**ELECTRONIC LETTER**

**LKB1 exonic and whole gene deletions are a common cause of Peutz-Jeghers syndrome**


**Background:** LKB1/STK11 germline mutations cause Peutz-Jeghers syndrome (PJS). The existence of a second PJS locus is controversial, the evidence in its favour being families unlinked to LKB1 and the low frequency of LKB1 mutations found using conventional methods in several studies. Exonic and whole gene deletion or duplication events cannot be detected by routine mutation screening methods.

**Objective:** To seek evidence for LKB1 germline deletions or duplications by screening patients meeting clinical criteria for PJS but without detected mutations on conventional screening.

**Methods:** From an original cohort of 76 patients, 48 were found to have a germline mutation by direct sequencing; the remaining 28 were examined using multiplex ligation dependent probe amplification (MLPA) analysis to detect LKB1 copy number changes.

**Results:** Deletions were found in 11 of the 28 patients (39%)—that is, 14% of all PJS patients (11/76). Five patients had whole gene deletions, two had the promoter and exon 1 deleted, and in one patient exon 8 was deleted. Other deletions involved: loss of exons 2–10; deletion of the promoter and exons 1–3; and loss of part of the promoter. No duplications were detected. Nine samples with deletions were sequenced at reported single nucleotide polymorphisms to exclude heterozygosity; homozygosity was found in all cases. No MLPA copy number changes were detected in 22 healthy individuals.

**Conclusions:** These results lessen the possibility of a second PJS locus, as the detection rate of germline mutations in PJS patients was about 80% (59/76). It is suggested that MLPA, or a suitable alternative, should be used for routine genetic testing of PJS patients in clinical practice.

The original report of LKB1 mutations in PJS demonstrated mutations in about 90% of cases (11/12) using direct sequencing of constitutional DNA and mRNA. Most subsequent screens for mutations in PJS have produced a similar, although slightly lower, frequency of patients with LKB1 mutations, although the methods used for mutation detection have varied. Two studies, however, found mutations in only 10% and 18% of PJS cases, although the proportion of familial cases in the latter study was low. These findings have led to claims that a single PJS locus cannot explain all cases of PJS. Support for this contention has been provided by linkage studies in PJS families, which have reported exclusion of the LKB1 locus (chromosome 19p13.3). Countervailing arguments have been that many tumour susceptibility genes harbour a large proportion of mutations which cannot be detected by routine screening methods, and that several conditions—even including normal variants—may mimic the pigmentation of PJS, leading to diagnostic misclassification.

Whole gene and exonic deletions and duplications cannot be detected using routine mutation screening methods. Given the high frequency of such changes in diseases such as von Hippel-Lindau syndrome, and the increasing realisation that conditions such as hereditary non-polyposis colon cancer (HNPCC) are often caused by such changes, we screened for gene and exon scale mutations in a set of PJS patients without detected LKB1 mutations. The results have implications for diagnostic genetic testing in PJS patients and for the hypothesised second PJS locus.

**METHODS**

A diagnosis of PJS was made when the patient presented with two or more PJS polyps, or one polyp and typical pigmented lesions, or one polyp and a family history of PJS. A cohort of 76 patients meeting these criteria had been screened previously for germline LKB1 mutations using direct sequencing of each exon plus intron–exon boundaries. In 48 patients, small scale mutations had been found, including protein truncating changes, missense variants targeting phosphorylation sites or other highly conserved residues, and splice site variants. In all, 28 patients without detected mutations (13 familial, 13 isolated cases, two unknown) were identified for the present study. The multiplex ligation dependent probe amplification (MLPA) LKB1/STK11 kit, designed to search for LKB1 deletions or duplications at exon or whole gene level, was obtained from MRC-Holland (Amsterdam, Netherlands). MLPA reactions were performed in the MRC-Holland laboratory, and results were obtained via the open access trial.

**Abbreviations:** MLPA, multiplex ligation dependent probe amplification; PJS, Peutz-Jeghers syndrome; SNP, single nucleotide polymorphism.
RESULTS AND COMMENT

Eleven of the 28 PJS patients tested (39%) had germline LKB1 mutations detected by MLPA (table 1). Five patients had whole gene deletions, two had the promoter region and exon 1 deleted, and in one patient exon 8 was deleted. The remaining detected deletions, each in a single patient, involved the following: loss of exons 2–10; deletion of the promoter region and exons 1–3; and loss of part of the promoter region. No duplications of any part of the gene were detected. Twenty two healthy individuals were screened by MLPA and no copy number changes detected.

For nine samples with deletions (75%), the appropriate primers were designed to detect deletion by MLPA. MLPA data were analysed using the Applied Biosystems PRISM™ 3100 DNA sequencer. MLPA data were analysed using the Applied Biosystems Genotyper software (PE Applied Biosystems, Foster City, California, USA). Finally, the MLPA data were evaluated by a Microsoft Excel based program originally designed to detect APC copy number changes (www.ngrl.org.uk/ManchesterPages/Downloads/Dosage) and adapted to evaluate copy number changes with the MLPA STX1I test kit. Samples were analysed alongside 22 normal healthy individuals to exclude detection of false positives. All samples with possible MLPA changes were tested at least twice to confirm the change. Single nucleotide polymorphism (SNP) analysis was undertaken by sequencing to exclude heterozygosity within deletions reported by MLPA.

<table>
<thead>
<tr>
<th>Patient ID(s)</th>
<th>Result</th>
<th>Family history</th>
</tr>
</thead>
<tbody>
<tr>
<td>11200</td>
<td>Whole gene deletion</td>
<td>Sporadic</td>
</tr>
<tr>
<td>11199</td>
<td>Whole gene deletion</td>
<td>Sporadic</td>
</tr>
<tr>
<td>11668</td>
<td>Whole gene deletion</td>
<td>Sporadic</td>
</tr>
<tr>
<td>24/1/1</td>
<td>Whole gene deletion</td>
<td>Unknown</td>
</tr>
<tr>
<td>02/551</td>
<td>Whole gene deletion</td>
<td>Familial</td>
</tr>
<tr>
<td>000/1/1, 52/1/1</td>
<td>Promoter and exon 1 deletion</td>
<td>Familial</td>
</tr>
<tr>
<td>59/1/1, 11181</td>
<td>Promoter and exon 1 deletion</td>
<td>Familial</td>
</tr>
<tr>
<td>13/1/1</td>
<td>Exon 8 deletion</td>
<td>Sporadic</td>
</tr>
<tr>
<td>7282</td>
<td>Exon 2–10 deletion</td>
<td>Familial</td>
</tr>
<tr>
<td>AXY</td>
<td>Promoter deletion</td>
<td>Sporadic</td>
</tr>
<tr>
<td>LEH</td>
<td>Promoter and exon 1–3 deletion</td>
<td>Familial</td>
</tr>
</tbody>
</table>

Table 1 MLPA results for patients with LKB1 changes

ACKNOWLEDGEMENTS

The study was supported by grants from the Academy of Finland (44870/Finnish Centre of Excellence Programme 2000–2005, 76227, 77547), the Sigrid Juselius Foundation, the Cancer Society of Finland, and Helsinki University Central Hospital. The support of Cancer Research UK is also acknowledged.

Authors’ affiliations
S Volkos, J Robinson, A Silver, Cancer Research UK Colorectal Cancer Unit, St Mark’s Hospital, Harrow, Middlesex, UK
K Aittomäki, Clinical Genetics, Haartman Institute, University of Helsinki, Helsinki, Finland
REFERENCES


2 Marignani PA. LKB1, the multitasking tumour suppressor kinase. J Clin Pathol 2005;58:15–19

3 Brugarolas J, Kaelin WG. Dysregulation of the protein kinase mutated in Peutz-Jeghers cancer syndrome, LKB1/STK11, at Ser431 by p90RSK and cAMP-dependent protein kinase, but not by farnesylation or Cys433, is essential for LKB1 to suppress cell growth. J Biol Chem 2001;276:19469–82


8 Buchet-Poyau M, Mehnki H, Radhakrishna U, Antonarakis SE. Phosphorylation of the protein kinase mutated in Peutz-Jeghers cancer syndrome, LKB1/STK11, at Ser431 by p90RSK and cAMP-dependent protein kinase, but not by farnesylation or Cys433, is essential for LKB1 to suppress cell growth. J Biol Chem 2001;276:19469–82


15 Brugarolas J, Marignani PA


18 Foret C, Etienne-Manneville S, Guad H, Fourrier L, Debili S, Salmi M, Boas A, Olschwang S, Clevers H, Biliard M. Functional analysis of Peutz-Jeghers mutations reveals that the LKB1 C-terminal region exerts a crucial role in regulating both the AMPK pathway and the cell polarity. Hum Mol Genet 2005;14:283–92


