Molecular, cytogenetic, and clinical characterisation of six XX males including one prenatal diagnosis

Ester Margarit, Anna Soler, Ana Carrió, Rafael Oliva, Dolors Costa, Teresa Vendrell, Jordi Rosell, Francisca Ballesta

Abstract
Cytogenetic analysis, fluorescent in situ hybridisation (FISH), and molecular amplification have been used to characterise the transfer of Yp fragments to Xp22.3 in six XX males. PCR amplification of the genes SRY, RPS4Y, ZFY, AMELY, KALY, and DAZ and of several other markers along the Y chromosome short and long arms indicated the presence of two different breakpoints in the Y fragment. However, the clinical features were very similar in five of the cases, showing a male phenotype with small testes, testicular atrophy, and azoospermia. All these patients have normal intelligence and a stature within the normal male range. In the remaining case, the diagnosis was made prenatally in a fetus with male genitalia detected by ultrasound and a 46,XX karyotype in amniocytes and fetal blood. Molecular analysis of fetal DNA showed the presence of the SRY gene. FISH techniques also showed Y chromosomal DNA on Xp22.3 in metaphases of placental cells. To our knowledge, this is the second molecular prenatal diagnosis reported of an XX male.

(Keywords: XX males; Xp-Yp interchanges; SRY; prenatal diagnosis)

The mechanism proposed to explain 46,XX males is the presence of a Y chromosome fragment transferred to the X chromosome short arm by unequal interchange between homologous regions in the short arms of the sex chromosomes during paternal meiotic division. This Y fragment would be a carrier of testicular determinants and would give male sexual characteristics to apparently XX subjects. In other patients, the presence of a low level mosaicism for an XY cell line accounts for the ambiguous phenotype. The existence of Y chromosome material in non-mosaic XX males was first detected as a hetrochromatin in the short arm of one X chromosome. More recently, studies on metaphase chromosomes by in situ hybridisation techniques located Y sequences to distal Xp in XX males, supporting the initial hypothesis of Ferguson-Smith. Subsequently, the use of molecular techniques has allowed the detection of Y sequences in most XX males either by Southern blot analysis or by PCR analysis, confirming the presence of the SRY gene. Some XX male cases have also been reported lacking any Y sequences. These cases usually have sexual ambiguities or hermaphroditism or both that may have arisen from a different mechanism, probably by a recessive mutation in a gene controlling the testicular pathway, since some cases are familial. This mutation would allow testicular development in the absence of SRY. Alternatively, Y sequences might be confined to testicular tissue, and therefore escape detection by the analysis of leucocyte DNA.

Here we present the characterisation of five new cases of XX males, not previously reported. Additionally, we provide new data for a previously reported case that was partially characterised. PCR amplification using markers along the Y chromosome has allowed the Y sequences present in each patient to be defined and correlations with the phenotype to be established. Subsequently, the location of Y fragments has been further determined by in situ hybridisation on metaphase chromosomes.

Methods
Cases
We included in this study five patients either attending our Genetics Service or referred from other centres for karyotyping, FISH, or molecular studies. The patients had pubertal hypogonadism, testicular atrophy, and azoospermia as the main clinical manifestations...
Table 1: Clinical, cytogenetic, and molecular data obtained from the six cases

<table>
<thead>
<tr>
<th>Case</th>
<th>Clinical features</th>
<th>Karyotype</th>
<th>Y markers</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Testicular atrophy, azoospermia, small testes</td>
<td>46,XX,t(X;Y)(p22.3;p11.2)</td>
<td>+ + + + + + + + +</td>
</tr>
<tr>
<td>2</td>
<td>Testicular atrophy, azoospermia, small testes</td>
<td>46,XX,t(X;Y)(p22.3;p11.2)</td>
<td>+ + + + + + + + +</td>
</tr>
<tr>
<td>3</td>
<td>Testicular atrophy, azoospermia, small testes, gynaecomastia, obesity</td>
<td>46,XX,t(X;Y)(p22.3;p11.2)</td>
<td>+ + + + + + + + +</td>
</tr>
<tr>
<td>4</td>
<td>Testicular atrophy, azoospermia, gynaecomastia, obesity</td>
<td>46,XX,t(X;Y)(p22.3;p11.2)</td>
<td>+ + + + + + + + +</td>
</tr>
<tr>
<td>5</td>
<td>Testicular atrophy, azoospermia</td>
<td>46,XX,t(X;Y)(p22.3;p11.2)</td>
<td>+ + + + + + + + +</td>
</tr>
<tr>
<td>6</td>
<td>Male genitalia (internal and external)</td>
<td>46,XX,t(X;Y)(p22.3;p11.2)</td>
<td>+ + + + + + + + +</td>
</tr>
</tbody>
</table>

n: not tested.

Table 2: Y specific primer pairs used in the PCR analysis of genomic DNA

<table>
<thead>
<tr>
<th>Primer pair</th>
<th>Gene locus</th>
<th>Location (deletion interval)</th>
<th>Band (%)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>PABY</td>
<td>Pseudoautosomal boundary</td>
<td>Yp11.31</td>
<td>947</td>
<td>26</td>
</tr>
<tr>
<td>PABX</td>
<td>Pseudoautosomal boundary</td>
<td>Xp22.3</td>
<td>771</td>
<td>26</td>
</tr>
<tr>
<td>SRY</td>
<td>SRY, sex determining region</td>
<td>Yp11.31 (1A)</td>
<td>336</td>
<td>3</td>
</tr>
<tr>
<td>Y53</td>
<td>SRY, sex determining region</td>
<td>Yp11.31 (1A)</td>
<td>470</td>
<td>1</td>
</tr>
<tr>
<td>sY238</td>
<td>ZFY, zinc finger protein</td>
<td>Yp11.31 (1)</td>
<td>350</td>
<td>36</td>
</tr>
<tr>
<td>sY59</td>
<td>DYS559S1</td>
<td>Yp11.3 (3)</td>
<td>267</td>
<td>22</td>
</tr>
<tr>
<td>sY76</td>
<td>AMELY, amelogenin</td>
<td>Yp11.2 (3)</td>
<td>200</td>
<td>36</td>
</tr>
<tr>
<td>sY78</td>
<td>DYZ2</td>
<td>Y centromere (4B)</td>
<td>170</td>
<td>22</td>
</tr>
<tr>
<td>sY90</td>
<td>KALY</td>
<td>Yq11.21 (5E)</td>
<td>176</td>
<td>36</td>
</tr>
<tr>
<td>sY130</td>
<td>DYS221</td>
<td>Yq11.23 (6A)</td>
<td>173</td>
<td>22</td>
</tr>
<tr>
<td>sY254</td>
<td>DAZ, deleted in azoospermia</td>
<td>Yq11.23 (6D)</td>
<td>107</td>
<td>35</td>
</tr>
</tbody>
</table>

FLUORESCENT IN SITU HYBRIDISATION
FISH analysis was performed using a WCP® chromosome painting system Y probe and SpectrumCEP® alpha satellite probes for X and Y (Vysis), labelled with different fluorescent dyes (Spectrum Green™ or Spectrum Orange™, Vysis). Hybridisations were performed on chromosome metaphases from lymphocyte culture or placental cell culture. Hybridisation conditions were: after an initial slide denaturation (five minutes in 70% formamide/2× SSC at 73°C) and dehydration (70/85/100% ethanol), 10 μl of the labelled probe hybridisation buffer mix were applied to each slide before sealing it with a coverslip. Hybridisation took place overnight in a humidified box at 37°C. After a rapid wash in 0.4× SSC at 73°C for two minutes and 2× SSC/0.1% NP-40 at room temperature for one minute, 10 μl of DAPI II counterstain was used. Slides were studied with a fluorescence microscope equipped with a CCD video camera and the Cytovision (Applied Imaging) image analyser.

RESULTS
CYTOGENETIC ANALYSES
Karyotypes were performed by standard procedures from peripheral blood lymphocytes in patients 1-5 (GAG and CBG banding). In the prenatal diagnosis, two successive cytogenetic analyses were performed on amniotic fluid cells at 12.4 and 20 weeks of gestation and confirmed on fetal lymphocytes.

MOLECULAR CHARACTERISATION
DNA was extracted from leucocytes by standard protocols, and from placental cells in the case of fetal DNA. Molecular amplification was performed by PCR using 12 different primer pairs from both arms and the centromere of the Y chromosome (table 2). The reactions contained 100 ng of DNA, 10 mmol/l tris-Cl, pH 8.3, 50 mmol/l KCl, 1.5 mmol/l MgCl₂, 200 μmol/l dNTPs, 10 pmol of each primer, and 1 unit of Taq polymerase in a final volume of 25 μl. Amplification conditions were initial denaturation for five minutes at 94°C, and 30 cycles for 20-30 seconds at 94°C, 30 seconds at 52-65°C, and 30-45 seconds at 72°C (depending on the primer pair used), with a final extension for five minutes at 72°C. After electrophoresis, PCR products were visualised under a UV transilluminator on a 2% agarose gel stained with ethidium bromide. Three oligonucleotides, PAB A, B, C, were simultaneously used in the reaction to detect both X specific and Y specific sequences from the proximal border of the pseudoautosomal region, giving two bands of different size on electrophoresis in normal males and PABY (+) XX males.

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RESULTS
CYTOGENETIC ANALYSES
G banded chromosome spreads showed a 46,XX karyotype in all patients. In the prenatal diagnosis (case 6), a male phenotype was detected prenatally by ultrasonography while the chromosome study on amniocytes showed a female karyotype. Therefore, additional cytogenetic analyses were performed on a second amniotic fluid sample and on fetal blood. After the discrepancy between the karyotype and the phenotype was confirmed, the parents decided to terminate the pregnancy. The examination of the conceptus showed normal external and internal male genitalia, with presence of prostate, epididymis, testes, vas deferens, and cavernous bodies, with no signs of congenital adrenal hyperplasia. The global fetal development was appropriate for the gestational age.
Characterisation of six XX males including one prenatal diagnosis

MOLECULAR STUDIES

PCR analysis proved that the SRY gene was present in all six cases (fig 1A). Other Yp genes or markers (PABY, RPS4Y, ZFY) were also detected in the five cases tested (cases 1-5) (table 1). The marker sY59, in contrast, was present in only one of the XX males tested, indicating the presence of different breakpoints on the Yp chromosome in different patients (fig 1B). As expected, the amplification using markers from the Y centromere (sY78) and from the long arm (KALY, sY130, DAZ) was negative in all patients.

FLUORESCENT IN SITU HYBRIDISATION

In all six cases, the Y chromosome fragment was located at the tip of the short arm of the X chromosome (Xp22.3), using FISH with a painting Y probe and an X centromere probe (fig 2). Hybridisation with a Y centromere probe was negative in all samples, indicating that only the short arm of the Y chromosome is implicated in the X-Y interchange.

Discussion

In this work, we have used cytogenetic analysis, FISH, and molecular amplification to characterise the Y chromosome sequences present in six XX males. All the cases in this study are positive for the SRY gene and other Y specific sequences, which is the most frequent type of XX male reported.7,8 The phenotype described in these cases is that of males with sterility owing to the absence of germinal cells and hypogonadism, without sexual ambiguities, consistent with the clinical data detected in our patients (table 1).

All our patients have the Y chromosome DNA transferred to Xp22.3, as found in all other reported cases.9,11-18,29 This confirms the relative frequency of an Xp/Yp interchange originating through unequal crossing over between homologous pseudoautosomal regions in the paternal meiosis, extending the exchange to sex specific sequences.31-37 Some cases of Y;autosome translocation have been described, conferring maleness to 45,X subjects.38-43 However, to our knowledge, no 46,XX male with a Y;autosome translocation has been reported.

In four cases (2, 3, 4, 5), PABY, SRY, RPS4Y, and ZFY sequences were amplified, while markers sY59, AMELY, sY78, and Yq were negative. In case 1, the sY59 marker was also positive, indicating a Yp breakpoint more proximally. Some authors have reported that the Y sequences present in the XX males extend from distal Yp to the Y centromere, showing a variation in the size of the fragment exchanged from less than 40 kb to more than 11 Mb.44,45 The similarity of the clinical features in all cases confirms that the SRY gene is responsible for testicular determination, and that other genes on the Y chromosome are not so important in defining the phenotype.

The case of a prenatally diagnosed XX male is especially interesting as an example of the problems that may arise in a laboratory when the sexual phenotype of a fetus is different from that expected based on prenatal cytogenetic analysis. In the present case, FISH and molecular studies allowed the confirmation of the XX male diagnosis in the fetus. To our knowledge, this is the first molecular prenatal diagnosis of a Y positive XX male, as the only other prenatal case reported was an XX male fetus lacking any Y sequence.45 Other cases...
were detected only after the birth of a male following a cytogenetic prenatal diagnosis of 46,XX,\(^{34}\) and where postnatal studies allowed the possibility of a sample error or maternal cell contamination to be ruled out.

Molecular and FISH techniques are very useful for detecting and locating Y sequences in cytogenetically XX males, allowing an accurate diagnosis and correct management of the patient. Testing new Y chromosome markers in XX males will make it possible to narrow the breakpoints further in each case and to establish correlations with the clinical features, identifying the Y regions implicated in the definition of the phenotype.

We are grateful to Drs A Rego and R V Garcia-Mayor for providing a blood sample from their patient.


