Calculating predictive values for the large repeat alleles at the SCA8 locus in patients with ataxia

V Juvonen, V Kairisto, M Hietala, M-L Savontaus

Since the original description of SCA8 in 1999, several reports have been published on the occurrence of the SCA8 gene CTG repeat expansion in various populations. These studies have shown that, in addition to finding the SCA8 expansion in familial and sporadic ataxia patients, expanded alleles can also be found in non-ataxic subjects, psychiatric patients, and in patients with various other neurological diseases with a known aetiological cause. Owing to the exceptionally low penetrance of the mutation, questions have been raised about the pathogenic role of the expansion, and there exists speculation about alternative mechanisms, such as linkage disequilibrium of the CTG expansion with another as yet unidentified causal mutation. Accordingly, caution in interpreting mutation findings in clinical samples has been stressed and some investigators discourage genetic testing for SCA8 until a pathological mechanism has been established.

SUBJECTS AND METHODS
We have investigated the occurrence of the SCA8 repeat expansion in 251 unrelated Finnish SCA patients and found 22 of them with the expansion. Based on our present and previous studies on controls and patients, we define the size range of 15–40 combined repeats as normal alleles and above 80 up to 800 as expanded alleles. Intermediate alleles between these groups are sometimes seen and we interpret them to be most likely non-pathogenic. We used a combination of PCR and Southern blotting methods as described previously in order to reach 100% sensitivity for the detection of expansions. None of the 22 SCA8 positive patients had expansions at the SCA1, 2, 3, 6, 7, 10, 12, 17, DRPLA, or FRDA loci. Thirteen of the SCA8 positive patients had a family history of the disease, and, in nine of them, it was compatible with a dominant inheritance pattern.

RESULTS AND DISCUSSION
The number of combined CTA/CTG repeats in the expanded alleles of the hereditary cases were 97, 118, 121, 125, 128, 151, 151, 196, 199, 345, and 660. Among the nine sporadic patients with expansions, three had expanded repeats on both alleles (101/156, 105/137, 134/151, 115, 168, 204, 504, 620, and 800 combined repeats on expanded alleles). Table 1 gives the frequencies of the SCA8 expansions and the respective 95% confidence intervals calculated using Freeman and Tukey’s approximation in the different subgroups. The frequency of subjects with SCA8 expansions was statistically significantly (p<0.002) higher in hereditary ataxias than among the 448 non-ataxic controls studied previously. The assumption that SCA8 has a prevalence of approximately 1/100 000 gives a penetrance of only 0.03% for the SCA8 expansion in Finland. It is obvious that genetic testing for SCA8 in clinical samples cannot be diagnostic on these premises.

However, as seen in table 1, the Finnish series shows that SCA8 expansions cluster in ataxia patients and this clustering is more conspicuous and statistically significant in the hereditary cases. Calculation of predictive values (PV), that is, the probability of disease after getting a positive test result, for each group of patients with ataxia symptoms and a defined family history further increases the predictive value of the test to above 80%

### Table 1 Frequencies of SCA8 expansion in the Finnish ataxia cohort and its subgroups and in non-ataxic controls

<table>
<thead>
<tr>
<th></th>
<th>Subjects with SCA8 expansion</th>
<th>SCA8 expansion frequency</th>
<th>95% confidence interval for frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>All ataxia patients</td>
<td>22</td>
<td>8.8%*</td>
<td>5.6% to 13.0%</td>
</tr>
<tr>
<td>Hereditary ataxia</td>
<td>13</td>
<td>15.1%*</td>
<td>9.2% to 23.1%</td>
</tr>
<tr>
<td>Dominant ataxia</td>
<td>9</td>
<td>18.4%*</td>
<td>10.0% to 30.1%</td>
</tr>
<tr>
<td>Sporadic ataxia</td>
<td>9</td>
<td>5.5%†</td>
<td>2.9% to 9.4%</td>
</tr>
<tr>
<td>Non-ataxic controls</td>
<td>13</td>
<td>2.9%</td>
<td>1.7% to 4.6%</td>
</tr>
</tbody>
</table>

* p<0.002 when the frequency is compared to non-ataxic controls by chi-square statistic with Yates’s continuity correction († not significant).
The concept of likelihood ratio (LR) is useful to derive predictive values (PV) for a disease from the estimated pre-test probability (Pr). It shows how much more probable it is for a diseased subject to obtain a true positive diagnostic test result than for a healthy person to get a false positive diagnostic test result. The likelihood ratio itself is not dependent on the prevalence of the disease. If clinical sensitivity (Se) and specificity (Sp) are known, the likelihood ratio can be calculated using the equation $LR = \frac{Pr \times Se}{(1 - Pr) \times (1 - Sp)}$.

When pre-test probability (Pr) and likelihood ratio (LR) are known, the predictive value (PV) can be calculated according to the following formula:

$$PV = \frac{(Pr \times LR) + (1 - Pr) \times LR}}{(1 - Pr) + (Pr \times LR)}.$$ 

As the likelihood ratio can be considered to be constant (34.5 in the Finnish material), predictive value is solely dependent, in a non-linear fashion, on pre-test probability. For the different ataxia patient groups in this study, the predictive values of a positive SCA8 repeat expansion result are the following: all ataxia patients 68.2%, inherited ataxia 82.7%, dominant inheritance pattern 86.3%, and sporadic ataxia 47.4% (fig 1). For a non-ataxic control, the PV is solely dependent, in a non-linear fashion, on pre-test probability. For 34.5 in the Finnish material, PV is solely dependent, in a non-linear fashion, on pre-test probability.

In comparison to many other populations, Finnish non-ataxic controls show an unusually high frequency of the SCA8 repeat expansion. Lower frequencies would result in a better likelihood ratio for SCA8 testing and an upward shift of the curve in fig 1. Thus, in other populations an even lower pre-test probability of SCA8 could result in a relatively high predictive value.

Despite its well established status in clinical chemistry, calculation of predictive values is not widely recognised or commonly used in genetic testing. Besides SCA8, it could, however, be applied to many genetic analyses with disease association.

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