Basic Study

Detection and analysis of common pathogenic germline mutations in Peutz-Jeghers syndrome

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BACKGROUND

Different types of pathogenic mutations may produce different clinical phenotypes, but a correlation between Peutz-Jeghers syndrome (PJS) genotype and clinical phenotype has not been found. Not all patients with PJS have detectable mutations of the \( \text{STK11/LKB1} \) gene, what is the genetic basis of clinical phenotypic heterogeneity of PJS? Do PJS cases without \( \text{STK11/LKB1} \) mutations have other pathogenic genes? Those are clinical problems that perplex doctors.

AIM

The aim was to investigate the specific gene mutation of PJS, and the correlation between the genotype and clinical phenotype of PJS.

METHODS

A total of 24 patients with PJS admitted to the Air Force Medical Center, PLA (formerly the Air Force General Hospital, PLA) from November 1994 to January 2020 were randomly selected for inclusion in the study. One hundred thirty-nine common hereditary tumor-related genes including \( \text{STK11/LKB1} \) were screened and analyzed for pathogenic germline mutations by high-throughput next-generation sequencing (NGS). The mutation status of the genes and their relationship with clinical phenotypes of PJS were explored.

RESULTS
patients (legal guardians of minors) understood the process and purpose of this study and signed an informed consent form. In the process of sample collection, follow the principles of informed consent in the Declaration of Helsinki, the Universal Declaration of Human Genome and Human Rights, and the Declaration of the Human Genome Ethics Committee on DNA Sampling, Control, and Acquisition. No additional data are available.

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Twenty of the 24 PJS patients in this group (83.3%) had STK11/LKB1 gene mutations, 90% of which were pathogenic mutations, and ten had new mutation sites. Pathogenic mutations in exon 7 of STK11/LKB1 gene were significantly lower than in other exons. Truncation mutations are more common in exons 1 and 4 of STK11/LKB1, and their pathogenicity was significantly higher than that of missense mutations. We also found SLX4 gene mutations in PJS patients.

CONCLUSION
PJS has a relatively complicated genetic background. Changes in the sites responsible for coding functional proteins in exon 1 and exon 4 of STK11/LKB1 may be one of the main causes of PJS. Mutation of the SLX4 gene may be a cause of genetic heterogeneity in PJS.

Key Words: Peutz-Jeghers syndrome; Genotype; Phenotype; STK11; Mutation

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Core Tip: It is currently believed that Peutz-Jeghers syndrome (PJS) is an autosomal dominant genetic disease predominantly caused by germline mutations in the STK11/LKB1 gene. No correlation of the PJS genotype and clinical phenotype has been found so far. The correlation of genotype and clinical phenotype and exploration of the internal molecular mechanism of different clinical phenotypes were studied in 24 treated PJS patients with different clinical phenotypes. Peripheral venous blood or normal tissue adjacent to polyps were collected for high-throughput next-generation sequencing (NGS) of 139 hereditary colorectal tumor-related genes including STK11/LKB1. A newly discovered likely pathogenic gene (SLX4) provided new data explaining the genetic heterogeneity of PJS.

INTRODUCTION
It is currently believed that Peutz-Jeghers syndrome (PJS) is an autosomal dominant genetic disease predominantly caused by germline mutations in the STK11/LKB1 gene. PJS is characterized by multiple hamartoma polyps in the gastrointestinal tract, pigmentation at specific sites, and hereditary tumors[1-4]. Pathogenic mutations of STK11/LKB1 lead to inactivation of its expression product and loss of inhibition of mammalian target of rapamycin (mTOR) activity, which leads to abnormal activation of the LKB1/mTOR signal pathway and the occurrence of black spots on the skin and gastrointestinal hamartoma polyps[5]. More than 400 different pathogenic STK11/LKB1 gene mutations are included in the Human Gene Mutation Database (HGMD), most of which are micromutation. Different types of pathogenic mutations may produce different clinical phenotypes, but no correlations of PJS genotype and clinical phenotype has been found so far[6]. Not all patients with PJS have detectable mutations in the STK11/LKB1 gene. What is the genetic basis of clinical phenotypic heterogeneity in PJS? Do PJS patients without STK11/LKB1 mutations have other pathogenic genes? These are clinical problems that perplex doctors[7,8]. We enrolled 24 patients treated for PJS. Peripheral venous blood and normal tissue adjacent to polyps were collected for high-throughput next-generation sequencing (NGS) of 139 hereditary colorectal tumor-related genes including STK11/LKB1 to study the correlation between genotype and clinical phenotype of PJS and explore the internal molecular mechanism of the clinical phenotypes.
MATERIALS AND METHODS

Study participants

Patients with PJS, from 18-70 years of age, met the clinical diagnostic criteria of PJS, had complete clinicopathological data, well preserved specimens, were eligible for inclusion. All participants gave their signed informed consent. Patients who could not provide experimental specimens or did not agree to participate in the study were excluded. Twenty-four PJS patients admitted to the Air Force Medical Center (formerly the Air Force General Hospital) from November 1994 to January 2020 met the above criteria and were enrolled. Their clinical information is shown in Table 1. Twenty-three were inpatients, one was an outpatient, 11 had family histories, and 12 had early onset pigment spots that had appeared when they were younger than 3 years of age. All patients met the PJS diagnostic criteria recommended by the National Comprehensive Cancer Network (NCCN)[9]. The experimental samples included 5 mL peripheral venous blood samples collected from 19 patients into tubes containing EDTA-2Na, and paraffin-embedded normal tissue surgically removed from areas adjacent to polyps in five patients. The study was reviewed and approved by the Ethics Committee of the Air Force Medical Center and the Second Affiliated Hospital of Zhejiang University School of Medicine. All patients or the legal guardians of minors, understood the process and purpose of this study and signed an informed consent form. Sample collection followed the ethical principles of the Declaration of Helsinki, the Universal Declaration of Human Genome and Human Rights, and the Declaration of the Human Genome Ethics Committee on DNA Sampling, Control, and Acquisition.

Methods

DNA was extracted from peripheral venous blood samples with TGuide Blood Genomic DNA Kits (CHI-TIANGEN) following the manufacturer’s instructions. DNA was extracted from paraffin-embedded tissue specimens with QIAamp DNA FFPE micro sample tissue kits (GER-QIAGEN). Nucleic acids were broken into small, random 150-200 bp fragments by ultrasonic fragmentation (Covaris S220) and separated and evaluated with a Tapestation 2200 electrophoresis working platform (Agilent) to check whether the fragments met the requirements for library construction. A standard gene library was constructed using KAPA HyperPlus Kit (Illumina). A panel of 139 common tumor genetic susceptibility genes including colorectal cancer (Table 2) was selected and provided by Genetron Health Co.(Beijing). The specific gene capture probe was hybridized with the library in the environment of a hybridization buffer, and purified by the magnetic bead method. High-throughput NGS was performed with a Novaseq 6000 sequencer (Illumina, United States). Trimomatic (version 0.33) was used to crop and filter the original data, which was stored in FastQ format, after sequencing. The reads at the end of each pair were aligned with the human reference sequence GRCh37 (hg19) using the BWA-MEM algorithm (BWA version 0.7.10-r789) and the default parameters. The Picard tool (version 1.103 http://broadinstitute.github.io/picard/) was used to delete duplicate readings, and GATK (version 3.1-0-g72492bb) was used to realign the sequences around the known insertion loss at the single sample level and to recalibrate the base quality. Integrative Genomics Viewer version 2.3.34 (https://software.broadinstitute.org/software/igv/) was used to check the mutations in the coding region.

The Chinese (1000 CN), general population (1000 MAF), and dbSNP (https://www.ncbi.nlm.nih.gov/) at 1000 Genome Project (http://ftp.ncbi.nih.gov/Snp/), ESP6500 AA/EA (NHBLI GO Exome Sequencing Project https://evs.gs.washington.edu/EVS/), ExAC MAF (The Exome Aggregation Consortium) and other population databases were searched for the mutation frequency of this gene. The location of genes with a mutation frequency < 0.01 in the HGMD database (HGMD-PUBLIC version 20152) were used for pathogenicity analysis.

The diseases that the variant gene was related to were searched in the OMIM disease database (https://omim.org/) by ClinVar (https://www.ncbi.nlm.nih.gov/clinvar/). HGMD (https://www.hgmd.cf.ac.uk) retrieved the description of the mutation. SIFT[10] (http://sift.jcvi.org), PolyPhen2[11] (http://genetics.bwh.harvard.edu/pph2), and Mutation Assessor (http://mutationassessor.org) make conservative predictions of amino acid sequences. The results were used to evaluate the pathogenicity of the mutations[12,13].

SPSS 24.0 was used for statistical analysis of the acquired data. Qualitative results were reported as numbers and percentages. The chi-square test or Fisher’s exact probability method was used for between-group comparisons. \( P < 0.05 \) was considered
Table 1 Clinical characteristics of 24 enrolled Peutz-Jeghers syndrome patients

| No. | Gender | Specimen   | Time since onset of pigment spots (yr) | Early or late onset | Family history (members) | Number of hospitalizations | Number of operations | Stomach and enteroscopy times | Age at initial diagnosis of polyps | Age at first treatment | Polyp pathology | Load of Gastric polyps/Max. diameter (mm) | Load of small intestinal polyps/Max. diameter (mm) | Load of colorectal polyps/Max. diameter (mm) |
|-----|--------|------------|----------------------------------------|---------------------|--------------------------|--------------------------|---------------------------|-----------------------------|-----------------------------------|---------------------|----------------|-------------------------------------------|-------------------------------------------------|-------------------------------------------------|
| 1   | Male   | Paraffin section | 20                                     | Late                | No                       | 2                        | 1                         | 6                           | 20                                | 15                  | 1             | /                                         | 20/30                                          | /                                              |
| 2   | Male   | Paraffin section | 6                                      | Late                | Yes (mother and sister)  | 1                        | 2                         | 3                           | 9                                 | 9                   | 1             | 2/16                                      | 20/40                                          | 1/8                                            |
| 3   | Female | Paraffin section | 4                                      | Late                | No                       | 2                        | 1                         | 4                           | 9                                 | 9                   | 1             | /                                         | 3/28                                           | /                                              |
| 4   | Male   | Paraffin section | 5                                      | Late                | No                       | 1                        | 2                         | 1                           | 21                                | 21                  | 3             | 20/4                                    | 6/50                                           | /                                              |
| 5   | Male   | Paraffin section | 1                                      | Early               | Yes (mother)             | 4                        | 2                         | 1                           | 4                                 | 4                   | 1             | 2/12                                      | 2/60                                           | /                                              |
| 6   | Female | Blood       | 5                                      | Late                | Yes (father)             | 1                        | 0                         | 1                           | 29                                | 29                  | 1             | /                                         | /                                              | /                                              |
| 7   | Female | Blood       | 1                                      | Early               | Yes (father and sister)  | 4                        | 0                         | 11                          | 7                                 | 7                   | 1             | 1/8                                      | 2/30                                           | 3/40                                           |
| 8   | Male   | Blood       | 0                                      | Early               | Yes (father and sister)  | 1                        | 0                         | 1                           | 10                                | 10                  | 1             | /                                         | 10/50                                          | /                                              |
| 9   | Male   | Blood       | 6                                      | Late                | Yes (mother and grandmother) | 4                       | 1                         | 7                           | 6                                 | 7                   | 1             | 5/12                                      | 2/30                                           | 3/35                                           |
| 10  | Female | Blood       | 2                                      | Early               | No                       | 1                        | 0                         | 3                           | 7                                 | 7                   | 1             | 2/15                                      | /                                               | 1/30                                           |
| 11  | Male   | Blood       | 3                                      | Late                | No                       | 1                        | 4                         | 0                           | 22                                | 32                  | 1             | /                                         | 1/30                                           | /                                              |
| 12  | Male   | Blood       | 2                                      | Early               | No                       | 2                        | 1                         | 10                          | 4                                 | 4                   | 1             | 1/6                                      | 2/50                                           | /                                              |
| 13  | Male   | Blood       | 2                                      | Early               | No                       | 1                        | 2                         | 1                           | 25                                | 24                  | 1             | /                                         | 10/20                                          | /                                              |
| 14  | Female | Blood       | 3                                      | Late                | No                       | 8                        | 2                         | 8                           | 6                                 | 6                   | 1             | 1/10                                    | 8/80                                           | 1/20                                           |
| 15  | Male   | Blood       | 5                                      | Late                | No                       | 1                        | 2                         | 3                           | 20                                | 19                  | 2             | 1/6                                      | 1/80                                           | 2/30                                           |
| 16  | Male   | Blood       | 1                                      | Early               | Yes (mother)             | 3                        | 0                         | 2                           | 10                                | 9                   | 1             | /                                         | 1/25                                           | /                                              |
| 17  | Male   | Blood       | 1                                      | Early               | No                       | 3                        | 1                         | 4                           | 6                                 | 6                   | 1             | 8/40                                    | 10/30                                          | /                                              |
| 18  | Female | Blood       | 1                                      | Early               | No                       | 6                        | 2                         | 9                           | 11                                | 10                  | 1             | 1/15                                    | 3/35                                           | 1/50                                           |
| 19  | Female | Blood       | 3                                      | Late                | Yes (mother)             | 2                        | 0                         | 4                           | 15                                | 15                  | 1             | 1/12                                    | 2/12                                           | 1/25                                           |
| No. | Name  | Gender | Age of Blood Sampling | Bone Marrow  | Polyp Pathology | Polyp Load | Genetic Mutations | Other Gene Mutations | STK11/LKB1 Gene Detection Results and Pathogenicity Analysis |
|-----|-------|--------|-----------------------|--------------|----------------|------------|-------------------|---------------------|--------------------------------------------------------|
| 20  | Female| Blood  | 3                     | Late         | Yes (father, uncle, and grandmother) | 2          | 2 5 7 7 1 /       | /                   | 18/50 /                                                 |
| 21  | Female| Blood  | 1                     | Early        | Yes (mother, uncle, and aunt)       | 2          | 0 4 31 31 1 /     | /                   | 10/50 10/40                                               |
| 22  | Female| Blood  | 2                     | Early        | Yes (father and brother)            | 1          | 0 1 6 6 1 10/10 8/50 / | /                   |
| 23  | Male  | Blood  | 5                     | Late         | No                                  | 1          | 0 2 11 11 1 1/30 5/70 1/30 | /                   |
| 24  | Male  | Blood  | 2                     | Early        | No                                  | 1          | 0 4 5 4 1 10/15 / | /                   |

(1) STK11 mutation, SLX4 mutation, other gene mutation groups: 0: None; 1: Yes; (2) Early onset: Pigment spots appeared at < 3 years of age; Late onset: Pigment spots appeared at ≥ 3 years of age; (3) Polyp pathology: 1 hamartoma, 2 hamartoma with adenoma, 3 hamartoma with cancer; (4) Polyp load is the number of polyps, the largest diameter unit is mm; and (5) 6 was an outpatient, the results of previous endoscopy are unknown.

RESULTS

**STK11/LKB1 gene detection results and pathogenicity analysis**
Twenty of the 24 PJS patients (83.3%) in this group had STK11/LKB1 gene mutations. All were heterozygous and ten were newly discovered mutation sites not included in the dbSNP database. There were eight frameshift mutations, five splice-site mutations, four missense mutations and three nonsense mutations. The mutations occurred in eight of the ten exons in the STK11/LKB1 gene, mutations in exons 1 and 4 and 4 each in exon 7, two in each exons 5 and 8, and one in exons 2, 3, and 6. Frameshift mutations, splice-site mutations, and nonsense mutations were all related to pathogenicity. Frameshift mutations accounted for 62.5% (5/8) that were clearly pathogenic, and 37.5% (3/8) that might cause disease. Splice-site mutations accounted for 40% (2/5) that are clearly pathogenic, and 60% (3/5) that might cause disease. All three nonsense mutations were clearly pathogenic, and the missense mutations were related to and might cause disease. Sites of unclear clinical significance accounted for 50% (2/4); of the 11 truncated mutations, eight cases were clearly pathogenic and three were likely to cause disease. The pathogenicity of STK11 gene mutations in exon 7 was significantly lower than that of other exons (P = 0.000). Truncation mutations were significantly more pathogenic than missense mutations (P = 0.012). The prediction results of bioinformatics tools for missense mutations are shown in Table 4, and the relevant database records and the pathogenicity judgment of all mutations are shown in Table 5.
Considering that the type of specimen may impact on the detection rate of STK11/LKB1 gene mutations, we analyzed the paraffin-embedded tissue and blood samples separately. The detection rate of STK11/LKB1 mutations in 60 patients with paraffin samples was 60% (3/5), slightly less than the 89.4% (17/19) of the blood samples from 19 patients. The difference in mutation detection rate of this gene in the two types of sample was not statistically different ($P = 0.116$).

### SLX4 gene detection results and pathogenicity analysis

SLX4 gene mutation (Table 6) was detected in 5 PJS patient samples in this group, with a total detection rate of 20.83% (5/24), all of which were heterozygous mutations. The mutation occurred in 4 of 15 exons of SLX4 gene. Mutation types include: 3 missense mutations, one splice-site mutation, and one non-frameshift mutation. No truncation mutation was found. The SLX4 gene is a tumor suppressor gene, and there are three newly discovered mutation sites. The prediction results of three cases of missense mutations by bioinformatics tools (Table 7), the collection of relevant databases and the judgment of the pathogenicity of all mutations (Table 8) are as follows.

### Other gene detection results and pathogenicity analysis

A total of 55 mutations of 46 genes other than STK11/LKB1 and SLX4 were detected in 21 cases (Table 9), a detection rate of 87.5% (21/24). Twenty-three of the genes were related to cancer suppression and had 32 different mutation sites. Two mismatch repair MMR genes were detected, MSH2, MSH6. Except for a frameshift mutation (frameshift deletion) in the BRIP1 gene detected in one patient (No. 18), the rest were missense mutations (Table 10).
### Table 3 Characteristics of STK11/LKB1 gene mutations

| No. | Mutation type | dbSNP RS | Mutation site | Amino acid change | Exon | Variant type |
|-----|---------------|----------|---------------|------------------|------|--------------|
| 2   | Frameshift    | rs372511774 | c.357delC     | p.N119Kfs        | 2|10 | SNV         |
| 4   | Splice-site variant | rs398123406 | c.921-1G>A    |                   | 8|10 | SNP         |
| 5   | Frameshift    | rs106049961 | c.131dupA     | p.L45Af          | 1|10 | INS         |
| 6   | Missense      | /         | c.869T>C      | p.L290P          | 7|10 | SNP         |
| 7   | Nonsense      | /         | c.658>T      | p.Q220X          | 5|10 | SNP         |
| 8   | Frameshift    | /         | c.548del     | p.L183Rfs        | 4|10 | DEL         |
| 9   | Splice-site variant | rs398123406 | c.921-1G>C    |                   | 8|10 | SNP         |
| 10  | Frameshift    | /         | c.471_472del | p.F157Lfs        | 4|10 | DEL         |
| 12  | Frameshift    | /         | c.180del     | p.Y60X           | 1|10 | DEL         |
| 13  | Missense      | /         | c.869T>A     | p.L290H          | 7|10 | SNP         |
| 14  | Splice-site variant | /         | c.598-2A>G    |                   | 5|10 | SNP         |
| 15  | Missense      | rs121913315 | c.580G>A     | p.D194N          | 4|10 | SNP         |
| 16  | Missense      | rs730881978 | c.890G>A     | p.R297K          | 7|10 | SNP         |
| 17  | Frameshift    | /         | c.577_578del | p.S193Rfs        | 4|10 | DEL         |
| 18  | Splice-site variant | /         | c.863-2A>G    |                   | 7|10 | SNP         |
| 19  | Splice-site variant | rs1555735080 | c.290+1G>T   |                   | 1|10 | SNP         |
| 20  | Nonsense      | /         | c.179dup     | p.Y60X           | 1|10 | INS         |
| 21  | Frameshift    | rs587782584 | c.842dup     | p.L822Af         | 6|10 | INS         |
| 23  | Frameshift    | rs786203886 | c.228dup     | p.V77Rfs         | 1|10 | INS         |
| 24  | Nonsense      | rs730881970 | c.409C>T     | p.Q137X          | 3|10 | SNP         |

DEL: Deletion; INS: Insertion; SNP: Single nucleotide polymorphism; SNV: Single nucleotide variation.

### Table 4 Prediction of protein function change caused by STK11/LKB1 mutation

| No. | PolyPhen Score | Prediction | Mutation Assessor Score | Prediction | SIFT Score | Prediction |
|-----|----------------|------------|-------------------------|------------|------------|------------|
| 6   | 1              | Probably damaging | 0.98351; 4.21 | High       | 0          | Deleterious |
| 13  | 1              | Probably damaging | 0.99415; 4.555 | High       | 0          | Deleterious |
| 15  | 1              | Probably damaging | 0.98178; 4.165 | High       | 0          | Deleterious |
| 16  | 1              | Probably damaging | 0.98818; 4.34 | High       | 0.01       | Deleterious |
| 23  | 0.022          | Benign      | 0.56769; 1.78 | Low        | 0.26       | Tolerated  |

**STK11/LKB1 genotype-phenotype correlation analysis**

Investigation of the relationship between genotype and family history found that the proportion of patients with truncated mutations was slightly higher in those with a family history than in those without a history (60% vs 50%). The proportion of splice-site mutations was lower in those with a family history (20% vs 30%), and the proportion of nonsense mutations was higher in patients with a family history (20.0% vs 11.1%). The proportions of missense mutations were the same (20% vs 20%), and the proportion of frameshift mutations were also equal (40% vs 10%). There were no significant difference between-group differences in $P_{\text{truncation mutation}} = 0.653$, $P_{\text{splice site mutation}} = 0.606$, $P_{\text{nonsense mutation}} = 0.371$, $P_{\text{missense mutation}} = 1.000$, and $P_{\text{frameshift mutation}} = 1.000$.

Evaluation of the relationship between genotype and early onset/late onset found that the proportion of truncated mutations in patients with early onset was higher than that in patients with late onset (72.7% vs 33.3%). In patients with early onset, the
Table 5 STK11/LKB1 mutation-related databases and pathogenicity analysis

| No. | cDNA/protein | Disease database | Pathogenic judgment |
|-----|-------------|------------------|---------------------|
|     |             | HGMD             | ClinVar             | OMIM                  |
| 2   | p.N119Kfs   | /                | (1/1) pathogenic    | Pathogenic            |
| 4   | c.921-1G>A  | √                | /                   | PJS                   |
| 5   | p.L45AfS    | /                | /                   | Pathogenic            |
| 6   | p.L290P     | √                | (1/1) pathogenic    | PJS                   |
| 7   | p.Q220X     | /                | (3/3) pathogenic    | PJS                   |
| 8   | p.L183Rfs   | /                | /                   | Pathogenic            |
| 9   | c.921-1G>C  | √                | (2/2) pathogenic    | PJS                   |
| 10  | p.F157Lfs   | /                | /                   | Likely pathogenic     |
| 12  | p.Y60X      | √                | √                   | PJS                   |
| 13  | p.L290H     | /                | /                   | Clinical significance unknown |
| 14  | c.598-2A>G  | /                | (1/1) pathogenic    | PJS                   |
| 15  | p.D194N     | √                | (4/6) likely pathogenic; (2/6) pathogenic | PJS | Likely pathogenic |
| 16  | p.R207K     | √                | (1/2) pathogenic; (1/2) unknown | PJS | Likely pathogenic |
| 17  | p.S193Rfs   | /                | /                   | PJS                   |
| 18  | c.863-2A>G  | /                | (1/1) pathogenic    | PJS                   |
| 19  | c.290+1G>T  | Pathogenic       | /                   | PJS                   |
| 20  | p.Y60X      | Pathogenic       | (2/2) pathogenic    | PJS                   |
| 21  | p.L282AfS   | Pathogenic       | (1/1) pathogenic    | PJS                   |
| 23  | p.V77Rfs    | /                | /                   | PJS                   |
| 24  | p.Q137X     | Pathogenic       | (1/1) pathogenic    | PJS                   |

(4/6) likely pathogenic: A total of six institutions have judged this mutation, four of which are judged as probably pathogenic, the same below. PJS: Peutz-Jeghers syndrome.

Table 6 Characteristics of SLX4 gene mutations

| No. | Mutation type | dbSNP RS      | Mutation site | Amino acid changes | Exon | Variant type |
|-----|---------------|---------------|---------------|-------------------|------|--------------|
| 1   | Missense      | rs551385115   | c.5072A>G     | p.N1691S          | 14/15| SNP          |
| 2   | Splice-site variant | /        | c.1683+1G>A   | splice            | 7/15 | SNP          |
| 3   | Missense      | rs774243118   | c.2900C>T     | p.P997L           | 12/15| SNP          |
| 18  | Missense      | /             | c.2425G>C     | p.E809Q           | 12/15| SNP          |
| 22  | Non-frameshift| /             | c.568_570del  | p.P190del         | 3/15 | DEL          |

DEL: Deletion; SNP: Single nucleotide polymorphism.

percentages of frameshift mutations (54.5% vs 22.2%) and sense mutations (18.2% vs 11.1%) were higher than those in late onset patients. The percentages of splice-site mutations (9% vs 44.4%) and missense mutations were lower (18.2% vs 22.2%). There were no significant between-group differences in $P_{\text{truncation mutation}} = 0.078$, $P_{\text{frameshift mutation}} = 0.142$, $P_{\text{nonsense mutation}} = 0.660$, $P_{\text{splice site mutation}} = 0.069$, $P_{\text{missense mutation}} = 0.822$.

**DISCUSSION**

The STK11/LKB1 gene located on chromosome 19p13.3 is considered to be a tumor
suppressor gene[14] and is widely expressed in human tissues. Pathogenic mutation of \(STK11\) can inactivate its expressed product, which results in the loss of its inhibitory effect on the activity of mammalian target of rapamycin (mTOR), leading to the occurrence of skin and mucous membrane black spots and gastrointestinal polyps[5]. Methylation of the \(STK11/LKB1\) gene promoter has an important role in the process of malignant transformation of gastrointestinal polyps[15]. At present, the comprehensive mutation rate of \(STK11/LKB1\) gene in PJS patients detected by multiple sequencing methods is about 80%-94%[8,15,16]. The detection rate of \(STK11/LKB1\) gene mutation in PJS patients in this study was 83.3% (20/24), 90% of which are related to pathogenicity. Analysis of the pathogenicity of all the detected mutation sites included in the Mendelian Inheritance in Man (OMIM) database found that about 90% of the \(STK11/LKB1\) mutations were related to PJS. Except for the \(STK11/LKB1\) gene and one case of \(SLX4\) gene mutation, no other gene mutations related to the disease or the possibility of disease were found.

Research on whether there is a correlation between the PJS genotype and clinical phenotype is ongoing. Although the correlation is currently unclear[6,17], some studies have reported positive results. For example, Forcet et al[18] reported that patients often present with only black spots and without gastrointestinal polyps when heterozygous mutations occur in exon 8 of the \(STK11\) gene. Amos et al[19] found that PJS patients with missense mutations had a first episode of polypectomy and appearance of other symptoms significantly later than those with truncated mutations or no detectable mutations. In a study including 116 PJS patients in 52 families, Wang et al[20] found that nearly 30% of the mutations occurred in exon 7, and some of those mutations affected the protein Kinase domain XI region, which is associated with 90% of cases with gastrointestinal polyp dysplasia. An analysis of the start region of the \(STK11/LKB1\) coding sequence by Hearle et al[21] found that a change in promoter sequence was unlikely to be the cause of PJS. In this study the time that dark spots first appeared, which is a relatively objective indicator, was the basis of clinical classification, and was used to determine whether there was a correlation between the appearance of the spots and any of the genotypes. Spots that appear in early childhood will be noticed. On the other hand, unless there are obvious clinical symptoms, it is extremely difficult to know about gastrointestinal polyps that appear in early childhood. Also, PJS is an autosomal dominant genetic disease and does not completely follow Mendelian inheritance[6]. In clinical practice, it is often found that neither parent has a family history but their child has the disease. This is difficult to fully explain if the disease is caused by a single gene. Therefore, whether the patient has a family history was also included in the basis of clinical classification.

This study did not found that patients with different clinical phenotypes (early onset/late onset and with or without a family history) had statistically significant differences in their \(STK11/LKB1\) gene mutations and loci. However, we found that the

![Table 7 Prediction of protein function change caused by SLX4 mutation](image)

| No. | cDNA/Protein | HGMD | ClinVar | OMIM | PolyPhen Score | PolyPhen Prediction | Mutation assessor Score | Mutation assessor Prediction | SIFT Score | SIFT Prediction |
|-----|-------------|------|---------|------|----------------|---------------------|------------------------|--------------------------|------------|----------------|
| 1   | p.N1691S    | /    | /       |      | 0.08118; 0     | Benign              | 0.08118; 0             | Neutral                  | 0.16       | Tolerated       |
| 2   | c.1683+1G>A | /    | /       |      | 0.05510; -0.035| Benign              | 0.05510; -0.035         | Neutral                  | 1          | Tolerated        |
| 18  | p.P190del   | /    | /       |      | 0.59436; 1.845 | Benign              | 0.59436; 1.845          | Neutral                  | 0.04       | Deleterious      |

Table 8 SLX4 mutation-related databases and pathogenicity analysis

| No. | cDNA/Protein | Disease database | HGMD | ClinVar | OMIM               | Pathogenic judgment |
|-----|-------------|------------------|------|---------|--------------------|---------------------|
| 1   | p.N1691S    | /                | (1/1)| Uncertain Significance | BTB/POZ domain containing 12\|SLX4 structure-specific | Clinical significance unknown |
| 2   | c.1683+1G>A | /                | /   | /       | BTB/POZ domain containing 12\|SLX4 structure-specific | Likely pathogenic    |
| 3   | p.P997L     | /                | /   | /       | BTB/POZ domain containing 12\|SLX4 structure-specific | Clinical significance unknown |
| 18  | p.E809Q     | √                | /   | /       | BTB (POZ) domain containing 12\|SLX4 structure-specific | Clinical significance unknown |
| 22  | p.P190del   | /                | /   | /       | BTB (POZ) domain containing 12\|SLX4 structure-specific | Clinical significance unknown |
| No. | Gene | Type | Mutation site | Amino acid changes | Exon | Disease database |
|-----|------|------|---------------|-------------------|------|------------------|
| 1   | BARD1 | TSG  | c.556A>G      | p.S186G           | 4 | (6/6) Uncertain Significance |
| 2   | EGFR  | /    | c.61G>A       | p.A21T            | 1  | /               |
| 3   | GEN1  | /    | c.181T>A      | p.S61T            | 3  | /               |
| 4   | BRCA1 | TSG  | c.2387C>T     | p.T796I           | 10 | (8/8) Uncertain Significance |
| 5   | NTRK1 | /    | c.1604A>G     | p.E475K           | 13 | /               |
| 6   | PDGFR | A    | c.521C>T      | p.S174L           | 6  | (2/2) Uncertain Significance |
| 7   | MSH6  | /    | c.1063G>A     | p.G355S           | 4  | (4/7) Uncertain Significance (3/7) likely benign |
| 8   | EGFR  | /    | c.3040G>A     | p.D1014N          | 25 | /               |
| 9   | MTUS1 | TSG  | c.2282G>A     | p.S761N           | 3  | /               |
| 10  | PTCH1 | TSG  | c.3475C>T     | p.R1159W          | 30 | (2/4) benign, (1/4) likely benign |
| 11  | SDHA  | TSG  | c.715A>G      | p.D239V           | 6  | (2/2) Uncertain Significance |
| 12  | MSH6  | /    | c.2944A>G     | p.T982A           | 30 | (2/2) Uncertain Significance |
| 13  | VHL   | TSG  | c.134C>T      | p.P45L            | 1  | /               |
| 14  | FANCA | TSG  | c.3940T>C     | p.W1314R          | 29 | (1/1) Uncertain Significance |
| 15  | TP53  | TSG  | c.620A>G      | p.D207G           | 6  | (3/3) Uncertain Significance |
| 16  | FANCA | /    | c.2944A>G     | p.R1314R          | 29 | (1/1) Uncertain Significance |
| 17  | FANCA | /    | c.3031C>T     | p.R1011C          | 31 | (1/1) likely benign |
| 18  | VEGFA | TSG  | c.109G>G      | p.G37W            | 1  | (1/1) Uncertain Significance |

**Table 9 Other gene mutations and inclusion in relevant database**

- **HGMD**
- **ClinVar**
- **OMIM**

**Disease database**

- Epidermal growth factor receptor
- Gen endonuclease homolog 1
- Mitochondrial tumor suppressor 1
- Ataxia telangiectasia mutated
- Von Hippel-Lindau syndrome
- MutL (E. Coli) homolog 3
- Ataxia telangiectasia and Rad3 related
- Vascular endothelial growth factor
| Gene  | Description | Mutation | Heterozygosity | Significance | Comments |
|-------|-------------|----------|---------------|-------------|----------|
| BRIP1 | /           | c.3072del | 20/20         | (1/2)likely pathogenic, (1/2)Uncertain significance | / |
| WRN   | /           | c.3778G>A | 32/35         | (2/2)Uncertain significance | Werner syndrome |
| RECQL | /           | c.166G>A  | 4/16          | /            | / |
| BARD1 | TSG         | c.1145T>G | 4/11          | /            | / |
| USHBP1| /           | c.1358C>T | 9/13          | /            | / |
| APC   | TSG         | c.2882A>G | 16/16         | (1/1)Uncertain Significance | Adenomatosis polyposis coli |
| BRCA1 | TSG         | c.1568A>G | 10/27         | (1/12)benign, (2/12)likely benign, (2/12)Uncertain Significance |Fanconi anemia |
| ATM   | TSG         | c.1555G>A | 10/63         | (3/3)Uncertain Significance | Ataxia telangiectasia mutated |
| BRCA2 | TSG         | c.1568A>G | 10/27         | (1/12)benign, (9/12)likely benign, (2/12)Uncertain Significance | Fanconi anemia |
| TP53  | TSG         | c.2144C>G | 4/11          | (5/5)Uncertain Significance | / |
| FLNC  | TSG         | c.1366C>G | 12/14         | /            | / |
| MSH2  | TSG         | c.1789G>C | 12/16         | (1/1)Uncertain Significance | Colon cancer, nonpolyposis type 1 |
| KIT   | /           | c.2263G>A | 16/21         | (1/2)Uncertain Significance, (1/2)Uncertain Significance |Piebald trait |
| BAP1  | TSG         | c.1154G>A | 12/17         | (2/2)Uncertain Significance | / |
| TSC2  | TSG         | c.1609C>T | 16/42         | (1/5)benign, (2/5)likely benign, (1/5)Uncertain Significance | / |

HGMD: Human Gene Mutation Database; OMIM: Online Mendelian Inheritance in Man; TSG: Tumor suppressor gene.

most truncation mutations of the STK11/LKB1 gene mostly occurred in exons 1 and 4, most missense mutations occurred in exon 7, and that truncation mutations were significantly more pathogenic than missense mutations. The results indicate that changes in the sites encoding functional proteins in exon regions 1 and 4 may be among the main causes of PJS. Also, the percentage of STK11/LKB1 truncation mutations in patients with early onset PJS was higher than that in patients with late onset PJS, and the between-group difference in the percentage of missense mutations was not significant. Because the evidence of a correlation with missense mutations was not strong, it suggests that early onset PJS is more likely to be caused by pathogenic mutations in STK11/LKB1, while late onset disease is likely to be clinically heterogeneous. The study results also suggest that analysis of the age of appearance of dark spots in a large sample of PJS patients would yield some interesting findings.

For the first time, we detected more concentrated mutations in the SLX4 gene in PJS patients. The SLX4 (FANCP) gene is a tumor suppressor gene located on chromosome 16p13.3[21]. It serves as a key scaffold element for the assembly of multiprotein complexes containing enzymes involved in DNA maintenance and repair[22] and has low to moderate expression in all adult and fetal tissues and specific adult brain regions[23]. It has been reported that[24] truncated mutations in the SLX4 gene were detected in families with Fanconi anemia, and it was determined that SLX4 mutations are clearly related to one of the subtypes of the disease. Fanconi anemia is a rare autosomal recessive genetic disease[25]. In addition to blood system-related manifestations, the clinical manifestations of FA include multiple congenital malformations, brown pigmentation of the skin, and tumor susceptibility[26]. There are many similarities with PJS, mutations in the SLX4 gene have been detected in patients with PJS in previous studies, the first of which was found in this group. SLX4 is considered
Table 10 Prediction of protein function changes caused by other gene mutations

| Gene  | SIFT Score | Prediction  | PolyPhen Score | Prediction  | Mutation Assessor Score | Prediction |
|-------|------------|-------------|----------------|-------------|-------------------------|------------|
| BARD1 | 0          | Deleterious | 0.144          | Benign      | 0.66939; 2.045          | Medium     |
| EGFR  | 0.4        | Tolerated   | 0.956          | Possibly damaging | 0.33485; 1.01         | Low        |
| GEN1  | 0          | Deleterious | 0.999          | Probably damaging | 0.34521; 1.04         | Low        |
| BRCA1 | 0.02       | Deleterious | 0.775          | Probably damaging | 0.78223; 2.4          | Medium     |
| NTRK1 | 0.01       | Deleterious | 0.639          | Probably damaging | 0.02685; -0.53       | Neutral    |
| PDGFRA| 0.1        | Tolerated   | 0.05           | Benign      | 0.38838; 1.175         | Low        |
| TSC2  | 0.15       | Tolerated   | 0.327          | Benign      | 0.57536; 1.79          | Low        |
| MSH6  | 0.45       | Tolerated   | 0.176          | Benign      | 0.08118; 0             | Neutral    |
| EGFR  | 0          | Deleterious | 0.814          | Possibly damaging | 0.83953; 2.67       | Medium     |
| MTUS1 | 0.09       | Tolerated   | 0.044          | Benign      | 0.27053; 0.805         | Low        |
| PTCH1 | 0          | Deleterious | 0.7            | Possibly damaging | 0.88377; 2.95       | Medium     |
| SDHA  | 0.01       | Deleterious low confidence | 0.078 | Benign | 0.49699; 1.58 | Low |
| MTUS1 | 0.01       | Deleterious | 0.096          | Benign      | 0.29908; 0.895         | Low        |
| RECQL4| /          | /           | /              | /           | /                      | /          |
| RECQL4| /          | /           | /              | /           | /                      | /          |
| ATM   | 0          | Deleterious | 0.294          | Benign      | 0.67953; 2.075         | Medium     |
| TSC2  | 0.01       | Deleterious | 0.226          | Benign      | 0.08118; 0             | Neutral    |
| FANCG | 0.03       | Deleterious | 0.018          | Benign      | 0.14661; 0.345         | Neutral    |
| SOD5  | 0.12       | Tolerated   | 0.051          | Benign      | 0.71920; 2.185         | Medium     |
| VHL   | 0.06       | Tolerated   | 0.012          | Benign      | 0.19112; 0.55          | Neutral    |
| FANCA | 0.24       | Tolerated   | 0              | Benign      | 0.02315; -0.6          | Neutral    |
| TP53  | 0.03       | Deleterious | 0.386          | Benign      | 0.45228; 1.405         | Low        |
| FANCA | 0.79       | Tolerated   | 0.007          | Benign      | 0.52573; 1.65          | Low        |
| PALLD | 0.7        | Tolerated   | 0.159          | Benign      | 0.00602; -1.34         | Neutral    |
| MLH3  | 0.47       | Tolerated   | 0              | Benign      | 0.55103; 1.725         | Low        |
| SMARCA4| 0.05      | Deleterious | 0.007          | Benign      | 0.29908; 0.895         | Low        |
| NFI   | 0.62       | Tolerated   | 0.015          | Benign      | 0.08118; 0             | Neutral    |
| PTCH1 | 0          | Deleterious | 0.626          | Possibly damaging | 0.88377; 2.95     | Medium     |
| GALNT2 | 0.11     | Tolerated   | 0.007          | Benign      | 0.51422; 1.61          | Low        |
| ATR   | 0          | Deleterious | 0.998          | Possibly damaging | 0.65975; 2.015     | Medium     |
| VEGFA | 0.25       | Tolerated low confidence | 0.695 | Benign | 0.08118; 0 | Neutral |
| DIS3L2| 0.05       | Tolerated   | 0.996          | Possibly damaging | 0.87328; 2.875   | Medium     |
| TSC1  | /          | /           | /              | /           | 0.00621; -1.32         | Neutral    |
| PTCH1 | 0.03       | Deleterious low confidence | 0.259 | Benign | 0.36672; 1.1 | Low |
| BRIP1 | /          | /           | /              | /           | /                      | /          |
| WRN   | 0.59       | Tolerated   | 0.164          | Benign      | 0.70959; 2.14          | Medium     |
| RECQL | 0.5        | Tolerated   | 0.005          | Benign      | 0.41079; 1.255         | Low        |
| BARD1 | 0.4        | Tolerated   | 0              | Benign      | 0.08118; 0             | Neutral    |
| USHBP1| 0.05       | Tolerated   | 0.521          | Possibly damaging | 0.56769; 1.78     | Low        |
| APC   | 0.16       | Tolerated   | 0.82           | Possibly damaging | 0.46157; 1.445   | Low        |
DICER1  0.29  Tolerated  0.664  Possibly damaging  0.34321; 1.04  Low  
FANCM  1  Tolerated  0  Benign  0.40543; 1.245  Low  
APC  0.57  Tolerated  low confidence  0.003  Benign  0.14461; 0.345  Neutral  
NSD1  0.03  Deleterious  0.684  Possibly damaging  0.66939; 2.045  Medium  
SDHA  0.02  Deleterious  low confidence  0.02  Benign  0.20574; 0.59  Neutral  
MTUS1  0.87  Tolerated  0  Benign  0.12746; 0.255  Neutral  
EXT2  0.03  Deleterious  0.993  Possibly damaging  0.82323; 2.985  Medium  
ATM  0.58  Tolerated  0.007  Benign  0.56769; 1.78  Low  
BRCA2  0.09  Tolerated  0.003  Benign  0.08618; 0  Neutral  
TP53  0.94  Tolerated  0  Benign  0.03608; -0.345  Neutral  
FLCN  0.03  Deleterious  0  Benign  0.47716; 1.5  Low  
MSH2  0.25  Tolerated  0.023  Benign  0.39692;1.235  Low  
KIT  0.15  Tolerated  0.472  Possibly damaging  0.03608; -0.345  Neutral  
BAP1  0  Deleterious  low confidence  0.968  Possibly damaging  0.59436; 1.845  Low  
TSC2  0.02  Deleterious  0.446  Possibly damaging  0.75777; 2.31  Medium  

to be an important regulator of DNA repair. Studies have shown that repairing specific types of DNA damage requires SLX4 and other endonucleases to participate together [22]. At present, it is believed that[27-29] the loss of DNA MMR genes causes the accumulation of mismatches in the process of DNA replication, resulting in the occurrence of microsatellite instability and partial junctions. Colorectal cancer has obvious genetic characteristics. We also detected mutations in some MMR genes (MSH2 and MSH6) in PJS, and the role of SLX4 gene is highly similar to that. Perhaps the mutation of the SLX4 gene may explain the genetic heterogeneity of PJS to some extent.

**CONCLUSION**

In conclusion, we discovered a series of new gene mutation sites, analyzed their pathogenicity, and enriched the mutation spectrum of PJS pathogenic genes. And through the summary of the clinical phenotypes with different STK11 genotypes, to explore whether they are related, and get some tendentious research results. The detection of SLX4 gene mutations in patients with PJS was reported for the first time. The relationship between SLX4 gene mutations and the occurrence of PJS is still unclear, but may help to explain the genetic heterogeneity of PJS.

**ARTICLE HIGHLIGHTS**

**Research background**

Different types of pathogenic mutations may produce different clinical phenotypes, but no exact correlation between Peutz-Jeghers syndrome (PJS) genotype and clinical phenotype has been found so far. So it is necessary to study the correlation between genotype and clinical phenotype of PJS, and explore the internal molecular mechanism of different clinical phenotypes.

**Research motivation**

The authors included 24 cases of treated PJS cases as study participants, collected peripheral venous blood or normal tissue adjacent to polyps for high-throughput next-generation sequencing (NGS) of 139 hereditary colorectal tumor-related genes including STK11/LKB1 to study the correlation between genotype and clinical phenotype of PJS.
Research objectives
To investigate the correlation between the genotype and clinical phenotype of PJS.

Research methods
Twenty-four patients with PJS were randomly selected for study inclusion. A total of 139 common hereditary tumor-related genes including STK11/LKB1 were screened and analyzed for pathogenic germline mutations by high-throughput next-generation sequencing (NGS), and the pathogenicity of these mutations was evaluated.

Research results
STK11/LKB1 gene mutations were identified in 20 PJS patients, 90% of which were pathogenic mutations. 10 cases had new mutation sites. Pathogenic mutations were significantly less frequent in exon 7 of the STK11/LKB1 gene than in other exons. Truncation mutations were more common in exons 1 and 4, and their pathogenicity was significantly higher than that of missense mutations. We also identified SLX4 gene mutations in PJS patients.

Research conclusions
PJS has a relatively complicated genetic background. Changes in the sites responsible for coding functional proteins in exon 1 and exon 4 of STK11/LKB1 may be one of the main causes of PJS. Mutation of the SLX4 gene may help to explain the genetic heterogeneity of PJS.

Research perspectives
Exploration of the relationships of clinical phenotypes with different STK11 genotypes, may help to interpret some controversial research results. The detection of SLX4 gene mutations in patients with PJS was reported for the first time.

REFERENCES
1 van Lier MG, Wagner A, Mathus-Vliegen EM, Kuipers EJ, Steyerberg EW, van Leerdam ME. High cancer risk in Peutz-Jeghers syndrome: a systematic review and surveillance recommendations. Am J Gastroenterol 2010; 105: 1258-64; author reply 1265 [PMID: 20051941 DOI: 10.1111/j.1399-0004.2009.00907.x]
2 Hearle N, Schumacher V, Menko FH, Olschwang S, Boardman LA, Gille JJ, Keller JJ, Westerman AM, Scott RJ, Lim W, Trimbath JD, Giardiello FM, Gruber SB, Offerhaus GJ, de Rooij FW, Wilson JH, Hansmann A, Moslein G, Royer-Pokora B, Vogel T, Phillips RK, Spigelman AD, Houlston RS. Frequency and spectrum of cancers in the Peutz-Jeghers syndrome. Clin Cancer Res 2006; 12: 3209-215 [PMID: 16707622 DOI: 10.1158/1078-0432.CCR-06-0083]
3 Lim W, Olschwang S, Keller JJ, Westerman AM, Menko FH, Boardman LA, Scott RJ, Trimbath J, Giardiello FM, Gruber SB, Gille JJ, Offerhaus GJ, de Rooij FW, Wilson JH, Spigelman AD, Phillips RK, Houlston RS. Relative frequency and morphology of cancers in STK11 mutation carriers. Gastroenterology 2004; 126: 1788-1794 [PMID: 15188174 DOI: 10.1053/j.gastro.2004.03.014]
4 Hemminki A, Markie D, Tomlinson I, Avizienyte E, Roth S, Loukola A, Bignell G, Warren W, Aminoff M, Höglund P, Järvinen H, Kristo P, Pelin K, Ridanpää M, Salovaara R, Toró T, Bodmer W, Olschwang S, Olsen AS, Stratton MR, de la Chapelle A, Aaltonen LA. A serine/threonine kinase gene defective in Peutz-Jeghers syndrome. Nature 1998; 391: 184-187 [PMID: 9428765 DOI: 10.1038/34432]
5 Jia Y, Fu H, Li N, Kang Q, Sheng J. [Diagnosis and treatment for 46 cases of Peutz-Jeghers syndrome]. Zhong Nan Da Xue Xue Bao Yi Xue Ban 2018; 43: 1323-1327 [PMID: 30643048 DOI: 10.11817/j.issn.1672-7347.2018.12.007]
6 Beggs AD, Latchford AR, Vasen HF, Moslein G, Alonso A, Aretz S, Bertario L, Blanco I, Biliou S, Burn J, Capella G, Colas C, Friedl W, Muller P, Hes FJ, Järvinen H, Mecklin JP, Nagengast FM, Parc Y, Phillips RK, Hyer W, Ponz de Leon M, Renkonen-Sinisalo I, Sampson JR, Tejpar S, Thomas HJ, Wijnen JT, Clark SK, Hodgson SV, Peutz-Jeghers syndrome: a systematic review and recommendations for management. Gut 2010; 59: 975-986 [PMID: 20581245 DOI: 10.1136/gut.2009.194899]
7 Riegert-Johnson DL, Westra W, Roberts M. High cancer risk and increased mortality in patients with Peutz-Jeghers syndrome. Gut 2012; 61: 322; author reply 322-322; author reply 323 [PMID: 21330574 DOI: 10.1136/gut.2011.238642]
8 de Leng WW, Jansen M, Carvalho R, Polak M, Musler AR, Milne AN, Keller JJ, Menko FH, de Rooij FW, Iacobuzio-Donahue CA, Giardiello FM, Weterman MA, Offerhaus GJ. Genetic defects underlying Peutz-Jeghers syndrome (PJS) and exclusion of the polarity-associated MARK/Par1 gene family as potential PJS candidates. Clin Genet 2007; 72: 568-573 [PMID: 17924967 DOI: 10.1111/j.1399-0004.2007.00907.x]
9 Williams CD, Grady WM, Zullig LL. Use of NCCN Guidelines, Other Guidelines, and Biomarkers
for Colorectal Cancer Screening. J Natl Compr Canc Netw 2016; 14: 1479-1485 [PMID: 27799515 DOI: 10.6004/jncnn.2016.0154]

10 Kumar P, Henikoff S, Ng PC. Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm. Nat Protoc 2009; 4: 1073-1081 [PMID: 19561590 DOI: 10.1038/nprot.2009.86]

11 Adzhubei IA, Schmidt S, Peshkin L, Ramensky VE, Gerasimova A, Bork P, Kondrashov AS, Sunyaev SR. A method and server for predicting damaging missense mutations. Nat Methods 2010; 7: 248-249 [PMID: 20354512 DOI: 10.1038/nmeth0410-248]

12 Thompson BA, Spurdle AB, Plazzer JP, Greenblatt MS, Akagi K, Al-Mulla F, Bapat B, Bernstein I, Capellà G, den Dunnen JT, du Sart D, Fabre A, Farrell MP, Farrington SM, Frayling IM, Freibourg T, Goldberg DE, Heinen CD, Holinski-Feder E, Kohonen-Corish M, Robinson KL, Leung SY, Martins A, Moller P, Morak M, Nystrom M, Peltomaki P, Pineda M, Qi M, Ramesar R, Rasmussen LJ, Royer-Pokora B, Scott RJ, Sijmons R, Tavtigian SV, Tops CM, Weber T, Wijnen J, Woods MO, Macrae F, Gemma M. Application of a 5-tiered scheme for standardized classification of 2,366 unique mismatch repair gene variants in the InSiGHT locus-specific database. Nat Genet 2014; 46: 107-115 [PMID: 24362816 DOI: 10.1038/ng.2854]

13 MacArthur DG, Manolio TA, Dimmock DP, Rehm HL, Shendure J, Abecasis GR, Adams DR, Altman RB, Antonarakis SE, Ashley EA, Barrett JC, Biesecker LG, Conrad DF, Cooper GM, Cox NJ, Daly MJ, Gerstein MB, Goldstein DB, Hirschhorn JN, Leal SM, Pennacchio LA, Stamatoyannopoulos JA, Sunyaev SR, Valle D, Voight BF, Winckler W, Gurley C. Guidelines for investigating causality of sequence variants in human disease. Nature 2017; 549: 406-414 [PMID: 27818037 DOI: 10.1038/nature23328]

14 Ale was listed in the previous content.}

15 Aretz S, Stiensten D, Uhlhaas S, Loff S, Back W, Pagensstecher C, McLeod DR, Graham GE, Mangold E, Santer R, Propping P, Friedl W. 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: 1283-1292 [PMID: 16000014 DOI: 10.1093/hmg/ddi359]

16 Amos CI, Keiteri-Chetser EB, Sabirpour M, Wei C, McGa rry JT, Seldin MF, Nations L, Lynch PM, Fidder HH, Friedman E, Frazier ML. Genotype-phenotype correlations in human disease. Hum Mutat 2003; 28: 327-333 [PMID: 15121768 DOI: 10.11136/jnms.897498]

17 Wang Z, Wu B, Mosis RA, Chen Y, Ye F, Zhang Y, Gong W, Gong L, Huang F, Wang X, Nie B, Zheng H, Cui M, Wang Y, Wang J, Chen C, Pol ydorides AD, Zhang DY, Martignetti JA, Jiang B. Functional analysis of Peutz-Jeghers syndrome. Med Sci Monit 2016; 22: 3628-3640 [PMID: 27721366 DOI: 10.12659/msm.897498]

18 Aretz S, Stiensten D, Uhlhaas S, Loff S, Back W, Pagenstecher C, McLeod DR, Graham GE, Mangold E, Santer R, Propping P, Friedl W. High proportion of large genomic STK11 deletions in Peutz-Jeghers syndrome. Hum Mutat 2009; 30: 2465-2472 [PMID: 2005; DOI: 10.1002/hum.22549]

19 Zheng H, Cui M, Wang Y, Wang J, Chen C, Polydorides AD, Zhang DY, Martignetti JA, Jiang B. Functional analysis of Peutz-Jeghers syndrome. Med Sci Monit 2016; 22: 3628-3640 [PMID: 27721366 DOI: 10.12659/msm.897498]

20 Aretz S, Stiensten D, Uhlhaas S, Loff S, Back W, Pagenstecher C, McLeod DR, Graham GE, Mangold E, Santer R, Propping P, Friedl W. High proportion of large genomic STK11 deletions in Peutz-Jeghers syndrome. Hum Mutat 2009; 30: 2465-2472 [PMID: 2005; DOI: 10.1002/hum.22549]

21 Wang Z, Wu B, Mosis RA, Chen Y, Ye F, Zhang Y, Gong W, Gong L, Huang F, Wang X, Nie B, Zheng H, Cui M, Wang Y, Wang J, Chen C, Pol ydorides AD, Zhang DY, Martignetti JA, Jiang B. Functional analysis of Peutz-Jeghers syndrome. Med Sci Monit 2016; 22: 3628-3640 [PMID: 27721366 DOI: 10.12659/msm.897498]

22 Aretz S, Stiensten D, Uhlhaas S, Loff S, Back W, Pagenstecher C, McLeod DR, Graham GE, Mangold E, Santer R, Propping P, Friedl W. High proportion of large genomic STK11 deletions in Peutz-Jeghers syndrome. Hum Mutat 2009; 30: 2465-2472 [PMID: 2005; DOI: 10.1002/hum.22549]
28 Bourhis A, De Luca C, Cariou M, Vigliar E, Barel F, Conticelli F, Marcorelles P, Nousbaum JB, Robaszkiewicz M, Samaison L, Badie B, Doucet L, Troncone G, Uguen A. Evaluation of KRAS, NRAS and BRAF mutational status and microsatellite instability in early colorectal carcinomas invading the submucosa (pT1): towards an in-house molecular prognostication for pathologists? J Clin Pathol 2020; 73: 741-747 [PMID: 32273401 DOI: 10.1136/jclinpath-2020-206496]

29 Vageli DP, Doukas SG, Markou A. Mismatch DNA repair mRNA expression profiles in oral melanin pigmentation lesion and hamartomatous polyp of a child with Peutz-Jeghers syndrome. Pediatr Blood Cancer 2013; 60: E116-E117 [PMID: 23677888 DOI: 10.1002/pbc.24579]
