similar trend was found for the 14-3-3 test; patients with high number of repeats had low percentage of abnormal tests: 1 \( \times \) 24 (1/1); 3 \( \times \) 24 (1/1); 4 \( \times \) 24 (5/5); 5 \( \times \) 24 (5/10) Fisher’s \( p \) value = 0.22.

**Effects of patient characteristics on abnormal findings**

The effect of clinical characteristics on percentage of abnormal findings in gCJD patients was the age at disease
onset ($p = 0.014$) and the PRNP codon 129 genotype (VV vs. MV $p = 0.043$). Sensitivity of 14-3-3 was higher in old patients compared to young ones (25.0% in patients younger than 40 years, 83.9 in patients aged 40–60 years, 86.5% in 60–80 years and 100% in patients older than 80 years).

Regarding the percentage of abnormal findings in the 14-3-3 test in relation to the PRNP codon 129 genotype, this was lower in gCJD patients homozygous for valine than in heterozygous patients (VV vs. MV $p = 0.043$). However, when we adjusted by type of mutation, this statistical significance was lost. Although the 14-3-3 test performed worse in homozygous for methionine than in heterozygous gCJD patients, this difference was not significant ($\chi^2$ test, $p = 0.08$) (Table 3). In E200K and V210I patients, the 14-3-3 sensitivity was higher in heterozygous (88.2 and 100%) than in methionine homozygous patients (78.1 and 77.8%), but these differences did not reach any significance (Table 2).

Disease duration had no influence on 14-3-3 test results (84.6% abnormal findings in patients with disease duration below the median, and 87.3% in patients with disease duration above the median survival time, Table 3). In gCJD patients, there was no significant influence of the disease stage at the time of lumbar puncture in relation to 14-3-3 results ($p = 0.4$) (100% in the first third of disease duration, 89% in the second third and 82% in the last third, Table 3, as reported in sporadic CJD [21].

Regarding the other CSF tests, there was a lower percentage of abnormal findings for the S100b test in gCJD patients homozygous for methionine than in heterozygous patients, while the opposite was found for tau and NSE (Table 3), though the differences were not statistically
significant (\(p = 0.06\) for tau, \(p = 0.92\) for S100b, and \(p = 0.24\) for NSE, \(\chi^2\) test).

Multivariate analysis, performed on all gTSE patients, included as variables disease duration, age at onset, gender, type of mutation and 129 genotype, and as covariates gender and country of residence. This analysis revealed that the type of mutation is the only variable that significantly influenced 14-3-3 test (\(p < 0.004\)). Particularly, in patients carrying the D178N-Met mutation (FFI), the percentage of abnormal findings of 14-3-3 decreased significantly in comparison to gCJD (\(p < 0.007\)) and insert gTSE (\(p < 0.001\)). Interestingly, regarding the 129 codon polymorphism, 14-3-3 had lower percentage of abnormal tests in patients homozygous for valine than in patients homozygous for methionine or heterozygous, though no significant differences were found (crude \(p\) value = 0.5; adjusted \(p\) value = 0.76). Table 4.

Multivariate analysis did not revealed any variables that influenced tau, NSE or S100b levels in gTSE patients.

In all gTSE there was a statistically significant negative correlation between tau levels and disease duration (Spearman \(\rho\) between duration and tau levels = -0.52 (\(p < 0.001\)). However, when the data were stratified by diagnostic groups, numbers become too low and were not significant (only borderline for gCJD: \(r^2 = -0.32, p = 0.057\)).

### Discussion

Data on brain-derived proteins in the CSF of patients with genetic TSE are limited and conflicting results have been reported, mostly because they are frequently based on single case observations (see Table 4). In these reports, sensitivity of biochemical markers in CSF is reported to be lower than in sporadic CJD and this was explained in terms of prolonged disease duration and relatively slow disease progression. Because of the limited numbers of patients, no detailed analysis on this topic is available.

In this study we provide data on four brain-derived proteins in a cohort of patients with various forms of genetic TSE. We found firm evidence for elevated concentrations of 14-3-3, tau, S100b and NSE in the CSF of patients with genetic CJD, but not in FFI or GSS patients. Of interest, the median concentrations for tau, S100b and NSE were similar to those detected in sporadic CJD in other studies [1, 16, 20]. In our previous study on sporadic CJD, we reported median tau levels in the range of

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Number of 14-3-3 positive patients/total</th>
<th>Number of tau positive patients/total</th>
<th>Number of S100b positive patients/total</th>
<th>Number of NSE positive patients/total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age at onset</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;40</td>
<td>1/4</td>
<td>1/1</td>
<td>1/1</td>
<td>1/1</td>
</tr>
<tr>
<td>40–60</td>
<td>47/57</td>
<td>18/19</td>
<td>9/11</td>
<td>11/15</td>
</tr>
<tr>
<td>60–80</td>
<td>46/53</td>
<td>18/21</td>
<td>9/9</td>
<td>6/11</td>
</tr>
<tr>
<td>&gt;80</td>
<td>2/2</td>
<td>1/1</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>(p) value</td>
<td>0.016</td>
<td>0.76</td>
<td>0.34</td>
<td>0.47</td>
</tr>
<tr>
<td>Codon 129</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MM</td>
<td>52/65</td>
<td>22/22</td>
<td>7/8</td>
<td>9/12</td>
</tr>
<tr>
<td>MV</td>
<td>32/35</td>
<td>11/14</td>
<td>9/10</td>
<td>6/12</td>
</tr>
<tr>
<td>VV</td>
<td>2/4</td>
<td>2/2</td>
<td>1/1</td>
<td>2/2</td>
</tr>
<tr>
<td>(p) value</td>
<td>0.74</td>
<td>0.06</td>
<td>0.93</td>
<td>0.25</td>
</tr>
<tr>
<td>Disease duration</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&gt; median</td>
<td>22/26</td>
<td>10/11</td>
<td>5/5</td>
<td>7/9</td>
</tr>
<tr>
<td>&lt; median</td>
<td>48/55</td>
<td>21/21</td>
<td>9/10</td>
<td>8/12</td>
</tr>
<tr>
<td>(p) value</td>
<td>0.74</td>
<td>0.16</td>
<td>0.46</td>
<td>0.58</td>
</tr>
<tr>
<td>Time point of LP during disease(^a)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Early stage</td>
<td>8/8</td>
<td>1/1</td>
<td>1/1</td>
<td>0/1</td>
</tr>
<tr>
<td>Middle stage</td>
<td>23/26</td>
<td>7/7</td>
<td>3/3</td>
<td>3/3</td>
</tr>
<tr>
<td>Advanced stage</td>
<td>28/34</td>
<td>7/7</td>
<td>3/3</td>
<td>2/2</td>
</tr>
<tr>
<td>(p) value</td>
<td>0.40</td>
<td>–</td>
<td>–</td>
<td>0.17</td>
</tr>
</tbody>
</table>

\(^a\) For the estimation of the disease stage when the LP was performed we divided the individual disease duration in thirds and calculated the time of lumbar puncture according to the first third of the total duration of the disease (early stage), the second (middle) or the third (advanced stage) of the disease.
6,000 pg/ml, which is not significantly different from what we found in gCJD patients [21]. These results are concordant with the observation that some gCJD might present clinical similarities with sporadic CJD [11, 15]. Indeed, these cases are often misclassified as sporadic CJD if family history and genetic testing are not done.

The rate of elevated levels of 14-3-3, tau, NSE and S100b in genetic CJD was comparable to that observed in sporadic CJD [3, 20, 26, 27]. In other forms of gTSE, such as FFI and GSS, these tests were consistently negative. Although levels of tau in FFI and GSS patients were lower than the cut-off levels given for CJD, they were still elevated if compared to non-demented controls [24].

The crude analyses of disease modifying factors of the 14-3-3 test in gCJD revealed that age at onset and PRNP codon 129 genotype influenced sensitivity. 14-3-3 test sensitivity was lower in patients with disease onset before 40 years. These data parallel the results performed on sporadic CJD [20]. However, while in the multivariate analysis age remained as an independent variable in sporadic CJD, in gCJD it did not. Interestingly, in gCJD the PRNP codon 129 genotype influences 14-3-3 sensitivity in a different way with respect to what has been observed in sporadic CJD. Valine homozygous gCJD patients had a lower sensitivity in the 14-3-3 test than heterozygous patients. Though there are too few patients to draw any definite conclusions, a possible explanation might be that the PRNP mutations coupled with the valine alleles (R208H, D178N, E196K) confer low sensitivity to 14-3-3.

The biological significance of brain-derived proteins in the CSF of patients with TSEs remains to be determined. It is generally assumed that the release of 14-3-3, tau and

<table>
<thead>
<tr>
<th>Table 4 CSF biomarker in genetic TSE (reports in the literature)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Author</td>
</tr>
<tr>
<td>--------</td>
</tr>
<tr>
<td>E200K</td>
</tr>
<tr>
<td>Sanchez-Valle [23] Eur J Neurol 2004</td>
</tr>
<tr>
<td>Huang [7] Arq neuropsiquiatr 2001</td>
</tr>
<tr>
<td>Sanchez-Valle [23] Eur J Neurol 2004</td>
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<tr>
<td>Rosenmann [18] Neurology 1999</td>
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<td>Zarrranz [29] JNNP 2005</td>
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<tr>
<td></td>
</tr>
<tr>
<td>Kotta [10] BMC Infect dis 2006</td>
</tr>
<tr>
<td>Elevated</td>
</tr>
<tr>
<td>Capellari [3] Neurology 2005</td>
</tr>
<tr>
<td>Sanchez-Valle [22] JNNP 2008</td>
</tr>
</tbody>
</table>

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NSE proteins in the CSF is a consequence of leakage into the CSF following rapid neuronal damage. Recently, a systematic analysis of brain-derived proteins in CSF and neuropathological lesions has shown that the levels of these proteins are the consequence of both the degree of neuronal damage and the localization of the most affected areas [2]. For example NSE levels correlated with damage of subcortical areas (such as the thalamus) and tau protein levels correlated with the degree of spongiform changes in the frontal cortex. Our findings on inverse correlation of tau levels and the number of octapeptide repeats are of interest, since the number of repeats has been correlated to the type of cerebellar PrPSc deposits [28].

In conclusion, the validity of the biomarkers varied among the different forms of gTSEs. Sensitivity of biomarkers was high in those forms, which are clinically more severe. Neurobiol Aging. doi:10.1016/j.neurobiolaging.2008.01.013

Acknowledgments

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Conflict of interest statement

The authors report no conflicts of interest.

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