Identification of novel MUNC13-4 mutations in familial haemophagocytic lymphohistiocytosis and functional analysis of MUNC13-4-deficient cytotoxic T lymphocytes


Background: Familial haemophagocytic lymphohistiocytosis (FHL) has an autosomal recessive mode of inheritance and consists of at least three subtypes. FHL2 subtype with perforin (PRF1) mutation accounts for 30% of all FHL cases, while FHL with MUNC13-4 mutation was recently identified and designated as FHL3 subtype.

Objective: To examine MUNC13-4 mutations and the cytotoxic function of MUNC13-4 deficient T lymphocytes in Japanese FHL patients.

Methods: Mutations of MUNC13-4 and the cytotoxicity of MUNC13-4-deficient cytotoxic T lymphocytes (CTL) were analysed in 16 Japanese families with non-FHL2 subtype.

Results: Five new mutations of the MUNC13-4 gene were identified in six families. The mutations were in the introns 4, 9, and 18, and exons 8 and 19. Two families had homozygous mutations, while the remaining four had compound heterozygous mutations. Cytotoxicity of MUNC13-4 deficient CTL was low compared with control CTL, but was still present. Clinically, the onset of disease tended to occur later; moreover, natural killer cell activity was not deficient in some FHL3 patients.

Conclusions: MUNC13-4 mutations play a role in the development of FHL3 through a defective cytotoxic pathway.

Haeomophagocytic lymphohistiocytosis is characterised by fever, hepatosplenomegaly associated with pancytopenia, hypertriglyceridaemia, and hypofibrinogenaemia. Familial haemophagocytic lymphohistiocytosis (FHL) has an autosomal recessive mode of inheritance and usually occurs in infancy. The pathogenesis of FHL has been associated with impairment of the cytotoxic pathway in lymphocytes, where uncontrolled activation of T lymphocytes results in raised levels of inflammatory cytokines.

With regard to the genetic defect in FHL, linkage analyses have indicated possible loci in 9q21.3–22, designated FHL1 (MIM 603552), and 10q12–22, designated FHL2 (MIM 603553). A mutation in the perforin gene (PRF1) was established as a cause of FHL2 in 1999. More recently, a mutation of MUNC13-4 mapped to 17q25 was identified as a causative gene of FHL3. The MUNC13-4 mutation leads to defective cytotoxic granule exocytosis followed by impaired cytotoxic activity of T lymphocytes in FHL3 patients.

In this study we examined MUNC13-4 mutations and the cytotoxic function of MUNC13-4 deficient T lymphocytes in Japanese FHL patients.

METHODS

Sixteen unrelated families with non-FHL2 (no mutation in PRF1) were eligible for the detection of MUNC13-4 mutations. All patients fulfilled the diagnostic criteria of HLH. Twelve of the 16 families had a positive family history, but consanguinity was noted in only one family. After informed consent had been obtained, genomic DNA and RNA were isolated from peripheral blood mononuclear cells. Samples from 62 healthy subjects were used as controls. In a comparative study of alloantigen specific CD4+ and CD8+ cytotoxic T lymphocytes (CTL), blood specimens were obtained from FHL2 and non-FHL2 patients as well as from their parents. The study was approved by the institutional review board at both Kyushu University and Saga University.

Genotyping of microsatellite markers was conducted as described earlier. Four microsatellite markers adjacent to MUNC13-4 (D17S1807, D17S1603, D17S785, and D17S937) were amplified using fluorescent labelled primers. Electrophoresis of polymerase chain reaction (PCR) products was effected on an ABI3100 DNA sequencer (PE-Applied Biosystems, Norwalk, Connecticut, USA). Analyses and assignment of marker alleles were carried out using Genotyper software (PE-Applied Biosystems). For the detection of MUNC13-4 mutation, 28 primer sets were designed employing the Primer3 program (Whitehead Institute for Biomedical Research, Cambridge, Massachusetts, USA) to amplify the 32 exons and flanking intronic sequences of MUNC13-4 gene from genomic DNA. These PCR products were used for sequence analysis with ABI3100 or ABI3730 DNA sequencer (PE-Applied Biosystems). Mutations are numbered according to GenBank XM_113950; additionally, the A of the ATG initiator codon is defined as nucleotide +1. Expression of MUNC13-4 was analysed by reverse transcriptase PCR. The PCR primers were designed to detect splicing variants generated by each mutation. PCR products were cloned into TA cloning vector (Invitrogen, San Diego, California, USA) and the sequences were verified on ABI3100 DNA sequencer.

Cytotoxic activities of alloantigen specific CD4+ and CD8+ CTLs were determined as shown previously. Peripheral blood mononuclear cells were obtained from the patients with MUNC13-4 deficiency (MUNC−/−) and their parents (MUNC−/+), as well as from normal controls. These cells were co-cultured with a mitomycin C treated B lymphoblastoid cell line (B-LCL) established from an HLA mismatched individual. Magnetisable polystyrene beads coated with anti-CD4 or anti-CD8 monoclonal antibody (Dynal, Oslo, Norway) were used to isolate CD4+ and CD8+ T lymphocytes, respectively, from peripheral blood mononuclear cells that had been stimulated with allogeneic B-LCL for six days. CD4+ and CD8+ T lymphocytes, which were cultured in medium

Abbreviations: B-LCL, B lymphoblastoid cell line; CTL, cytotoxic T lymphocytes; FHL, familial haemophagocytic lymphohistiocytosis; HLA, human leucocyte antigen
Figure 1  Identification of MUNC13-4 mutations associated with familial haemophagocytic lymphohistiocytosis (FHL). (A) Schematic representation of the MUNC13-4 protein and corresponding genomic organisation of the MUNC13-4 gene. The positions of two C2 domains (C2A and C2B) are indicated by amino acid number. The mutations 322-1G>R, 640C>R, 754-1G>R, 1596+1G>C, and 1723insA identified in this study are designated M1, M2, M3, M4, and M5, respectively. Nucleotides are numbered from A of the initiation codon (ATG); X, stop; ins, insertion; fs, frame shift. (B) Haplotype analysis of MUNC13-4 variants and microsatellite markers adjacent to MUNC13-4 in the five families characterised by FHL. The markers were ordered according to the Genome Browser of UCSC Genome Bioinformatics (http://genome.ucsc.edu/index.html). The pedigree of family 6 is not shown in this figure. Wt, no mutation.

Figure 2  Reverse transcriptase polymerase chain reaction (RT-PCR) analysis of MUNC13-4 in patients with familial haemophagocytic lymphohistiocytosis (FHL). (A) Outcome of 322-1G>A mutation of MUNC13-4. A 370 base pair (bp) RT-PCR product of MUNC13-4 exons 3-7 was detected in control (lane 2) and family 1-I-2 (heterozygote for this mutation; lane 3), whereas an extra 303 bp product was detected exclusively in family 1-I-2 (lane 3). Sequence analysis of a 303 bp fragment revealed that 322-1G>A caused skipping of exon 5 (67 bp), resulting in frame shift and translational arrest after an additional 14 amino acids. (B) Outcome of 754-1G>C mutation of MUNC13-4. A 610-bp RT-PCR product of MUNC13-4 exons 5-11 was detected in control (lane 2), family 4-II-2 (heterozygous for this mutation, lane 4), and in family 5-I-1 and -2, who do not carry this mutation (lanes 5 and 6). An extra 648 bp product was detected in family 3-II-1 (homozygous for this mutation) and family 4-II-2 (lanes 3 and 4). Sequence analysis of a 648 bp fragment revealed that the 754-1G>C mutation retains the entire intron 18 (77 bp) in the cDNA. This 77 bp insertion is predicted to cause translational arrest after an additional 40 amino acids. Sequence analysis of a 459 bp product showed that this mutation caused skipping of exon 18 (52 bp), resulting in frame shift and translational arrest after an additional 15 amino acids.

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with interleukin-2 (Genzyme, Boston, Massachusetts, USA), were stimulated with allogeneic B-LCL three times at one week intervals; subsequently, these lymphocytes served as effector cells. Cytotoxic activity was determined using a five hour \(^{51}\)Cr release assay. To evaluate the role of perforin in CTL mediated cytotoxicity, effector cells were pretreated with an inhibitor of the perforin based cytotoxic pathway, concanamycin A (CMA) (Wako Pure Chemical Industries, Osaka, Japan), at a concentration of 100 nM for two hours before incubation with target cells.

**RESULTS**

Five different sequence alterations were identified in six of 16 non-FHL2 families; these alterations were neither detectable in control subjects nor in a previous report which described six mutations, including 274delC (exon 3), 753+1G→T (intron 9), C766T (exon 10), 1389+1G→A (intron 15), 1755insT (exon 20), and 1822del12 bp (exon 20) in seven families.\(^{11}\) Mutations identified in this study were in introns 4, 9, and 18, and in exons 8 and 19, which included a nonsense change (640C→T, resulting in R214X), a single base insertion (1723insA, resulting in E575fsX584), an alteration occurring at the splice donor site (1596+1G→C), and aberrations at the splice acceptor sites (322-1G→A and 754-1G→C). Two families had homozygous aberrations (families 3 and 5) while the remaining four had compound heterozygous abnormalities (fig 1A and 1B). An interval of 2.3 Mb between \(D17S1807\) and \(D17S785\) was homozygous in two families (one with the 754-1G→C allele (family 3) and one with the 1596+1G→C allele (family 5)), although they were not consanguineous. In addition, families 2 and 4 shared a common haplotype for the 1596+1G→C allele, suggesting a common founder (fig 1B). The patient of family 6 was compound heterozygous for 1596+1G→C and 1723insA. Because DNA samples of parents were not available, we could not determine the haplotype of microsatellite markers in family 6.

Expression of \(MUNC13-4\) was analysed in four families carrying mutations at splice acceptor or donor sites. By sequencing, the 322-1G→A mutation in intron 4 resulted in skipping of exon 5 (67 bases) (fig 2A). This deletion caused a frame shift and translational arrest at the site with an additional 14 amino acids apart. The 754+1G→C mutation in intron 9 led to inclusion of the 38 bases flanked by a nearby cryptic splice acceptor site and exon 10 in cDNA (fig 2B). This 38 base insertion induced translational arrest at the site with additional 88 amino acids apart. The 1596+1G→C mutation in intron 18 generated two abnormal transcripts: the long form which incorporated the entire intron 18 (77 bases), and the short form in which exon 18 (52 bases) was skipped (fig 2C). In both cases, a premature stop codon appeared at the site with additional amino acids apart (40 and 15 amino acids in the long and short forms, respectively). As the truncated proteins generated by these mutations do not contain C2A and/or C2B domains which mediate \(Ca^{2+}\)
must facilitate understanding of the distinct molecular
determination of precise genotype–phenotype association
for FHL1 or other subtypes is a major concern; thus future
mutations in approximately 30% of HLH patients.9–10 In this
PRF1 FHL2 and FHL3 subtypes. We previously found
cytotoxicities in MUNC13-4 deficient T lymphocytes.
detectable NK function could be associated with residual
patients,9–10 age at onset tended to occur late (after five
summarised in table 1. Relative to that observed in FHL2
homogeneous and indistinguishable among various types of
mechanisms involved in the development of various FHL
subtypes.

### Table 1 Clinical and laboratory findings of 6 FHL3 patients

<table>
<thead>
<tr>
<th>Family</th>
<th>Age/sex</th>
<th>Family history</th>
<th>MUNC13-4 mutations</th>
<th>CNS involvement</th>
<th>NK activity*</th>
<th>Treatment†</th>
<th>Outcome</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>11 mo/M</td>
<td>+</td>
<td>1596+1G→C</td>
<td>322:1G→A</td>
<td>29%</td>
<td>VP16, CSA, PSL</td>
<td>Alive</td>
</tr>
<tr>
<td>2</td>
<td>2 mo/M</td>
<td>+</td>
<td>640C→T</td>
<td>–</td>
<td>2.2%</td>
<td>VP16, CSA, PSL</td>
<td>Dead</td>
</tr>
<tr>
<td>3</td>
<td>6 mo/M</td>
<td>–</td>
<td>754:1G→C</td>
<td>–</td>
<td>1–10%</td>
<td>VP16, CSA, PSL</td>
<td>Alive</td>
</tr>
<tr>
<td>4</td>
<td>5 mo/M</td>
<td>+</td>
<td>1596+1G→C</td>
<td>–</td>
<td>1–19%</td>
<td>VP16, CSA, PSL</td>
<td>Dead</td>
</tr>
<tr>
<td>5</td>
<td>6 mo/F</td>
<td>+</td>
<td>1596+1G→C</td>
<td>–</td>
<td>1–3.2%</td>
<td>VP16, CSA, PSL</td>
<td>Alive</td>
</tr>
<tr>
<td>6</td>
<td>5 mo/M</td>
<td>+</td>
<td>1596+1G→C</td>
<td>1723insA</td>
<td>5–7%</td>
<td>VP16, CSA, PSL</td>
<td>Dead</td>
</tr>
</tbody>
</table>

*Normal value >5% when effector to target ratio is 20:1.
†The combination of VP16, CSA, and PSL was used as the HLH94 protocol, as proposed by the Histiocyte Society.

Data access

Accession numbers and URLs for data presented herein are as follows:

- GenBank accession number: MUNC13-4 gene sequence, XM_113950.
- The Genome Browser of UCSC Genome Bioinformatics: http://genome.ucsc.edu/index.html.

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Conflicts of interest: none declared

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