Table I Proportion of IFNγ-expressing T and NK cells in the patient

Age	$IFN\gamma^+/IL\text{-}4^-$		
	CD4 (%)	CD8 (%)	CD56 (%)
8 months	1.14	8.83	2.00
11 months	3.18	70.40	66.29
3 years 11 months	11.89	65.48	82.79
Healthy control	15	60–80	80–90

reduced by flow cytometer (Fig. 1b), but the activity of mutant NEMO was almost defective which was confirmed by a mutant NEMO-NF-κB luciferase reporter assay (Fig. 1c). He has been prescribed prophylactic cotrimoxazole before and after the diagnosis.

He presented with chest pain, erythema, polyarthritis, continuous high fever refractory to antibiotics, and marked elevation of C-reactive protein (7.4 mg/dL) at 4 years of age. Autoantibodies such as anti-centromere antibody were detected transiently. Chest computed tomography revealed multiple nodular shadows resembling bronchiolitis obliterans organizing pneumonia. The repertoire of T cell receptor showed high expression of limited Vβ subsets (Supplementary Fig. 2). Combination therapy using corticosteroids, cyclosporine A, and methotrexate was effective and was continued to control his symptoms.

Severe abdominal pain and intractable frequent diarrhea recurred when the corticosteroid dose was reduced, and he presented perianal fistula at 8 years of age. A mild elevation was observed in both erythrocyte sedimentation rate and C-reactive protein under the preceding immunosuppressive treatments (Table II). No significant pathogen was detected by stool culture and the use of antibiotics and antifungal drugs resulted in no improvement in clinical symptoms.

Endoscopic and Microscopic Findings of the Colon

Colonic endoscopy revealed many polyp-like lesions with mucosal redness and edema at the sigmoid/descending junction (Fig. 2). A longitudinal ulcerative lesion found in the sigmoid colon was suggestive of Crohn's disease. Passing the endoscope beyond these obstructive clusters of polyps was difficult; therefore, we could not observe the upper part of the colon. Neither stenosis nor ulcer formation was observed by intestinal radiocontrast analysis.

Histopathological examination of the colonic biopsied specimens showed diffuse lymphoplasmacytic infiltration, superficial edema, and hyperemia in lamina propria. Foamy cells and some eosinophils were also seen (Fig. 3a, b). No definite neutrophilic infiltration, crypt abscesses, or granulomatous lesions were observed. Cultures from biopsied specimens yielded neither bacterial nor fungal growth.

Immunohistochemical staining revealed predominant infiltration of CD79a-positive, plasma cells in the lamina propria. Infiltration of CD68-positive macrophages and CD3-positive T cells was also observed (Fig. 3c–g).

Detection of TNFα-Producing Cells in the Lamina Propria and Peripheral Blood

To investigate the possibility that TNFα blockade therapy can ameliorate inflammatory colitis as well as NEMO-deficient mice as suggested by previous analysis [15], we analyzed TNFα-producing mononuclear cells in the lamina propria in the colon of our patient. Immunohistochemical staining showed abundant TNFα in infiltrated mononuclear cells in the lamina propria (Fig. 3h) which would be associated with progression of inflammatory colitis.

We also analyzed TNFα-producing T cells and monocytes in the peripheral blood (Fig. 4a). The majority (72.49%) of CD4-positive T cells in our patient expressed intracellular TNFα, while 40% to 70% of CD4-positive T cells expressed TNFα in adults with IBD in our study. Forty-eight percent of CD8-positive T cells in our patient expressed TNFα. CD14-positive monocytes from our patient expressed small amounts of intracellular TNFα after LPS stimulation, while similarly treated CD14-positive cells from healthy subjects expressed abundant TNFα (Fig. 4b).

Reversion Analysis

Nishikomori et al. reported that in an X-EDA-ID patient, the mutation had been reverted to the normal state in IFNγ-

Table II Laboratory data on admission (8 years old)

WBC	13,600/μL	CD3	76.2%	IgG	790 mg/dL
Neutrophils	10,200/μL	CD4	22.2%	IgA	666 mg/dL
Lymphocytes	1,632/μL	CD8	58.3%	IgM	71 mg/dL
Monocytes	952/μL	CD19	4.8%	IgD	<0.6 mg/dL
Hemoglobin	12.0 g/dL	CD20	3.8%	C3	134 mg/dL
Platelets	84.7×10^4/μL	CD16	0.5%	C4	46 mg/dL
		CD56	33.6%	CH50	56 U/mL
		HLA-DR	26.5%	ESR	43 mm/h

WBC white blood cell, *CH50* total complement activity, *ESR* erythrocyte sedimentation rate

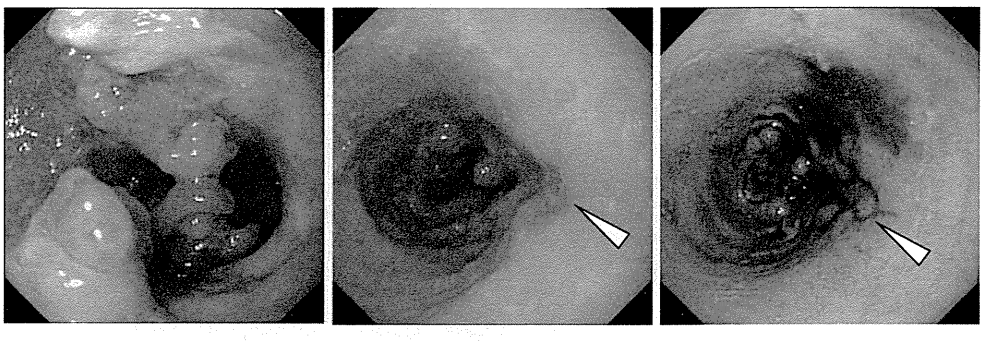


Fig. 2 Findings of colonoscopy performed before initial treatment with infliximab. Colonoscopy revealed polyp-like lesions with mucosal redness and edema at the sigmoid/descending junction (*left panel*). A longitudinal ulcer (*arrowhead*) was found in the sigmoid colon (*center panel*). Same segment as in the *center panel* after indigo carmine dye (*right panel*)

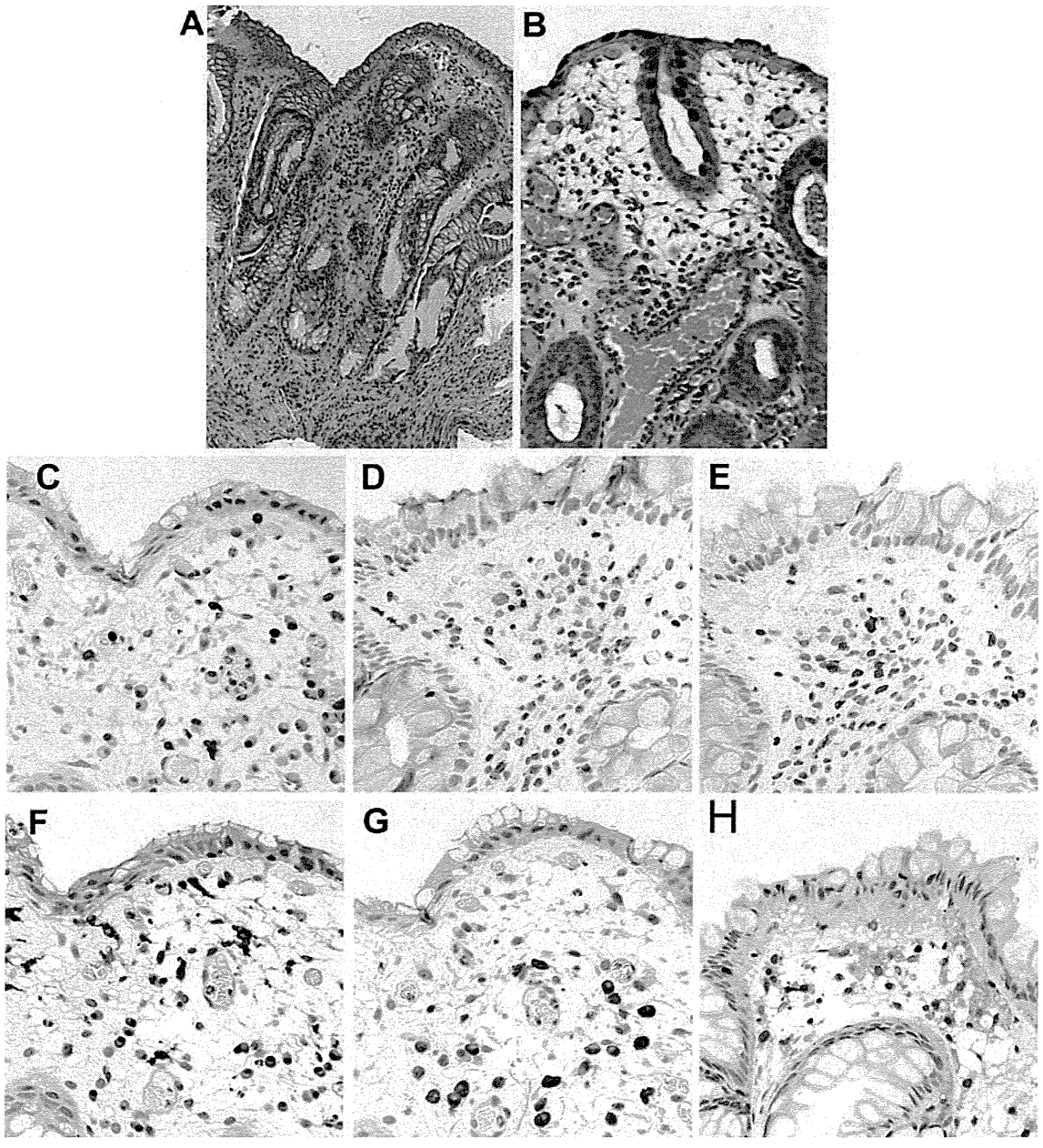


Fig. 3 Microscopic findings of affected colonic specimens. **a**, **b** Hematoxylin and eosin staining. **a** and **b** are low-power field and high-power field views, respectively. **c**–**h** Staining profiles of cellular surface antigens: **c** CD3ε, **d** CD4, **e** CD8, **f** CD68, and **g** CD79a. **h** Staining with anti-human TNFα antibody

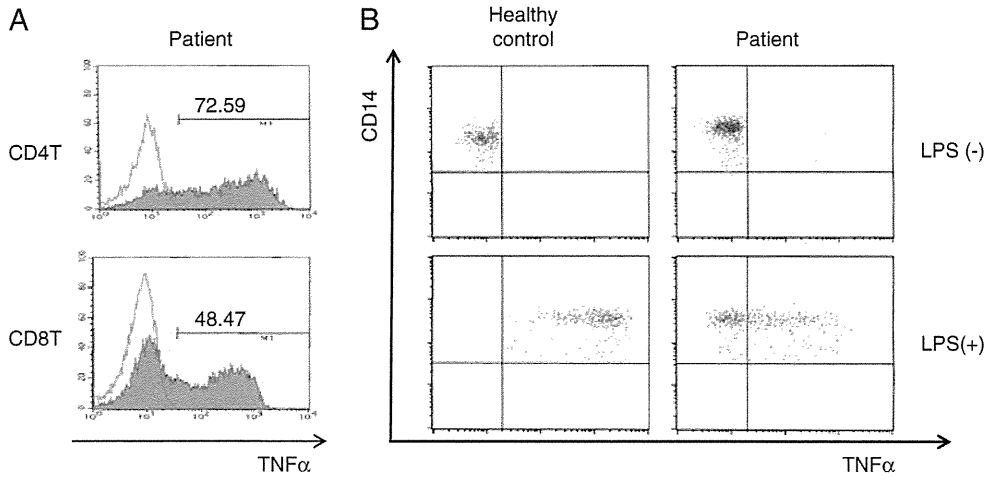


Fig. 4 Analysis of TNFα-producing mononuclear cells in peripheral blood. **a** TNFα-expressing T cells increased markedly before infliximab treatment. PBMCs were stimulated with ionomycin and PMA for 4 h in the presence of brefeldin A then stained for intracellular TNFα. For FACS analysis, gates were set on lymphocytes according to forward and side scatter properties. Representative histograms of TNFα expression in stimulated (*solid histograms*) or unstimulated (*black line histograms*) T cells. The proportion of TNFα-positive CD4-positive T cells in adult IBD patients is 40–70%. **b** The percentage of TNFα-positive monocytes was examined. Cells from our patient and healthy volunteer were incubated with or without LPS for 4 h in the presence of brefeldin A. Monocytes were identified by CD14. Approximately 50% of stimulated monocytes produced a small amount of TNFα

expressing T cells [18]. Our patient showed expansion of IFNγ-expressing T cells during infancy and an increase in TNFα-producing T cells at that time. We hypothesized that the A169P mutation in the *IKBKG* gene had been reverted to wild type and that the reverted T cells had expanded in our patient. Indeed, before initiating infliximab treatments, reversion mutation was detected in 23/67 (34%) from non-stimulated PBMCs (Table III). At 24 months after the initiation, reversion mutation was detected in both messenger RNA (mRNA) and genomic DNA from lymphocytes stimulated with PHA and IL-2 for 10 days, whereas only mutated mRNA was identified from non-stimulated lymphocytes (Fig. 5). Reverted mRNA was observed in CD3-positive T cells. Sex chromosome analysis with fluorescent in situ hybridization revealed no maternal cells and therefore graft-versus-host disease secondary to maternal–fetal transfusion was unlikely. These findings suggest that reverted T cells activated NF-κB in response to growth signals and had a growth advantage over mutant cells.

Table III Frequency of reverted clones before and after initiation of infliximab treatments

	Before	After 12 months	After 24 months
PBMCs	23/67 (34%)	nd	2/6 (33%)[a]
CD3	nd	3/16 (19%)	nd
CD14	nd	0/19 (0%)	nd
CD19	nd	0/47 (0%)	nd

nd not done

[a] A result using stimulated mononuclear cells

Reverted T cells decreased with repeated administrations of anti-TNFα monoclonal antibody. In contrast, CD14-positive monocytes and GM-CSF-induced monocyte-derived dendritic cells had no reversion (Table III).

Anti-TNFα Treatment Improved NEMO Colitis

We initially treated NEMO colitis with high dose corticosteroid therapy (2 mg/kg prednisolone, daily) (Fig. 6). However, steroid therapy did not improve clinical symptoms and resulted in compression fracture in the thoracic spine from corticosteroid-induced osteoporosis.

The increase in TNFα-producing T cells suggested the possibility that TNFα blockade therapy would be an effective treatment for the intractable NEMO colitis. After confirming the absence of severe bacterial or mycobacterial infection, we initiated administration of the chimeric anti-TNFα monoclonal antibody, infliximab, to our patient.

Soon after the first infusion of infliximab, abdominal pain disappeared and his appetite recovered. Frequency of diarrhea decreased as administrations of infliximab were repeated (Fig. 6). Colonoscopy after his third administration showed mild improvement of both mucosal redness and edema (Fig. 7a). These mucosal inflammatory findings had almost disappeared after 1-year treatment with infliximab, although polyp-like lesions remained (Fig. 7b).

The proportion of TNFα-producing cells in CD4-positive and CD8-positive T cells markedly decreased by his third infliximab infusion (from 72.6% to 26.7% in CD4-positive T cells and from 48.5% to 23.1% in CD8-positive T cells), and reduction of TNFα-producing cells was

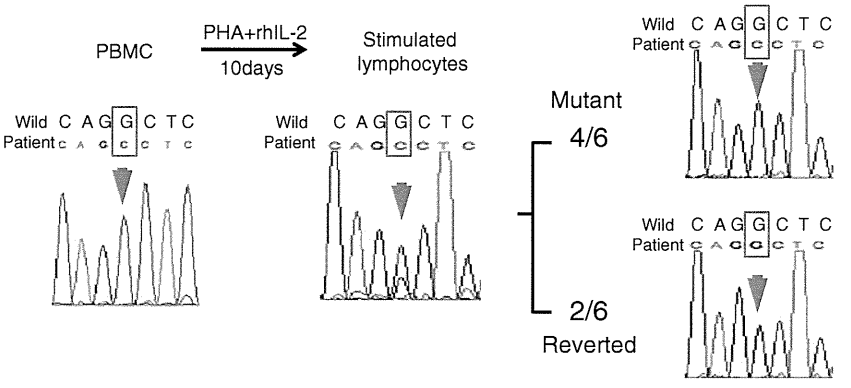


Fig. 5 Reversion analysis of cDNA of gene encoding NEMO isolated from mononuloclear cells after 24 months of infliximab treatment. PBMC was obtained from our patient and incubated with PHA and IL-2 for 10 days. Direct sequence for mRNA encoding NEMO was performed using PBMC and the stimulated mononuclear cells. Before stimulation, no reverted mononuclear cells were detected. After PHA and IL-2 stimulation, reverted mononuclear cells apparently increased. Subcloning of cDNA from stimulated cells showed that two of six cells had reversion of mutation in the gene

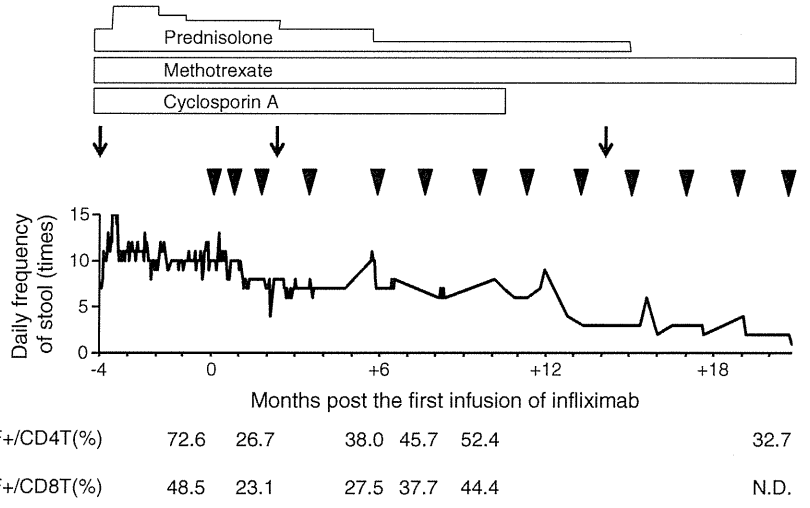
associated with improvement of clinical symptoms (Fig. 6). Administration of cyclosporine A was discontinued by the eighth infliximab treatment, and corticosteroid was reduced and then discontinued by the tenth infliximab infusion.

Our patient had one serious adverse event, pneumonia, after his fourth administration of infliximab. *Campylobacter jejuni* was isolated from his blood culture at that time. He was successfully treated with antibiotics and infliximab administration was resumed after confirming resolution of pneumonia. He has been treated safely for more than 2 years with regular administrations of infliximab (once every 7–8 weeks). Neither mycobacterial infections nor severe infusion reactions have been observed.

Discussion

Our patient showed immunodeficiency with very low IFNγ-production during his younger years as shown in Table I and suffered from many opportunistic infections (Zoster virus infection, penicillin-resistant *Streptococcus pneumoniae* meningitis, and other undetermined infections). A novel missense mutation, A169P, in the first coiled-coil domain resulted in defective NEMO function (Fig. 1) and was responsible for recurrent severe infections. However, he later suffered from autoimmune diseases at 4 years of age (bronchiolitis obliterans organizing pneumonia, severe arthritis, and vasculitis) and severe chronic inflammatory colitis at 8 years. Based on the facts that, in the mice model, TNFα played a major role in the pathogenesis of NEMO colitis [15], and that, in our patient, TNFα-producing mononuclear cells in the peripheral blood were markedly increased (Fig. 4a), infliximab was employed for the patient's treatment. This treatment led to improvement in his symptoms and colonoscopic findings for 2 years.

Increases in TNFα-producing cells similar to that seen in other IBD [19] were detected (Fig. 4). We confirmed G/C



TNF+/CD4T(%)	72.6	26.7	38.0	45.7	52.4	32.7
TNF+/CD8T(%)	48.5	23.1	27.5	37.7	44.4	N.D.

Fig. 6 Clinical course of NEMO colitis after infliximab treatment in our patient. Colonoscopy (*arrows*), administrations of infliximab (*arrowheads*), and other immunosuppressive drugs (*bars*) are indicated. Daily frequency of stools (times) is graphed at the *center*. Changes in the proportion of TNFα-producing T cells in CD4-positive and CD8-positive cells are also indicated at the *bottom*

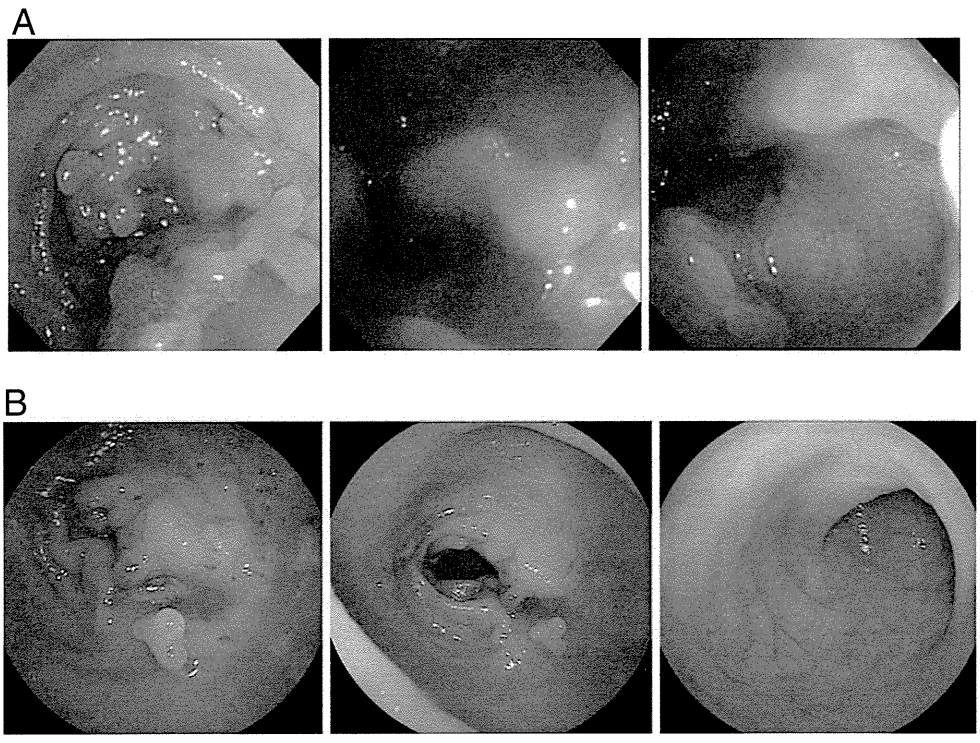


Fig. 7 Findings of colonoscopy after infliximab treatment. **a** Colonoscopy performed after the third infliximab treatment. Mild improvement was observed. Both mucosal redness and edema decreased. However, polyp-like lesions remained. At this point, the patient showed neither abdominal pain nor watery diarrhea. **b** Colonoscopy after 1-year treatment. Almost no mucosal redness or edema. A clear vascular pattern was also observed. Inflammatory polyps could still be found

reversion in T cells after co-stimulation with PHA and IL-2 before and even after infliximab therapy (Table III and Fig. 5). Reversion mosaicism has been reported in primary immunodeficiencies such as X-linked severe combined immunodeficiency [20, 21], adenosine deaminase deficiency [22], *RAG1* deficiency [23], and Wiskott–Aldrich syndrome [24]. Most of these patients reduced the frequency of severe infections and showed survival for longer periods. Our patient also had very few episodes of severe infection after expansion of IFNγ-producing peripheral blood mononuclear cells, contrary to increased susceptibility to diverse pathogens in X-EDA-ID [5, 25]. However, none of the patients with reversion mosaicism involving reverted T cells developed IBD other than X-EDA-ID. Our patient and patients with Omenn's syndrome [21, 23] developed systemic inflammatory conditions and exhibited a restricted TCR repertoire. In our patient, oligoclonal expansion of reverted T cells caused impairment of immune regulation.

According to the report by Nenci et al. in a murine model of intestinal epithelium-specific NEMO deficiency, intestinal epithelial cells exhibit increased sensitivity to TNFα-induced apoptosis and cause disruption of the epithelial barrier if mucosal immune cells have normal immune functions and produce proinflammatory cytokines [15]. They also showed that an additional TNF receptor-1 knockout ameliorated this intestinal inflammation [15]. The pathogenesis of severe colitis in the mouse model seems to be similar to that of our patient. Specifically, NEMO-deficient intestinal epithelium was damaged by TNFα produced from both T cells and macrophages in the lamina propria (shown in Fig. 3c–e, h), and anti-TNFα antibody suppressed progression of intestinal inflammation. Although reversion in peripheral blood monocytes was not confirmed after culture with GM-CSF and analysis of TNFα expression after LPS stimulation, submucosal and peripheral macrophages produced a fair amount of TNFα detectable by immunohistochemistry and flow cytometry (Figs. 3 and 4). Production of TNFα from lamina propria macrophages may be augmented by IFNγ released from reverted T cells.

In addition to the amelioration of clinical symptoms and colonic mucosal inflammation, in our patient, TNF blockade therapy restored his dry skin with thick epidermis to moderately moist skin of normal thickness. Nenci et al. described in another paper using the epidermis-specific NEMO-deficient mice that mice showed severe skin inflammation with thick epidermis and predominant infiltration of inflammatory cells and showed further that an additional knockout of TNFR1 suppressed the inflammatory condition [26]. We postulate that TNFα is also a key cytokine in the pathogenesis of inflammation in diverse epithelial tissues and that infliximab treatment suppresses the TNFα-mediated inflammatory response by inducing apoptosis of TNFα-producing cells [27]. In fact, the patient's peripheral blood TNFα-producing cells reduced along with the improvement of clinical symptoms, and this reduction provided an available marker to assess inflammatory status. Reverted cells in peripheral blood also decreased after repeated anti-TNFα antibody administrations. Unfortunately, we could not obtain consent for re-biopsy so we could not

confirm a vulnerability for apoptosis of intestinal epithelium and lamina propria after the treatment.

Since patients with X-EDA-ID were well known to have increased susceptibility to mycobacterium, and in addition, anti-TNFα monoclonal antibody indeed caused infection-related deaths in a few patients with inflammatory colitis associated with primary immunodeficiencies [28–30], the side effects of anti-TNFα monoclonal antibody treatment should be paid attention to, especially, mycobacterial infections. Before infliximab treatment, we confirmed the absence of active mycobacterial infections by culture tests for mycobacterium including atypical mycobacteria, laboratory examinations, and chest radiographs. He also has no history of Bacillus Calmette-Guérin immunization. Although the patient experienced bacterial pneumonia after his third infliximab infusion, he has not suffered from severe infections for several years. This may be because of the patient's mosaicism of mutated and reverted cells. The risks concerning severe infections and oncogenic effects [31–33] should be considered before employing infliximab for NEMO colitis.

Conclusion

Reversion of mutation in T cells contributes to the pathogenesis of mucosal immunity in NEMO-deficient patients. Moreover, treatment with anti-TNFα monoclonal antibody therapy can improve the symptoms of the disease by both preventing exposure of the mucosa to TNFα and reducing the number of T cells carrying the reverted gene. Anti-TNFα monoclonal antibody therapy provides a promising treatment for intractable NEMO colitis.

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Conflict of Interests The authors declare no competing financial interests.

References

1. Zonana J, Elder M, Schneider L, et al. A novel X-linked disorder of immune deficiency and hypohidrotic ectodermal dysplasia is allelic to incontinentia pigmenti and due to mutations in IKK-gamma (NEMO). Am J Hum Genet. 2000;67:1555–62.
2. Döffinger R, Smahi A, Bessia C, et al. X-linked anhidrotic ectodermal dysplasia with immunodeficiency is caused by impaired NF-kappaB signaling. Nat Genet. 2001;27:277–85.
3. Jain A, Ma CA, Liu S, et al. Specific missense mutations in NEMO result in hyper-IgM syndrome with hypohydrotic ectodermal dysplasia. Nat Immunol. 2001;2:223–8.
4. Orange JS, Brodeur SR, Jain A, et al. Deficient natural killer cell cytotoxicity in patients with IKK-gamma/NEMO mutations. J Clin Invest. 2002;109:1501–9.
5. Orange JS, Jain A, Ballas ZK, et al. The presentation and natural history of immunodeficiency caused by nuclear factor kappaB essential modulator mutation. J Allergy Clin Immunol. 2004;113:725–33.
6. Pai S, Levy O, Jabara H, et al. Allogeneic transplantation successfully corrects immune defects, but not susceptibility to colitis, in a patient with nuclear factor-kappaB essential modulator deficiency. J Allergy Clin Immunol. 2008;122:1113–1118.e1111.
7. Tono C, Takahashi Y, Terui K, et al. Correction of immunodeficiency associated with NEMO mutation by umbilical cord blood transplantation using a reduced-intensity conditioning regimen. Bone Marrow Transplant. 2007;39:801–4.
8. Mancini AJ, Lawley LP, Uzel G. X-linked ectodermal dysplasia with immunodeficiency caused by NEMO mutation: early recognition and diagnosis. Arch Dermatol. 2008;144:342–6.
9. Fish J, Duerst R, Gelfand E, et al. Challenges in the use of allogeneic hematopoietic SCT for ectodermal dysplasia with immune deficiency. Bone Marrow Transplant. 2009;43:217–21.
10. Permaul P, Narla A, Hornick J, et al. Allogeneic hematopoietic stem cell transplantation for X-linked ectodermal dysplasia and immunodeficiency: case report and review of outcomes. Immunol Res. 2009;44:89–98.
11. Cheng L, Kanwar B, Tcheurekdjian H, et al. Persistent systemic inflammation and atypical enterocolitis in patients with NEMO syndrome. Clin Immunol. 2009;132:124–31.
12. Hanson E, Monaco-Shawver L, Solt L, et al. Hypomorphic nuclear factor-kappaB essential modulator mutation database and reconstitution system identifies phenotypic and immunologic diversity. J Allergy Clin Immunol. 2008;122:1169–1177.e1116.
13. Takada H, Nomura A, Ishimura M, et al. NEMO mutation as a cause of familial occurrence of Behçet's disease in female patients. Clin Genet. 2010;78:575–9.
14. Marks DJ, Miyagi K, Rahman FZ, et al. Inflammatory bowel disease in CGD reproduces the clinicopathological features of Crohn's disease. Am J Gastroenterol. 2009;104:117–24.
15. Nenci A, Becker C, Wullaert A, et al. Epithelial NEMO links innate immunity to chronic intestinal inflammation. Nature. 2007;446:557–61.
16. Nagano M, Kimura N, Ishii E, et al. Clonal expansion of alphabeta-T lymphocytes with inverted Jbeta1 bias in familial hemophagocytic lymphohistiocytosis. Blood. 1999;94:2374–82.
17. Kimura N, Toyonaga B, Yoshikai Y, et al. Sequences and repertoire of the human T cell receptor alpha and beta chain variable region genes in thymocytes. Eur J Immunol. 1987;17:375–83.
18. Nishikomori R, Akutagawa H, Maruyama K, et al. X-linked ectodermal dysplasia and immunodeficiency caused by reversion mosaicism of NEMO reveals a critical role for NEMO in human T-cell development and/or survival. Blood. 2004;103:4565–72.
19. Ogura Y, Imamura Y, Murakami Y, et al. Intracellular cytokine patterns of peripheral blood T cells as a useful indicator of activeness of Crohn's disease. Hiroshima J Med Sci. 2005;54:1–8.
20. Stephan V, Wahn V, Le Deist F, et al. Atypical X-linked severe combined immunodeficiency due to possible spontaneous reversion of the genetic defect in T cells. N Engl J Med. 1996;335:1563–7.
21. Wada T, Yasui M, Toma T, et al. Detection of T lymphocytes with a second-site mutation in skin lesions of atypical X-linked severe combined immunodeficiency mimicking Omenn syndrome. Blood. 2008;112:1872–5.
22. Hirschhorn R, Yang D, Puck J, et al. Spontaneous in vivo reversion to normal of an inherited mutation in a patient with adenosine deaminase deficiency. Nat Genet. 1996;13:290–5.
23. Wada T, Toma T, Okamoto H, et al. Oligoclonal expansion of T lymphocytes with multiple second-site mutations leads to

Omenn syndrome in a patient with RAG1-deficient severe combined immunodeficiency. Blood. 2005;106:2099–101.
24. Ariga T, Kondoh T, Yamaguchi K, et al. Spontaneous in vivo reversion of an inherited mutation in the Wiskott–Aldrich syndrome. J Immunol. 2001;166:5245–9.
25. Filipe-Santos O, Bustamante J, Haverkamp MH, et al. X-linked susceptibility to mycobacteria is caused by mutations in NEMO impairing CD40-dependent IL-12 production. J Exp Med. 2006;203:1745–59.
26. Nenci A, Huth M, Funteh A, et al. Skin lesion development in a mouse model of incontinentia pigmenti is triggered by NEMO deficiency in epidermal keratinocytes and requires TNF signaling. Hum Mol Genet. 2006;15:531–42.
27. Van den Brande J, Braat H, van den Brink G, et al. Infliximab but not etanercept induces apoptosis in lamina propria T-lymphocytes from patients with Crohn's disease. Gastroenterology. 2003;124:1774–85.
28. Nos P, Bastida G, Beltran B, et al. Crohn's disease in common variable immunodeficiency: treatment with antitumor necrosis factor alpha. Am J Gastroenterol. 2006;101:2165–6.
29. Chua I, Standish R, Lear S, et al. Anti-tumour necrosis factor-alpha therapy for severe enteropathy in patients with common variable immunodeficiency (CVID). Clin Exp Immunol. 2007;150:306–11.
30. Uzel G, Orange JS, Poliak N, et al. Complications of tumor necrosis factor-α blockade in chronic granulomatous disease-related colitis. Clin Infect Dis. 2010;51:1429–34.
31. Mackey AC, Green L, Liang LC, et al. Hepatosplenic T cell lymphoma associated with infliximab use in young patients treated for inflammatory bowel disease. J Pediatr Gastroenterol Nutr. 2007;44:265–7.
32. Mackey AC, Green L, Leptak C, et al. Hepatosplenic T cell lymphoma associated with infliximab use in young patients treated for inflammatory bowel disease: update. J Pediatr Gastroenterol Nutr. 2009;48:386–8.
33. Diak P, Siegel J, La Grenade L, et al. Tumor necrosis factor alpha blockers and malignancy in children: forty-eight cases reported to the Food and Drug Administration. Arthritis Rheum. 2010;62:2517–24.

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High Incidence of *NLRP3* Somatic Mosaicism in Patients With Chronic Infantile Neurologic, Cutaneous, Articular Syndrome

Results of an International Multicenter Collaborative Study

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Objective. **Chronic infantile neurologic, cutaneous, articular (CINCA) syndrome, also known as neonatal-onset multisystem inflammatory disease (NOMID), is a dominantly inherited systemic autoinflammatory disease. Although heterozygous germline gain-of-function *NLRP3* mutations are a known cause of this disease, conventional genetic analyses fail to detect disease-causing mutations in ~40% of patients. Since somatic *NLRP3* mosaicism has been detected in several mutation-negative NOMID/CINCA syndrome patients, we undertook this study to determine the precise contribution of somatic *NLRP3* mosaicism to the etiology of NOMID/CINCA syndrome.**

Methods. **An international case–control study was performed to detect somatic *NLRP3* mosaicism in NOMID/CINCA syndrome patients who had shown no mutation during conventional sequencing. Subcloning and sequencing of *NLRP3* was performed in these mutation-negative NOMID/CINCA syndrome patients and their healthy relatives. Clinical features were analyzed to identify potential genotype–phenotype associations.**

Results. **Somatic *NLRP3* mosaicism was identified in 18 of the 26 patients (69.2%). Estimates of the level of mosaicism ranged from 4.2% to 35.8% (mean ± SD 12.1 ± 7.9%). Mosaicism was not detected in any of the 19 healthy relatives (18 of 26 patients versus 0 of 19**

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Dr. Goldbach-Mansky has served as an expert witness on behalf of Biovitrum, Novartis, and Regeneron.

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relatives; $P < 0.0001$). In vitro functional assays indicated that the detected somatic *NLRP3* mutations had disease-causing functional effects. No differences in *NLRP3* mosaicism were detected between different cell lineages. Among nondescript clinical features, a lower incidence of mental retardation was noted in patients with somatic mosaicism. Genotype-matched comparison confirmed that patients with somatic *NLRP3* mosaicism presented with milder neurologic symptoms.

***Conclusion.* Somatic *NLRP3* mutations were identified in 69.2% of patients with mutation-negative NOMID/CINCA syndrome. This indicates that somatic *NLRP3* mosaicism is a major cause of NOMID/CINCA syndrome.**

Chronic infantile neurologic, cutaneous, articular (CINCA) syndrome (MIM no. #607715), also known as neonatal-onset multisystem inflammatory disease (NOMID), is a dominantly-inherited autoinflammatory disease that is characterized by neonatal onset and the triad of urticarial-like skin rash, neurologic manifestations, and arthritis/arthropathy. Patients often experience recurrent fever and systemic inflammation. NOMID/CINCA syndrome is the most severe clinical phenotype of the cryopyrin-associated periodic syndromes (CAPS) that also include the 2 less severe but phenotypically similar syndromes familial cold autoinflammatory syndrome (FCAS; MIM no. #120100) and Muckle-Wells syndrome (MIM no. #191900). CAPS are caused by mutations in the *NLRP3* gene, which is a member of the nucleotide-binding oligomerization domain–like receptor (NLR) family of the innate immune system (1,2).

NLRP3 is an intracellular "sensor" of danger signals arising from cellular insults, such as infection, tissue damage, and metabolic deregulation, and it has been highly conserved throughout evolution. NLRP3 associates with ASC and procaspase 1 to constitute a large multiprotein complex termed the NLRP3 inflammasome. When activated, the NLRP3 inflammasome converts the biologically inactive procaspase 1 into active caspase 1. Caspase 1 produces the cytokines interleukin-1β (IL-1β) and IL-18, which are mainly involved in the inflammatory response (3). Available research suggests that mutated *NLRP3* induces autoactivation of the NLRP3 inflammasome in CAPS patients, resulting in an uncontrolled overproduction of IL-1β.

Most CAPS patients carry heterozygous germline missense mutations in the *NLRP3* coding region ("mutation-positive" patients) (4,5). More than 80 different disease-causing mutations have been reported to date (6). However, ~40% of clinically diagnosed NOMID/CINCA syndrome patients show no heterozygous germline *NLRP3* mutation during conventional Sanger-sequencing-based genetic analyses ("mutation-negative" patients). Comparisons of NOMID/CINCA syndrome patients with and without heterozygous germline *NLRP3* mutations have revealed no differences in clinical features or response to treatment (4,7).

In a previous study, we identified a high incidence of somatic *NLRP3* mosaicism in "mutation-negative" NOMID/CINCA syndrome patients in Japan (8). We therefore hypothesized that somatic *NLRP3* mosaicism may be implicated in the etiology of the disorder, although its precise contribution remains unclear. The aim of the present study was to evaluate both the frequency of *NLRP3* somatic mosaicism in NOMID/CINCA syndrome patients and the association between somatic mosaicism and clinical phenotype using an international cohort of mutation-negative NOMID/CINCA syndrome patients.

PATIENTS AND METHODS

Study design and participants. International collaborators were contacted to identify mutation-negative NOMID/CINCA syndrome cases. A total of 20 DNA samples were received from 4 centers: France (n = 6), The Netherlands (n = 4), Spain (n = 3), and the US (n = 7). DNA samples had been extracted from peripheral blood mononuclear cells or whole blood. All 20 samples had been subjected to conventional sequencing, and no *NLRP3* mutations had been identified. In each case, the accuracy of the clinical diagnosis had been confirmed according to the diagnostic criteria (7). The 6 previously reported Japanese cases and 1 Spanish case with *NLRP3* somatic mosaicism were also included (8,9). DNA samples were also collected from 19 healthy relatives of 8 patients (8 from France, 5 from Japan, 2 from Spain, and 4 from the US) to evaluate the causality of somatic *NLRP3* mosaicism in a case–control manner, since the clinical features may be modified by genetic and environmental factors.

Written informed consent for *NLRP3* gene analysis was obtained from all patients and controls. The study was approved by the Institutional Review Board of the Kyoto University Graduate School of Medicine and was conducted in accordance with the Declaration of Helsinki.

Data collection. *Demographic and clinical data.* The clinicians responsible for each mutation-negative NOMID/CINCA syndrome patient completed a questionnaire to document characteristics such as age, sex, race, symptoms, clinical findings, clinical course, and prognosis. No clinical data were obtained from the healthy controls.

Investigation of NLRP3 gene mosaicism. Disease-causing mutations in NOMID/CINCA syndrome patients have

only been reported in exons 3, 4, and 6 of *NLRP3* (6). Thus, the present sequencing was focused on a search for somatic mosaicism of these 3 exons and their flanking intronic regions. After amplifying these genomic regions with the proofreading polymerase chain reaction (PCR) enzyme KOD-Plus polymerase (Toyobo) and dA addition with an LA *Taq* polymerase (Takara Bio), the amplicons were subcloned into pCR2.1-TOPO vector (Invitrogen). Ninety-six clones were selected at random for each amplicon. The subcloned amplicons were retrieved by PCR with LA *Taq* polymerase. They were then treated with ExoSAP-IT (USB) and proteinase K (Promega) prior to direct sequencing. The cloned exons were sequenced at the Kazusa DNA Research Institute using a BigDye Terminator kit (version 3.1) and an ABI 3730 DNA sequencer (Life Technologies). Mosaicism was indicated by the detection of >2 subclones carrying the same base variation at the same position in 96 clones.

To purify leukocyte subpopulations, freshly drawn whole blood was separated using sequential dextran and Ficoll-Hypaque density-gradient centrifugation methods. Cell sorting to select T cells, B cells, and monocytes was performed with an AutoMACS Pro Separator (Miltenyi Biotec) or a FACSVantage System (BD Biosciences), as described elsewhere (8,9). The purity of each cell lineage was >90%. The level of mosaicism was determined by sequencing each source of genomic DNA from 80 clones.

Plasmids and cell lines. To determine whether the identified NLRP3 mutants cause disease, experiments for assessing 2 pathologic functions were performed as described elsewhere (8). Briefly, ASC-dependent NF-κB activation was performed by a dual-luciferase reporter assay in HEK 293FT cells transfected with NLRP3 mutants. Transfection-induced cell death in the human monocytic cell line THP-1 was performed by transfecting green fluorescent protein–fused mutant NLRP3 into THP-1 cells and then measuring the dead cells with 7-aminoactinomycin D.

Statistical analysis. The study was designed to detect mosaicism at a 5% allele frequency with >95% possibility. To satisfy this condition, it was necessary to sequence at least 93 clones per patient. The following calculation was used to estimate the number of clones that had to be sequenced: $P = 1 - (1 - 0.05)^n - n(0.05)(1 - 0.05)^{n-1}$ ($n = 93$, $P = 0.956$). The study was designed to analyze 96 PCR-fragment clones from each patient. The error rate of the PCR reactions was estimated using a proofreading KOD-Plus enzyme. We analyzed a plasmid vector carrying a normal *NLRP3* exon 3, in which 2 distinct errors were detected by sequencing 91 clones. The calculated error rate for this result was 1/87,451 (2/[1,922 bp × 91 clones]). Thus, the probability was negligible that the same errors would be detected more than twice in 96 clones from 1 patient.

To calculate the sample size, we calculated the prevalence of somatic mosaicism among mutation-negative NOMID/CINCA syndrome patients. Eight cases of somatic mosaicism were identified among 15 mutation-negative NOMID/CINCA syndrome patients who were subsequently analyzed by the subcloning method described above. It was assumed that the maximum number of possible somatic mosaicism cases among family controls was 1. On the basis of these data and this assumption, it was calculated that 19 controls were required to ensure a 2-sided alpha level of 0.05 and a power of 0.8.

Continuous variables are presented as the mean ± SD or as the median and interquartile range. Categorical variables are presented as numbers and ratios (with percentages). To compare clinical data between patients with and patients without mosaicism, the Wilcoxon rank sum test was used for continuous variables and Fisher's exact test was used for categorical variables. Fisher's exact test was used to compare the difference in mosaicism ratio between cases and controls. The chi-square test was used to compare the difference in the level of mosaicism between different sources of genomic DNA from each patient.

Table 1. Somatic mosaicism among mutation-negative NOMID/CINCA syndrome patients*

Country, patient	Sequence variant	Protein variant	Mosaicism, %
France			
F1	1298C>T	T433I	5.2
F2	907G>C	D303H	4.2
F3	1315G>C	A439P	21.9
F4	1216A>G	M406V	9.2
F5	1698C>A	F566L	11.5
F6	None	–	–
Japan			
J1	1709A>G	Y570C	12.2
J2	790C>T	L264F	4.3
J3	919G>A	G307S	10.7
J4	1699G>A	E567K	6.5
J5	907G>C	D303H	11.9
J6	None	–	–
Spain			
S1	920G>T	G307V	9.6
S2	907G>C	D303H	19.1
S3	None	–	–
S4	None	–	–
US			
A1	1065A>T	K355N	18.8
A2	1698C>A	F566L	14.6
A3	1704G>C	K568N	9.4
A4	2263G>A	G755R	35.8
A5	None	–	–
A6	None	–	–
The Netherlands			
N1	1699G>A	E567K	6.3
N2	2263G>A	G755R	6.3
N3	None	–	–
N4	None	–	–

* *NLRP3* mosaicism was detected in 18 of 26 patients (69.2%) with neonatal-onset multisystem inflammatory disease (NOMID)/chronic infantile neurologic, cutaneous, articular syndrome (CINCA syndrome). When samples from 19 healthy relatives of these patients were investigated, no somatic mosaicism was detected. The *P* value from the comparison of the cases and the controls (18 of 26 versus 0 of 19) was statistically significant ($P < 0.0001$).

RESULTS

Somatic *NLRP3* mosaicism in mutation-negative NOMID/CINCA syndrome patients. A heterozygous germline *NLRP3* mutation was detected in 1 of the 27 samples, and this was therefore excluded from the analyses. For each patient, 96 clones were selected at random for each amplicon. These were then sequenced. *NLRP3* mosaicism was detected in 18 of 26 patients (69.2%), and the level of allelic mosaicism ranged from 4.2% to 35.8% (mean ± SD 12.1 ± 7.9%; median 10.2%) (Table 1). Seven of the detected *NLRP3* mutations were novel (p.G307S, p.K355N, p.M406V, p.T433I, p.F566L, p.E567K, and p.K568N). The remaining mutations have been reported previously in NOMID/CINCA syndrome patients as disease-causing heterozygous germline mutations (p.L264F, p.D303H, p.G307V, p.A439P, p.Y570C, and p.G755R). Each of the 3 *NLRP3* mutations, p.F566L, p.E567K, and p.G755R, was detected in 2 unrelated patients. *NLRP3* mutation p.D303H was detected in 3 unrelated patients.

Analyses in family controls. To validate the clinical relevance of the *NLRP3* mosaicism identified in mutation-negative NOMID/CINCA syndrome patients, samples from 19 healthy relatives were investigated. No somatic mosaicism was detected in any of these samples. The *P* value from the comparison of cases and controls (18 of 26 versus 0 of 19) was statistically significant ($P < 0.0001$).

Functional effects of the identified somatic *NLRP3* mutations. Since disease-causing heterozygous germline mutations in *NLRP3* have been implicated in necrosis-like programmed cell death and ASC-dependent NF-κB activation (8), experiments were performed to determine whether the mutations identified in patients with somatic mosaicism showed the same effects. All of the identified mutations induced both THP-1 cell death (Figure 1A) and ASC-dependent NF-κB activation (Figure 1B). The in vitro effects of these novel mutations were similar to or even more pronounced than those of previously reported *NLRP3* mutations. This strongly suggests that all mutations showing somatic mosaicism have pathogenic effects, including the novel mutations identified in the present study.

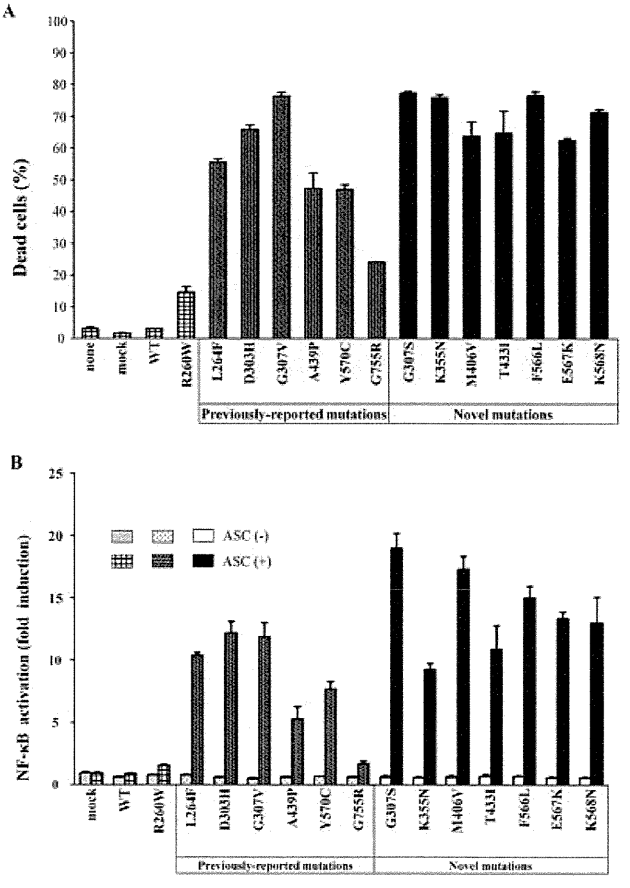

Figure 1. In vitro functional assessment of the identified *NLRP3* mosaicism mutations. **A,** Necrotic cell death of THP-1 cells induced by the identified somatic *NLRP3* mosaicism mutations. Green fluorescent protein (GFP)–fused mutant NLRP3 was transfected into THP-1 cells. The percentage of dead cells (7-aminoactinomycin D positive) among GFP-positive cells is shown. Values are the mean ± SD of triplicate experiments, and data are representative of 2 independent experiments. None = nothing transfected; mock = vector without NLRP3; WT = wild-type NLRP3; R260W = NLRP3 with p.R260W (frequent mutations in patients with cryopyrin-associated periodic syndromes). **B,** ASC-dependent NF-κB activation induced by the identified somatic *NLRP3* mosaicism mutations. HEK 293FT cells were cotransfected with WT or mutant NLRP3 in the presence or absence of ASC. The induction of NF-κB is shown as the fold change compared with cells that were transfected with a control vector without ASC (set at 1). Values are the mean ± SD of triplicate experiments, and data are representative of 2 independent experiments.

Mutation frequency of *NLRP3* among various cell lineages and 1 tissue type. To explore the origin of the *NLRP3* mosaicism, mutational frequency was evaluated in various cell lineages and 1 tissue type from 4 Japanese patients with *NLRP3* somatic mosaicism. In each patient, the same mutations were found in all of the cell lineages investigated (neutrophils, monocytes, T cells, B cells) and in the buccal mucosa tissue, and no significant difference in mutation frequency was observed between these sources (Table 2).

Table 2. Distribution and quantification of *NLRP3* mutations among sources of genomic DNA (4 cell lineages and 1 tissue type)*

Patient	Sequence variant	Protein variant	Mosaicism, %				
			Neutrophils	Monocytes	T cells	B cells	Buccal mucosa
J1	1709A>G	Y570C	12.6	9.8	8.0	9.5	8.3
J3	919G>A	G307S	9.1	10.8	6.9	10.6	9.0
J4	1699G>A	E567K	3.5	2.3	3.7	3.4	2.2
J5	907G>C	D303H	14.4	8.7	7.7	8.5	13.5

* No significant differences in the level of mosaicism were observed among the sources of genomic DNA.

Phenotype–genotype analysis. Given the previously reported genotype–phenotype association between the *NLRP3* gene and CAPS, the clinical characteristics of NOMID/CINCA syndrome patients with somatic *NLRP3* mutations were compared with those of patients from previous reports who had the same *NLRP3* mutations but with heterozygous germline status (1,4,10–13) (Figure 2) (further information is available at http://web16.kazusa.or.jp/download/). All of the patients in these 2 groups had an early onset of the disease, fever, and urticarial rash. The presence of arthritis, bony overgrowth, contractures, hearing loss, and seizure varied in each group of patients, and no significant difference was detected. However, whereas most patients with heterozygous germline *NLRP3* mutations presented with mental retardation, this was not the case for patients with somatic *NLRP3* mosaicism. A comparison was also made between the clinical data from patients with somatic *NLRP3* mosaicism and the data from patients with neither germline nor somatic *NLRP3* mutations. Again, a lower incidence of mental retardation was observed in patients with somatic *NLRP3* mosaicism

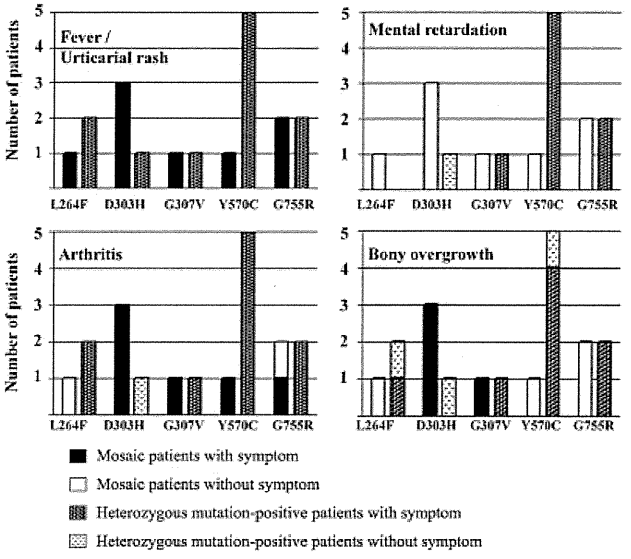

Figure 2. Comparison of the clinical profiles of patients carrying somatic *NLRP3* mutations and patients carrying the same mutation, but with germline status. Clinical profiles of patients with mosaicism and those of patients with heterozygous germline mutations are compared for each protein variant (L264F, D303H, G307V, Y570C, and G755R). The data on 4 typical clinical symptoms are shown. Total numbers of patients with mosaicism and total numbers of patients with heterozygous mutation examined are shown as a bar for each protein variant. Each bar is stratified according to the presence or absence of the symptom. For the protein variant L264F, no data on mental retardation were available for the patient with a heterozygous germline mutation.

Table 3. Clinical profiles of patients with somatic *NLRP3* mosaicism and patients with neither germline nor somatic *NLRP3* mutations*

	Patients with somatic *NLRP3* mosaicism (n = 18)	Patients with neither germline nor somatic *NLRP3* mutations (n = 8)
Age, median (IQR) years	12 (1–30)	10 (3–21)
No. of men/women	10/8	3/5
Age at onset, median (IQR) months	0 (0–24)	0.5 (0–33)
Fever	17/17	7/7
Urticarial rash	14/14	8/8
Mental retardation	4/17	6/8
Meningitis	13/17	5/8
Seizures	2/18	1/7
Hearing loss	10/18	2/7
Arthritis	14/17	7/8
Bony overgrowth	12/17	6/7
Contractures	7/17	4/7
Walking disability	8/18	3/7
Biologic therapy	10/15	3/8

* Except where indicated otherwise, values are the number with the feature/the total number of patients assessed. A lower incidence of mental retardation was observed in patients with somatic *NLRP3* mosaicism ($P = 0.03$). No other significant differences were detected between the groups. IQR = interquartile range.

($P = 0.03$). No other significant differences were detected (Table 3) (further information is available at http://web16.kazusa.or.jp/download/).

DISCUSSION

The present international multicenter study investigated 26 NOMID/CINCA syndrome patients who were mutation negative according to conventional sequencing along with 19 family controls to determine whether low-level mosaicism is a disease-causing genetic mechanism. Following our first report of low-level somatic mosaicism in a NOMID/CINCA syndrome patient (14), we reported a new method of detecting low-level *NLRP3* mosaicism, in which lipopolysaccharide (LPS) induced cell death specifically in *NLRP3* mutation–positive monocytes (8). However, this method requires fresh live monocytes, special equipment such as a cell sorter, and experience in its use due to the rapid time course of LPS-induced necrotic monocytic death. For these reasons, application of this method was not feasible in an international collaborative study. We therefore opted to use genomic DNA, since it is easier to handle and can be stored and shipped. Based on our previous study in Japanese patients showing that the frequency of mutant alleles could be <5%, we designed a subcloning and Sanger-sequencing strategy that could detect this very low allelic mutation frequency.

Presuming that the present cohort is representative of the 40% of NOMID/CINCA syndrome patients who are mutation negative according to conventional sequencing, the results suggest that ~28% of all NOMID/CINCA syndrome patients may carry somatic *NLRP3* mosaicism. CAPS patients present with a continuous spectrum of symptoms, and a degree of genotypic overlap is observed between disease subtypes. Although the present study focused on the most severe NOMID/CINCA syndrome phenotype, it is possible that somatic *NLRP3* mosaicism may also occur in milder forms of CAPS. The presence of somatic mosaicism should also be investigated in patients with other dominantly inherited autoinflammatory diseases caused by gain-of-function mutations and who are mutation negative according to conventional sequencing.

Among the 18 patients with somatic *NLRP3* mosaicism, we found 6 mutations that have previously been identified in NOMID/CINCA syndrome patients as heterozygous germline mutations. We also identified 7 novel mutations, which were confirmed as being functionally active and presumably pathogenic. Functional in vitro assays showed that these novel mutations had greater disease-causing capacity than the previously described mutations. This suggests that the novel mutations may be deleterious and unrecognized if inherited as heterozygous germline mutations.

The present study also addressed the important question of how somatic *NLRP3* mosaicism modifies clinical presentation. Although no statistically significant differences in age at disease onset, skin symptoms, joint involvement, or response to IL-1 blockade were detected, milder neurologic involvement was observed in patients with somatic mosaicism. Comparisons with NOMID/CINCA syndrome patients carrying the same *NLRP3* mutations but with heterozygous germline status made this tendency more prominent. Although the level of somatic mosaicism in blood leukocytes was relatively low, it remains unclear how these low-level mutations influence clinical presentation, including disease severity. One interesting hypothesis is that the difference in the severity of neurologic manifestations is a function of the level of mosaicism. For ethical and technical reasons, it was not possible to evaluate the level of mosaicism in central nervous system (CNS) cells or glial cells in the present study, and this therefore awaits investigation in future studies.

The mechanism through which *NLRP3* somatic mosaicism occurs also requires elucidation. The present study demonstrated that similar proportions of neutrophils, T cells, B cells, monocytes, and buccal cells carried the mutated allele. Therefore, the mutation leading to mosaicism must have arisen before the pluripotent stem cells committed to hematopoietic progenitor stem cells or ectoderm-derived nonhematopoietic cells. Several mechanisms for mosaicism have been proposed, including chimerism due to cell fusion with an aborted dizygotic twin and a mutational event during early embryogenesis (15). The latter mechanism is more likely in the present cohort, since mosaicism at similar frequency was detected in several cell types. To verify the hypothesis of a mutational event during embryogenesis, and to determine the point at which this occurred, it would be helpful to analyze other tissues. However, obtaining such tissues from patients may be ethically problematic.

Approximately 12% of the patients in the present cohort carried neither germline nor somatic *NLRP3* mutations and may therefore be considered to be genuinely mutation negative. However, it is possible that these patients have *NLRP3* mutations that have been overlooked. A recent report described a mutation in the 5′-untranslated region of *NLRP3* in a patient with FCAS

(16), although it remains unclear how this noncoding mutation causes disease. Another possibility is that an extremely low frequency of NLRP3 mosaicism may have been missed. The subcloning and Sanger-sequencing strategy used in this study set the detection limit of mosaicism at 5%. Considering the range of *NLRP3* mosaicism detected (4.2–35.8%), the median (10.2%), and the identification of 2 patients with <5% mosaicism, it is indeed likely that patients with an even lower level of *NLRP3* mosaicism may have been overlooked. Recent advances in next-generation DNA sequencing technology may resolve this technical problem, although the associated error rate could be problematic. Another possibility is that *NLRP3* mutations were present in uninvestigated cell lineages, such as those from CNS tissue, bone tissue, or skin. Future studies of NOMID/CINCA syndrome should investigate these tissues while searching for mutations in other genes.

In conclusion, the present study has clearly demonstrated that a significant proportion of NOMID/CINCA syndrome patients who were mutation negative according to conventional sequencing carried somatic *NLRP3* mutations with a variable degree of mosaicism. Clinicians should therefore consider somatic mosaicism as a possible cause of disease in mutation-negative NOMID/CINCA syndrome patients and implement appropriate therapy. The early diagnosis of NOMID/CINCA syndrome and prompt initiation of therapy would improve clinical outcome. Further goals in this research field are the refinement of genetic screening and the verification of the functional consequences of all detected somatic mutations. Systematic screening for somatic mosaicism will provide new insights into the etiology of human disease.

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AUTHOR CONTRIBUTIONS

All authors were involved in drafting the article or revising it critically for important intellectual content, and all authors approved the final version to be published. Drs. Ohara and Nishikomori had full access to all of the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

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Acquisition of data. Tanaka, Izawa, Saito, Oshima, Ohara, Nishikomori, Goldbach-Mansky, Aksentijevich, de Saint Basile, Neven, van Gijn, Frenkel, Aróstegui, Yagüe, Merino, Ibañez, Pontillo, Takada, Imagawa.

Analysis and interpretation of data. Sakuma, Morimoto, Kawai, Yasumi, Nakahata, Heike.

ROLE OF THE STUDY SPONSOR

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REFERENCES

1. Neven B, Callebaut I, Prieur AM, Feldmann J, Bodemer C, Lepore L, et al. Molecular basis of the spectral expression of CIAS1 mutations associated with phagocytic cell-mediated autoinflammatory disorders CINCA/NOMID, MWS, and FCU. Blood 2004;103:2809–15.
2. Stojanov S, Kastner DL. Familial autoinflammatory diseases: genetics, pathogenesis and treatment. Curr Opin Rheumatol 2005; 17:586–99.
3. Schroder K, Zhou R, Tschopp J. The NLRP3 inflammasome: a sensor for metabolic danger? Science 2010;327:296–300.
4. Aksentijevich I, Nowak M, Mallah M, Chae JJ, Watford WT, Hofmann SR, et al. De novo CIAS1 mutations, cytokine activation, and evidence for genetic heterogeneity in patients with neonatal-onset multisystem inflammatory disease (NOMID): a new member of the expanding family of pyrin-associated autoinflammatory diseases. Arthritis Rheum 2002;46:3340–8.
5. Hoffman HM, Mueller JL, Broide DH, Wanderer AA, Kolodner RD. Mutation of a new gene encoding a putative pyrin-like protein causes familial cold autoinflammatory syndrome and Muckle-Wells syndrome. Nat Genet 2001;29:301–5.
6. Milhavet F, Cuisset L, Hoffman HM, Slim R, El-Shanti H, Aksentijevich I, et al. The Infevers autoinflammatory mutation online registry: update with new genes and functions. Hum Mutat 2008;29:803–8.
7. Goldbach-Mansky R, Dailey NJ, Canna SW, Gelabert A, Jones J, Rubin BI, et al. Neonatal-onset multisystem inflammatory disease responsive to interleukin-1β inhibition. N Engl J Med 2006;355: 581–92.
8. Saito M, Nishikomori R, Kambe N, Fujisawa A, Tanizaki H, Takeichi K, et al. Disease-associated CIAS1 mutations induce monocyte death, revealing low-level mosaicism in mutation-negative cryopyrin-associated periodic syndrome patients. Blood 2008;111:2132–41.
9. Arostegui JI, Lopez Saldana MD, Pascal M, Clemente D, Aymerich M, Balaguer F, et al. A somatic NLRP3 mutation as a cause of a sporadic case of chronic infantile neurologic, cutaneous, articular syndrome/neonatal-onset multisystem inflammatory disease: novel evidence of the role of low-level mosaicism as the pathophysiologic mechanism underlying Mendelian inherited diseases. Arthritis Rheum 2010;62:1158–66.
10. Rosen-Wolff A, Quietzsch J, Schroder H, Lehmann R, Gahr M, Roesler J. Two German CINCA (NOMID) patients with different clinical severity and response to anti-inflammatory treatment. Eur J Haematol 2003;71:215–9.
11. Aksentijevich I, Putnam CD, Remmers EF, Mueller JL, Le J, Kolodner RD, et al. The clinical continuum of cryopyrinopathies: novel CIAS1 mutations in North American patients and a new cryopyrin model. Arthritis Rheum 2007;56:1273–85.
12. Matsubayashi T, Sugiura H, Arai T, Oh-Ishi T, Inamo Y. Anakinra

therapy for CINCA syndrome with a novel mutation in exon 4 of the CIAS1 gene. Acta Paediatr 2006;95:246–9.
13. Jesus AA, Silva CA, Segundo GR, Aksentijevich I, Fujihira E, Watanabe M, et al. Phenotype–genotype analysis of cryopyrin-associated periodic syndromes (CAPS): description of a rare non-exon 3 and a novel CIAS1 missense mutation. J Clin Immunol 2008;28:134–8.
14. Saito M, Fujisawa A, Nishikomori R, Kambe N, Nakata-Hizume M, Yoshimoto M, et al. Somatic mosaicism of CIAS1 in a patient with chronic infantile neurologic, cutaneous, articular syndrome. Arthritis Rheum 2005;52:3579–85.
15. Erickson RP. Somatic gene mutation and human disease other than cancer: an update. Mutat Res 2010;705:96–106.
16. Anderson JP, Mueller JL, Misaghi A, Anderson S, Sivagnanam M, Kolodner RD, et al. Initial description of the human NLRP3 promoter. Genes Immun 2008;9:721–6.

Case Report

Sepsis and spontaneous bacterial peritonitis in Thailand

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In June, 2007, a 66-year-old man (case 1), an alcohol misuser with alcoholic liver cirrhosis who habitually ate raw pork, was referred to Uttaradit Hospital, northern Thailand. He had a fever and massive ascites. His leucocyte count was $4{\cdot}4\times10^9$/L, and total bilirubin and albumin concentrations were 23·7 mg/L, and 26 g/L, respectively. Polymorphonuclear leucocyte count of ascitic fluid was $4{\cdot}1\times10^8$/L and culture was positive despite a negative blood culture. This patient was diagnosed with spontaneous bacterial peritonitis,[1] and successfully treated with ceftriaxone. Testing of this isolate with the API 20 Strep Kit (BioMérieux, Marcy l'Etoile, France) suggested *Streptococcus equi* subspecies *zooepidemicus* with 91·8% identification. However, there was 99% similarity of the 16S rDNA sequence with known *S suis* strains. Confirmation that this isolate belonged to this species was further supported by a positive reaction for *S suis*-specific PCR amplification of the *S suis* 16S rRNA gene.[2]

In May, 2007, a 62-year-old woman (case 2), with liver cirrhosis who had had repeated episodes of spontaneous bacterial peritonitis in 2006, was admitted to Phetchabul Hospital, northern Thailand, with a fever. Physical examination showed cutaneous jaundice and ascites. Her leucocyte cell count, total bilirubin, and albumin were $15{\cdot}1\times10^9$/L, 108·2 mg/L, and 18 g/L, respectively. Culture of ascitic fluid was negative, blood culture was positive, and she was diagnosed with sepsis. The isolate was identified as *S suis* by the API 20 Strep Kit. This patient also improved on treatment with ceftriaxone.

The isolates from these two cases were confirmed by a co-agglutination test as serotype 5 for case 1 and serotype 24 for case 2 (table), and were assigned to the novel sequence types by multilocus sequence typing.[2]

We report the first human cases of *S suis* infection with serotypes 5 and 24. *S suis* is a zoonotic pathogen that can cause invasive infections in human beings who consume raw pork products or are in close contact with infected pigs.[3] Although serotype 2 is the most prevalent in human beings, cases with serotypes 1, 4, 14, and 16 have been reported.[2–4] In Thailand between 2006 and 2008, 179 human isolates of *S suis* were collected from sterile sites eg, blood, cerebrospinal fluid. Of these isolates, 165 (92·2%) were serotype 2, and 12 (6·7%) were serotype 14.[2] The differential diagnosis of our two cases includes melioidosis and leptospirosis. Bacterial translocation has an important role in the pathogenesis of spontaneous bacterial peritonitis in cirrhosis, and the most common pathogens are enterobacteriaceae.[1] Previous reports on human infections after recent consumption of raw pork products suggested that the gastrointestinal tract is a major route of entry in cases of *S suis* infections in Thailand and Vietnam.[2,3,5] In this region, the occurrence of spontaneous bacterial peritonitis through bacterial translocation of *S suis* after consumption of raw pork products is possible in patients with liver cirrhosis. A similar case of spontaneous bacterial peritonitis caused by serotype 16 strain of *S suis* in a patient with alcoholic liver cirrhosis was reported from Vietnam.[4] Although the isolation rates for serotypes 5 and 24 are low (2/179 cases; 1·1%), *S suis*-specific PCR is recommended for identification of streptococcal isolates from sterile sites, and a serious caution against eating raw pork products should be given to patients with liver cirrhosis, especially in southeast Asian countries.

	Case 1	Case 2
Source of isolate	Ascites	Blood
Clinical diagnosis	Spontaneous bacterial peritonitis	Sepsis
Comorbid illness	Alcholic liver cirrhosis	Liver cirrhosis
Identification with API 20 Strep	*S equi* subspecies *zooepidemicus*	*S suis*
S suis-specific PCR	Positive	Positive
Sequencing of 16S rRNA gene	*S suis* (99%)	*S suis* (99%)
Serotype	5	24
Multilocus sequence typing	ST181	ST221

ST: sequence type.

Table: **Microbiological features of two human cases of *Streptococcus suis* infection**

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Patient care: AB, SS. Microbiology: AK, WN, SC, YA. Serotyping: MG. Study coordination: SD. Writing: PS, DS, KO. Written consent to publish was obtained.

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References

1 Koulaouzidis A, Bhat S, Karagiannidis A, Tan WC, Linaker BD. Spontaneous bacterial peritonitis. *Postgrad Med J* 2007; 83: 379–83.
2 Kerdsin A, Dejsirilert S, Puangpatra P, et al. Genotypic profile of *Streptococcus suis* serotype 2 and clinical features of infection in humans, Thailand. *Emerg Infect Dis* 2011; 17: 836–42.
3 Gottschalk M, Xu J, Calzas C, Segura M. *Streptococcus suis*: a new emerging or an old neglected zoonotic pathogen? *Future Microbiol* 2010; 5: 371–91.
4 Nghia HDT, Hoa NT, Linh LD, et al. Human case of *Streptococcus suis* serotype 16 infection. *Emerg Infect Dis* 2008; 14: 155–57.
5 Ho DTN, Le TPT, Wolbers M, et al. Risk factors of *Streptococcus suis* infection in Vietnam. A case-control study. *PLoS One* 2011; 6: e17604.