46,XX, inv(6)(p21.1p23) in a pedigree with hereditary haemochromatosis

Charles P Venditti, Nicole K Seese, Glenn S Gerhard, Amy E Ten Elshof, Karen A Chorney, Philip N Mowrey, Paul G Lacey, Joan H M Knoll, Michael J Chorney

Abstract
Hereditary haemochromatosis (HFE) is a recessive genetic disease of iron overload which has been shown by linkage analysis to reside on the short arm of chromosome 6, close to the major histocompatibility complex (MHC). Positional cloning of the putative HFE locus has been hampered, in part, by the lack of a structural alteration on 6p. In this report, we describe a pedigree with HFE which carries a balanced paracentric inversion of chromosome 6, inv(6)(p21.1p23), a rarely reported chromosomal rearrangement in this region. We have determined the inheritance of the chromosome harbouring the inversion, which segregates as an HFE chromosome. Because the HFE locus has been mapped distal to the HLA-F class I locus at 6p21.3, the breakpoints associated with this chromosomal rearrangement may provide a significant genomic landmark for positional cloning of the HFE gene.

Keywords: hereditary haemochromatosis; human chromosome 6 inversion; major histocompatibility complex.

Idiopathic or hereditary haemochromatosis (HFE) (McKusick No 235200) is an autosomal recessive disease of progressive iron accumulation which can result in cirrhosis, carbohydrate intolerance, cutaneous hyperpigmentation, cardiomyopathy, arthritis, and hypogonadotropic hypogonadism. In certain white populations, the carrier frequency may approximate 5%. Because the expression of the HFE defect is partially dependent on dietary factors and gender, the definitive diagnosis of HFE can be clinically challenging in predisposed people. The identification of the mutation(s) causing HFE may allow for the assignment of more certain clinical diagnoses.

The genetic defect in HFE has been linked to the human leucocyte antigen A locus (HLA-A), which resides at the telomeric end of the major histocompatibility complex (MHC) class I region. The precise location of the HFE gene is not known at present, but has been the subject of several recent genetic mapping experiments. The results of a series of linkage and linkage disequilibrium studies indicate that the HFE gene is associated with polymorphisms defined by the microsatellite D6S105, but, based on defined recombinants, may reside anywhere between the HLA-F gene and the telomeric microsatellite D6S299, which is approximately 4 cM from the HLA-A locus. Our own data, based on the study of an American patient collection, support the localisation of the HFE locus between markers D6S464 and D6S1558, but most likely close to D6S1260; this is in general agreement with data obtained by Raha-Chowdhury et al. Aside from an HLA-A locus subregional deletion, no other structural rearrangement of chromosome 6 has been reported in a patient with HFE.

In the present report, we describe a pedigree with HFE which carries an inv(6)(p21.1p23) chromosome. We show by cytogenetic and molecular genetic analysis the inheritance of this chromosome in this family and discuss the relevance of the chromosomal abnormality to the mapping of the HFE disease gene.

Materials and methods
In order to establish cell lines, 20 cc of peripheral blood was obtained from volunteer patients (consent forms, approved by the Institutional Review Board of the Pennsylvania State University College of Medicine (IRB Protocol No 93-140 EP) were reviewed and signed by all participants). Lymphocytes were purified from these samples using Ficoll-Paque Plus (Pharmacia, Uppsala, Sweden) according to the manufacturer’s protocol and immobilised with Epstein-Barr virus (EBV). Each line used in this study was then serologically typed for HLA-A and HLA-B antigens in the Milton S Hershey Medical Center’s Histocompatibility Laboratory.

Standard PHA stimulated lymphocyte chromosome preparations were made from peripheral blood lymphocytes from the proband and her brother. Karyotypes of the proband’s children were performed as part of a conventional amniocentesis protocol. Analysis of prometaphase chromosomes from the proband’s established B lymphocyte lines using GTG banding (Giemsa-trypsin) was performed as previously described. DNA was isolated from the proband’s cell line by conventional methods.

DNA was also obtained from paraffin-embedded tissue sections from archival (1992) necropsy material from the proband’s mother and from similar archival (1979) material from a prostate biopsy from the proband’s father. Ten μm sections were deparaffinised in xylene followed by proteinase K digestion at 55°C.
Haemochromatosis and inv(6)(p21.1p23)

Table 1  Response of proband (patient 1.2) to phlebotomy treatment. Following repeated abnormal serum iron indices, 1900 ml of blood were withdrawn over an almost two year period resulting in normalisation of iron parameters

<table>
<thead>
<tr>
<th>Date</th>
<th>Ferritin (10-100 ng/ml)</th>
<th>Iron (50-125 μg/ml)</th>
<th>TIBC (200-352 μg/ml)</th>
<th>Saturation (20-50%)</th>
<th>Phlebotomy</th>
</tr>
</thead>
<tbody>
<tr>
<td>July 1990</td>
<td>107</td>
<td>199</td>
<td>210</td>
<td>94.8</td>
<td></td>
</tr>
<tr>
<td>January 1991</td>
<td>108</td>
<td>217</td>
<td>210</td>
<td>99.1</td>
<td></td>
</tr>
<tr>
<td>September 1991</td>
<td>114</td>
<td>222</td>
<td>214</td>
<td>100</td>
<td>&lt; -1000 ml</td>
</tr>
<tr>
<td>September 1992</td>
<td>57</td>
<td>163</td>
<td>237</td>
<td>69</td>
<td>&lt; -900 ml</td>
</tr>
<tr>
<td>July 1993</td>
<td>7</td>
<td>83</td>
<td>271</td>
<td>31</td>
<td></td>
</tr>
</tbody>
</table>

DNA was then purified by standard phenol-chloroform extraction.
Polymerase chain reaction (PCR) analysis of DNA was performed using primers to amplify 12 polymorphic microsatellite markers spanning the MHC to D6S299 interval as described previously.8

Case report
The proband (patient 1.2) is a 43 year old, G2 P2002, premenopausal female with a history of infertility and polycystic ovarian disease. Her menstrual history was completely regular (28 day cycle, five day period) until the birth of her children, when the cycle length shortened. Following surgical removal of one ovary and fallopian tube and wedge resection of the other ovary, patient 1.2 became pregnant in 1985 by artificial insemination and a routine amniocentesis performed during this pregnancy showed a fetal 46,XX, inv(6)(p21.1p23) karyotype. Subsequent chromosomal analysis showed that the mother (proband) carried the same inverted chromosome as the fetus. The proband’s second pregnancy was without complications; the healthy infant (born in 1987) also carried the inversion chromosome.

Apart from polycystic ovarian disease, the proband had no other documented or suspected medical problems until 1990. At that time, a routine laboratory panel indicated several abnormal iron indices; these included a raised total iron of 199 μg/dl (range 50–125 μg/dl), total iron binding capacity of 210 μg/dl (range 200–352 μg/dl), a transferrin saturation of 94.8% (range 20–55%), and a ferritin level of 107 ng/ml (range 10–300 ng/ml) in an otherwise asymptomatic, healthy female. Over the following years, these tests were repeated every two months and on all occasions total iron and transferrin saturation remained abnormally high. During this period, the proband’s 82 year old mother (patient 1.1) died and necropsy showed cardiomegaly with underlying cardiac fibrosis and hypertrophy, haemochromatosis with diffuse 4⁺ hepatic cellular iron deposition (evidenced through Prussian Blue staining based upon a severity score range of 1–4⁺), and bronchopneumonia. The cause of death was attributed to dysrhythmia. After considering the maternal necropsy results and available data which suggest that raised transferrin saturation is a sensitive and specific indicator of homozygous haemochromatosis,15–17 the diagnosis of idiopathic haemochromatosis in patient 1.2 was assigned. The HFE disease status of the proband’s dead father is not known.

The proband’s 57 year old brother (patient 1.3) was examined and noted to have an increased total serum iron (195 μg/dl), an increased transferrin saturation (77.4%), raised levels of ferritin (484 ng/ml) and transferrin (248 mg/dl), and a total iron binding capacity of 252 μg/dl. Karyotype analysis showed that he also carried the same paracentric inversion as patient 1.2. The proband’s two children, carriers of the inversion chromosome, were also tested and found to be normal with respect to serum iron indices (serum irons of 86 and 85 μg/dl, total iron binding capacities of 294 and 309 μg/dl, transferrin saturations of 29.3 and 27.5%, and ferritin levels of 18 and 9 ng/ml).

Both the proband and her brother are currently being treated by phlebotomy with appropriate restoration of serum iron indices towards normal values (table 1). Liver biopsies have been offered and refused by both patients.

HLA, cytogenetic, and molecular genetic results
Fourteen metaphase cells from the proband’s immortalised lymphocytes were re-examined. Representative chromosome 6 pairs are shown in fig 1 and the paracentric inversion of chro-

![Figure 1](http://example.com/figure1.png)

Figure 1  Representative G banded chromosomes 6 from the proband. Pairs of G banded chromosomes are shown on the left; the chromosomes carrying the paracentric inversion (inv(6)(p21.1p23)) is marked by an asterisk. An ideogram of chromosome 6 is shown. The breakpoints are indicated by arrows.
mosome 6 (inv(6)(p21.1p23)) was confirmed. A pedigree is presented in fig 2 along with HLA typing, karyotype, and transferrin saturation results. By combining the results of HLA haplotype and karyotype studies (fig 2), we determined that the inversion chromosome possesses the HLA-A24 and HLA-B51 MHC class I alleles. The results of PCR microsatellite analysis of the proband and her parents are shown in table 2. Marker D6S265, located 70 kb centromeric to HLA-A18, is tightly linked to various HLA-A alleles. The occurrence of allele 1 in marker D6S265, in addition to other markers through D6S1260 (700 kb telomeric to D6S105), indicates that the proband inherited a "common" HFE HLA-A3 associated chromosome from her mother. The atypical HLA-A24 associated HFE inversion chromosome appears to be of paternal origin (fig 3).

Discussion

Mapping and positional cloning efforts to identify the HFE gene have recently accelerated. Several linkage disequilibrium studies and recombinant subjects have narrowed the HFE critical region to the genomic expanse between the HLA-F locus (centromeric) and the microsatellite marker D6S299 (telomeric). Results using geographically and ethnically different control and patient populations point towards different areas within this region. Whether the breakpoints of the inversion chromosome reported here fall within this region is of prime interest.

The paucity of reported inversions associated with the short arm of chromosome 6 suggests an enhanced stability of such rearrangements within this region. The location of the MHC and the lack of meiotic recombination associated with certain HLA haplotypes supports this observation. Recombination in paracentric inversion heterozygotes is also reduced because acentric and deletion products resulting from crossing over within the inversion loop of meiotically paired homologous chromosomes are usually lost. The occurrence of this inversion in two sibs and in the children of the proband suggests that this particular chromosomal rearrangement has been stably transmitted through at least two generations.

The serological markers encoded by the polymorphic HLA genes could not conclusively predict the parental origin of the chromosome.

Table 2 Results of PCR analysis of polymorphic microsatellite loci in DNA from the proband and her parents. VNDR allele assignments and PCR conditions have been previously described. The configuration of alleles the proband inherited from her mother are consistent with an HFE-associated HLA-A3 carrying chromosome. The inversion chromosome is thus inferred to have been transmitted by the father.

<table>
<thead>
<tr>
<th>Locus</th>
<th>Marker name</th>
<th>Type</th>
<th>Allele sizes (bp)</th>
<th>Mother</th>
<th>Proband</th>
<th>Father</th>
</tr>
</thead>
<tbody>
<tr>
<td>D6S265</td>
<td>AFM101X1A1</td>
<td>(CA)n</td>
<td>122-144</td>
<td>1.1</td>
<td>1.3</td>
<td>3.3</td>
</tr>
<tr>
<td>D6S306</td>
<td>AFM248XH1</td>
<td>(CA)n</td>
<td>236-250</td>
<td>4.4</td>
<td>4.4</td>
<td>4.5</td>
</tr>
<tr>
<td>D6S105</td>
<td>MFD61</td>
<td>(CA)n</td>
<td>116-138</td>
<td>5.5</td>
<td>5.10</td>
<td>10.5</td>
</tr>
<tr>
<td>D6S464</td>
<td>AFM243VB5</td>
<td>(CA)n</td>
<td>202-230</td>
<td>3.3</td>
<td>3.3</td>
<td>3.8</td>
</tr>
<tr>
<td>D6S1260</td>
<td>CS-S</td>
<td>(CA)n</td>
<td>144-166</td>
<td>4.4</td>
<td>4.4</td>
<td>4.3</td>
</tr>
<tr>
<td>D6S1558</td>
<td>AFMA99WG9</td>
<td>(CA)n</td>
<td>251-271</td>
<td>4.5</td>
<td>5.5</td>
<td>5.5</td>
</tr>
<tr>
<td>D6S1016</td>
<td>GGA101G12</td>
<td>Tetra</td>
<td>236-260</td>
<td>1.1</td>
<td>1.6</td>
<td>6.5</td>
</tr>
<tr>
<td>D6S1281</td>
<td>GATA9PB7</td>
<td>Tetra</td>
<td>176-208</td>
<td>7.5</td>
<td>5.5</td>
<td>5.4</td>
</tr>
<tr>
<td>D6S1545</td>
<td>AFMA11Z1E1</td>
<td>(CA)n</td>
<td>225-233</td>
<td>2.2</td>
<td>2.2</td>
<td>2.4</td>
</tr>
<tr>
<td>D6S1554</td>
<td>AFMA183WB5</td>
<td>(CA)n</td>
<td>162-176</td>
<td>2.1</td>
<td>1.1</td>
<td>1.2</td>
</tr>
<tr>
<td>D6S276</td>
<td>158.3/158.5</td>
<td>(CA)n</td>
<td>198-228</td>
<td>8.9</td>
<td>9.9</td>
<td>9.8</td>
</tr>
<tr>
<td>D6S299</td>
<td>AFM217XG7</td>
<td>(CA)n</td>
<td>210-234</td>
<td>10.10</td>
<td>10.7</td>
<td>7.1</td>
</tr>
</tbody>
</table>

Figure 2: Pedigree of the family with inv(6). The proband is indicated with an arrow. Shadowing refers to the haemochromatosis state (questionable in the proband's father, although he must be considered to be at least an obligate carrier), with half shading illustrating carriers in the pedigree. Inv indicates that the subject harbour the inv(6) chromosome. Iron saturation in the table on the right indicates the percentage of transferrin bound with iron; the normal range of this value is 20-55%. NA = not available for analysis.

Figure 3: Scale map of the MHC class I region and distal markers used to determine the inheritance of the inversion chromosome. The order and relative positions of the markers are approximate but based on available mapping data. Previous linkage disequilibrium mapping analysis showed the probable position for the haemochromatosis disease gene to be close to marker D6S1260.
Haemochromatosis and inv(6)(p21.1p23)

This work was supported by grants from the Hackett Foundation (MJC), the March of Dimes (Basic Research Award) (MJC), the NIH (NIDDK No 1 R01 DK43734-01A2; MJC); HD 16468 (JHMK)); a Penn State College of Medicine Clinical Research Grant 95-43 (GSG), and the Beth Israel Pathology Foundation, Inc (JHMK). The authors would like to thank Dr John-Ves Le Gall, Dr Roger Ladda, and Ms Patricia Plana for their helpful suggestions. The authors also thank the Department of Pathology of Queen’s Medical Center of Honolulu (HA) and Prince George’s Hospital Center (CQ) (NIH/CEPH) for archival material. Dr Magdik Krikker (President of the Haemochromatosis Foundation) and Ms Roberta Crawford (President of the Iron Overload Diseases Association, Inc) are also acknowledged for their continued interest and support.