Disseminated cryptococcosis in two boys with novel mutation of CD40 Ligand-Associated X-linked hyper-IgM syndrome

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Abstract

X-linked hyper-IgM syndrome (XHIM) caused by CD40L mutations is a primary immunodeficiency condition that increases susceptibility to opportunistic infections. Disseminated cryptococcosis in XHIM is rarely reported in children. Here, we report two related boys who have a novel hemizygous frameshift c.208delC mutation of CD40L. They live in the western region of Thailand and developed disseminated cryptococcosis while receiving regular intravenous immunoglobulin supplementation.

Key words: Thailand, disseminated cryptococcosis, novel mutation, CD40 ligand, X-linked hyper-IgM syndrome

Introduction

X-linked hyper-IgM syndrome (XHIM; OMIM 308230) is a rare primary immunodeficiency disorder, but it is the most common type of hyper-IgM syndrome (HIGM). XHIM is caused by mutations of the CD40 ligand (CD40L; OMIM 300386), which is located at Xq26.3-27.1.¹ To date, more than 130 mutations have been identified throughout the CD40L.² As a result of the class-switching defect and T-cell dysfunction, patients are susceptible to opportunistic infections (OI), including Pneumocystis jirovecii pneumonia (PJP), Cryptosporidium infection, and infections by members of the herpesvirus family.³ Cryptococcus neoformans is a commonOI that is mostly found in patients with cell-mediated immunodeficiency, but it is rarely reported in patients with XHIM.

Here, we report two male cousins with a novel mutation of the CD40L that developed disseminated cryptococcosis while receiving regular intravenous immunoglobulin (IVIG) supplementation.

Report of case

Patient A was diagnosed with XHIM at 3 years of age. He presented at our center with oroesophageal candidiasis. Immunologic investigations revealed IgG < 7 mg/dl, IgA 17.5 mg/dl, IgM 431 mg/dl, IgE < 3.36 mg/dl, CD4 1,290 cells/mm³ (35.4%), CD8 1,158 cells/mm³ (31.7%), CD3 2,814 cells/mm³ (77.13%), CD19 516 cells/mm³ (14.15%). Lymphocyte proliferation in response to phytohemagglutinin (PHA) was normal.

Patient B, a younger cousin of patient A (Figure 1), was diagnosed with XHIM at 6 months of age. He presented with severe pneumonia and oral ulcer. Immunologic investigations revealed IgG 17.3 mg/dl, IgA 6.86 mg/dl, IgM 37.1 mg/dl,

List of abbreviations

- ANC: absolute neutrophil count
- CI: confidence interval
- CSF: cerebrospinal fluid
- ECU domain: extracellular unique domain
- G-CSF: granulocyte-colony stimulating factor
- GXM: glucuronoxylomannan
- Hct: hematocrit
- IVIG: intravenous immunoglobulin
- MAbs: monoclonal antibodies
- MIC: minimum inhibitory concentration
- NETs: neutrophil extracellular traps
- PHA: phytohaemagglutinin
- PJP: Pneumocystis jirovecii pneumonia
- ROS: reactive oxygen species
- TNF-H domain: extracellular C-terminal TNF homology domain
- WBC: white blood cell
- XHIM: X-linked Hyper-IgM syndrome
or c.208delC mutation in exon 2 of CD40L (Figure 1A). This frameshift mutation resulted in a premature termination codon at position 83 (p.Glu70Argfs*13). Molecular analysis of maternal DNA revealed heterozygosity of the same mutation (Figure 1B), which indicates that this mutation was inherited from his mother. The genetic testing of the mother and other available family members was performed. Other affected males and carrier females were identified (Figure 2). The reference sequences were NM_000074 and NP_000065 for CD40L cDNA and amino acid positions, respectively.

Disseminated cryptococcal infection

At 12 years of age, patient A presented with fever and severe headache. Physical examination revealed signs of meningeal irritation. Laboratory investigations revealed white blood cell (WBC) count 4,050 cells/mm³ (neutrophils 14.3%, lymphocytes 77.6%), the absolute neutrophil count (ANC) was 580 cells/mm³. Cerebrospinal fluid (CSF) examination revealed WBC 130 cells/mm³, protein 89 mg/dl, and sugar < 4.32 mg/dl. Encapsulated budding yeasts were identified or c.208delC mutation in exon 2 of CD40L (Figure 1A). This frameshift mutation resulted in a premature termination codon at position 83 (p.Glu70Argfs*13). Molecular analysis of maternal DNA revealed heterozygosity of the same mutation (Figure 1B), which indicates that this mutation was inherited from his mother. The genetic testing of the mother and other available family members was performed. Other affected males and carrier females were identified (Figure 2). The reference sequences were NM_000074 and NP_000065 for CD40L cDNA and amino acid positions, respectively.

Mutation analysis of the CD40L gene

After written informed consent was obtained, molecular analysis of the CD40L was performed for the probands and their mothers in 2014. Briefly, genomic DNA was extracted from peripheral blood lymphocytes using commercially available kits according to manufacturer's instructions. Five coding exons and exon/intron junctions of CD40L were separately amplified by polymerase chain reaction (PCR) using previously described primers. The results revealed a novel hemizygous deletion of cytosine at nucleotide position 208

Figure 1. DNA sequence analysis in exon 2 of the CD40L gene. (A) Direct DNA sequencing revealed a novel hemizygous frameshift c.208delC mutation in patient A whom was earlier diagnosed with X-linked hyper IgM syndrome (XHIGM); (B) A heterozygous c.208delC mutation in the proband’s mother; and, (C) A normal DNA sequence.

IgE < 4.25 mg/dL, CD4 5,889 cells/mm³ (35.9%), CD8 3,642 cells/mm³ (22.2%), CD3 10,401 cells/mm³ (63.4%), CD19 4,126 cells/mm³ (25.15%). Lymphocyte proliferation in response to PHA was normal.

Since the diagnosis of XHIM, based on the clinical presentations and immunological findings, both patients have been receiving monthly IVIG supplementation and daily trimethoprim-sulfamethoxazole for PJP prophylaxis. IgG trough levels have been consistently above 600 mg/dL in both patients.

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Figure 2. Pedigree of the proband’s family.
Cryptococcus neoformans is an encapsulated yeast that is predominantly isolated from pigeon droppings, and from soil contaminated with avian excreta. It causes life-threatening meningoencephalitis mainly in patients with cell-mediated immune deficiency, such as human immune deficiency virus (HIV) infection. However, it has only rarely been reported in patients with XHIM.

Many factors predispose patients to cryptococcal infection, including host immunologic defect and environmental factors. Although disseminated cryptococcosis can be found in immunocompetent children, it is more common in patients that have abnormality in cell-mediated immunity. The patients in this study had normal T-cell counts and normal in vitro T-cell function, as tested by PHA stimulation. However, they may have T-cell dysfunction that is specific to the cryptococcal antigen. In fact, not only T cell that plays role against host defense to cryptococcal infection, but also humoral and innate immune systems such as macrophages, dendritic cells, neutrophils, natural killer cells, eosinophils.

We report 2 boys cousins that harbor a novel mutation of CD40L, and both have been regularly treated with monthly IVIG and daily trimethoprim-sulfamethoxazole prophylaxis since XHIM diagnosis. In spite of our efforts to avert OI in these two patients, both developed disseminated cryptococcosis within 2 months of each other.

Mutations in the CD40L are highly heterogenous, Missense mutations and small deletions are the main types, accounting for 50-70% of mutations. We identified a novel hemizygous cytokine deletion at nucleotide position 208 (c.208delC) in exon 2 of the CD40L in our patients. This mutation is predicted to result in premature termination at codon 83 (p.Glu70Argfs*13), which causes truncation of a portion of the extracellular unique (ECU) domain and the entire extracellular C-terminal TNF homology (TNFH) domain, both of which play an important role in the function of CD40L. Based on our review of the literature, this frameshift mutation has never been reported.

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Presence of neutropenia may predispose a patient to develop cryptococcosis. The mechanism of neutropenia is defect in myeloid cell development that is mediated by CD40-CD40L interaction. Neutrophils kill C. neoformans primarily via NADPH oxidase-mediated ROS production, and through the release of neutrophil extracellular traps (NETs). A previous study in C. neoformans-infected mice found that survival was increased after treatment with G-CSF.

The recommended antifungal treatment for disseminated cryptococcosis is amphotericin B plus flucytosine. However, flucytosine is more widely available and less expensive than flucytosine. In this study, both patients responded well to treatment, but breakthrough infection occurred with lower-dose flucytosine in patient A. Breakthrough infection occurred in 4% of adults with HIV/AIDS who were receiving flucytosine 200 mg/day (equivalent to 6 mg/kg/day in children), and flucytosine at this dosage has been recommended as maintenance suppressive therapy. Although there is no standard guideline for secondary cryptococcal prophylaxis in primary immunodeficiency patients, we decided to continue the suppressive therapy due to the severity of the disease. It remains unclear whether flucytosine resistance played a role in his relapse of cryptococcal infection despite prescribing the prophylaxis therapy. A recent systematic review of fluconazole resistance found that 24% of relapsed strain were resistant to fluconazole.
Therefore, we decided to increase the maintenance dose to 12 mg/kg/day to overcome the possibility of elevated minimum inhibitory concentration (MIC), and there has been no recurrent episode.

In conclusion, patients with XHIM are at increased risk of developing disseminated cryptococcal infection. In settings where fluconazole is not available or accessible, combination therapy consisting of amphotericin B and fluconazole yielded good outcomes. Low-dose fluconazole may not be sufficient to prevent recurrence.

Ethical approval and consent to participate

Written informed consent was obtained from the parents of the two males profiled herein to report their history and the results of investigations. The reporting of clinical data was approved by the Ethics Committee of the Siriraj Institutional Review Board (SIRB) Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, Thailand (COA no. Si 479/2017; approved 4 September 2017).

Consent for publication

The individual described in this case report completed and signed a consent form authorizing publication and presentation of this manuscript.

Funding

Siriraj Grant for Research Development, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, Thailand

Authors’ contributions

• PP wrote the manuscript.
• BB performed genetic testing and wrote the manuscript.
• OJ and NV provided clinical care to the patients.
• WP and KC revised the manuscript.
• All authors read and approved the final manuscript to be submitted for publication.

Acknowledgements

The authors gratefully acknowledge Dr. Voravich Leungwedchakarn of the Division of Allergy and Immunology, Department of Pediatrics, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, Thailand.

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