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Nationwide Survey of Patients with Primary Immunodeficiency Diseases in Japan

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Abstract To determine the prevalence and clinical characteristics of patients with in Japan, we conducted a nationwide survey of primary immunodeficiency disease (PID) patients for the first time in 30 years. Questionnaires were sent to 1,224 pediatric departments and 1,670 internal medicine departments of Japanese hospitals. A total of 1,240 patients were registered. The estimated number of patients with PID was 2,900 with a prevalence of 2.3 per 100,000 people and homogenous regional distribution in Japan. The male-to-female ratio was 2.3:1 with a median age of 12.8 years. Adolescents or adults constituted 42.8% of the patients. A number of 25 (2.7%) and 78 (8.5%) patients developed malignant disorders and immune-related diseases, respectively, as complications of primary immunodeficiency disease. Close monitoring and appropriate management for these complications in addition to prevention of infectious diseases is important for improving the quality of life of PID patients.

Keywords Primary immunodeficiency disease · epidemiology · nationwide survey · Japan

Abbreviations

APECED	Autoimmune polyendocrinopathy with candidiasis and ectodermal dystrophy
BTK	Bruton's tyrosine kinase
CGD	Chronic granulomatous disease
CID	Combined T and B cell immunodeficiency
CVID	Common variable immunodeficiency disease
FMF	Familial Mediterranean fever
IPEX	Immune dysregulation polyendocrinopathy enteropathy X-linked
NEMO	Nuclear factor kappa B essential modulator
PID	Primary immunodeficiency disease
SIgAD	Selective IgA deficiency
SLE	Systemic lupus erythematosus

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TRAPS	Tumor necrosis factor receptor-associated periodic syndrome
WAS	Wiskott–Aldrich syndrome
WHIM	Warts hypogammaglobulinemia, infections, and myelokathexis

Introduction

Patients with primary immunodeficiency disease (PID) show susceptibility to infections due to congenital immune system defects. These patients are also associated with noninfectious complications including autoimmune diseases and malignant disorders. Recent studies have revealed the causes of many PIDs to be mutations in various genes encoding molecules involved in the host defense mechanisms [1]. In addition, various new PIDs including defects in innate immunity and autoinflammatory disorders were identified under the recent progress in immunology and molecular genetics [2]. PID classification has been revised according to the identification of new PIDs and on the basis of new findings in PID pathophysiology. For a more precise clinical analysis, data should be obtained in accordance with the latest PID classifications.

The first nationwide survey of patients with PID in Japan was conducted between 1974 and 1979, which included 497 registered cases [3]. By 2007, a total of 1,297 patients were cataloged by a small number of PID specialists into a registration system [4]. The approximate prevalence of PID patients in Japan in the first nationwide survey was 1.0 in 100,000 people, which was much lower than that in other countries [5–7]. This difference in PID prevalence between Japan and other countries suggested that some PID patients in Japan remained unregistered. To determine the prevalence and clinical characteristics of patients with PID in Japan on the basis of the recent international classification system for PID, we conducted a nationwide survey of PID for the first time in 30 years.

Methods

This study was performed according to the nationwide epidemiological survey manual of patients with intractable diseases (2nd edition 2006, Ministry of Health, Labour, and Welfare of Japan) as described previously [8]. PID classification was based on the International Union of Immunological Societies Primary Immunodeficiency Diseases Classification Committee in 2007 [2]. Patients with chronic benign neutropenia and syndrome of periodic fever, aphthous stomatitis, pharyngitis, and cervical adenitis were excluded because these were considered to be acquired diseases. The survey was conducted on PID patients who were alive on December 1, 2008 and those who were newly diagnosed and dead between December 1, 2007 and November 30, 2008 in Japan. Among the 2,291 pediatric departments and 8,026 internal medicine departments in Japan, hospitals participating in the survey were randomly selected after setting the selection ratio according to the number of beds (overall selection rate: 53.4% for pediatric departments, 20.8% for internal medicine departments; Table I). University hospitals and pediatric training hospitals, where many PID patients were considered to be treated, were stratified separately (Table I). Primary questionnaires regarding the number of patients and disease names based on PID classification were sent to the selected hospitals. Secondary questionnaires regarding age, gender, clinical manifestations, and complications of individual PID patients were sent to respondents who answered that they observed at least one PID patient with characteristics listed in the primary questionnaires.

Results

Questionnaires were distributed to 1,224 pediatric departments and 1,670 internal medicine departments of hospitals in Japan, and the response rate was 55.0% and 20.1%, respectively (Table I). A total of 1,240 patients (1,146 patients from pediatric departments and 94 patients from internal medicine departments) were registered (Table I). The estimated number of patients with PIDs in Japan was 2,900 (95% confidence interval: 2,300–3,500), and the prevalence was 2.3 per 100,000 inhabitants. We also determined the regional distribution on the basis of the patients' addresses. The estimated regional prevalence ranged from 1.7 to 4.0 per 100,000 inhabitants, and no significant differences were observed between different regions in Japan (Fig. 1). The most common form of PID was predominantly antibody deficiencies (40%), followed by congenital defects of phagocyte number, function, or both (19%) and other well-defined immunodeficiency syndromes (16%; Table II). Autoinflammatory disorders were observed in 108 cases (9%). The most common PID was Bruton's tyrosine kinase (BTK) deficiency (182 cases, 14.7%), followed by chronic granulomatous disease (CGD; 147 cases, 11.9%). However, common variable immunodeficiency disease (CVID) and selective IgA deficiency (SIgAD) were observed only in 136 (11.0%) and 49 cases (4.0%), respectively. Among patients registered from internal medicine departments, antibody deficiencies were the most common disorder (71%).

In the secondary survey, 923 cases were registered. The male-to-female ratio was 2.3:1 (n=914, unanswered: 9 cases) with a median age of 12.8 years (range: 0 to 75 years; n=897, unanswered: 26 cases). The number of adolescent or

Table I Stratification and selection of hospitals and the survey results

	Stratification	Departments in Japan	Departments selected	Selection rate (%)	Return[a]	Response	Response rate (%)	PID Patient	Patients per department	Patients estimated
Pediatrics	University hospital	118	118	100	0	80	67.8	661	8.3	975
	Training hospital	402	402	100	4	242	60.8	376	1.6	618
	≥500 beds	92	92	100	5	48	55.2	24	0.5	44
	400–499 beds	118	118	100	3	63	54.8	42	0.7	77
	300–399 beds	287	230	80.1	4	122	54.0	31	0.3	72
	200–299 beds	289	116	40.1	4	53	47.3	6	0.1	32
	100–199 beds	486	98	20.2	0	44	44.9	4	0.1	44
	<99 beds	499	50	10.0	1	10	20.4	2	0.2	100
	Subtotal	2,291	1,224	53.4	21	662	55.0	1,146	1.7	1,961
Internal medicine	University hospital	156	156	100	1	47	30.3	37	0.8	122
	≥500 beds	374	374	100	1	86	23.1	35	0.4	152
	400–499 beds	328	263	80	1	54	20.6	6	0.1	36
	300–399 beds	692	278	40.2	6	49	18.0	10	0.2	140
	200–299 beds	1,008	202	20.0	0	36	17.8	2	0.1	56
	100–199 beds	2,460	246	10.0	1	36	14.7	1	0.0	68
	<99 beds	3,008	151	5.0	6	24	16.6	3	0.1	375
	Subtotal	8,026	1,670	20.8	16	332	20.1	94	0.3	950
Total		10,317	2,894	28.1	37	994	34.8	1,240		2,911

[a] Due to the closure of departments

adult cases (≥15 years) was 384 (42.8%; Fig. 2a). The male-to-female ratio of the younger generation (<15 years) was 2.7:1, while that of the older generation (≥15 years) was 2.0:1. Combined T and B cell immunodeficiencies (CIDs) were predominantly observed in the younger generation, while antibody deficiencies were more common with

Region	Reported PID Patients	Population ($x10^5$)	Estimated prevalence per 10^5 (95% C.I.)
Hokkaido	73	55.4	4.0 (0.2-7.8)
Tohoku	81	94.3	2.1 (0.9-3.3)
Kanto	387	419.8	1.8 (1.2-2.5)
Chubu	236	236.9	2.3 (1.4-3.1)
Kinki	158	208.4	2.0 (1.2-2.8)
Chugoku/Shikoku	105	116.1	1.7 (1.0-2.3)
Kyushu/Okinawa	200	146.0	2.5 (1.7-3.3)
Total	1240	1276.9	2.3 (1.8-2.7)

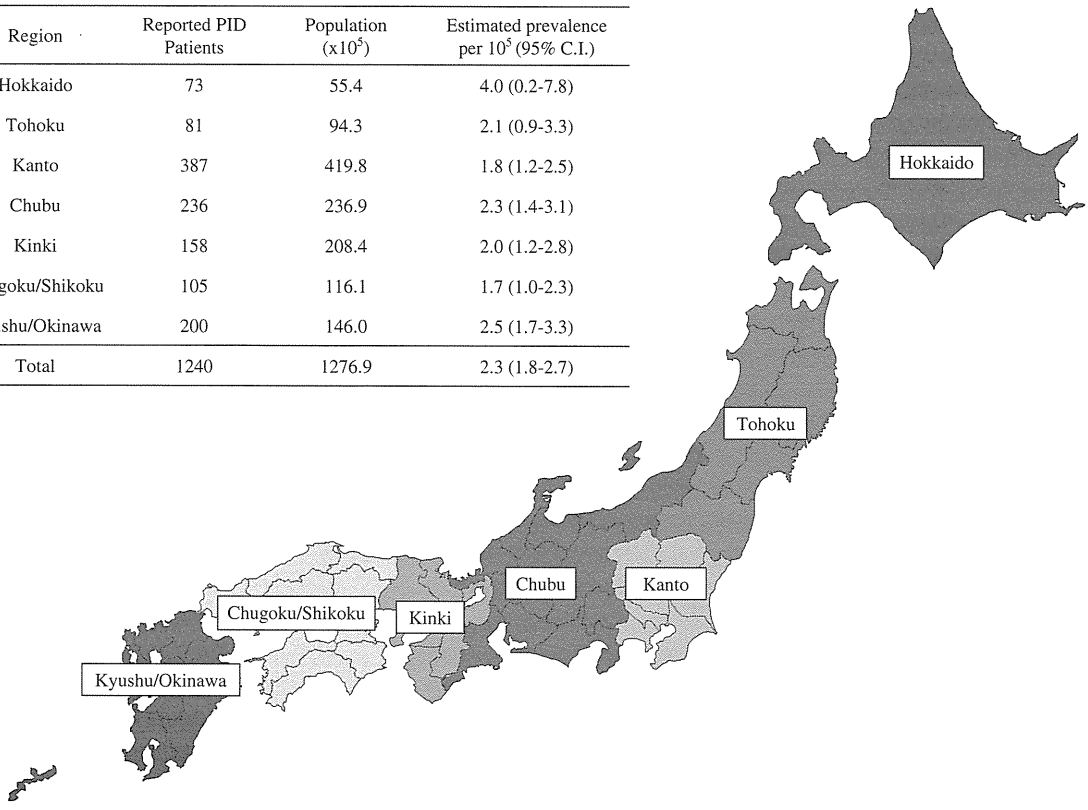

Fig. 1 Regional distribution of PID patients. *CI* Confidence interval

Table II Reported number of PID

Category	Total number	Pediatric department	Internal medicine department
I. Combined T and B cell immunodeficiencies	93 (7%)	93 (8%)	0 (0%)
γc deficiency	47	47	0
Adenosine deaminase deficiency	9	9	0
Omenn syndrome	4	4	0
Others	23	23	0
Untested or undetermined	10	10	0
II. Predominantly antibody deficiencies	501 (40%)	434 (38%)	67 (71%)
BTK deficiency	182	173	9
Common variable immunodeficiency disorders	136	107	29
Selective IgG subclass deficiency	66	58	8
Selective IgA deficiency	49	34	15
Hyper IgM syndrome	34	34	0
Transient hypogammaglobulinemia of infancy	7	7	0
Others	11	7	4
Untested or undetermined	16	14	2
III. Other well-defined immunodeficiency syndromes	194 (16%)	189 (17%)	5 (5%)
Wiskott–Aldrich syndrome	60	60	0
DNA repair defects (other than those in category I)	15	15	0
DiGeorge anomaly	38	38	0
Hyper-IgE syndrome	56	52	4
Chronic mucocutaneous candidiasis	17	16	1
Others	5	5	0
Untested or undetermined	3	3	0
IV. Diseases of immune dysregulation	49 (4%)	48 (4%)	1 (1%)
Chediak–Higashi syndrome	9	8	1
Familial hemophagocytic lymphohistiocytosis syndrome	5	5	0
X-linked lymphoproliferative syndrome	8	8	0
Autoimmune lymphoproliferative syndrome	8	8	0
APECED	4	4	0
IPEX syndrome	7	7	0
Others	2	2	0
Untested or undetermined	6	6	0
V. Congenital defects of phagocyte number, function, or both	230 (19%)	223 (19%)	7 (8%)
Severe congenital neutropenia	44	42	2
Cyclic neutropenia	19	17	2
Chronic granulomatous disease	147	144	3
Mendelian susceptibility to mycobacterial disease	5	5	0
Others	9	9	0
Untested or undetermined	6	6	0
VI. Defects in innate immunity	15 (1%)	15 (1%)	0
Anhidrotic ectodermal dysplasia with immunodeficiency	7	7	0
Interleukin-1 receptor-associated kinase 4 deficiency	2	2	0
Others	5	5	0
Untested or undetermined	1	1	0
VII. Autoinflammatory disorders	108 (9%)	101 (9%)	7 (8%)
Familial Mediterranean fever	44	40	4
TNF receptor-associated periodic syndrome	13	12	1
Hyper IgD syndrome	4	4	0
Cryopyrin-associated periodic syndrome	22	22	0

Table II (continued)

Category	Total number	Pediatric department	Internal medicine department
Others	3	3	0
Untested or undetermined	22	20	2
VIII. Complement deficiencies	32 (3%)	29 (3%)	3 (3%)
IX. Undetermined	18 (1%)	14 (1%)	4 (4%)
Total	1,240	1,146	94

APECED Autoimmune polyendocrinopathy with candidiasis and ectodermal dystrophy, *IPEX* immune dysregulation, polyendocrinopathy, enteropathy, X-linked

increasing age (Fig. 2b). The median age of CID, BTK deficiency, CVID, and CGD patients was 5.2, 12.8, 25.1, and 14.7 years, respectively.

It is well known that PID patients are susceptible to many pathogens and experience community-acquired or opportunistic infections. In this study, we focused on noninfectious complications of PID because they have been less well studied on a large scale and may provide important information for improving the quality of life of PID patients. Twenty-five PID patients developed malignant disorders (2.7%; Table III). Lymphoma, in particular, Epstein–Barr virus-related, and leukemia were dominant, while there were no patients with gastric carcinoma. CVID, Wiskott–Aldrich syndrome (WAS), and ataxia telangiectasia were more frequently associated with malignant diseases among PID patients. A case of Mendelian susceptibility

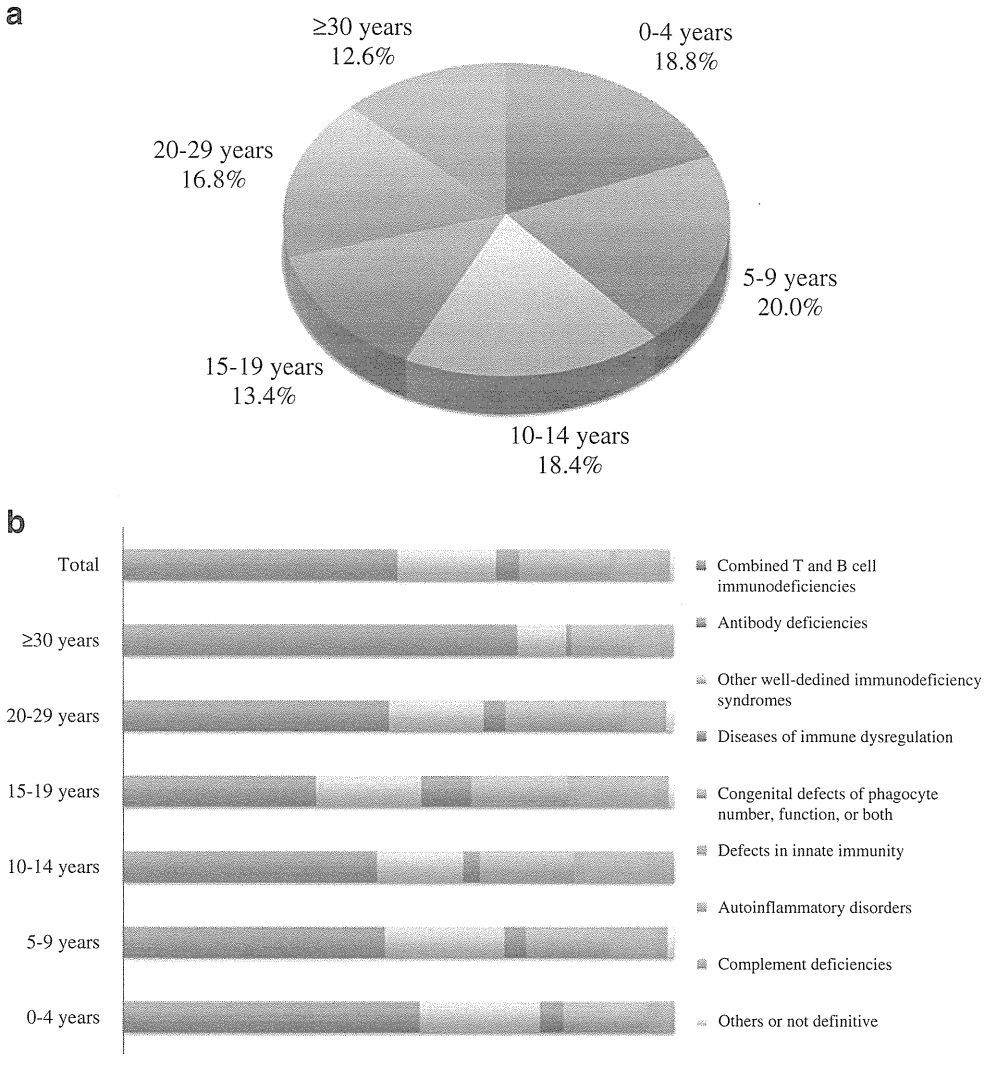

Fig. 2 **a** Age distribution of PID patients. **b** Distribution of PID in each age group

to mycobacterial disease with squamous cell carcinoma was also observed [9] (Table III).

Seventy-eight PID patients had immune-related (autoimmune) diseases (8.5%; Table IVa). Autoimmune lymphoproliferative syndrome, immune dysregulation, polyendocrinopathy, enteropathy X-linked (IPEX) syndrome, and nuclear factor kappa B essential modulator (NEMO) deficiency were associated with immune-related diseases at a very high incidence. In addition, immune-related diseases were relatively common in CGD and CVID patients (Table IVa). The most commonly observed immune-related disease was inflammatory bowel disease (33 cases), which was most frequently observed in CGD patients, followed by immune thrombocytopenic purpura (13 cases), autoimmune hemolytic anemia (8 cases), and systemic lupus erythematosus (SLE; 8 cases; Table IVa and b). Kawasaki disease occurred in WAS and CGD patients. In addition, this is the first report of Kawasaki disease in patients with complement deficiency (C9) and familial Mediterranean fever (FMF). A patient with warts, hypogammaglobulinemia, infections, and myelokathexis (WHIM) syndrome and a patient with tumor necrosis factor receptor-associated periodic syndrome (TRAPS) were first reported as cases of type 1 diabetes mellitus and SLE, respectively [10, 11].

Discussion

We conducted a nationwide survey of PID for the first time in 30 years and report the prevalence of PID in Japan. We registered 1,240 PID patients and found that the estimated prevalence of PID (2.3/100,000) is higher than that previously reported (1.0/100,000) in Japan. Our results are equivalent to those reported in Singapore (2.7/100,000) and Taiwan (0.77–2.17/100,000) [12–14]. However, our values are lower than those reported in Middle Eastern countries such as Kuwait (11.98/100,000) or in European countries such as France (4.4/100,000) [5–7, 15]. The high rate of consanguinity may be a cause of the high prevalence rate of PID reported in Middle Eastern countries [6, 15]. There may has been sample selection bias in this study because some asymptomatic cases (SIgAD, etc.), clinically recovered cases (transient hypogammaglobulinemia of infancy, etc.), and cases in which patients were deceased were not registered. In addition, lack of recognition of PID in internal medicine departments, not just the low response rate, might also have influenced the estimated prevalence of PID as well as the age and disease distribution. The regional prevalence of PIDs in Japan was homogenous, unlike in other countries in which a higher prevalence was

Table III Malignancies in PID patients

Primary immunodeficiency	Total	*n*	Malignancy
I. Combined T and B cell immunodeficiencies	75	2	(2.7%)
Ommen syndrome	3	1	NHL (EBV+) 1[a]
Adenosine deaminase deficiency	4	1	Breast carcinoma 1
II. Predominantly antibody deficiencies	378	8	(2.1%)
Common variable immunodeficiency disorders	93	7	HL 2, ML 2, ALL 1, Basal cell carcinoma 1, Cervical carcinoma 1
Good syndrome	4	1	Double primary carcinoma of breast and colon 1
III. Other well-defined immunodeficiency syndromes	165	7	(4.2%)
Wiskott–Aldrich syndrome	57	5	NHL 3, NHL/HL 1, LPD (EBV-) 1
Ataxia telangiectasia	13	2	T-ALL 1, MDS 1
IV. Diseases of immune dysregulation	38	4	(10.5%)
X-linked lymphoproliferative syndrome	5	2	Burkitt lymphoma 2
Autoimmune lymphoproliferative syndrome	6	2	HL (EBV+) 1, Brain tumor 1
V. Congenital defects of phagocyte number, function, or both	153	4	(2.6%)
Severe congenital neutropenia	35	3	MDS 3 (including 2 cases with monosomy 7)
MSMD	7	1	Squamous cell carcinoma of finger 1
VI. Defects in innate immunity	12	0	(0%)
VII. Autoinflammatory disorders	74	0	(0%)
VIII. Complement deficiencies	23	0	(0%)
IX. Undetermined	5	0	(0%)
Total	923	25	(2.7%)

n Number of PID patients who had malignant disorders, *ALL* acute lymphoblastic leukemia, *EBV* Epstein-Barr virus, *HL* Hodgkin lymphoma, *LPD* lymphoproliferative disease, *MDS* myelodysplastic syndrome, *ML* malignant lymphoma, *MSMD* Mendelian susceptibility to mycobacterial disease, *NHL* non-Hodgkin lymphoma

[a] The number of patients

Table IV Immune-related diseases in PID patients

(a) Immune-related diseases with each PID

Primary immunodeficiency	Total	*n*	Immune-related disease
I. Combined T and B cell immunodeficiencies	75	2	(2.6%)
MHC class II deficiency (suspected)	1	1	ITP with AIHA 1[a]
CD4 deficiency	1	1	Hashimoto disease 1
II. Predominantly antibody deficiencies	378	24	(6.3%)
Common variable immunodeficiency disorders	93	16	ITP 3, RA 2, AIHA 2, Hashimoto's disease 2, IBD 2, SLE 1, MG 1, ADEM 1, Autoimmune hepatitis 1, Uveitis 1
Hyper-IgM syndrome	32	3	JIA 1, SLE (complicated with C1q deficiency) 1, IBD 1
Selective IgA deficiency	28	3	SLE 1, SLE with Kikuchi disease 1, RA 1
IgG subclass deficiency	50	2	ITP with AIHA 1, ITP with MS 1
III. Other well-defined immunodeficiency syndromes	165	5	(3.0%)
Wiskott–Aldrich syndrome	57	3	AIHA 2, Kawasaki disease 1
DiGeorge syndrome	33	2	AIHA 1, ITP 1
IV. Diseases of immune dysregulation	38	10	(26.3%)
X-linked lymphoproliferative syndrome	5	1	IBD 1
Autoimmune lymphoproliferative syndrome	6	4	ITP 3, Graves' disease with IBD 1
APECED	5	1	T1DM with Hashimoto's disease and Vogt–Koyanagi–Harada disease 1
IPEX syndrome	6	4	T1DM 1, T1DM with ITP, AIN and IBD 1, Autoimmune enteritis 1, AIHA with Autoimmune enteritis and Hashimoto's disease 1
V. Congenital defects of phagocyte number, function, or both	153	25	(16.3%)
Chronic granulomatous disease	87	25	IBD 20, ITP 2, JIA 1, MCTD 1, Kawasaki disease 1
VI. Defects in innate immunity	12	5	(41.7%)
NEMO deficiency	7	4	IBD 3, IBD with JIA 1
WHIM syndrome	3	1	T1DM 1
VII. Autoinflammatory disorders	74	3	(4.0%)
Familial Mediterranean fever	36	2	SLE 1, Kawasaki disease 1
TNF receptor associated periodic syndrome	9	1	SLE 1
VIII. Complement deficiencies	23	3	(13.0%)
C4 deficiency	1	1	SLE with RA 1
C6 deficiency	1	1	IBD 1
C9 deficiency	11	1	Kawasaki disease 1
IX. Undetermined	5	1	(20%)
Nakajo syndrome	1	1	SLE 1
Total	923	78	(8.5 %)

(b) Immune-related manifestations associated with PID

Immune-related diseases	*n*
IBD (including autoimmune enteritis)	33
ITP	13
AIHA	8
SLE	8
RA/JIA	6
Hashimoto's disease/Graves' disease	5
Kawasaki disease	4
T1DM	4
Uveitis (including Vogt–Koyanagi–Harada disease)	2
ADEM/MS	2
Others	5

n Number of PID patients who had immune-related disorders, *ADEM* acute disseminated encephalomyelitis, *AIHA* autoimmune hemolytic anemia, *AIN* autoimmune neutropenia, *APECED* autoimmune polyendocrinopathy candidiasis ectodermal dystrophy, *IBD* inflammatory bowel disease, *IPEX* immunodysregulation, polyendocrinopathy, enteropathy X-linked, *ITP* immune thrombocytopenic purpura, *JIA* juvenile idiopathic arthritis, *MCTD* mixed connective tissue disease, *MG* myasthenia gravis, *MS* multiple sclerosis, *RA* rheumatoid arthritis, *SLE* systemic lupus erythematosus, *T1DM* type 1 diabetes mellitus, *WHIM* warts, hypogammaglobulinemia, infections, and myelokathexis

[a] The number of patients

observed in urban areas [5, 7, 16]. This may be because many PID patients were treated or followed by PID specialists distributed nationwide in Japan; this is assumed by the location of hospitals with which they were affiliated.

The distribution ratios of BTK deficiency (14.7%) and CGD (11.9%) in Japan were higher than those in a previous report from Europe (5.87% and 4.33%, respectively), while those of CIDs and other well-defined immunodeficiency syndromes were comparable [17]. The prevalence of BTK deficiency was previously reported to be 1/900,000–1,400,000 in a European cohort study [18]. In contrast, this value was estimated to be 1/300,000 in Japan in our study. BTK deficiency appears to be common in Japan, although this may be partially because more patients, including those showing atypical clinical manifestations, were diagnosed more accurately by the recently established genetic diagnostic network in Japan [19]. This is supported by the highest proportion of Japanese patients in the international mutation database for X-linked agammaglobulinemia (BTKbase) [20]. The reason for the low number of registered CGD patients in Europe in a recent report (1/620,000) [17] is unknown; the prevalence of CGD was 1 in 250,000 in a previous European survey [21], which was similar to our results (1 in 380,000 in this study and 1 in 280,000 in our previous study [22]). The percentage of BTK deficiency and CGD would be lower if more adult cases were registered because the prevalence of these disorders is low in adults. CVID was the most commonly reported PID (20.7%) in Europe, and the onset of symptoms was observed most commonly in the third decade of life in these patients [17, 23]. In this study, CVID constituted 11.0% (136 cases) of PID cases, and only 29 cases were reported from internal medicine departments (Table II). A lower number of registered CVID patients may have led to a lower number of reported patients with antibody deficiency and a lower prevalence of PID, although it is still possible that CVID is not as common in Japan as in European countries. There was no significant difference in the distribution rate of SIgAD between Japanese and Europeans, although SIgAD is rare in Japanese (1/18,500) compared with Caucasians (1/330–2,200) according to seroepidemiologic studies [24]. This may be because most SIgAD patients lack clinical manifestations. The distribution ratio of autoinflammatory disorders in Japan (9%) was much higher than that in Europe (1.02%) [17] (Table II). Considering the disease type of the autoinflammatory disorders was not specified in 22 cases (20%), it is possible that many other patients with autoinflammatory disorders remain undiagnosed in Japan as well as in other countries.

The percentage of men (69.7%) with PID is higher in Japan than in Europe (60.8%) or Kuwait (61.8%), but is equivalent to that in Taiwan (70.2%) [6, 13, 17]. The higher ratio of men, particularly in younger generation (<15 years), appears to be due to the larger number of X-linked PID patients (BTK deficiency, X-CGD, γc deficiency, etc.) in this study compared to that in Europe or Kuwait. Adolescents or adults (≥15 years) constituted 42.8% of the patients in this study, which is equivalent to the number in the European study (≥16 years: 46.6%), while those >16 years constituted only 10.9% in the previous survey [3, 17]. In this study, it was found that CVID and SIgAD are common in adults (Table II) and that antibody deficiencies are more common with increasing age (Fig. 2b). A reason for the increased number of adult PID patients may be long-term survival of PID patients due to improved treatments such as immunoglobulin replacement therapy. In addition, an increased likelihood of patients being diagnosed by internists as having late-onset PID, e.g., CVID and SIgAD, may have contributed to these values [17, 25, 26]. Therefore, it is important for internists to be well-informed regarding PID. In contrast, CIDs are fatal during infancy without hematopoietic stem cell transplantation or gene therapy. Because hematopoietic stem cell transplantation has been widely performed in Japan since the 1990s, surviving patients with CID are limited to the younger generation, similar to French patients (Fig. 2b) [5, 27, 28].

It has been reported that PID patients are at increased risk of developing malignant diseases, in particular, non-Hodgkin lymphoma, leukemia, and stomach cancer [29]. Although lymphoma and leukemia were relatively common, stomach cancer was not observed in our study. In the previous survey in Japan, eight of nine PID patients with malignant disorders (including one gastric cancer patient) died [3]. It is possible that some PID patients with malignant disorders were not registered because they were deceased. PID is also associated with immune-related diseases because of a defect in the mechanisms to control self-reactive B and T cells. The frequency of immune-related manifestations varied among individual PID patients, as reported previously [30, 31]. Four PID patients who had developed Kawasaki disease, one patient with WHIM syndrome and type 1 diabetes mellitus, and one patient with TRAPS and SLE in our study may provide new pathophysiological insights of these diseases and the association between PID and autoimmune diseases.

Conclusions

We report the prevalence and clinical characteristics of PIDs in Japan. Although the advances in diagnostic technologies and treatments have improved the prognoses of PID, many patients continue to experience severe complications such as malignancy and immune-related diseases as well as infections. To improve the quality of life of PID patients, it is necessary to pay attention to

complications and treat them appropriately. Web-based PID databases and consultation systems have been created in Japan (Primary Immunodeficiency Database in Japan [4] and Resource of Asian Primary Immunodeficiency Diseases in Asian countries [32]) to reveal precise information regarding PID and to promote cooperation between doctors and researchers [19].

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Conflict of Interest There is no actual or potential conflict of interest in relation to the study.

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Gain-of-function human *STAT1* mutations impair IL-17 immunity and underlie chronic mucocutaneous candidiasis

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Abbreviations used: AD, autosomal dominant; AR, autosomal recessive; CMC, chronic mucocutaneous candidiasis; CMCD, CMC disease; EMSA, electrophoretic mobility shift assay; GAS, γ-activated sequence; ISRE, IFN-stimulated response element; MSMD, Mendelian susceptibility to mycobacterial disease; WB, Western blotting.

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Chronic mucocutaneous candidiasis disease (CMCD) may be caused by autosomal dominant (AD) IL-17F deficiency or autosomal recessive (AR) IL-17RA deficiency. Here, using whole-exome sequencing, we identified heterozygous germline mutations in *STAT1* in 47 patients from 20 kindreds with AD CMCD. Previously described heterozygous *STAT1* mutant alleles are loss-of-function and cause AD predisposition to mycobacterial disease caused by impaired STAT1-dependent cellular responses to IFN-γ. Other loss-of-function *STAT1* alleles cause AR predisposition to intracellular bacterial and viral diseases, caused by impaired STAT1-dependent responses to IFN-α/β, IFN-γ, IFN-λ, and IL-27. In contrast, the 12 AD CMCD-inducing *STAT1* mutant alleles described here are gain-of-function and increase STAT1-dependent cellular responses to these cytokines, and to cytokines that predominantly activate STAT3, such as IL-6 and IL-21. All of these mutations affect the coiled-coil domain and impair the nuclear dephosphorylation of activated STAT1, accounting for their gain-of-function and dominance. Stronger cellular responses to the STAT1-dependent IL-17 inhibitors IFN-α/β, IFN-γ, and IL-27, and stronger STAT1 activation in response to the STAT3-dependent IL-17 inducers IL-6 and IL-21, hinder the development of T cells producing IL-17A, IL-17F, and IL-22. Gain-of-function *STAT1* alleles therefore cause AD CMCD by impairing IL-17 immunity.

Chronic mucocutaneous candidiasis (CMC) is characterized by persistent or recurrent disease of the nails, skin, oral, or genital mucosae caused by *Candida albicans* (Puel et al., 2010b). CMC may be caused by various inborn errors of immunity. CMC is one of a multitude of infectious diseases observed in patients with broad and profound T cell deficiencies. In contrast, patients with the autosomal dominant (AD) hyper IgE syndrome, caused by dominant-negative mutations of *STAT3*, are susceptible principally to CMC and staphylococcal diseases of the lungs and skin (Minegishi, 2009). These patients have very low proportions of circulating IL-17A– and IL-22–producing T cells, probably because of impaired responses to IL-6, IL-21, and/or IL-23 (de Beaucoudrey et al., 2008; Ma et al., 2008; Milner et al., 2008; Renner et al., 2008; Minegishi et al., 2009). Patients with autosomal recessive (AR) IL-12p40 or IL-12Rβ1 deficiency suffer from Mendelian susceptibility to mycobacterial disease (MSMD) and occasionally develop mild CMC (Filipe-Santos et al., 2006; de Beaucoudrey et al., 2010). Some have low proportions of IL-17A– and IL-22–producing T cells, presumably because of the abolition of IL-23 responses (de Beaucoudrey et al., 2008, 2010). The proportion of IL-17A–producing T cells was also found to be low in a family with AR CARD9 deficiency, dermatophytosis, invasive candidiasis, and CMC (Glocker et al., 2009). Finally, CMC is the only infection in patients with autoimmune polyendocrinopathy syndrome type 1, who have high titers of neutralizing autoantibodies against IL-17A, IL-17F, and IL-22 (Kisand et al., 2010; Puel et al., 2010a). Thus, regardless of the underlying illness, CMC pathogenesis apparently involves the impairment of IL-17A, IL-17F, and IL-22 immunity (Puel et al., 2010b).

The pathogenesis of CMC was eventually deciphered through investigations of patients with CMC disease (CMCD), in which CMC is isolated, with no other infectious or autoimmune signs (Kirkpatrick, 2001; Puel et al., 2010b). The definition of CMCD is not absolute, as illustrated in some patients by cutaneous staphylococcal disease, which is milder than that in patients with AD hyper IgE syndrome (Herrod, 1990), or by autoimmune features affecting the thyroid in particular, although fewer such features are observed than in patients with autoimmune polyendocrinopathy syndrome type 1 (Atkinson et al., 2001). It is unclear whether CMCD, with these or other manifestations (Shama and Kirkpatrick, 1980; Bentur et al., 1991; Germain et al., 1994), is immunologically and genetically related to pure CMCD. Low proportions of IL-17A–producing T cells have been documented in five patients with CMCD (Eyerich et al., 2008). Moreover, a candidate gene approach centered on IL-17 immunity recently revealed the first genetic etiologies of pure CMCD. In a consanguineous family from Morocco, a child with CMCD was found to display AR complete IL-17RA deficiency (Puel et al., 2011). His leukocytes and fibroblasts did not respond to IL-17A or IL-17F homodimers, or to IL-17A/F heterodimers. Four patients from an Argentinean family were shown to harbor dominant-negative mutations in the *IL17F* gene (Puel et al., 2011). Mutated IL-17F–containing homodimers and heterodimers were produced in normal amounts but were not biologically active, as they were unable to bind to the IL-17 receptor. Morbid mutations in *IL17RA* and *IL17F* demonstrated that CMCD could be caused by inborn errors of IL-17 immunity. However, no genetic etiology has yet been identified for most patients with CMCD. We set out to identify new genetic etiologies of CMCD through a recently developed genome-wide approach based on whole-exome sequencing (Alcaïs et al., 2010; Bolze et al., 2010; Byun et al., 2010; Ng et al., 2010).

RESULTS

We investigated one sporadic case and the probands from five multiplex kindreds with AD CMCD, by whole-exome sequencing. The annotated data were analyzed with sequence analysis software that had been developed in-house and made it possible to analyze and compare several exome sequences simultaneously. A hierarchy of candidate variations was generated by filtering out known polymorphisms reported in dbSNP and 1,000-genome databases. We also used our own database of 250 exomes to filter out unreported polymorphisms (Table S1). The only relevant gene displaying heterozygous variations in at least four of the six unrelated patients with AD CMCD was *STAT1* (Fig. 1, A and B, Kindreds A, B, G, and L; Table I; and Table S2). Three different *STAT1* mutations were found in four patients; they were confirmed by Sanger

sequencing and shown to be missense mutations. All these mutations affected the coiled-coil domain, which plays a key role in unphosphorylated STAT1 dimerization and STAT1 nuclear dephosphorylation (Fig. 1, A and C; Chen et al., 1998; Levy and Darnell, 2002; Braunstein et al., 2003; Zhong et al., 2005; Hoshino et al., 2006; Mertens et al., 2006). We therefore sequenced the corresponding coding region of *STAT1* (exons 6 to 10) in another 106 patients, including 57 with sporadic CMCD and 49 from 22 multiplex kindreds with AD CMCD. 29 patients from 16 kindreds were heterozygous for a *STAT1* missense mutation (Fig. 1, A and B, Kindreds C-F, H-K, and M-T; Fig. 1 C; and Table I; Table S3). In total, 36 patients from 20 kindreds were heterozygous for 1 of the 12 missense mutations identified that affected the coiled-coil domain of STAT1. 11 other CMCD patients in these kindreds were not genotyped. The intrafamilial segregation of the mutations was consistent with an AD trait, as all patients with CMCD from the kindreds tested were heterozygous, whereas none of these mutations was found in the heterozygous state in any of the healthy relatives tested (Fig. 1 B). Moreover, the *STAT1* haplotypes for common SNPs indicated that the five recurrent mutations were caused by mutation hotspots rather than founder effects (unpublished data). Finally, the mutations were found to have occurred de novo in at least four kindreds, which is consistent with a high clinical penetrance of these alleles. The mutations were not found in the National Center for Biotechnology Information, Ensembl, and dbSNP databases. They were also absent from 1,052 controls from 52 ethnic groups in the Centre d'Etude du Polymorphisme Humain and Human Genome Diversity panels, suggesting that they were rare, CMCD-inducing variants rather than irrelevant polymorphisms.

The 12 missense mutations were not conservative and were therefore predicted to affect protein structure and function. Moreover, most of the affected residues were found to have been conserved throughout evolution in the species in which *STAT1* had been sequenced (Table S3). Accordingly, POLYphen II predicted that all but one of these mutations would be possibly or probably damaging (Adzhubei et al., 2010; Table S3). None of the previously described nine patients with AD STAT1 deficiency and MSMD was heterozygous for mutations affecting the coiled-coil domain (Fig. 1, A and C; Dupuis et al., 2001; Chapgier et al., 2006a; Averbuch et al., 2011; unpublished data). However, three of the eight patients with AR STAT1 deficiency and susceptibility to intracellular bacterial and viral diseases, who, like their heterozygous relatives, did not display CMC, carried mutations affecting the coiled-coil domain (Fig. 1, A and C; Chapgier et al., 2009; Chapgier et al., 2006b; Dupuis et al., 2003; Kong et al., 2010; Kristensen et al., 2011; Averbuch et al., 2011). These three patients from two kindreds carried the K201N or K211R mutation (Kong et al., 2010; Kristensen et al., 2011). Nevertheless, the three-dimensional structure of phosphorylated STAT1 molecules revealed that the 12 CMCD-linked missense mutations affected a cluster of residues located in a specific pocket of the coiled-coil domain, near residues essential for STAT1 dephosphorylation (Fig. 1 C; Chen et al., 1998; Zhong et al., 2005; Mertens et al., 2006). In contrast, the other two morbid mutations (K201N and K211R) affect residues located on the other side of the coiled-coil domain (Fig. 1 C). Moreover, these two hypomorphic alleles were shown to be pathogenic not because they were missense, but because they promoted the splicing out of exon 8, resulting in AR partial STAT1 deficiency, with the production of small amounts of intrinsically functional STAT1 molecules (Kong et al., 2010; Kristensen et al., 2011). These genetic data strongly suggest that heterozygous missense mutations in the coiled-coil domain of STAT1 may cause AD CMCD in a large fraction of patients. Nevertheless, the occurrence of other germline mutations in *STAT1* in patients without CMC and with an AD or AR predisposition to other infectious diseases raised questions about whether these mutations were really responsible for CMCD and the underlying mechanism of disease.

We functionally characterized the CMCD-causing *STAT1* allele R274Q, which was found in four kindreds (Fig. 1 B and Table I). We compared it with a WT and an MSMD-causing loss-of-function *STAT1* allele (L706S; Dupuis et al., 2001). We transfected STAT1-deficient U3C fibrosarcoma cells with WT, R274Q, or L706S *STAT1* alleles. Upon stimulation with IFN-α, IFN-γ, or IL-27, cells transfected with the R274Q allele responded two to three times more strongly than those transfected with the WT allele, as shown by measurement of the induction of γ-activated sequence (GAS)–dependent reporter gene transcription activity, with mock- and L706S-transfected cells serving as negative controls (Fig. 2 A and Fig. S1 A). All *STAT1* alleles were expressed at an equal strength, as shown by Western blotting (WB; Fig. 2 B). Higher levels of STAT1 phosphorylation were observed for the R274Q allele than for the WT allele after stimulation with IFN-γ, IFN-α, and IL-27, whereas STAT3 phosphorylation levels were similar for the two alleles (Fig. 2 B). In contrast, the induction of IFN-stimulated response element (ISRE)–dependent transcription activity by IFN-α was normal (Fig. S1, B and C). In the same experimental conditions, the other 10 CMCD-associated *STAT1* alleles tested were also gain-of-function, unlike the K201N and K211R alleles (Fig. S1 D). Upon stimulation with IFN-γ, IFN-α, or IL-27, an increase in GAS-binding activity was detected in cells transfected with the R274Q allele (Fig. S1 E). Accordingly, the transcription of the *CXCL9* and *CXCL10* target genes was enhanced (Fig. 2, C and D). Overall, these data indicate that at least 11 of the 12 CMCD-linked *STAT1* missense alleles are intrinsically gain-of-function.

The mechanism involved an increase in STAT1 tyrosine 701 residue phosphorylation, as shown for R274Q by WB after stimulation with IFN-α, IFN-γ, and IL-27 (Fig. 2 B). STAT1 was not constitutively activated, and STAT3 was normally activated in R274Q-transfected cells (Fig. 2 B and not depicted). Almost all the mutant STAT1 molecules, which were phosphorylated in response to IFN-γ, translocated to and accumulated in the nucleus, as shown by immunofluorescence (Fig. S1 F). WB showed R274Q STAT1 to be more

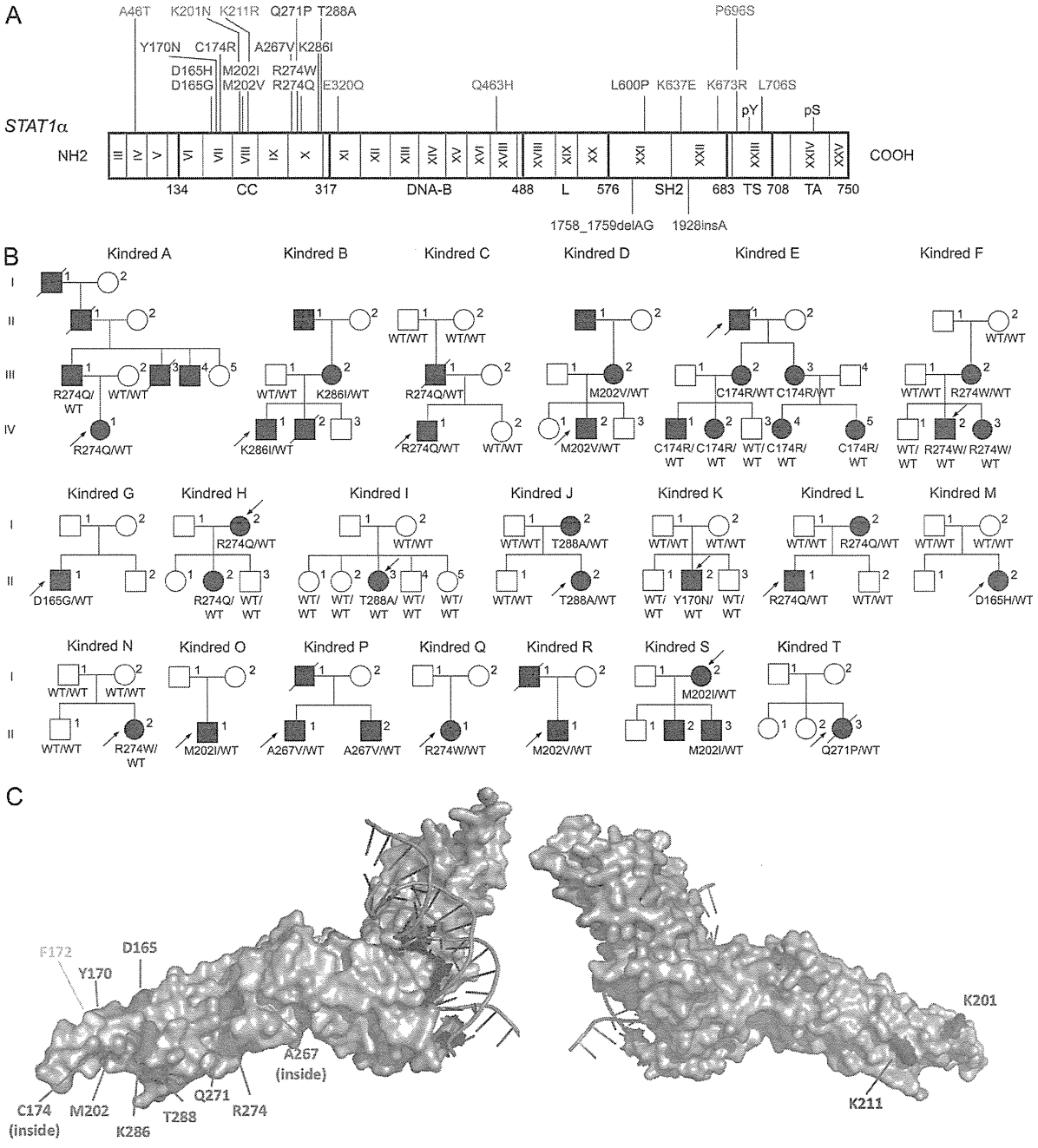

Figure 1. Heterozygous missense mutations affecting the STAT1 coiled-coil domain in kindreds with AD CMCD. (A) The human *STAT1* α isoform is shown, with its known pathogenic mutations. Coding exons are numbered with roman numerals and delimited by a vertical bar. Regions corresponding to the coiled-coil domain (CC), DNA-binding domain (DNA-B), linker domain (L), SH2 domain (SH2), tail segment domain (TS), and transactivator domain (TA) are indicated, together with their amino-acid boundaries, and are delimited by bold lines. Tyr701 (pY) and Ser727 (pS) are indicated. Mutations in green are dominant and associated with partial STAT1 deficiency and MSMD. Mutations in brown are recessive and associated with complete STAT1 deficiency and intracellular bacterial and viral disease. Mutations in blue are recessive and associated with partial STAT1 deficiency and intracellular bacterial and/or viral disease. Mutations in red are dominant and associated with a gain-of-function of STAT1 and CMCD. (B) Pedigrees of 20 families with AD "gain-of-function" *STAT1* mutations. Each kindred is designated by a letter (A to T), each generation is designated by a roman numeral (I-II-III-IV), and each individual is designated by an Arabic numeral (each individual studied is identified by a code of this type, organized from left to right). Black indicates CMCD patients. The probands are indicated by arrows. When tested, the genotype for *STAT1* is indicated below each individual. (C) Three-dimensional structure of phosphorylated STAT1 in complex with DNA. Connolly surface representation, with the following amino acids highlighted: red, amino acids mutated in patients with CMCD; blue, amino acids located in the coiled-coil domain and mutated in patients with MSMD and viral diseases; yellow, amino acids identified in vitro as affecting the dephosphorylation process.

Table I. Summary of the clinical and genetic data for the patients

Patient	Age at presentation	Origin	Clinical features of CMC	Cause of death (age/yr)	Autoimmunity	Genotype
A-I-1	-	France	Nails	Not related to the disease (old age)	None	-
A-II-1	-	France	Nails	Not related to the disease (old age)	None	-
A-III-1	1 mo	France	Nails, oral cavity, oropharynx, genital mucosa		None	WT/R274Q
A-III-3	-	France	Nails, oral cavity	Not related to the disease (40)	None	-
A-III-4	-	France	Nails, oral cavity		None	-
A-IV-1	1 mo	France	Nails, oral cavity, oropharynx		None	WT/R274Q
B-II-1	-	France	-		None	-
B-III-2	3 yr	France	Skin, nails, oral cavity, oropharynx, genital mucosa		None	WT/K286I
B-IV-1	5 yr	France & Congo	Skin, nails, oral cavity, oropharynx		None	WT/K286I
B-IV-2	5 mo	France & Congo	Skin, nails, oral cavity, oropharynx	Cerebral aneurysm (8)	None	-
C-III-1	-	Turkey	Nails, oral cavity, genital mucosa	Cerebral aneurysm (34)	Thyroid autoimmunity	WT/R274Q
C-IV-1	-	Turkey	Nails, oral cavity		None	WT/R274Q
D-II-1	-	France	Nails, oral cavity, genital mucosa		-	-
D-III-2	7 yr	France	Skin, oral cavity, oropharynx		None	WT/M202V
D-IV-2	1 mo	France	Skin, nails, oropharynx		Thyroid autoimmunity	WT/M202V
E-II-1	1 yr	Germany	Skin, oral cavity, oropharynx	Squamous cell carcinoma (54)	-	-
E-III-2	1 yr	Germany	Nails, oral cavity, oropharynx, genital mucosa		Thyroid autoimmunity	WT/C174R
E-III-3	9 mo	Germany	Skin, nails, oral cavity, oropharynx, genital mucosa		Thyroid autoimmunity	WT/C174R
E-IV-1	18 mo	Germany	Skin, oral cavity, oropharynx, genital mucosa		None	WT/C174R
E-IV-2	2 yr	Germany	Skin, oral cavity, oropharynx		Thyroid autoimmunity	WT/C174R
E-IV-4	2 yr	Germany	Skin, oral cavity, oropharynx, genital mucosa		None	WT/C174R
E-IV-5	1 yr	Germany	Skin, nails, oral cavity, oropharynx		None	WT/C174R
F-III-2	1 mo	Argentina	Nails, oral cavity, oropharynx, genital mucosa		-	WT/R274W
F-IV-2	1 mo	Argentina	Skin, nails, oral cavity, oropharynx		-	WT/R274W
F-IV-3	6 mo	Argentina	Nails, oral cavity, genital mucosa		-	WT/R274W
G-II-1	3 mo	Ukrainian	Nails, skin, oral cavity, oropharynx, esophagus		None	WT/D165G
H-I-2	1 yr	Japan	Skin, oropharynx, esophagus		-	WT/R274Q
H-II-2	5 yr	Japan	Oral cavity, oropharynx		-	WT/R274Q
I-II-3	9 mo	Mexico	Skin, nails, oral cavity, genital mucosa		None	WT/T288A
J-I-2	-	Switzerland	Oral cavity, oropharynx		None	WT/T288A
J-II-2	3 mo	Switzerland	Oral cavity, oropharynx		-	WT/T288A
K-II-2	11 mo	Switzerland	Nails, oral cavity, oropharynx		Thyroid autoimmunity	WT/Y170N
L-I-2	7 yr	France	Skin, nails, oropharynx, esophagus		Thyroid autoimmunity	WT/R274Q
L-II-1	1 mo	France	Skin, nails, oropharynx, esophagus		None	WT/R274Q
M-II-2	6 mo	Germany	Skin, nails, oropharynx, genital mucosa		Thyroid autoimmunity	WT/D165H

Table I. Summary of the clinical and genetic data for the patients *(Continued)*

Patient	Age at presentation	Origin	Clinical features of CMC	Cause of death (age/yr)	Autoimmunity	Genotype
N-II-2	1 yr	Germany	Skin, nails, oropharynx	Squamous cell carcinoma (54)	None	WT/R274W
O-II-1	18 mo	Germany	Oral cavity, oropharynx		None	WT/M202I
P-I-1	1 yr	Israel	Oropharynx, genital mucosa	Not related to the disease (46)	None	-
P-II-1	<2 yr	Israel	Skin, nails, oropharynx		None	WT/A267V
P-II-2	<2 yr	Israel	Skin, nails, oropharynx		None	WT/A267V
Q-II-1	1 mo	France	Skin, oral cavity, oropharynx, genital mucosa		None	WT/R274W
R-I-1	4 yr	France	Skin, nails, oropharynx	Squamous cell carcinoma (55)	None	-
R-II-1	18 mo	France	Lips, oropharynx		None	WT/M202V
S-I-2	6 mo	France	Skin, oral cavity, oropharynx		Systemic lupus erythematosus	WT/M202I
S-II-2	1 yr	France	Nails		None	-
S-II-3	1 mo	France	Skin, oropharynx		None	WT/M202I
T-II-3	1 yr	Germany	Skin, nails, oropharynx	Squamous cell carcinoma (41)	None	WT/Q271P

None of the patients displays autoantibodies against IL-17A, IL-17F, and IL-22. -, unknown.

strongly phosphorylated than the WT protein in both cytoplasmic and nuclear extracts (Fig. S1 G). The mechanism underlying the gain of R274Q phosphorylation was explored with the tyrosine kinase inhibitor staurosporine and the phosphatase inhibitor pervanadate. The dephosphorylation of IFN-γ–activated R274Q STAT1 was impaired by staurosporine, but less than that of the known dephosphorylation mutant F77A (Fig. 2 E; Zhong et al., 2005). In contrast, pervanadate normalized the phosphorylation of R274Q to WT levels (Fig. 2 F). Another CMCD-linked mutation, D165G (Fig. 1, A–C), also resulted in impaired dephosphorylation that could be normalized by adding pervanadate (Fig. 2 F and Fig. S1 H). Thus, at least two CMCD-linked *STAT1* missense alleles (R274Q and D165G) are gain-of-function caused by the impairment of nuclear dephosphorylation. These alleles may therefore enhance cellular responses to cytokines activating STAT1 predominantly and STAT3 to a lesser extent, such as IFN-α/β, IFN-γ, IFN-λ, and IL-27, and possibly also responses to cytokines activating STAT3 predominantly and STAT1 to a lesser extent, such as IL-6, IL-21, IL-22, and IL-23 (Fig. S2).

We investigated the dominance of the *STAT1* alleles at the cellular level by testing EBV-B–transformed (EBV-B) cells and SV-40–transformed dermal fibroblasts from a CMCD patient heterozygous for the *STAT1* R274Q allele. We observed enhanced IFN-α/β–, IFN-γ–, and IL-27–dependent STAT1 phosphorylation in EBV-B cells from a patient heterozygous for the *STAT1* R274Q allele, as shown by WB (Fig. 3, B and D). Phospho-STAT1 accumulated in the nucleus of R274Q heterozygous SV-40 fibroblasts upon IFN-γ stimulation, as well as in EBV-B cells (Fig. 3 I and Fig. S3 D). Moreover, the IFN-α/β–, IFN-γ–, and IL-27–induced DNA-binding activity of GAF was stronger in cells from the CMCD patient than in those from a healthy control or from a MSMD patient carrying the L706S mutant allele, as shown by electrophoretic mobility shift assay (EMSA; Fig. 3, A and C). In contrast, the DNA-binding activity of ISGF-3 seemed to be normal in cells from the patient stimulated with IFN-α/β (Fig. S3 A). These data strongly suggest that the heterozygous R274Q allele is dominant for STAT1-dependent responses and gain-of-function for GAF-dependent cellular responses to key STAT1-activating cytokines, such as IFN-α/β, IFN-γ, and IL-27. The mutation may also affect IFN-λ responses.

We then tested cytokines that predominantly activate STAT3, rather than STAT1, such as IL-6, IL-21, IL-22, and IL-23 (Hunter, 2005; Kishimoto, 2005; Kastelein et al., 2007; Spolski and Leonard, 2008; Donnelly et al., 2010; Sabat, 2010; Ouyang et al., 2011). Peripheral T cell blasts from a patient displayed normal STAT3 activation in response to IL-23, as shown by WB (Fig. S3 B). No increase in STAT1 phosphorylation was detected in cells from a patient or controls upon IL-23 stimulation. Furthermore, fibroblasts from a patient displayed normal activation of STAT3 in response to IL-22 (Fig. S3 C). In the same conditions, no STAT1 phosphorylation was detected in cells from the patient or controls (unpublished data). In contrast, the levels of STAT1 phosphorylation in response to IL-6 and IL-21 were higher in the patient's EBV-B cells than in cells from healthy controls and from a patient with MSMD heterozygous for the L706S allele, whereas STAT3 activation was normal as shown by WB (Fig. 3, F and H). Consistent with these findings, stronger GAS activity was observed in cells from the patient in response to IL-6 and IL-21 stimulation (Fig. 3, E and G). These data suggest that heterozygous missense mutations in the coiled-coil domain of STAT1 are dominant and gain-of-function for GAF-dependent cellular responses for cytokines that predominantly activate STAT3, such as IL-6 and IL-21. Overall, these data suggest that the *STAT1* alleles are truly responsible for CMCD in these kindreds and raise questions about the immunological basis of CMCD.

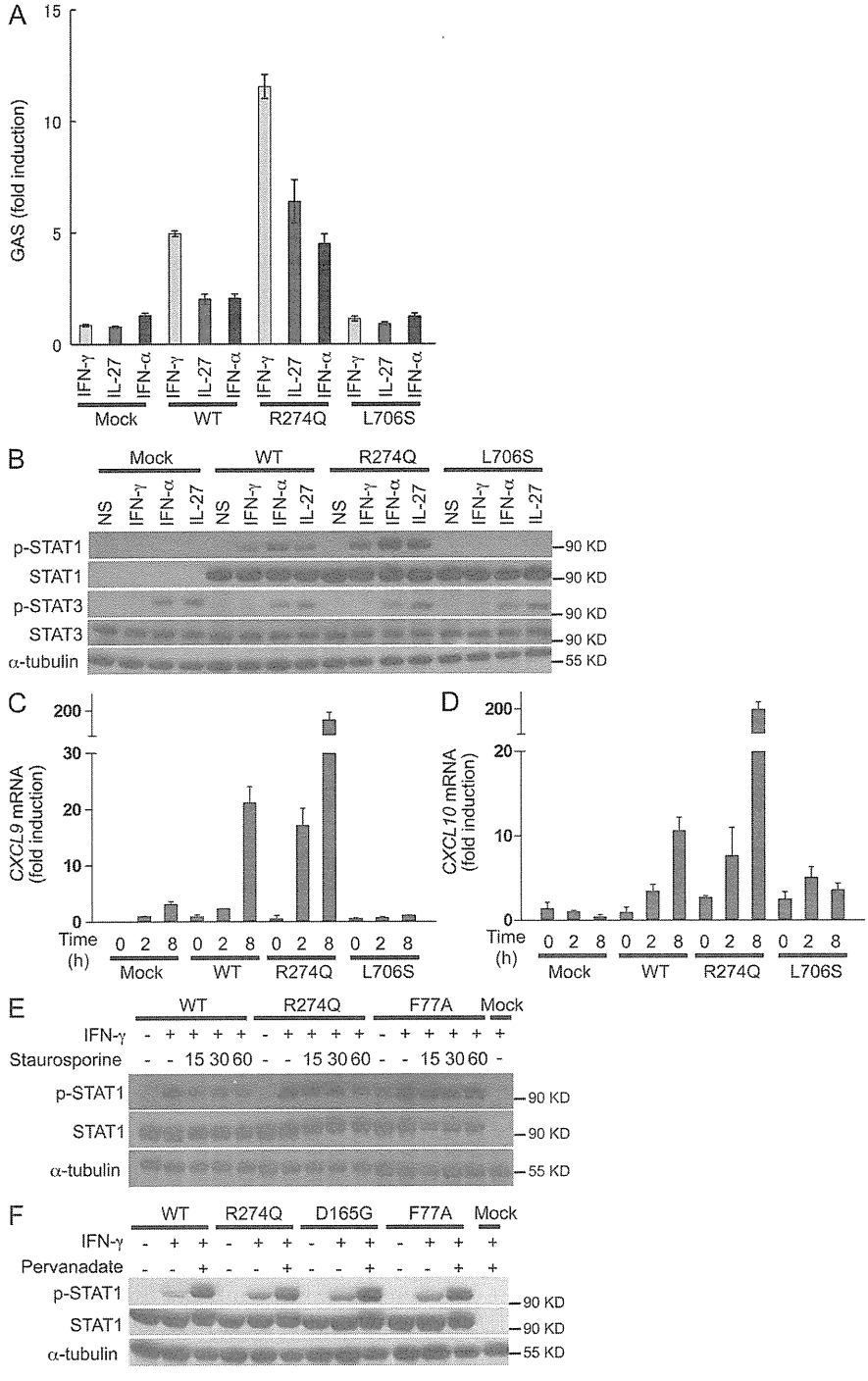

Figure 2. The mutant R274Q *STAT1* allele is gain-of-phosphorylation and gain-of-function for GAF-dependent cellular responses. U3C cells were transfected with a mock vector, a WT, or two mutant alleles of *STAT1* (R274Q and L706S). The response to IFN-γ, IL-27, and IFN-α was then evaluated by determining luciferase activity of a reporter gene under the control of the GAS promoter (A), and by determining STAT1 and STAT3 phosphorylation by Western blot (B). Experiments were performed at least three times independently. (C and D) Quantitative RT-PCR was used to measure the induction of *CXCL9* (C) and *CXCL10* (D) 2–8 h after stimulation with IFN-γ. Experiments were performed two times independently. (E) The nuclear dephosphorylation of STAT1 was tested by WB in U3C cells transfected with a mock vector, WT *STAT1*, the R274Q, or the F77A (a known loss-of-dephosphorylation mutant) *STAT1* mutant alleles, and treated with IFN-γ with or without the tyrosine kinase inhibitor staurosporine for the indicated periods of time (in minutes). Three independent experiments were performed. (F) Western blot of U3C cells transfected with mock, WT, R274Q, D165G, and F77A alleles of *STAT1*, nontreated or treated with IFN-γ in the absence or presence of the phosphatase inhibitor pervanadate. Two independent experiments were performed. Error bars represent SD of one experiment done in triplicate (Fig. S1 D).

IL-27 is a potent inhibitor of the development of IL-17–producing T cells in mice (Batten et al., 2006; Stumhofer et al., 2006; Yoshimura et al., 2006; Amadi-Obi et al., 2007; Diveu et al., 2009; El-behi et al., 2009; Villarino et al., 2010) and humans (Diveu et al., 2009; Liu and Rohowsky-Kochan, 2011), through a mechanism dependent on STAT1 (Amadi-Obi et al., 2007; Batten et al., 2006; Diveu et al., 2009; Liu and Rohowsky-Kochan, 2011; Stumhofer et al., 2006; Villarino et al., 2010). Moreover, mouse IFN-γ (Feng et al., 2008; Tanaka et al., 2008; Villarino et al., 2010) and human IFN-α/β (Chen et al., 2009; Ramgolam et al., 2009) have been shown to antagonize the development of IL-17–producing T cells via STAT1. In addition, IL-6, IL-21, and IL-23 are prominent inducers of IL-17–producing T cells, via a mechanism dependent on STAT3 and antagonized by STAT1 (Hirahara et al., 2010). Finally, we recently showed that inborn errors of IL-17F or IL-17RA were genetic etiologies of CMCD (Puel et al., 2010b, 2011). We thus determined the proportion of IL-17A– and IL-22–producing T cells by flow cytometry in patients with heterozygous *STAT1* mutations and AD CMCD. The 18 CMCD patients carrying gain-of-function mutations in *STAT1* that were tested had lower proportions of circulating IL-17A– and IL-22–producing T cells ex vivo than 28 healthy controls ($P < 10^{-4}$) and six patients bearing loss-of-function *STAT1* alleles ($P < 2.10^{-3}$; Fig. 4, A and B; and Fig. S4 G). In contrast, they displayed normal proportions of IFN-γ–producing T cells (Fig. S4 F).

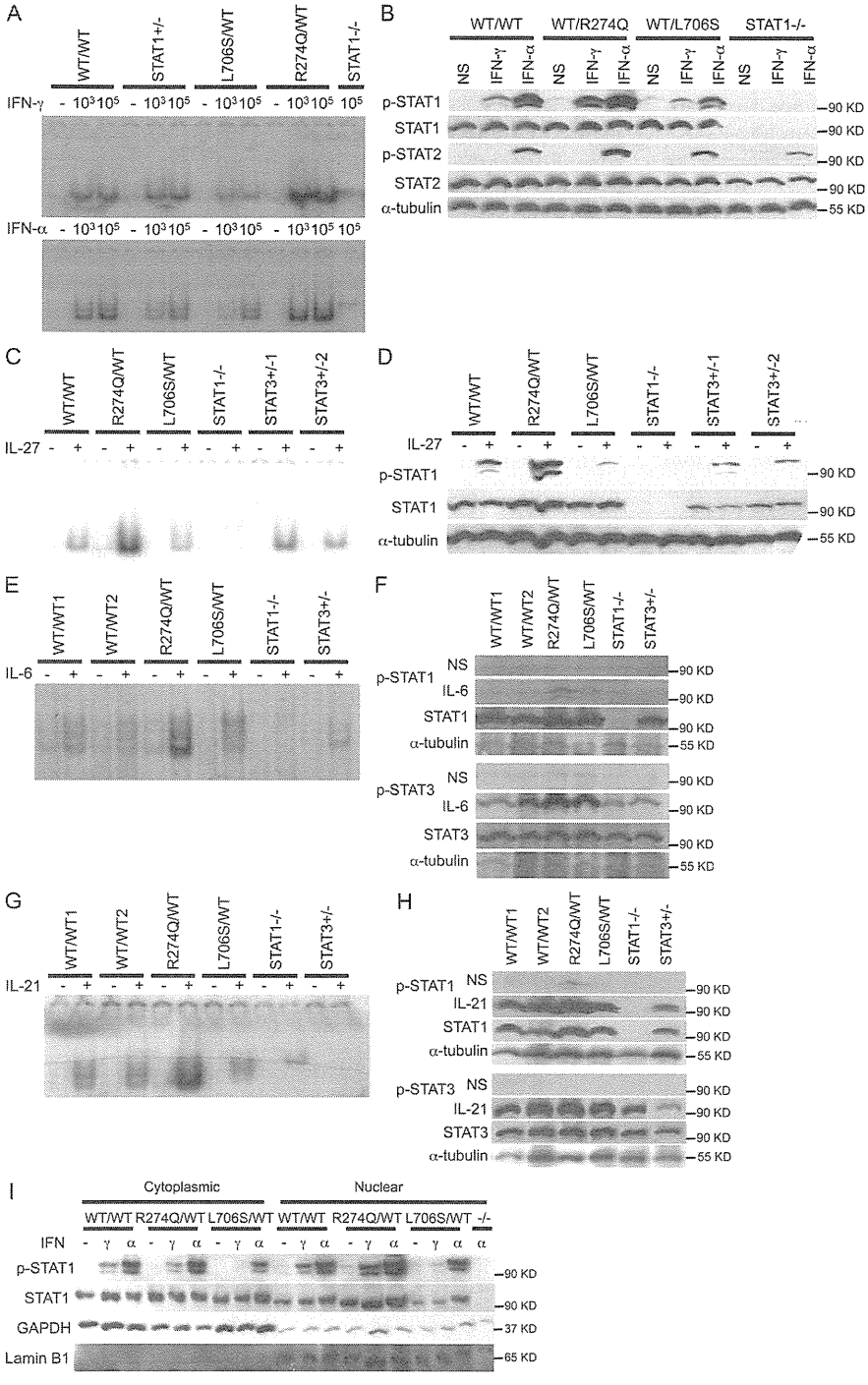

Figure 3. The mutant R274Q *STAT1* allele is dominant for GAF-dependent cellular responses at the cellular level. The responses of the patient's EBV-B cells (R274Q/WT) were evaluated independently at least twice, by EMSA, with a GAS probe (A, C, E, and G), and by Western blot (B, D, F, and H). This response was compared with that of one or two healthy controls (WT/WT1 and WT/WT2), heterozygous cells with a WT and a loss-of-function *STAT1* allele ($STAT1^{+/-}$), cells heterozygous for a dominant loss-of-function mutation of *STAT1* (L706S/WT), cells with complete STAT1 deficiency ($STAT1^{-/-}$), and cells from two patients heterozygous for dominant loss-of-function mutations of *STAT3* ($STAT3^{+/-1}$ and $STAT3^{+/-2}$). Cells were left nonstimulated (NS) or stimulated, as indicated, with IFN-γ, IFN-α, IL-27, IL-6, and IL-21. pSTAT is an antibody specific for STAT with a phosphorylated tyrosine residue. (I) The nuclear and cytoplasmic fractions of EBV-B cells from a control (WT/WT), a CMCD patient (R274Q/WT), a heterozygous patient with a dominant loss-of-function mutation of *STAT1* (L706S/WT) and a patient with complete STAT1 deficiency ($^{-/-}$) stimulated with IFN-γ and IFN-α were tested for the presence of phosphorylated STAT1 and STAT1 by WB. Antibodies directed against GAPDH and Lamin B1 were used to normalize the amount of cytoplasmic and nuclear proteins, respectively. The experiment was performed twice.

Moreover, only very small amounts of IL-17A, IL-17F, and IL-22 were secreted by freshly prepared leukocytes after ex vivo stimulation with PMA and ionomycin ($P < 8.10^{-3}$), as shown by ELISA (Fig. 4, C–E). In contrast, the amounts of secreted IL-17A, IL-17F, and IL-22 were normal in patients heterozygous or homozygous for loss-of-function or hypomorphic *STAT1* mutations (Fig. 4, C–E). Interestingly, in all assays, the proportions of IL-17A– and IL-22–producing T cells and the amounts of IL-17A, IL-17F, and IL-22 secreted were smallest for the four patients with the most apparently severe clinical phenotype (Fig. 4, A–E and not depicted).

After the culture of PBMCs in vitro in the presence of various cytokines, including IL-6, TGF-β, IL-1β, and IL-23, the proportion of IL-17A– and IL-22–producing T cell blasts remained significantly lower ($P < 10^{-4}$) in CMCD patients carrying *STAT1* mutations than in controls (Fig. S4, A and B; and not depicted). In contrast, the proportions of IL-17A– and IL-22–producing T cell blasts were normal in patients with loss-of-function *STAT1* mutations (Fig. S4, A and B; and not depicted). The amounts of IL-17A, IL-17F, and IL-22 in the supernatant of T cell blasts stimulated with PMA and ionomycin after culture in vitro were also significantly lower in patients with *STAT1* mutations and CMCD ($P < 4.10^{-4}$; Fig. S4, C–E; and not depicted). In contrast, patients with loss-of-function mutant *STAT1* alleles displayed normal levels of cytokine secretion (Fig. S4, C–E; and not depicted). Finally, levels of IL-12p70 and

IL-12p40 production by whole blood stimulated with IFN-γ were higher in CMCD patients bearing gain-of-function *STAT1* alleles than in patients bearing loss-of-function *STAT1* alleles and healthy controls (Fig. 4 F and not depicted). Thus, patients with familial or sporadic AD CMCD heterozygous for mutations affecting the coiled-coil domain of STAT1, including the dominant gain-of-function R274Q mutant allele, displayed lower levels of IL-17 cytokine production by peripheral T cells, providing a molecular mechanism for the disease.

DISCUSSION

We have shown that several germline missense mutations affecting the coiled-coil domain of STAT1 may cause sporadic and familial AD CMCD. The underlying mechanism involves a gain of STAT1 phosphorylation caused by the loss of nuclear dephosphorylation, resulting in a gain-of-function of GAF in response to various cytokines. Impaired dephosphorylation may not be the only mechanism influencing the impact of these mutations on the transcription of STAT1 target genes, as these mutations may also affect other processes, such as the dimerization of unphosphorylated STAT1. Moreover, the gain-of-function, which manifests itself in terms of DNA-binding activity, reporter gene induction, and target gene induction, may not necessarily increase the transcription of all target genes, possibly even resulting in the repression of some genes. In addition, the various *STAT1* mutations, although they all affect the coiled-coil domain and are probably all loss-of-dephosphorylation and gain-of-function, may somewhat differ from each other in terms of their functional impact. The genome-wide impact of these mutations on the transcriptome remains to be assessed in various cell types stimulated with a range of cytokines. In any case, the gain-of-function mutant *STAT1* alleles were dominant for GAF activation in all cell types tested. They affected cellular responses to various cytokines, including IFN-α/β, IFN-γ, and IL-27, which predominantly activate STAT1 over STAT3, and IL-6 and IL-21, which predominantly activate STAT3 over STAT1. These mutations probably also strengthen cellular responses to IFN-λ. However, they do not seem to affect STAT1-containing ISGF-3 activation by IFN-α/β, at least in the conditions tested. Moreover, STAT3 activation by IL-6, IL-21, IL-22, and IL-23 is maintained, suggesting that STAT3 activation by IL-26 is also intact.

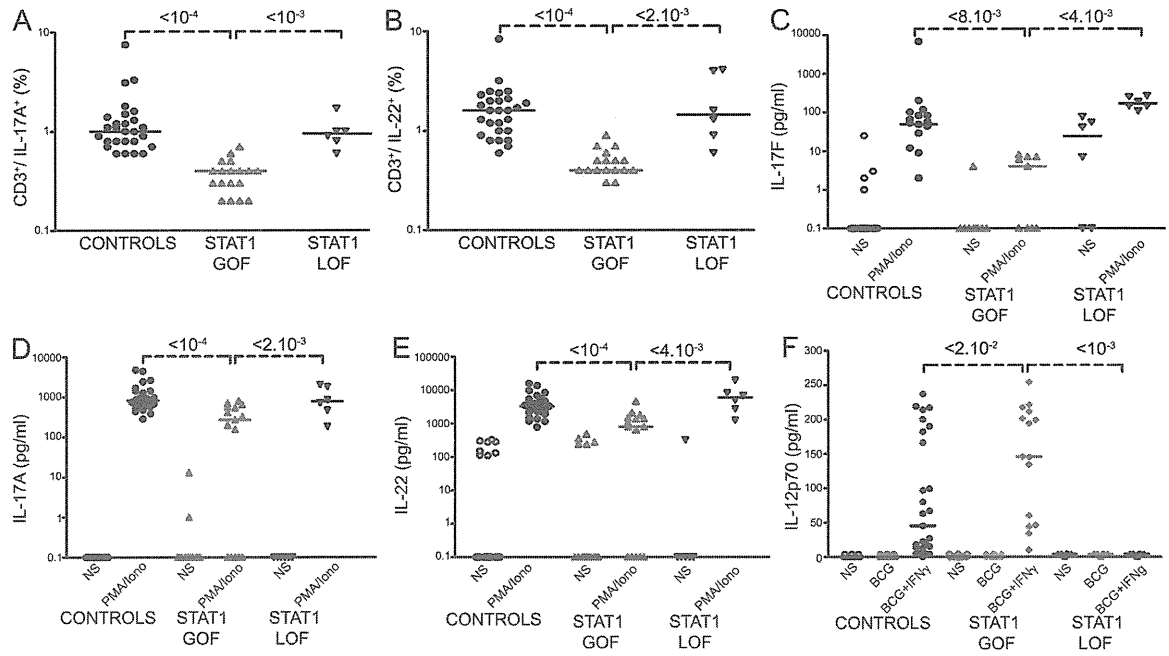

Figure 4. Impaired development and function of IL-17– and IL-22–producing T cells ex vivo in patients with AD CMCD and *STAT1* mutations. Each symbol represents a value from a healthy control individual (black circles), a patient bearing a *STAT1* gain-of-function (GOF) allele (red upright triangles), or a patient bearing one or two *STAT1* loss-of-function (LOF) alleles (black upside-down triangles). (A and B) Percentage of $CD3^+/IL\text{-}17A^+$ (A) and $CD3^+/IL\text{-}22^+$ (B) cells, as determined by flow cytometry, in nonadherent PBMCs activated by incubation for 12 h with PMA and ionomycin. (C–E) Secretion of IL-17F (C), IL-17A (D) and IL-22 (E) by whole blood cells, as determined by ELISA, in the absence of stimulation (open symbols) and after stimulation with PMA and ionomycin for 48 h (closed symbols). Horizontal bars represent medians. The p-values for the nonparametric Wilcoxon test, between patients with *STAT1* GOF mutations ($n = 18$) and controls ($n = 28$) and patients with *STAT1* LOF mutations ($n = 6$) are indicated. All differences between healthy controls and patients with *STAT1* LOF alleles were not significant. (F) Secretion of IL-12p70 by whole blood cells, as determined by ELISA, in the absence of stimulation (open symbols), after stimulation with BCG (lightly colored symbols), or BCG + IFN-γ for 48 h (closed symbols). Horizontal bars represent medians. The p-values for differences between patients with *STAT1* GOF mutations ($n = 15$) and controls ($n = 23$) and patients with *STAT1* LOF mutations ($n = 6$) are indicated and were calculated in nonparametric Wilcoxon tests. All experiments were performed at least two times independently.

The mutant *STAT1* alleles described herein enhance cellular responses to cytokines such as IFN-α/β, IFN-γ, and IL-27, which potently inhibit the development of IL-17–producing T cells via STAT1 (Batten et al., 2006; Yoshimura et al., 2006; Stumhofer et al., 2006; Amadi-Obi et al., 2007; Feng et al., 2008; Kimura et al., 2008; Tanaka et al., 2008; Chen et al., 2009; Ramgolam et al., 2009; Crabé et al., 2009; Diveu et al., 2009; El-behi et al., 2009; Guzzo et al., 2010; Villarino et al., 2010; Liu and Rohowsky-Kochan, 2011). These mutant alleles also increase cellular responses to IL-6 and IL-21, which normally induce IL-17–producing T cells via STAT3 rather than STAT1 (Hirahara et al., 2010). Enhanced STAT1-dependent cellular responses to these two groups of cytokines probably impair the development of IL-17–producing T cells. It remains unclear whether this mechanism predominantly involves IL-17–inhibiting cytokines (IFN-α/β, IFN-γ, and IL-27), either individually or in combination. The available data from the mouse model suggest that IL-27 is the most potent of the three inhibitors. There is also evidence that these cytokines inhibit IL-17–producing T cell development in humans (Ramgolam et al., 2009; Liu and Rohowsky-Kochan, 2011). Enhanced STAT1 and GAF activation in response to the IL-17 inducers IL-6 and IL-21, and perhaps IL-23, may also play a key role in disease, by antagonizing STAT3 responses. The effect of the aryl hydrocarbon receptor on IL-17 T cell development might also be enhanced by gain-of-function *STAT1* alleles (Kimura et al., 2008). Moreover, enhanced STAT1 activity downstream from IL-22 and IL-26 in cells, not detected in our study, might also contribute to the CMCD phenotype. Finally, thyroid autoimmunity in eight patients and systemic lupus erythematosus in another patient in our series probably resulted from the enhancement of IFN-α/β responses, as such autoimmunity is a frequent adverse effect of treatment with recombinant IFN-α or IFN-β (Oppenheim et al., 2004; Selmi et al., 2006). Importantly, no autoantibodies against IL-17A, IL-17F, or IL-22 were detected in the patients' serum (Table I and unpublished data).

Remarkably, germline mutations in human *STAT1* underlie susceptibility to three different types of infectious disease: mycobacterial diseases, viral diseases, and CMC. Patients bearing *STAT1* mutations and displaying mycobacterial and/or viral disease do not suffer from CMC, and the patients with CMCD caused by other *STAT1* alleles described here present no mycobacterial or viral disease. The pathogenic mechanisms involved are clearly different, with loss-of-function mutations in *STAT1* underlying mycobacterial and viral diseases (Dupuis et al., 2001, 2003; Chapgier et al., 2006b, 2009; Kong et al., 2010; Averbuch et al., 2011; Kristensen et al., 2011). Human AR STAT1 deficiency impairs cellular responses to IFN-α/β, IFN-γ, IFN-λ, and IL-27 (Dupuis et al., 2003; Chapgier et al., 2006b, 2009; Kong et al., 2010; Kristensen et al., 2011). Viral diseases probably result from impaired IFN-α/β and, perhaps, IFN-λ immunity, although impaired IFN-γ and IL-27 immunity may also contribute to the phenotype. Patients with AD MSMD, heterozygous for loss-of-function dominant-negative mutations of *STAT1*, suffer from mycobacterial disease caused by the impairment of IFN-γ immunity (Chapgier et al., 2006a; Dupuis et al., 2001). Overall, mutations impairing STAT1 function confer AD or AR susceptibility to intracellular agents, through the impairment of IFN-α/β (viral diseases) and/or IFN-γ immunity (mycobacterial diseases). In contrast, the gain-of-function *STAT1* mutations reported here confer AD CMCD because of the enhancement of STAT1-mediated cellular responses to STAT1-dependent repressors and STAT3-dependent inducers of IL-17–producing T cells. These studies neatly demonstrate that severe infectious diseases in otherwise healthy patients may be subject to genetic determinism (Casanova and Abel, 2005, 2007; Alcaïs et al., 2009, 2010). They also highlight the profoundly different effects that germline mutations in the same human gene may have, resulting in different infectious diseases through different molecular and cellular mechanisms.

MATERIALS AND METHODS

Massively parallel sequencing

DNA (3 µg) extracted from EBV-B cells from the patient was sheared with a S2 Ultrasonicator (Covaris). An adapter-ligated library was prepared with the Paired-End Genomic DNA Sample Prep kit (Illumina). The SureSelect Human All Exon kit (Agilent Technologies) was then used for exome capture. Single-end sequencing was performed on a Genome Analyzer IIx (Illumina), generating 72-base reads.

Sequence alignment, variant calling, and annotation

BWA aligner (Li and Durbin, 2009) was used to align the sequences obtained with the human genome reference sequence (hg18 build). Downstream processing was performed with the Genome analysis toolkit (GATK; McKenna et al., 2010), SAMtools (Li et al., 2009), and Picard Tools (http://picard.sourceforge.net). Substitution calls were made with a GATK UnifiedGenotyper, whereas indel calls were made with a GATK IndelGenotyperV2. All calls with a read coverage ≤2x and a Phred-scaled SNP quality of ≤20 were filtered out. All the variants were annotated with annotation software that was developed in-house. The data were further analyzed with sequence analysis software that had been developed in-house (SQL database query–driven system).

Molecular genetics

EBV-B cells and the STAT1-deficient cell line U3C were cultured as previously described (Chapgier et al., 2006a). Primary fibroblasts were cultured in DME supplemented with 10% fetal calf serum. Cells were stimulated with the indicated doses (in IU/ml or ng/ml) of IFN-γ (Imukin; Boehringer Ingelheim), IFN-α2b (IntronA; Schering-Plough), IL-27 (R&D Systems), IL-21 (R&D Systems), IL-22 (R&D Systems), IL-23 (R&D Systems), and IL-6 (R&D Systems). Genomic DNA and total RNA were extracted from cell lines and fresh blood cells, as previously described (Chapgier et al., 2006a). Genomic DNA was amplified with specific primers encompassing exons 6–10 of *STAT1* (available upon request), sequenced with the Big Dye Terminator cycle sequencing kit (Applied Biosystems), and analyzed on an ABI Prism 3730 (Applied Biosystems). We used the various alleles of *STAT1* in the pcDNA3 *STAT1*-V5 vector (Chapgier et al., 2006a; Kong et al., 2010). We generated the various *STAT1* mutations by site-directed mutagenesis (QuikChange Site-Directed Mutagenesis kit; Stratagene) with the mismatched primers listed in Table S4. U3C cells were harvested by trypsin treatment 24 h before transfection and replated at a density of 2.5×10^5 cells/ml in 6-well plates. Plasmid DNA (5 µg per plate) carrying the WT or all the various mutant *STAT1* alleles was used for cell transfection with the Calcium Phosphate Transfection kit (Invitrogen).

Luciferase reporter assay

U3C cells were dispensed into 96-well plates (1×10^4/well) and transfected with reporter plasmids (Cignal GAS and ISRE Reporter Assay kit;

SABiosciences) and plasmids carrying the various alleles of *STAT1* or a mock vector, in the presence of Lipofectamine LTX (Invitrogen). 6 h after transfection, the cells were transferred back into medium containing 10% FBS and cultured for 24 h. The transfectants were then stimulated with IFN-γ (500 and 1,000 IU/ml), IL-27 (20 and 100 ng/ml), and IFN-α (500, 1,000, and 5,000 IU/ml) for 16 h and subjected to luciferase assays with the Dual-Glo luciferase assay system (Promega). Experiments were performed in triplicate and firefly luciferase activity was normalized with respect to *Renilla* luciferase activity. The data are expressed as fold induction with respect to nonstimulated cells.

Immunoblot analysis and electrophoretic mobility shift assays

The following optimal stimulation conditions were used. EBV-B or U3C cells were stimulated by incubation for 20 min with 100 µg/ml IL-21 or 25 ng of IL-22; 30 min with 10^3 or 10^5 IU/ml IFN-γ and IFN-α; 15 min with 50 ng/ml IL-6; or 30 min with 50 or 100 ng/ml IL-27. WB was performed as previously described (Dupuis et al., 2003). In brief, cell activation was blocked with cold 1X PBS, cells were lysed in 1% NP-40 lysis buffer, and the proteins were recovered and subjected to SDS-PAGE. We used antibodies directed against phosphorylated STAT1 (pY701; BD), STAT1 (C-24; Santa Cruz Biotechnology), V5 (Invitrogen), α-tubulin (Santa Cruz Biotechnology), phosphorylated STAT3 (Cell Signaling Technology), lamin B1 (Santa Cruz Biotechnology), GAPDH (Santa Cruz Biotechnology), and STAT3 (Santa Cruz Biotechnology). EMSA was performed as previously described (Chapgier et al., 2006a). In brief, cell activation was blocked by incubation with cold 1X PBS, and the cells were gently lysed to remove cytoplasmic proteins while keeping the nucleus intact. We then added nuclear lysis buffer and recovered the nuclear proteins, which were subjected to nondenaturing electrophoresis with radiolabeled GAS (from the FCγR1 promoter: 5′-ATGTATTTCCCAGAAA-3′) and ISRE (from the ISG15 promoter: 5′-GATCGGGAAAGGGAAACCGAAACTGAA-3′) probes.

Staurosporine and pervanadate treatment of cells

We assessed dephosphorylation by stimulating U3C transfectants with 10^5 IU/ml IFN-γ. The cells were then washed and incubated with 1 µM staurosporine in DME for 15, 30, or 60 min. The cells were then lysed with 1% NP-40 lysis buffer, and the proteins recovered were subjected to immunoblot analysis.

Pervanadate was prepared by mixing orthovanadate with H_2O_2 for 15 min at 22°C. U3C transfectants were treated with pervanadate (0.8 mM orthovanadate and 0.2 mM H_2O_2) 5 min before stimulation. They were then stimulated with IFN-γ for 20 min. The stimulation was stopped by adding cold 1X PBS. The proteins were recovered and subjected to immunoblot analysis.

Extraction of nuclear and cytoplasmic proteins

U3C transfectants or EBV-B cells were stimulated with IFN-γ or IFN-α for 20 min and subjected to nuclear and cytoplasmic protein extraction with NE-PER Nuclear and Cytoplasmic Extraction Regents (Thermo Fisher Scientific) according to the manufacturer's protocol.

Immunofluorescence staining

Immunofluorescence experiments were performed as previously described (Chapgier et al., 2006a). In brief, cells (transfected U3C or SV-40 fibroblasts) were stimulated for the times indicated with 10,000 IU/ml of IFN-γ. Cells were then washed with cold PBS and fixed with 4% PFA. The cells were washed and incubated with an antibody against STAT1, which was then detected by incubation with an Alexa Fluor 488–conjugated anti–mouse antibody.

T cell blast differentiation and stimulation

PBMCs were recovered by centrifuging blood samples on Ficoll gradients, as previously described (Chapgier et al., 2006a). They were then cultivated, at a density of 1 million cells per ml in RPMI supplemented with 10% fetal calf serum and stimulated with phytohemagglutinin (1 µg/ml) for 3 d. Cells were then recovered, centrifuged on a Ficoll gradient, cultivated (at a density of 0.2 million cells/ml) to Panserin 401 supplemented with 10% FCS and glutamine 1X, and stimulated with 40 IU/ml IL-2 (Roche). Cells were then incubated for 30 min with 100 ng/ml IL-23. Activation was stopped by adding 1X cold PBS, and cells were processed for immunoblot analysis.

Modeling

Images of the three-dimensional structure of STAT1 (Chen et al., 1998) were generated with the 2002 PyMOL Molecular Graphics System (DeLano Scientific), using PDB accession no. 1BF5.

Whole-blood assay of the IL-12–IFN-γ circuit

Whole-blood assays were performed as previously described (Feinberg et al., 2004). Heparin-treated blood samples from healthy controls and patients were stimulated in vitro with live *Mycobacterium bovis* BCG (Pasteur) alone or with IFN-γ (5,000 IU/ml; Boehringer Ingelheim). Supernatants were collected after 48 h of stimulation, and ELISA were performed with specific antibodies directed against IL-12p40 or IL-12p70, using kits from R&D Systems according to the manufacturer's instructions.

Production of IL-17A, IL-17F, and IL-22 by leukocytes

Cell activation. IL-17A– and IL-22–producing T cells were evaluated by intracellular staining or by ELISA, as previously described (de Beaucoudrey et al., 2008). In brief, PBMCs were purified by centrifugation on a gradient (Ficoll-Paque PLUS; GE Healthcare) and resuspended in RPMI supplemented with 10% FBS (RPMI/10% FBS; Invitrogen). Adherent monocytes were removed from the PBMC preparation by incubation for 2 h at 37°C, under an atmosphere containing 5% CO_2.

For ex vivo evaluation of IL-17– and IL-22–producing T cells by flow cytometry, we resuspended 5×10^6 nonadherent cells in 5 ml RPMI/10% FBS in 25 cm^2 flasks and stimulated them by incubation with 40 ng/ml PMA (Sigma-Aldrich) and 10^{-5} M ionomycin (Sigma-Aldrich) in the presence of a secretion inhibitor (1 µl/ml GolgiPlug; BD) for 12 h.

For evaluation of the IL-17– and IL-22–producing T cell blasts after in vitro differentiation, the nonadherent PBMCs were dispensed into 24-well plates at a density of 2.5×10^6 cells/ml in RPMI/10% FBS and activated with 2 µg/ml of an antibody directed against CD3 (Orthoclone OKT3; Janssen-Cilag) alone, or together with 5 ng/ml TGF-β1 (240-B; R&D Systems), 20 ng/ml IL-23 (1290-IL; R&D Systems), 50 ng/ml IL-6 (206-IL; R&D Systems), 10 ng/ml IL-1β (201-LB; R&D Systems), or combinations of these four cytokines. After 3 d, the cells were restimulated in the same activation conditions, except that the anti-CD3 antibody was replaced with 40 IU/ml IL-2 (Proleukin i.v.; Chiron). We added 1 ml of the appropriate medium, resuspended the cells by gentle pipetting, and then split the cell suspension from each well into two. Flow cytometry was performed on one of the duplicated wells 2 d later, after stimulation by incubation for 12 h with 40 ng/ml PMA and 10^{-5} M ionomycin in the presence of 1 µl/ml GolgiPlug. FACS analysis was performed as described in the following section. The other duplicated well was split into two, with one half left unstimulated and the other stimulated by incubation with 40 ng/ml PMA and 10^{-5} M ionomycin for another 2 d. Supernatants were collected after 48 h of incubation, for ELISA.

Flow cytometry. Cells were washed in cold PBS, and surface labeling was achieved by incubating the cells with PECy5-conjugated anti–human CD3 antibody (BD) in PBS/2% FBS for 20 min on ice. Cells were then washed twice with 2% FBS in cold PBS, fixed by incubation with 100 µl of BD Cytofix for 30 min on ice, and washed twice with BD Cytoperm (Cytofix/Cytoperm Plus, fixation/permeabilization kit; BD). Cells were then incubated for 1 h on ice with Alexa Fluor 488–conjugated anti–human IL-17A (53–7179-42; eBioscience), PE-conjugated anti–human IL-22 (IC7821P; R&D Systems), or PE-conjugated anti–human IFN-γ (IC285P; R&D Systems) antibodies, washed twice with Cytoperm, and analyzed with a FACSCanto II system (BD).

ELISA. IL-17A, IL-17F, and IL-22 levels were determined by ELISA on the supernatants harvested after 48 h of whole-blood stimulation with 40 ng/ml PMA and 10^{-5} M ionomycin, or after in vitro PHA blast differentiation and