A new locus for hereditary haemorrhagic telangiectasia (HHT3) maps to chromosome 5
S G Cole, M E Begbie, G M F Wallace, C L Shovlin

Patients with hereditary haemorrhagic telangiectasia (HHT, or Osler-Weber-Rendu syndrome) have variable presentation patterns and a high risk of preventable complications. Diagnostic tests for mutations in endoglin (HHT type 1) and ALK-1 (HHT type 2) are available. Some HHT patients are known to have HHT-jugular polypsis overlap syndrome due to Smad4 mutations. Families were ascertained following the presentation of probands for embolization of pulmonary arteriovenous malformations. Genome-wide linkage studies using over 700 polymorphic markers, and sequencing of candidate genes, were performed. In a previously described HHT family, linkage to endoglin was excluded, and no mutations were identified in the endoglin, ALK-1, or Smad4 genes. Two point LOD scores and recombination mapping identified a 5.4 cM HHT3 disease gene interval on chromosome 5 in which a single haplotype was inherited by all affected members of the pedigree. The remainder of the genome was under investigation. We are currently studying a further family potentially linked to HHT3. We conclude that classical HHT with pulmonary involvement can result from mutations in an unidentified gene on chromosome 5. Identification of HHT3 should further illuminate HHT pathogenic mechanisms in which aberrant transforming growth factor (TGF)-β signalling is implicated.

Hereditary haemorrhagic telangiectasia (HHT, also known as Osler-Weber-Rendu syndrome) is one of the most common autosomal dominant disorders, affecting between 1 in 5000 and 1 in 8000 people in Europe and Japan.3,4 HHT is a genetically heterogeneous group of disorders that lead to common vascular phenotypes. HHT types 1 and 2 have been recognised for more than a decade. HHT1 (OMIM 187300) results from mutations in endoglin on chromosome 9, whereas the disease gene for HHT2 (OMIM 600376) is ALK-1 on chromosome 12.5 In addition, mutations in Smad4/MADH4 causing a juvenile polypsis/HHT overlap syndrome (JPHT; OMIM 175050) have been described recently.6 Although the existence of a third “pure” HHT locus has been suggested twice,7,8 the first family was subsequently demonstrated to have an ALK-1 mutation,9 and further data on the family described by Wallace and Shovlin10 have not been presented.

All forms of HHT result in the development of abnormal blood vessels including telangiectasia of the oral mucous membranes, nose, and gastrointestinal tract, and visceral arteriovenous malformations (AVMs). Nosebleeds and chronic gastrointestinal bleeding leading to iron deficiency anaemia and transfusion dependence are the features of HHT most appreciated by clinicians. Visceral AVMs are usually silent, but screening programmes indicate that pulmonary AVMs occur in 30–50% of HHT patients,10–12 cerebral AVMs in 10%,13 and hepatic AVMs in 20–30%.14 Pulmonary AVM-induced embolic strokes and brain abscesses, and cerebral AVM-induced haemorrhagic strokes make HHT a common cause of inherited stroke in young adults,15 and complications from other visceral involvement, including hepatic failure, also occur. There are subtle differences in the phenotype between HHT1 and HHT2, with HHT2 patients exhibiting fewer pulmonary AVMs and a milder HHT phenotype,16 but carrying a higher risk of development of HHT related pulmonary arterial hypertension17 (table 1).

Importantly, many of the complications of HHT can be prevented or limited by clinical screening programmes. Since HHT is a disease with late onset penetrance (≈90% by 40 years; 97% by 60 years15), genetic screening programmes have been introduced.18 Patients without detectable mutations in endoglin or ALK-1 are recognised by the HHT genetic centres. It would be predicted that some of these, particularly from smaller families will have Smad4 mutations since routine colonoscopies that would exclude juvenile polypsis are not a feature of HHT management. In this group, there would be additional clinical screening implications, since for at risk members of juvenile polypsis (JP) families, the British Society of Gastroenterology recommends surveillance colonoscopies and upper gastrointestinal endoscopies, with therapeutic interventions to reduce later risks of colon cancer.19

The pathogenic mechanisms involved in the development of the HHT vessels are of interest to scientists and clinicians alike. Endoglin and ALK-1 encode proteins expressed predominantly on vascular endothelial cells. Endoglin, ALK-1, and the ubiquitously expressed Smad4 are involved in signalling by the transforming growth factor (TGF)-β superfamily that regulates a diverse series of fundamental pathways in development and pathophysiology. A simplified model of Smad dependent signalling by this superfamily is presented in fig 1, indicating the interactions and functions of the HHT gene products. Ligands signal through heteromeric complexes comprised of type I and type II cell surface receptor serine-threonine kinases.20 Activated type I receptors phosphorylate cytoplasmic receptor associated Smad proteins (R-Smads). These oligomerise with a co-Smad molecule, Smad4, and translocate to the nucleus to act as transcription factors and alter gene expression.

In view of the clinical implications of the new molecular association of HHT with juvenile polypsis, we consider it important to report the linkage analysis in the classical HHT pedigree described by Wallace and Shovlin.7 This identifies a

Abbreviations: AVMs, arteriovenous malformations; CM-AVM, capillary malformation-artefiovenous malformation; EBV, Epstein-Barr virus; EC, endolethelial cells; HBT, hereditary benign telangiectasia; HHT, hereditary haemorrhagic telangiectasia; HHT1, HHT type 1; HHT2, HHT type 2; JP, juvenile polypsis; JPHT, juvenile polypsis/HHT overlap syndrome; R-Smads, receptor-associated Smad proteins; TGF-β, transforming growth factor-β
new HHT gene locus (HHT3) on chromosome 5, resulting in four known types of HHT (table 1).

**METHODS**

**Pedigrees**

The proband (fig 2, III.3) was referred to the Hammersmith Hospital for embolization of pulmonary arteriovenous malformations (AVMs). Extended pedigree analysis was performed with informed consent and Multicentre and Local Research Ethics Committee approval (MREC/98/0/42; LREC 99/5637M). The diagnosis of HHT was assigned by the presence of three international consensus diagnostic criteria, that is: affected first degree relative; recurrent, spontaneous nosebleeds; mucocutaneous telangiectasia; and in the case of III.3 and III.4, documented visceral manifestations (pulmonary AVMs). Importantly, telangiectasia were considered diagnostic only if in the correct distribution for HHT (that is, nose, lips, tongue, oral mucosa, finger tips, or ears) and persistent, having developed from late childhood or during adult life. In view of nosebleeds affecting 8–10% of children, with nocturnal nosebleeds a common feature, occasional nosebleeds occurring purely in childhood were not considered a diagnostic criterion.

**Genotyping and molecular analyses**

Genomic DNA was extracted from peripheral venous blood or Isocode mouth swabs (Schleicher and Schuell, Dassel, Germany) using standard procedures. cDNA was derived from Ebstein-Barr virus (EBV) immortalised lymphocyte cell lines which were established on four family members as previously.

A total of 400 fluorescently labelled primer pairs from the ABI Prism Linkage MD-10 Mapping Set (Applied Biosystems, Foster City, CA) were used according to the manufacturer’s instructions for a first genome-wide linkage screen. An additional 312 fluorescently labelled polymorphic markers pre-labelled from Applied Biosystems and Research Genetics (Huntsville, AL), or custom synthesised by Sigma-Genosys (Cambridge, UK), were used to fine-map the identified interval, and exclusion map the remainder of the genome. PCR products were size separated on a ABI 7700 capillary sequencer, and analysed using GeneScan software (Applied Biosystems). Candidate genes were analysed by PCR amplification of all exons, exon-intron boundaries, and 40–50 bp of flanking intronic sequence (endoglin, ALK-1, Smad4, Smad5), or by sequencing the entire cDNA from EBV immortalised lymphocyte cell lines (SPARC). Primer details are available on request.

Two point LOD scores between a putative disease locus and each marker were calculated assuming autosomal dominant inheritance, a disease gene frequency of 0.0001, and equal recombination rates in both sexes. LOD scores were calculated initially with equal allele frequencies. Based on previously published estimates, for unaffected individuals,

<table>
<thead>
<tr>
<th>Table 1</th>
<th>HHT genes and pattern of HHT</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>HHT</strong></td>
<td><strong>HHT features</strong></td>
</tr>
<tr>
<td>HHT1</td>
<td>Classical HHT</td>
</tr>
<tr>
<td>HHT2</td>
<td>Classical HHT</td>
</tr>
<tr>
<td>JPHT</td>
<td>Juvenile polyposis</td>
</tr>
<tr>
<td>HHT3</td>
<td>Classical HHT</td>
</tr>
</tbody>
</table>

AD, autosomal dominant.
RESULTS
Exclusion of known HHT disease genes
Linkage analyses were performed to confirm the exclusion of *endoglin* and *ALK-1* in the extended pedigree, and to exclude the new JP-HHT gene, *Smad4* (table 2).

*Endoglin* had been sequenced in full in affected members of the pedigree. The other two HHT genes were sequenced in four affected family members (III.3, II.3, II.4, III.3, and III.4). No mutations were found in any of the *ALK-1* coding regions or intron-exon boundaries. Although the JP-HHT mutations predominantly occur in the 3' exons of *Smad4*, all 11 exons and intron-exon boundaries were sequenced. No mutations were found.

Exclusion of core components of the TGF-β signalling pathways
Recognising that the data from the other HHT genes strongly suggested that the disease gene in this pedigree would encode a protein affecting TGF-β signalling, other core components of TGF-β signalling pathways were excluded by linkage analyses (see fig 1). Literature and database searches revealed that in addition to the proteins illustrated in fig 1, over 100 further proteins are known to interact with the TGF-β superfamily signalling pathways, precluding an exhaustive candidate gene approach. A genome-wide screen was therefore undertaken.

Linkage analyses define the HHT3 locus on chromosome 5
An initial genome-wide scan excluded 70% of the genome, and identified a 12 cM interval where LOD scores exceeded +2. Information from initial markers was limited due to non-informative meioses. Supplementary adjacent markers were fully informative, generating a two point *Z*max of 3.45 at a recombination fraction (θ) of 0.00, and refining the interval. The series of two point LOD scores (table 3) and recombination mapping using affected individuals. The series of two point LOD scores (table 3) and recombination mapping using affected individuals (fig 3) defined the 5.4 cM/6 Mb *HHT3* locus. In this region, all affected family members had inherited a conserved disease associated haplotype (fig 2).

In order to assess the likely frequency of HHT3, we studied three families (including two previously unreported) with theoretical *Z*max of 1.87, a maximum two point LOD score of 1.17 at θ = 0.00 was obtained with *D5S436* on a different disease-segregating haplotype to that.

![Family pedigree and haplotype analysis](image-url)
Table 2 Exclusion of known HHT genes

<table>
<thead>
<tr>
<th>Marker</th>
<th>Mb</th>
<th>cM</th>
<th>Z (θ=0.00)</th>
<th>Z (θ=0.05)</th>
<th>Z (θ=0.10)</th>
<th>Z (θ=0.50)</th>
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<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
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<tr>
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<td>-2.95</td>
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<tr>
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<td>61</td>
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<tr>
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</tbody>
</table>

Haplotype and multipoint data for endoglin and ALK-1 are presented in Wallace and Shovlin. Mb and cM refer to position on respective chromosomes.

Table 3 LOD scores (Z) spanning the HHT3 interval

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<tr>
<th>Marker</th>
<th>cM</th>
<th>Mb</th>
<th>0</th>
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<th>0.05</th>
<th>0.1</th>
<th>0.2</th>
<th>0.3</th>
<th>0.4</th>
<th>0.5</th>
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<td>3.45</td>
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<td>145.23</td>
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<td>3.41</td>
<td>3.25</td>
<td>3.01</td>
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<td>1.69</td>
<td>0.84</td>
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<tr>
<td>DSS2033</td>
<td>148.63</td>
<td>145.98</td>
<td>0.40</td>
<td>0.46</td>
<td>0.59</td>
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<td>0.62</td>
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<td>0.34</td>
<td>0.38</td>
<td>0.25</td>
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</table>

Marker positions ranked according to the Marshfield map.

DISCUSSION

We have identified a novel locus for the autosomal dominant disorder hereditary haemorrhagic telangiectasia (HHT). In the presented family, the disease affects both sexes equally and is indistinguishable from that in other families with HHT. The pulmonary AVM frequency (13%) was not as high as in HHT type I families with endoglin mutations, but numbers are too small to suggest that HHT3 resembles HHT2 more than HHT1. Importantly, no family members have experienced cancer of any form, and none are known to have developed pulmonary hypertension.

Our data do not allow us to address the proportion of HHT families which are due to HHT3, as in our four “unassigned” large families, only one categorically maps to chromosome 5. Most HHT families will have mutations in endoglin or ALK-1, and mutational screening programmes should detect the majority of these. Data from labs employing sensitive quantitative genomic exon PCR screening methods have not detected mutations in as many as 10–15% of classical HHT families (Dr Michelle Letarte, personal communication). In these families, linkage analyses with the chromosome 5 markers should begin to address the likely frequency of HHT3.

The HHT3 locus (5q13.1–5q32) is not the same as that recently identified for hereditary benign telangiectasia (HBT; OMIM 187260) on chromosome 5 (5q14), for which the causative gene, RASA1, encoding Ras GTPase activating protein 1, has been identified. HBT is therefore part of the capillary malformation-arteriovenous malformation (CM-AVM) syndrome, and should not be considered a benign allelic variant of HHT as proposed. The importance of making this clear distinction is that HHT patients are at significant risk of pulmonary and cerebral AVMs. The diseases can be distinguished clinically by the distinctive skin lesions. In HBT, randomly distributed cutaneous vascular malformations over the head, trunk, and limbs are often congenital (40%) or develop from early childhood. In contrast, HHT telangiectasia have a highly restricted distribution on the mucosa of the nose, lips, oral cavity, conjunctiva, finger tips, ears, and face, develop from teenage years, and become more numerous with age.

As all three identified HHT genes encode proteins involved in TGF-β superfamily signalling, we anticipate that the disease gene responsible for HHT3 will also encode a protein involved in Smad dependent TGF-β signalling. In keeping with the expression patterns of endoglin and ALK-1 which are transmembrane proteins predominantly expressed on vascular endothelial cells (EC), we predict that the disease gene for this “pure” form of HHT will also display EC restricted expression. Identification of this gene will be illustrated in fig 2. The reduction from the theoretical Zmax was due to a single young unaffected recombinant.

Exclusion mapping

To exclude the possibility that an alternative locus had been missed, the remainder of the genome was formally examined. A further 290 polymorphic markers were selected and analysed to ensure that at least two double recombination events would have had to occur in a 2–5 cM interval for a putative locus to have been missed. Highly conservative estimates (excluding genetic interference) based on 500 intervals indicated that the probability of this occurring was 3.1×10^{-3} and 8×10^{-5} (that is, p<0.0031).

Candidate gene analysis

Ensembl identifies 28 genes within the 5.4 cM HHT3 interval, including 10 of unknown function. Furthermore, the gene for Smad5, a strong candidate based on its role in ALK-1 signalling pathways (fig 1), is assigned on current mapping to within 5 Mb of the HHT3 interval (fig 3). The Smad5 gene had been excluded by linkage analyses using markers either side of the published gene locus. However, in view of its strong candidate status due to functional considerations, and the possibility that the precise database positional assignment of Smad5 was erroneous, all coding exons and flanking intronic sequence were sequenced in affected members of the possibility that the precise database positional assignment of Smad5 was erroneous, all coding exons and flanking intronic sequence were sequenced in affected members of both families. No pathogenic mutations were identified. In addition, the initial 12 cM mapping interval contained SPARC, a further attractive candidate gene due to endothelial cell expression and roles in TGF-β1 mediated proliferative responses. SPARC cDNA was amplified from EBV immortalised lymphocyte cell lines. The complete transcript was sequenced and no mutations identified.
important not only for clinical diagnostic services but also to elucidate the mechanisms of TGF-β superfamily signalling in vascular endothelium.

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ELECTRONIC-DATABASE INFORMATION


**Authors' affiliations**

S G Cole, C L Shovlin, The Eric Bywaters Centre, Respiratory Section, National Heart and Lung Institute, Imperial College Faculty of Medicine, Hammersmith Hospital, London W12 ONN, UK

M E Begbie, Respiratory Medicine, National Heart and Lung Institute, Imperial College Faculty of Medicine, Hammersmith Hospital, London W12 ONN, UK

G M F Wallace, Respiratory Medicine Unit, University of Edinburgh, Edinburgh, UK

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Competing interests: none declared

Correspondence to: Dr Claire Shovlin, The Eric Bywaters Centre, Respiratory Section, National Heart and Lung Institute, Imperial College Faculty of Medicine, Hammersmith Hospital, Du Cano Road, London W12 ONN, UK; c.shovlin@imperial.ac.uk

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**Figure 3** Recombination mapping of interval using affected family members. Pedigree numbers as in fig 2. Black bars indicate definite recombination events; shaded bars indicate uninformative markers. The locations of the candidate genes Smad5 and SPARC (but not RASA1 at 86.6 Mb) are illustrated.
CORRECTION

doi: 10.1136/jmg.2005.19224corr1

It has come to our attention that in figure 3 of BE Baysal et al (J Med Genet 2004;41:703-9) that some of the lines were displaced. Below is a corrected figure. The journal apologises for this error.
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