Low frequency of BMPR2 mutations in a German cohort of patients with sporadic idiopathic pulmonary arterial hypertension


Methods

Patients

Between March 2002 and January 2004, 99 consecutive non-related patients >20 years of age with IPAH and negative family history were evaluated. In all cases, diagnosis of IPAH was made by experienced and specialised cardiologists or pulmonologists according to WHO criteria. Other causes of pulmonary hypertension such as illicit drug abuse or anorectic drug use were excluded by careful medical history evaluation. Underlying heart and lung diseases (recurrent pulmonary embolism, connective tissue disease, obstructive or restrictive lung disease) and HIV were excluded by a cascade of clinical examinations including laboratory tests, arterial blood gas analysis, chest x ray, pulmonary function tests, echocardiography, ventilation perfusion scanning, chest computed tomography, pulmonary angiography (when indicated), and cardiac catheterisation (table 1). EDTA blood samples were collected for genetic analysis in all patients. The study protocol was approved by the Ethics Committee of the Medical Faculty of the University of Heidelberg and written informed consent was given by each patient.

BMPR2 mutation analysis

Mutation analysis of the BMPR2 coding sequence and intron/exon boundaries was performed in two independent laboratories using two different detection methods. In one laboratory (RK, BJ) the entire BMPR2 coding sequence and all intron/exon boundaries were analysed by dHPLC (WAVE, Transgenomic, Omaha, NE, USA). Primer sequences used for dHPLC are listed in table 2. Genomic DNA samples of all 99 patients were analysed using at least two different dHPLC protocols per PCR fragment according to the manufacturer’s instructions. Any fragments demonstrating aberrant proper-}

Key points

- Idiopathic pulmonary arterial hypertension (IPAH) is a rare progressive disorder in which elevated pulmonary artery pressure, in the absence of secondary causes, leads to right heart failure and death. Mutations of the bone morphogenetic protein receptor type II gene (BMPR2) have been identified in both familial and sporadic cases.
- This study, the first to investigate the frequency of BMPR2 mutations in a German cohort, analysed 99 patients with sporadic IPAH. BMPR2 mutations were identified in only 11 cases (~11%).
- These data suggest that BMPR2 mutations may be less frequent than previously reported in sporadic IPAH and that the role of BMPR2 mutations in the sporadic phenotype may have been overestimated.

RT-PCR

cDNA analysis was performed by RT-PCR to determine the significance of the potential splice-site mutation. RNA was prepared from peripheral blood leukocytes using TRIzol reagent, as described by the manufacturer (Life Technologies, Carlsbad, CA, USA). Total RNA (1 µg) was reverse transcribed using random hexamer primers (Pharmacia Biotech Piscataway, NJ, USA) and 200 units of MMLV reverse transcriptase (SuperScript, Life Technologies) for 1 h at 42°C. RT-PCR products were obtained using region specific primer data are available at http://www.med.uni-heidelberg.de/humangen/ger/humgen/pph-scl.htm. The analyses were conducted concurrently in a blinded fashion and the results were compared only after analyses were completed by each laboratory.

Diastolic pulmonary arterial hypertension (IPAH; formerly known as primary pulmonary hypertension, PPH) is a rare disorder characterised by pulmonary vascular proliferation and remodelling resulting in loss of patency of the pulmonary arteries. This leads to sustained elevation of pulmonary artery pressures with subsequent progressive right heart failure and often death. While the majority of cases (>90%) have no known family history of the disease, ~6% of the cases are known to be familial and are inherited in an autosomal dominant manner with markedly reduced penetrance. In previous studies, linkage analysis identified a familial IPAH locus on chromosome 2q33. Subsequent heterozygous germline mutations in the bone morphogenetic protein receptor, type II (BMPR II) gene (BMPR2) were identified in at least 50% of familial cases. BMPR-II is a member of the transforming growth factor-β (TGF-β) receptor superfamily signalling pathway, which is critical in both cell differentiation and cell growth mediated through transcriptional regulation. Interestingly, germline mutations were also identified in 26–40% of sporadic cases. This study was performed to establish the frequency of BMPR2 mutations in a different population of patients with sporadic IPAH.
Deletion of exon 10 results in the frameshift G426fs (intron 10 (IVS10 +MHH10 demonstrated a change at the third nucleotide of mutation on the protein level. The genomic DNA of patient No RNA was available to test the consequence of this splice substitution at the first nucleotide of intron 8 (IVS8 + mutations. The genomic DNA of patient K3771A had a (R584X). Additionally, we identified two novel splice site substitutions (A) cDNA analysis of patient MHH10 (Pat.) in comparison with wildtype cDNA (WT). Patient MHH10 shows two different PCR fragments, both predicted to result in premature termination of the wildtype cDNA sequence with a predicted normal amino acid sequence as indicated. Fragment F2 demonstrated a deletion of exon 10 and predicts a frameshift at the protein level illustrated by italicised letters.

RESULTS
Heterozygous germline BMPR2 mutations were identified in 11 of the 99 (11.1%; 95% confidence interval: 5.7 to 19%, calculated by exact approximation) sporadic IPAH patients (table 3). We identified five novel nonsense mutations (E31X, R321X, Q450X, W466X, Q495X), one known missense mutation (R491W), and one known nonsense mutation (E31X). Additionally, we identified two novel splice site mutations. The genomic DNA of patient K3771A had a substitution at the first nucleotide of intron 8 (IVS8+1G→T).

BMPR-II peptide. In the first case, K4690A, we found a 4 bp deletion (c.1313–1316 del CAGA) in exon 10 that generates a stop codon 35 amino acids downstream of the mutation. In patient MHH52, we detected a 1 bp insertion (c.1388 insA), which results in a stop codon six amino acids downstream of the mutated codon E464. We detected an unclassified variant (UV) in patient MHH07 which results in the substitution of glutamic acid for glycine at codon 386 (fig 2). It seems likely that the substitution of glycine for glutamic acid in the kinase domain of BMPR-II, a change from an acidic to an aliphatic amino acid, has functional relevance. In the absence of functional data, however, the substitution E386G has been characterised as a UV. Analysis of parental DNA samples for the E31X mutation detected in patient K4518A confirmed the mutation in the non-symptomatic mother. No parental DNA was available for any of the other cases in which BMPR2 mutations were identified. All results were confirmed by both laboratories; each mutation was detected by both of the methods described above.

<table>
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<tr>
<th>Exon</th>
<th>Primer Forward</th>
<th>Primer Reverse</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>5’-GGT ATT TGG ATA AGA CAA AG-3’</td>
<td>5’-TTT AAC ATA TCT CCA TGT CC-3’</td>
</tr>
<tr>
<td>2</td>
<td>5’-GGG TAC AGC CTT TCT AAA GG-3’</td>
<td>5’-GAT ACT ATT GAG GCT GGG TG-3’</td>
</tr>
<tr>
<td>3</td>
<td>5’-GCT CCT AAT TCT TCA GCA GC-3’</td>
<td>5’-GAA TGA AGT CAC TGT TCC AG-3’</td>
</tr>
<tr>
<td>4</td>
<td>5’-CAG AGA GCT GTA GCA TTC TG-3’</td>
<td>5’-AAG TGA TCC ACC TGC ATG AG-3’</td>
</tr>
<tr>
<td>5</td>
<td>5’-GCG ATT TTT TCC TCT AAT A-3’</td>
<td>5’-TCG ATT TCA TGC TGA TCA TTC C-3’</td>
</tr>
<tr>
<td>6</td>
<td>5’-GCA GAA AAA TAA TAC TAC TCT TAT A-3’</td>
<td>5’-GAT GTT TTT AAT TAA ATT ATC ATT TC-3’</td>
</tr>
<tr>
<td>7</td>
<td>5’-AGA ATA TGC TAC GTT CTC ATC-3’</td>
<td>5’-ACA CTA GAT AGC AAT GAA CTA AAG G-3’</td>
</tr>
<tr>
<td>8</td>
<td>5’-GCC TGG AGG GGA TGA AAA A-3’</td>
<td>5’-GCC ATT AGG CAA CTC CAA AA-3’</td>
</tr>
<tr>
<td>9</td>
<td>5’-CCT CAT GTG GTA ACC TGA AAA GCC-3’</td>
<td>5’-TGC ATT TGT ACC AAA CAA AAA TG-3’</td>
</tr>
<tr>
<td>10</td>
<td>5’-TTT AAC ATA CTC CCA TGT CC-3’</td>
<td>5’-TTT AAC ATA CTC CCA TGT C-3’</td>
</tr>
<tr>
<td>11</td>
<td>5’-GGA ATT TCT TCG TCA TTA TTA-3’</td>
<td>5’-AGT CCT GCT CTC CAG TG-3’</td>
</tr>
<tr>
<td>12</td>
<td>5’-GCA GAA AAA TAA TAC TAC TCT TAT A-3’</td>
<td>5’-GAT GTT TTT AAT TAA ATT ATC ATT TC-3’</td>
</tr>
<tr>
<td>13</td>
<td>5’-TTA CAT CCC TTA CCC GTT AT-3’</td>
<td>5’-TTA AAG CAA GCT TTT GTT GC-3’</td>
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</table>
12 mutations in a group of 30 Japanese patients (40%).

They found familial form of the disease. Morisaki and colleagues found mutations predispose to sporadic IPAH as they do in the familial form of the disease. Our findings of 11 heterozygous germline BMPR2 mutations in 50 sporadic IPAH patients and found germline mutations in 13 of the patients (26%).

Their conclusion was that germline mutations in the BMPR2 gene are responsible for the clinical phenotype in those patients for whom no parental DNA was available. Our findings of only an 11% mutation rate in our cohort of 99 adults for whom no parental DNA was available. Our cohort and theirs are of Northern European descent. Thus, we conclude that the disparity between the estimated frequencies of mutations in the three studies is not due to differences in methodology.

Recent studies have tried to determine the role of BMPR2 in the pathogenesis of pulmonary arterial hypertension (PAH). Atkinson and coworkers reported a reduced expression of BMPR2 in lung tissue in all patients with PAH. The reduction in expression was reported by more than 50% in patients with a BMPR2 mutation. This reduction is due to low grade mosaicism or sequencing artefacts, two different methods were used in two independent laboratories: direct sequencing and dHLPC. However, it cannot be ruled out in any of the three studies that undetected gene rearrangements, large deletions, insertions, or intronic mutations in the BMPR2 gene are responsible for the clinical phenotype in those patients for whom no mutations were identified. Thus, we conclude that the disparity between the estimated frequencies of mutations in the three studies is not due to differences in methodology.

BMPR2 mutations, can explain this phenomenon. Geraci and colleagues have used microarray analysis to characterise the gene expression pattern in PAH patients. Interestingly, comparison of expression patterns could be used to distinguish between sporadic IPAH and familial

Table 3

<table>
<thead>
<tr>
<th>No</th>
<th>Patient ID</th>
<th>Exon</th>
<th>Mutation type</th>
<th>Nucleotide change</th>
<th>Amino acid change</th>
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<tbody>
<tr>
<td>1</td>
<td>K451B</td>
<td>2</td>
<td>Nonsense</td>
<td>c.91 G→T</td>
<td>E31X</td>
</tr>
<tr>
<td>2</td>
<td>K5429A</td>
<td>7</td>
<td>Nonsense</td>
<td>c.961 C→T</td>
<td>K321X</td>
</tr>
<tr>
<td>3</td>
<td>K3771A</td>
<td>8</td>
<td>Donor splice</td>
<td>IVS8 +1 G→T</td>
<td>ND</td>
</tr>
<tr>
<td>4</td>
<td>MHH10</td>
<td>10</td>
<td>Donor splice</td>
<td>IVS10 +3 A→T</td>
<td>G426fs(–27)</td>
</tr>
<tr>
<td>5</td>
<td>K4609A</td>
<td>10</td>
<td>Frameshift</td>
<td>c.1313-1316 del CAGA</td>
<td>T438fs(–35)</td>
</tr>
<tr>
<td>6</td>
<td>MHH69</td>
<td>10</td>
<td>Nonsense</td>
<td>c.1348 C→T</td>
<td>Q450X</td>
</tr>
<tr>
<td>7</td>
<td>MHH52</td>
<td>10</td>
<td>Frameshift</td>
<td>c.1388-1389 insA</td>
<td>E464fs(–6)</td>
</tr>
<tr>
<td>8</td>
<td>K5943A</td>
<td>10</td>
<td>Nonsense</td>
<td>c.1397 G→A</td>
<td>W466X</td>
</tr>
<tr>
<td>9</td>
<td>K6361A</td>
<td>11</td>
<td>Missense</td>
<td>c.1471 C→T</td>
<td>R491W</td>
</tr>
<tr>
<td>10</td>
<td>K5909A</td>
<td>11</td>
<td>Missense</td>
<td>c.1483 C→T</td>
<td>Q495X</td>
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<tr>
<td>11</td>
<td>MHH18</td>
<td>12</td>
<td>Nonsense</td>
<td>c.1720 C→T</td>
<td>R584K</td>
</tr>
<tr>
<td>12</td>
<td>MHH07</td>
<td>9</td>
<td>UV (missense)</td>
<td>c.1157 A→G</td>
<td>E386G</td>
</tr>
</tbody>
</table>

*Nucleotide numbers are according to published cDNA, with the A of the ATG designated as +1.
†Frameshifts are denoted with the amino acid, position, and number of amino acids until new stop codon.

DISCUSSION

Our findings of 11 heterozygous germline BMPR2 mutations in 99 sporadic IPAH patients (11%) are significantly different from those of previously published studies. Thomson et al determined the frequency of BMPR2 mutations in a cohort of 50 sporadic IPAH patients and found germline mutations in 13 of the patients (26%). Their conclusion was that germline mutations predispose to sporadic IPAH as they do in the familial form of the disease. Morisaki and colleagues found 12 mutations in a group of 30 Japanese patients (40%). They hypothesised that some of these cases might actually be familial in nature, since most of their samples were from adults for whom no parental DNA was available. Our findings of only an 11% mutation rate in our cohort of 99 IPAH patients is significantly different from both the studies by Thomson et al (p = 0.0196) and Morisaki et al (p = 0.0003). There are several potential explanations for this discrepancy. The first is population differences between the three cohorts. Regarding the study by Thomson et al, both our cohort and theirs are of Northern European descent. Despite this seemingly common ancestry, it is possible that different environmental factors and lifestyles could affect the penetrance and fitness of BMPR2 mutations as well as the phenocopy rate. In comparison to the study by Morisaki et al, the population difference is more pronounced in that their cohort is of Japanese ancestry. Therefore, genetic differences affecting penetrance of BMPR2 mutations between the two populations may also play a role. Second, the smaller sample size of both the Thomson et al and the Morisaki et al studies introduces the potential for overestimation of the prevalence of BMPR2 mutations in sporadic IPAH due to sampling error. Third, patient recruitment differences may have occurred between the three studies. Any other causes of pulmonary hypertension were thoroughly excluded in our cohort. Finally, to ensure that no mutations were missed in our patients due to low grade mosaicism or sequencing artefacts, two different methods were used in two independent laboratories: direct sequencing and dHLPC. However, it cannot be ruled out in any of the three studies that undetected gene rearrangements, large deletions, insertions, or intronic mutations in the BMPR2 gene are responsible for the clinical phenotype in those patients for whom no mutations were identified. Thus, we conclude that the disparity between the estimated frequencies of mutations in the three studies is not due to differences in methodology.

Amino acid alignment of type II TGF-β superfamily receptors surrounding E386 in BMPR-II. Patient MHH07 has an amino acid substitution E386G (dark grey), which is located in the kinase domain of the BMPR-II protein. The alignment showed a wholly conserved region of nine amino acids (light grey) in different mammalian species (mouse, human, rat, sheep) for several type II receptors. The alignment showed a wholly conserved region of nine amino acids (light grey) in different mammalian species (mouse, human, rat, sheep) for several type II receptors. The alignment showed a wholly conserved region of nine amino acids (light grey) in different mammalian species (mouse, human, rat, sheep) for several type II receptors.
IPAH. They conclude that sporadic and familial IPAH are mechanistically distinct. Taken together, both the published expression data and our mutation data suggest that while reduction of BMPR2 expression is common in pulmonary hypertension patients, additional factors other than germline BMPR2 mutations may lead to the development of sporadic IPAH.

Although BMPR2 plays an important role in the pathogenesis of IPAH, our data indicate that in most cases of sporadic IPAH BMPR2 mutations are not the primary cause of the disease. However, identification of individuals with BMPR2 mutations could enable more accurate risk assessment in other family members. Therefore, despite the low mutation frequency in sporadic IPAH, genetic screening for germline BMPR2 mutations may be warranted.

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ELECTRONIC-DATABASE INFORMATION

The PCR conditions and primer data mentioned in this study are available at http://www.med.uni-heidelberg.de/humangen/ger/humgen/pph-cl.htm.

Conflict of interest: none declared.

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