Autosomal recessive erythropoietic protoporphyria in the United Kingdom: prevalence and relationship to liver disease


Erythropoietic protoporphyria (EPP; MIM 177000) is an inherited disorder of haem biosynthesis characterised by the onset in early childhood of lifelong acute photosensitivity of sun-exposed skin. It results from partial deficiency of ferrochelatase (FECH; E.C. 4.99.1.1.), which leads to accumulation of protoporphyrin IX in erythrocytes, plasma, skin, and liver. Up to 35% of patients have mildly abnormal biochemical tests of liver function, while liver failure caused by the hepatotoxic action of protoporphyrin complicates about 2% of cases. Over 70 mutations in the FECH gene have been identified in EPP families (Human Gene Mutation Database: http://www.hgmd.org/). Most individuals who are heterozygous for these mutations are asymptomatic, despite having normal FECH activities. For protoporphyrin to accumulate sufficiently to cause photosensitivity, reduction of FECH activity to below a critical threshold of about 35% of normal is required.

In most patients, this additional reduction results from inheritance of a low expression FECH allele trans to a severe mutation. The low expression allele is the C variant of a single nucleotide polymorphism (SNP; IVS3-48C/T) in intron 3 of the FECH gene. Because the IVS3-48C allele is common in the general population, being present in about 11% of the white inhabitants of France, inheritance trans to a severe FECH mutation occurs within EPP families at a frequency that is high enough to produce a pattern of inheritance of overt EPP resembling an autosomal dominant disease with incomplete penetrance.

Although co-inheritance of an IVS3-48C allele appears to explain the occurrence of photosensitivity in most EPP families, alternative mechanisms may reduce FECH activity to below threshold activity in some patients. These include autosomal recessive inheritance with an FECH mutation on both alleles, deletion of an FECH gene secondary to haematological malignancy, and a dominant-negative effect from the mutant FECH allele.

The prevalence of autosomal recessive EPP has not been established. FECH measurements in small numbers of families suggest that up to 20% of patients may have autosomal recessive disease, but mutational analysis of patients with EPP suggests a lower frequency of mutations on both alleles have been identified in only three families. In one of these families, two siblings developed liver failure and it has been suggested that severe FECH mutations on both alleles may predispose to end stage liver disease during adolescence. This suggestion has been disputed on the grounds that protoporphyric liver disease was not present in the two other families with autosomal recessive EPP and that all other patients with severe liver disease in whom mutations have been identified have been heterozygotes.

Here we describe the molecular investigation of 105 randomly selected patients with EPP and one patient with liver disease caused by EPP. We show that the prevalence of autosomal recessive disease among patients with EPP in the United Kingdom is 3% (95% confidence interval: 1 to 7); that this mode of inheritance is the usual explanation for overt EPP in patients without an IVS3-48C allele; autosomal recessive EPP may carry a much higher risk of severe liver disease than the more usual form; and that EPP in patients with an FECH mutation on one allele is indistinguishable from EPP in which an FECH mutation on the other allele.

Key points

- Erythropoietic protoporphyria (EPP) is an inherited disorder of haem biosynthesis resulting from partial deficiency of ferrochelatase (FECH) and characterised by early onset of lifelong acute photosensitivity.
- Over 70 mutations in the FECH gene have been identified in EPP families. Inheritance of an IVS3-48C allele trans to the mutation appears to explain photosensitivity in most families, though alternative mechanisms sometimes may be involved.
- A total of 105 randomly selected patients with EPP and one patient with liver disease caused by EPP were molecularly investigated.
- The prevalence of autosomal recessive disease among patients with EPP in the United Kingdom is 3% (95% confidence interval: 1 to 7). This mode of inheritance is the usual explanation for overt EPP in patients without an IVS3-48C allele; autosomal recessive EPP may carry a much higher risk of severe liver disease than the more usual form.
- Autosomal recessive EPP appears to be clinically indistinguishable from EPP in which an FECH mutation on one allele is trans to a low expression IVS3-48C allele.

Abbreviations: ALT, alanine aminotransferase; AST, aspartate transaminase; EPP, erythropoietic protoporphyria; FECH, ferrochelatase; GGT, gamma glutamyl transpeptidase; SNP, single nucleotide polymorphism

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Quikchange mutagenesis (Stratagene) was employed to characterise the in vitro activity of the mutant FECHs.

RESULTS

Case report

Patient A presented at 4 years of age with itching, painful erythema and swelling affecting sun-exposed skin which had been occurring from the age of 1 year. The eruption started each year in early spring, persisted during the summer months, and then subsided. There was no family history of photosensitivity. On examination, there was mild linear and varioliform scarring over the nose. His erythrocyte protoporphyrin concentration was increased at 17.4 μmol/l with normal urinary porphyrin, porphobilinogen, and 5-aminolaevulinate concentrations, confirming the clinical diagnosis of EPP. Advice was given about the use of sunblock creams and appropriate protective clothing. At 6 years of age, he was commenced on beta-carotene due to worsening symptoms during the summer months. Biochemical tests of liver function were mildly deranged: aspartate transaminase (AST) 59 IU/l (normal: 5–45 IU/l), alanine aminotransferase (ALT) 75 IU/l (normal: 5–40 IU/l), total bilirubin 16 μmol/l (normal: 1–22 μmol/l).

At the age of 9 years, he was admitted to hospital during July with a painful, red, swollen face, abdominal discomfort, and loose stools. On examination, he had tender erythema and oedema of his face, associated with linear scarring on the nose and cheeks, and extensive varioliform scarring on the forehead and dorsal aspects of his hands. His haemoglobin was 11 g/dl with mild hypochromia and microcytosis. Biochemical tests of liver function were normal. His symptoms settled rapidly and annual desensitisation with ultraviolet-B phototherapy was initiated to improve his restricted lifestyle.

Evidence of increasing liver damage was first noted at the age of 12 years: AST 109 IU/l, ALT 184 IU/l, gamma glutamyl transpeptidase (GGT) 131 IU/l (normal: 5–30 IU/l), and total bilirubin 7 μmol/l. Erythrocyte protoporphyrin was 36.0 μmol/l, plasma protoporphyrin 83 nmol/l (normal: <10 nmol/l). He complained of recurrent abdominal discomfort over the next 3 months. An abdominal ultrasound scan was normal. He was started on cholestyramine 4 g daily. By the age of 13 years, his symptoms had worsened, with an episode of painful, swollen arms after walking outside for just 10 min on a cloudy day. His erythrocyte and plasma protoporphyrin had increased to 45.7 μmol/l and 727 nmol/l, respectively, and there was evidence of further liver damage: AST 219 IU/l, ALT 319 IU/l, GGT 255 IU/l, and total bilirubin 18 μmol/l. His haemoglobin was 11.2 g/l and ferritin 18 μg/l. He was referred for early assessment as a potential candidate for liver transplantation. A liver biopsy was not considered necessary at this stage. His symptoms are well controlled 1 year later (AST 106 IU/l, ALT 164 IU/l, GGT 125 IU/l).

Analysis of genomic DNA from patient A and his asymptomatic mother (erythrocyte protoporphyrin: 1.2 μmol/l) showed him to be a compound heterozygote for the IVS3-48C/T polymorphism and the IVS3-48C/T SNP. The mutation was confirmed by sequencing both strands. Fluorescence dosage analysis of exon 4 of the FECH gene was carried out using exon 17 of the DMD gene as an internal standard and exon-specific primers, one of each pair labelled with 5′FAM. Fluorescent PCR products were separated and quantified with an ABI Genescan 310 analyser.

Expression and characterisation of mutant FECHs

To characterise the in vitro activity of the mutant FECHs, Quikchange mutagenesis (Stratagene) was employed to recreate the mutations in the previously described wild type ferrochelatase expression plasmid, pHiStTF20E. The mutant enzymes were purified as described previously. Enzyme activity was measured using a real time direct spectroscopic assay.

Other methods

Erythrocyte and plasma porphyrins were determined by standard methods.

Numbering system

Nucleotides are numbered from the cDNA sequence of human FECH (GenBank accession number D00726) with the A of the ATG initiation codon as “+1”.
Table 1  
FECH alleles in autosomal recessive EPP

<table>
<thead>
<tr>
<th>Patient</th>
<th>Allele 1</th>
<th>Allele 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>215T&gt;C</td>
<td>[L299]; IVS3-48T</td>
</tr>
<tr>
<td>B</td>
<td>416A&gt;T</td>
<td>[Q139L]; IVS3-48T</td>
</tr>
<tr>
<td>C</td>
<td>707G&gt;A</td>
<td>[C236Y]; IVS3-48T</td>
</tr>
<tr>
<td>E</td>
<td>1636G&gt;T</td>
<td>[G55C]; IVS3-48C or T*</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>FECH expression in E. coli of mutant and wild type</th>
</tr>
</thead>
<tbody>
<tr>
<td>FECH</td>
<td>Percent wild type activity</td>
</tr>
<tr>
<td>mutation</td>
<td>min/nmol mesohaem/100</td>
</tr>
<tr>
<td>Wild type</td>
<td>2.5, 2.7</td>
</tr>
<tr>
<td>C[139L]</td>
<td>0.46</td>
</tr>
<tr>
<td>C[236Y]</td>
<td>0.36</td>
</tr>
<tr>
<td>F[260L]</td>
<td>1.36</td>
</tr>
<tr>
<td>K[379N]</td>
<td>0.97</td>
</tr>
</tbody>
</table>

*Heterozygous for IVS3-48C/T SNP, phase not determined.

Identification of autosomal recessive EPP

Three unrelated patients (patients B, C, and D) with overt EPP had not inherited the low expression IVS3-48C allele (table 3). Patients B and C had a sibling with EPP, but none had any other family history of the disease or parents known to be consanguineous. To investigate the molecular mechanism for EPP in these patients, we sequenced their FECH genes. Sequence and allele dosage analysis showed that patient B was homozygous for a novel missense mutation in exon 4 (416A>T [Q139L]) (table 1). Patient C was found to be a compound heterozygote for novel missense mutations in exon 7 (707G>A [C236Y]) and exon 10 (1137G>C [K379N]) (table 1). Activities of the Q139L, C236Y, and K379N mutants ranged from 12% to 50% of the activity of wild type enzyme (table 2).

Family investigation showed that the low expression IVS3-48C allele was present in only 13% of the control group (allele frequency: 6.5%), a figure close to the 11% found for the white French population.19

Table 3 shows that there is a strong association between the low expression IVS3-48C allele and clinically manifest EPP in UK patients (χ² = 97; p<0.001), as recently reported for French20 and Swedish21 patients. A total of 102 (97%) of our 105 patients had at least one IVS3-48C allele whereas this allele was present in only 13% of the control group (allele frequency: 6.5%), a figure close to the 11% found for the white French population.19

DISCUSSION

Previously, only three EPP families have been identified in which patients had mutations on both alleles.20–22 Here we describe an additional four unrelated patients with autosomal recessive EPP, as defined by the presence of a deleterious FECH mutation on both alleles (tables 1 and 2).

To determine the prevalence of autosomal recessive EPP, we have carried out the first investigation of a large, randomly selected group of unrelated patients for the presence of mutations on both FECH alleles. Because detailed analysis of the complete 45 kb FECH gene in such a large group of patients was not practicable, we initially screened for the presence of IVS3-48C alleles and then carried out mutational analysis on patients lacking this allele. Implicit in this strategy is the assumption that all patients having an IVS3-48C allele are heterozygous for a disabling FECH mutation. Although there is support for this assumption from previous studies of EPP families,16–18 we checked that it held for our patients by sequencing the FECH gene in a randomly selected subgroup of 14 patients who had inherited an IVS3-48C allele.

Using this approach, we identified autosomal recessive EPP in three of 105 patients to give a minimum prevalence of 3% (95% confidence interval: 1 to 7%) for this pattern of inheritance in UK families. This figure is consistent with previous evidence from molecular analysis of the FECH gene that autosomal recessive EPP is uncommon.20–22 It suggests that family studies based on FECH activity alone20–22 overestimated its frequency, possibly due to the inherent imprecision of FECH measurement and the consequent difficulty of distinguishing between the effect of a low expression IVS3-48C allele and an FECH mutation.

Our data also provide independent confirmation of the recent report by Gouya et al23 that clinically overt disease is strongly associated with inheritance of an IVS3-48C allele (table 3). This finding supports the hypothesis that clinical expression of EPP usually requires this allele trans to a severe FECH mutation.18 In the small number of patients with the IVS3-48C/T genotype, other mechanisms must be responsible for decreasing FECH activity to below the threshold for photosensitivity. In our series, three of four patients with this genotype had FECH mutations on both alleles suggesting that autosomal recessive disease is the usual explanation. The most important complication of EPP is liver disease, caused by accumulation of protoporphyrin in the liver and usually progressing rapidly to death from end stage liver failure unless treated by orthotopic liver transplantation.24–25 This complication occurs in about 2% of patients but, at present, there is no reliable method for the early detection of those at high risk.

One of our patients (patient A) with autosomal recessive disease was identified because molecular analysis was prompted by clinical and biochemical features characteristic of the initial phase of protoporphyric liver disease during which failure of hepatic excretion leads to increasing
accumulation of protoporphyrin in the liver and progressive liver damage.\textsuperscript{5,57} Liver disease in EPP may be associated with particularly low FECH activities.\textsuperscript{2,21} The missense mutation (F260L) in our patient decreased FECH activity to 50\% of normal (table 2) and was trans to a null (L72X) mutation. Assuming a similar effect in human cells in vivo, the predicted FECH activity in this patient would be about 25\% compared to about 34\% for L72X trans to an IVS3-48C allele.

Our findings support the view that autosomal recessive EPP carries a higher risk of severe liver disease than other forms of EPP.\textsuperscript{21} Liver disease has complicated EPP in two of the seven families proven by molecular analysis to have autosomal recessive disease\textsuperscript{20,21,23} (table 1). Analysis of the mutations in 19 unrelated patients with severe liver disease who were heterozygous for FECH mutations has shown that missense mutations are present in only two of 19 patients, whereas about 25\% of all mutations identified in EPP are missense mutations.\textsuperscript{9,22} In this context, it is intriguing that two of the three patients with autosomal recessive EPP who did not have missense mutations on both alleles have both had liver disease\textsuperscript{21} (table 1).

All our patients with autosomal recessive disease had a missense mutation on at least one allele (table 1). Of the six missense mutations in our patients, only two have previously been identified: G55C in a compound heterozygote with autosomal recessive disease\textsuperscript{20,21,23} and P334L as the only mutation in a patient with EPP.\textsuperscript{6} The P334L mutant was shown to have 19\% of normal activity.\textsuperscript{6} The four novel mutations that we identified all retained some FECH activity (12–50\% of normal; table 2). In contrast, functional studies of missense mutations previously identified on only one allele in EPP, apart from P334L, have shown much lower or undetectable FECH activities.\textsuperscript{9,22,24} Some or all of the milder mutations that we identified may only cause disease in homozygotes or when trans to another FECH mutation and thus be truly recessive. The functionally most severe missense mutation that we identified (C236Y) (table 2) had not caused clinically overt EPP when trans to an IVS3-48C allele in the father of patient C indicating that this combination, and presumably similar combinations with less severe mutations, may not lead to disease in heterozygotes.

In conclusion, autosomal recessive EPP appears to be clinically indistinguishable from EPP in which an FECH mutation on one allele is trans to a low expression IVS3-48C allele but may carry a much higher risk of severe liver disease. In practice, screening all new patients with EPP for absence of the IVS3-48C allele to select those with the T/T genotype for mutational analysis of the FECH gene should identify most patients with autosomal recessive disease. Such patients can then be managed clinically with particular attention to their high risk of liver disease.

ACKNOWLEDGEMENTS
We thank Professor J-C Deybach, INSERM U 409, Hopital Louis Mourier, Colomnes, France, for providing information about the FECH IVS3-48C/T SNP in advance of publication. Part of the work was carried out as the project component of the MSc in Clinical Biochemistry and Molecular Biology of the University of Surrey undertaken by MK.


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