Announcement of population data

Population data on the X chromosome short tandem repeat loci DXS10011, DXS101, DXS6789, DXS7132, DXS8377, and DXS9895 in Taiwan

Meng-Yi Chen, Chang-En Pu *

Scientific and Technical Research Center, Ministry Justice Investigation Bureau, 74, Chung-Hua Road, Hsin-Tien City, Taipei County, 231 Taiwan ROC

Received 3 September 2003; received in revised form 19 March 2004; accepted 31 March 2004

Available online 1 June 2004

Abstract

X chromosome linked short tandem repeat (STR) are powerful auxiliary systems to genomic STR, they are helpful for differentiating if two women have the same father directly, avoiding some of the ambiguity generated from sibship estimation. This report contains the results of population studies on the X chromosome STR DXS10011, DXS101, DXS6789, DXS7132, DXS8377 and DXS9895 carried out in Taiwan. The common alleles of each locus were sequenced and used in a control ladder to type unknown samples. The numbers of unrelated individuals were 273 (female 92 and male 181) for DXS10011 locus, 448 (female 135 and male 313) for DXS101 locus, 447 (female 135 and male 312) for DXS6789 locus, 414 (female 119 and male 295) for DXS7132 locus, 450 (female 135 and male 315) for DXS8377 locus and 413 (female 120 and male 293) for DXS9895 locus. These STR polymorphisms will be a useful marker for parentage testing especially when disputed blood relative is female.

Keywords: Forensic science; Short tandem repeats; X chromosome; DXS10011; DXS101; DXS6789; DXS7132; DXS8377; DXS9895; Population data

Population: Unrelated volunteer donors living in Taiwan.

Extraction: DNA was extracted by using BioGene-Fast™ 30 min DNA extraction kit (Texas BioGene Inc., TA, USA) and quantities by a Fluorometer (DyNA Quant 200, Hoefer Pharmacia Biotech, San Francisco, CA, USA).

PCR: PCR amplifications were performed using primer sequences according GeneBank information (http://

<table>
<thead>
<tr>
<th>Allele</th>
<th>DXS10011</th>
<th>DXS101</th>
<th>DXS6789</th>
<th>DXS7132</th>
<th>DXS9895</th>
<th>Allele</th>
<th>DXS8377</th>
</tr>
</thead>
<tbody>
<tr>
<td>8</td>
<td>0.002</td>
<td></td>
<td>33</td>
<td>0.003</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>11</td>
<td>0.004</td>
<td>0.002</td>
<td>38</td>
<td>0.002</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>0.086</td>
<td>0.002</td>
<td>40</td>
<td>0.003</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>13</td>
<td>0.208</td>
<td>0.286</td>
<td>41</td>
<td>0.009</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>14</td>
<td>0.005</td>
<td>0.351</td>
<td>0.380</td>
<td>42</td>
<td>0.019</td>
<td></td>
<td></td>
</tr>
<tr>
<td>15</td>
<td>0.168</td>
<td>0.255</td>
<td>0.197</td>
<td>43</td>
<td>0.031</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* Corresponding author. Tel.: +886-2-2911-2241; fax: +886-2-2913-8599.
E-mail address: pu4431@ms14.hinet.net (C.-E. Pu).

0379-0738/ – see front matter © 2004 Elsevier Ireland Ltd. All rights reserved.
doi:10.1016/j.forsciint.2004.03.020
Typing: ABI 310 (Applied Biosystem) with sequenced ladders referred from [1–4] and made by authors.

Results: See Table 1.

Analysis of data: POPGENE [5] and PowerStats Excel Template [6].

Access to the data: Mail to pu4431@ms14.hinet.net.

Other remarks: The presented data do not consider linkage and linkage disequilibrium among loci. The frequency of DXS9895 was found with no significant difference from that of reported Chinese population study [7]. This paper follows the guidelines for publication data requested by the journal [8].

References


