Prevalence of Mefv Gene Mutations and their Association with Clinical Phenotypes in 102 Caucasian Children with Henoch-Schönlein Purpura

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Abstract

Aim: To assess the prevalence of MEFV mutations in Caucasian children with Henoch-Schönlein purpura (HSP) and to investigate a possible association between the two diseases in a population with presumably low incidence of familial Mediterranean fever (FMF).

Methods: One hundred and two children diagnosed with HSP between January 2002 and February 2009 were included in the study. Clinical data were obtained from medical charts. Children were tested for 6 common MEFV mutations. To find out the carrier rate of mutations in MEFV gene in Slovenian population a control group of 105 apparently healthy adults was screened.

Results: Heterozygous MEFV gene mutations were found in 6% of children with HSP and in 7% of apparently healthy adults. The most common allelic variants found in both groups were as follows: V726A in 5 participants, K695R in 4 participants, E148Q in 3 participants and M694V in 1 participant. No significant differences in HSP clinical picture between the group of children with and without mutations in MEFV were found. HSP patients with MEFV mutations were younger than patients without MEFV mutations.

Conclusion: In contrast to previously published researches, MEFV mutations are not more frequent in children with HSP comparing to apparently healthy population and have no influence on the clinical presentation of HSP.

Keywords: Familial Mediterranean fever; Henoch-Schönlein purpura; MEFV mutations

Abbreviations: CRP: C-reactive protein; DNA: Deoxyribonucleic Acid; ECE: Countries: Eastern and Central European Countries; ESR: Erythrocyte Sedimentation Rate; EULAR: European League Against Rheumatism; FMF: Familial Mediterranean Fever; GIT: Gastrointestinal; HSP: Henoch- Schönlein Purpura; MEFV: Familial Mediterranean Fever Gene; PRES: Paediatric Rheumatology European Society

Introduction

Henoch-Schönlein purpura (HSP) is the most common systemic vasculitis in childhood with estimated incidence of 12.9-20.1/100.000 children [1,2]. It is characterized by palpable purpura, arthritis and arthralgias, abdominal pain, occult or manifest gastrointestinal bleeding and nephritis ranging from microscopic hematuria and proteinuria to nephrotic or nephritic syndrome or even acute renal failure [3,4]. HSP is also the most common vasculitis in Slovenian children. On the other hand Familial Mediterranean Fever (FMF), the most common periodic fever syndrome, is a very rare disease in Slovenia with only few diagnosed cases in adult population.

FMF is an autosomal recessive disease caused by mutations in MEFV gene localized on chromosome 16. MEFV gene is composed of 10 exons encoding a 781 amino acid protein known as pyrin, which is expressed mainly in innate immune cells, but not lymphocytes. Pyrin has several domains that have a distinct role in interactions with different proteins related to inflammation [5]. Mutation in MEFV gene causes the clinical picture of FMF, which is characterized by recurrent fever accompanied by arthritis, serositis, myalgias and rash [6,7]. So far, 100 disease associated mutations have been described [8].

Studies investigating the MEFV mutations in children with HSP performed in populations, where FMF prevalence is high, reported MEFV gene mutations to be more common in patients with HSP than in general population, thus making it an important predisposing factor for HSP [9-11]. It was also shown that FMF patients develop vasculitides, most commonly HSP, more often than general population [6]. Aims of the present study were to determine the prevalence of MEFV mutations in children with HSP in a population with presumably low incidence of FMF and to investigate the possible associations between the two diseases.

Methods

Study design was a retrospective data collection of children diagnosed with HSP between January 2002 and February 2009 at the University Children's Hospital, Ljubljana, Slovenia. Study population consisted of 102 children who were available for genetic testing and were willing to participate in the study. To be diagnosed as having HSP, children had to fulfil the EULAR/PReS endorsed consensus criteria for classification of childhood vasculitides that were valid at the time of diagnosis and had to be younger than 18 years at the time of diagnosis [12,13]. The exclusion criteria were leukocytoclastic vasculitis of other aetiology or suspected periodic fever syndrome. Data were collected from medical charts, including sex, age at diagnosis, cutaneous manifestations, joint, GIT and/or renal involvement, and laboratory parameters at the time of diagnosis- ESR, CRP and the number of leukocytes. Control group consisted of 105 apparently healthy adults, who donated their DNA for research purposes.

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the number of all persons with mutations is 13

A written informed consent for participation in the study, drawing of blood for DNA isolation and genetic testing of MEVF mutations was obtained from the parents of the children or from the patients themselves if older than 18 years at the time of drawing blood. Patients were invited for a control visit. Blood sample was obtained at the time of a clinical examination. The study was approved by the Ethics' Committee of the Slovenian Ministry of Health and was conducted according to the principles of the Helsinki Declaration.

Clinical and laboratory data were collected using Microsoft Excel 2003 and statistical tests were performed using SPSS 13.0. A p value <0.05 was considered statistically significant.

Molecular analysis

DNA isolation was performed from peripheral blood using FlexiGene isolation kit (Qiagen, Germany), following the manufacturer's instructions. Polymerase chain reaction of part of exons 2 and 10 was performed using the AmpliTaq polymerase (Applied Biosystems, USA) and corresponding reagents. Six most common mutations in MEVF gene were tested including V726A, K695R, M694V, M694I, M680I in exon 10 and E148Q in exon 2 [15]. Primers used for the amplification were FMF2f5' AAAACGGCACAGATGATTCC 3' / FMF2e 5'

CCTTCTCTCTGCAGTGCCTC3' and FMFe10f5'

TTGGAGACAAGACAGCATGG 3'/FMFe10r5'

AGCAGGAAGAGAGATGCGT 3' (Invitrogen, USA).

Our protocol mixture consisted of 4 ng/μL double stranded DNA, 0.2 μM of each deoxynucleoside triphosphate (dNTP), 0.4 μM primers, 1 mM MgCl2, 1/10 of corresponding reaction buffer and 0.08 U/ μL AmpliTaq DNA polymerase (Applied Biosystems, USA).

After the initial preincubation of DNA for 5 minutes at 95°C, 35 cycles of amplification were performed. Three steps PCR protocol was chosen, with DNA denaturation at 94°C for 30 seconds, annealing at 58°C for 30 seconds and primer extension at 72°C for 30 seconds. Seven minutes primer extension at 72°C was allowed at the end of 35 cycles.

PCR products (201bp for exon2 and 400bp for exon10) were purified and concentrated using the QIAquick PCR purification kit (Qiagen, Germany), following the manufacturer’s instructions and subjected to direct nucleotide sequencing using the Big Dye Terminator cycle sequencing kit and ABI PRISM 310 automated sequencer (Applied Biosystems, Foster City, CA, USA). We compared the obtained sequences with the gene sequence published in GenBank (NG_007871.1) [14].

Results

MEVF mutations in the group of children with HSP and in the control group

Heterozygous mutations were found in 6/102 (6%) of children with HSP and in 7/105 (7%) subjects in a control group. The distribution of MEVF genotypes in both groups is shown in Table 1. There were no homozygous or compound heterozygous mutations found in either group. The difference in the frequency of mutations between the groups was not statistically significant (χ²=0.048, p= 0.8271).

Clinical features of HSP and association with MEVF gene mutations

Among 102 children with medical history of HSP 48 patients were male and 54 female. The mean age at diagnosis was 7.1 ± 3.9 years; range 0.5–17.3 years. Palpable purpura was present in all patients (100%), arthritis or periarticular edema in 58 patients (57%), mild gastrointestinal involvement in 22 patients (22%), severe gastrointestinal involvement necessitating methylprednisolone therapy in 11 patients (11%) and kidney involvement in 11 patients (11%). The mean value of leukocytes at the time of hospitalization was 9.7 ± 3.8 × 10⁹/L. Elevated values of ESR (>15 mm/h) were found in 66% (38/58) of patients, mean value was 32.8 ± 19.6 mm/h and CRP values (>8 mg/L) were elevated in 28% (28/100) of patients, mean value was 31.8 ± 21.7 mg/L.

Patients with MEVF mutations were in average younger than patients without MEVF mutations, but the difference was not statistically significant. No other statistically significant difference was found between patients with and without mutations. The clinical manifestations in the group of children with MEVF mutations and in the group of children without mutations are shown in Table 2.

Clinical presentation of HSP in children, carriers of MEVF mutations, was very diverse and their clinical data is shown in Table 3.

Discussion

Present study is the first to evaluate the prevalence of MEVF mutations in children with HSP in a population where FMF is very rare. There was no difference in the MEVF carrier rate between the group

*CRP value was higher than 5mg/L in only one patient with MEVF mutation

Table 1: MEVF genotypes.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Patients with HSP</th>
<th>Controls</th>
<th>Total (% of all persons with mutations)*</th>
</tr>
</thead>
<tbody>
<tr>
<td>null/null</td>
<td>96</td>
<td>99</td>
<td>194</td>
</tr>
<tr>
<td>M694V/null</td>
<td>1</td>
<td>0</td>
<td>1 (8)</td>
</tr>
<tr>
<td>M694I/null</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>M680I/null</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>V726A/null</td>
<td>1</td>
<td>4</td>
<td>5 (38)</td>
</tr>
<tr>
<td>K695R/null</td>
<td>2</td>
<td>2</td>
<td>4 (31)</td>
</tr>
<tr>
<td>E148Q/null</td>
<td>2</td>
<td>1</td>
<td>3 (23)</td>
</tr>
<tr>
<td>Total</td>
<td>102</td>
<td>105</td>
<td>207</td>
</tr>
</tbody>
</table>

* the number of all persons with mutations is 13

Table 2: Clinical manifestations in group of children with and without MEVF mutations.

<table>
<thead>
<tr>
<th>Clinical features</th>
<th>Patients without MEVF mutations (n=96)</th>
<th>Patients with MEVF mutations (n=6)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean age at diagnosis (years):</td>
<td>7.1±3.9 (5.8±2.6)</td>
<td></td>
</tr>
<tr>
<td>Gender, n(%)</td>
<td>51 (53)</td>
<td>3 (50)</td>
</tr>
<tr>
<td>Male</td>
<td>45 (47)</td>
<td>3 (50)</td>
</tr>
<tr>
<td>Clinical features, n(%)</td>
<td>96 (100)</td>
<td>6 (100)</td>
</tr>
<tr>
<td>Palpable purpura</td>
<td>55 (57)</td>
<td>3 (50)</td>
</tr>
<tr>
<td>Mild GIT involvement</td>
<td>21 (22)</td>
<td>1 (17)</td>
</tr>
<tr>
<td>Severe GIT involvement</td>
<td>11 (12)</td>
<td>0</td>
</tr>
<tr>
<td>Renal involvement</td>
<td>10 (10)</td>
<td>1 (17)</td>
</tr>
</tbody>
</table>

Laboratory findings:

<table>
<thead>
<tr>
<th>Laboratory findings</th>
<th>Patients without MEVF mutations (n=96)</th>
<th>Patients with MEVF mutations (n=6)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Leukocytes, n=196, n=6</td>
<td>9.7±3.9</td>
<td>3±1±2.9</td>
</tr>
<tr>
<td>Elevated ESR, n=51, n=4</td>
<td>26.0±19.3</td>
<td>26.8±21.1</td>
</tr>
<tr>
<td>Elevated CRP, n=27, n=1</td>
<td>32.3±21.9</td>
<td>18*</td>
</tr>
</tbody>
</table>

* CRP value was higher than 5mg/L in only one patient with MEVF mutation

n1- number of data available for patients without MEVF mutations
n2- number of data available for patients with MEVF mutations

of children with HSP and apparently healthy controls. Six out of 102 (6%) patients and 7 out of 105 (7%) apparently healthy controls were found to be heterozygous for one of the screened MEFV mutations. No homozygous or compound heterozygous mutations were found in either group.

Studies evaluating MEFV mutations in children with HSP have, so far, only been published in Israeli and Turkish populations where the carrier rate of MEFV mutation is high [9-11]. In an Israeli population, Gershoni-Baruch et al. found a single mutation in 17.3% and two mutations in 9.6% of patients with HSP and concluded that the prevalence of mutated alleles significantly exceeds the prevalence in general Israeli population [9]. MEFV mutations as an important predisposing factor for HSP were reported also in a study published by Özçakar et al. who found that the proportion of MEFV mutation carriers among Turkish patients exceeds that in general population [10]. Recently, another study conducted in Turkish population confirmed that MEFV mutations are more frequent in HSP patients than in the general population [11]. Our results do not support findings of previously published studies.

The present study is also the first study in the region of eastern and central European (ECE) countries evaluating carrier rate of MEFV mutations in a population where FMF is a rare disease. FMF mainly differs when the search of MEFV mutations in a population where FMF is a rare disease. FMF mainly appears that in western European caucasian patients the prevalence of mutated alleles significantly exceeds the prevalence in general population [11]. Our results do not support findings of previously published studies.

In conclusion, our study demonstrated that MEFV mutations are present also in Slovenian children with HSP but there was no significant difference in the carrier rate of MEFV mutations comparing to apparently healthy Slovenian population. These results are in contrast to previously published studies in populations with a high carrier rate of MEFV mutations, where the presence of MEFV mutation presents a risk factor for development of HSP.

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**Disclosure statement:** The authors have declared no conflicts of interest.

**References**


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<table>
<thead>
<tr>
<th>Patient - gender</th>
<th>genotype</th>
<th>age at diagnosis (y)</th>
<th>Clinical manifestations</th>
</tr>
</thead>
<tbody>
<tr>
<td>M</td>
<td>M694V/null</td>
<td>7.6</td>
<td>purpura, articular involvement, mild gastrointestinal involvement</td>
</tr>
<tr>
<td>F</td>
<td>V726A/null</td>
<td>5.0</td>
<td>purpura, articular involvement, mild gastrointestinal involvement</td>
</tr>
<tr>
<td>M</td>
<td>K695R/null</td>
<td>8.9</td>
<td>purpura, articular involvement, kidney involvement</td>
</tr>
<tr>
<td>F</td>
<td>K695R/null</td>
<td>3.1</td>
<td>purpura, kidney involvement</td>
</tr>
<tr>
<td>F</td>
<td>E148Q/null</td>
<td>2.7</td>
<td>purpura, kidney involvement</td>
</tr>
<tr>
<td>M</td>
<td>E148Q/null</td>
<td>7.6</td>
<td>purpura, articular involvement</td>
</tr>
</tbody>
</table>

M- male, F- female, y- years


