A polymorphic DNA marker at the D10S106 locus

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Source and Description: G2-2E is a single copy 200 bp subfragment of G2 cloned into the EcoRV site of Bluescript KSII(+). Clone G2 was isolated from a library highly enriched for (TTAGGG)n-associated sequences (1).

Polymorphisms:
TaqI identifies a two allele polymorphism as assessed in 29 unrelated Caucasians.

<table>
<thead>
<tr>
<th>Allele</th>
<th>Size</th>
<th>No. of Chromosomes</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1</td>
<td>900 bp</td>
<td>31</td>
<td>(0.54)</td>
</tr>
<tr>
<td>A2</td>
<td>700 bp</td>
<td>27</td>
<td>(0.46)</td>
</tr>
</tbody>
</table>

PstI identifies a two allele polymorphism as assessed in 34 unrelated Caucasians and 25 unrelated East Indians, respectively. There is an invariant band at 2.0 kb.

<table>
<thead>
<tr>
<th>Allele</th>
<th>Size</th>
<th>No. of Caucasians</th>
<th>Frequency</th>
<th>No. of East Indians</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1</td>
<td>2.5 kb</td>
<td>36</td>
<td>(0.53)</td>
<td>30</td>
<td>(0.60)</td>
</tr>
<tr>
<td>A2</td>
<td>2.3 kb</td>
<td>32</td>
<td>(0.47)</td>
<td>20</td>
<td>(0.40)</td>
</tr>
</tbody>
</table>

Polymorphism For: BglII, HincII.

Not Polymorphic For: BglIII, EcoRI, Msapl, SstI, RsaI, all tested on a panel of 8 unrelated individuals.

Chromosomal Localisation: 10q22.1 - 10q24.3 by PCR-mapping using a somatic cell hybrid panel (BIOS Inc., New Haven) and hybrids containing various fragments of chromosome 10 (2).

Mendelian Inheritance: Codominant segregation has been shown for the TaqI polymorphism in five and for the PstI polymorphism in four families.

Probe Availability: Contact B. Weber or M. R. Hayden.

Acknowledgements: We thank Dr. P. J. Goodfellow for the chromosome 10 deletion panel. This work was supported by grants from MRC Canada, the Canadian Genetic Disease Network and Deutsche Forschungsgemeinschaft (We 1259/1-1).


A polymorphic DNA marker at the D8S131 locus

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Source and Description: Y19-1D is a single copy 836 bp subclone of Y19. Y19 was isolated from a library highly enriched for (TTAGGG)n-associated sequences (1). The subclone is ligated into the EcoRV site of Bluescript KSII(+), and it is free of any telomeric repeats.

Polymorphism: BamHI digestion yields two polymorphic bands as assessed in 28 unrelated Caucasians and 77 parents from the CEPH panel.

<table>
<thead>
<tr>
<th>Allele</th>
<th>Size</th>
<th>No. of Chromosomes</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1</td>
<td>7 kb</td>
<td>170</td>
<td>(0.81)</td>
</tr>
<tr>
<td>A2</td>
<td>6 kb</td>
<td>40</td>
<td>(0.19)</td>
</tr>
</tbody>
</table>


Chromosomal Localisation: Y19-1D has been localised using a somatic cell hybrid panel (BIOS Inc., New Haven) to chromosome 8 (1). Screening a total genomic cosmid library (Stratagene) with Y19-1D yielded one positive cosmid cY19. Competitive fluorescent in situ hybridisation mapped cosmids clone cY19 to 8p21 (2).

Mendelian Inheritance: Codominant segregation has been shown in 15 CEPH families.

Probe Availability: Contact B. Weber or M. R. Hayden.

Acknowledgements: This work was supported by grants from MRC Canada, the Canadian Genetic Disease Network, and the Deutsche Forschungsgemeinschaft (We 1259/1-1).