X-linked susceptibility to mycobacteria is caused by mutations in NEMO impairing CD40-dependent IL-12 production.


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Germline mutations in five autosomal genes involved in interleukin (IL)-12–dependent, interferon (IFN)–γ–mediated immunity cause Mendelian susceptibility to mycobacterial diseases (MSMD). The molecular basis of X-linked recessive (XR)–MSMD remains unknown. We report here mutations in the leucine zipper (LZ) domain of the NF-κB essential modulator (NEMO) gene in three unrelated kindreds with XR–MSMD. The mutant proteins were produced in normal amounts in blood and fibroblastic cells. However, the patients’ monocytes presented an intrinsic defect in T cell–dependent IL-12 production, resulting in defective IFN-γ secretion by T cells. IL-12 production was also impaired as the result of a specific defect in NEMO– and NF-κB/c-Rel–mediated CD40 signaling after the stimulation of monocytes and dendritic cells by CD40L–expressing T cells and fibroblasts, respectively. However, the CD40-dependent up-regulation of costimulatory molecules of dendritic cells and the proliferation and immunoglobulin class switch of B cells were normal. Moreover, the patients’ blood and fibroblastic cells responded to other NF-κB activators, such as tumor necrosis factor–α, IL-1β, and lipopolysaccharide. These two mutations in the NEMO LZ domain provide the first genetic etiology of XR–MSMD. They also demonstrate the importance of the T cell– and CD40L–triggered, CD40–, and NEMO/NF-κB/c-Rel–mediated induction of IL-12 by monocyte–derived cells for protective immunity to mycobacteria in humans.
Mendelian susceptibility to mycobacterial diseases (MSMD) (MIM 209950) is a congenital syndrome resulting in predisposition to clinical disease caused by weakly virulent mycobacterial species, such as BCG vaccines and nontuberculous, environmental mycobacteria (EM) (1–4). Patients are also susceptible to the more virulent species Mycobacterium tuberculosis (5). Diseases caused by nontyphoidal Salmonella serotypes have been observed in just under half the cases (4). Other infectious diseases have only rarely been reported, mostly in single patients. A few patients have suffered from viral infections, including cytomegalovirus and human herpes virus-8 infections, and others have had fungal infections with species such as Histoplasma capsulatum and Paracoccidioidomyces brasiliensis. MSMD was initially thought to be autosomal recessive in most, if not all kindreds, as a result of the high frequency of both multiple-case sibships and consanguineous kindreds (2, 3).

Figure 1. Clinical phenotypes and NEMO genotypes of patients. (A) Pedigrees of three kindreds with NEMO mutations (A, B, and C). Each generation is designated by a Roman numeral, and each individual is designated by an Arabic numeral. Male patients (in black squares) present mycobacterial infections and hemizygous NEMO mutations; asymptomatic female carriers are represented by black dots. The probands are indicated by arrows. (B) The teeth of patient P1 (Kindred A, II.4, sparse teeth), patient P2 (Kindred B, II.1, conical decidual incisors), and patient P3 (Kindred C, II.1, normal teeth). (C) Sequence electrophoregram of NEMO complementary DNA in the region corresponding to the mutation. Kindred A, P1 presents the mutation A→C leading to the replacement at residue 315 of Glu (E) by Ala (A) (E315A). Kindred B, P2 and kindred C, P3 present the mutation G→A resulting in the replacement of an Arg (R) at position 319 by Gln (Q) (R319Q). (D) Schematic representation of the NEMO coding region, from exons 2 to 10, and corresponding domains, shown in dark gray: the coil-coiled domain 1 (CC1, Leu 93 to Gln 194) and coil-coiled domain 2 (CC2, Met 258 to Lys 292), and the leucine zipper (LZ, Tyr 308 to Lys 344) and zinc finger (ZF, Cys 397 to Cys 417) domains. All published hypomorphic NEMO mutations (associated with the various forms of EDA-ID) are represented (reference 43). Missense and nonsense mutations (amino-acid code) are shown on top, whereas splice and frameshift mutations (nucleotide code) are shown on the bottom. NEMO mutations in red represent mutations associated with mycobacterial infections.
After the identification in 1996 of germline mutations in *IFNGR1*, encoding the IFN-γ receptor ligand-binding chain (IFN-γR1) (6, 7), recessive mutations were reported in three other autosomal genes: *IFNGR2*, encoding the accessory chain of the IFN-γ receptor (8); *IL12B*, encoding the p40 subunit shared by IL-12 and IL-23 (9); and *IL12RB1*, encoding the β1 chain shared by the receptors for IL-12 and IL-23 (10, 11). Defects in *IFNGR1* and IFNGR2 are associated with impaired cellular responses to IFN-γ, whereas defects in *IL12B* and *IL12RB1* are associated with impaired IFN-γ production. Allelic heterogeneity at these four loci accounts for the existence of nine autosomal recessive disorders. After the identification of complete defects in which no protein is expressed (6–8, 10, 11), partial forms of IFN-γR1 (12) and IFN-γR2 (13) deficiency and complete forms of IFN-γR1 (14), IFN-γR2 (15), and IL-12Rβ1 (16) deficiency with surface receptor expression were identified.

The identification of MSMD-causing recessive alleles in these four autosomal genes led to the discovery of an autosomal dominant form of MSMD, caused by dominant-negative mutations in *IFNGR1* (17). The mutant alleles exert a dominant-negative effect as the result of overexpression, at the cell surface, of truncated chains that cannot transduce signals. Dominant mutations in *STAT1*, another autosomal gene encoding the signal transducer and transactivator of transcription 1 (Stat-1), were subsequently identified (18). There are two forms of partial Stat-1 deficiency, depending on whether the mutation impairs the phosphorylation of Tyr 701 (18) or DNA-binding activity (unpublished data). The two forms of partial Stat-1 deficiency are associated with MSMD because these mutations affect the activation of IFN-γ–induced Stat-1 homodimers, but not of IFN-α/β–induced Stat-1–Stat-2–IRF-9 trimers, in heterozygous cells. A dominant-negative mutant allele of *IFNGR2* has also been identified, resulting in the aberrant subcellular distribution of IFN-γR2, as the result of a mutation affecting the transmembrane domain (19).

In one family first reported in 1991, and more extensively in 1994, it was suggested that MSMD might display X-linked recessive inheritance (1, 20–22). Four maternally related male patients were found to suffer from severe EM disease. These patients’ monocytes were found to be intrinsically unable to produce normal levels of IL-12 upon stimulation by PHA and T cells (21, 22). Despite the identification of this immunological phenotype, the molecular basis of XR-MSMD has remained elusive. We report here the identification of MSMD-causing *NEMO* mutations in this kindred and in two other, unrelated kindreds. These mutations do not affect NF-κB activation in response to most classical activators tested, accounting for the narrow spectrum of infections in patients. The two NF-κB essential modulator (NEMO) mutations identified selectively impair the CD40-triggered and NF-κB/c-Rel–mediated induction of IL-12 production by monocytes and monocyte-derived dendritic cells, accounting for the susceptibility to mycobacteria.

RESULTS

**New germline mutations in NEMO in three kindreds**

We studied an American multiplex kindred, a French kindred, and a German kindred, each containing one male patient with sporadic mycobacterial disease (Fig. 1 A). None of the six patients in these kindreds displayed the classical developmental and infectious features of anhidrotic ectodermal dysplasia with immunodeficiency (EDA-ID) (23–25). Conical incisors in one proband (P2, kindred B, Fig. 1 B) and in a second patient (patient III.8, kindred A) nevertheless led us to study the X-linked EDA-ID–causing *NEMO* gene (26) (unpublished data). New mutations were found in the coding region of *NEMO* in the three probands (Fig. 1 C). P1 from kindred A presented a nucleotide substitution at position 944 (A→C) (Fig. 1 C, left), leading to the replacement of a Glu by an Ala at residue 315 (E315A) (Fig. 1 D). P2 and P3 from kindreds B and C, respectively, presented a nucleotide substitution at position 956 (G→A) (Fig. 1, C and D).
and right) resulting in the replacement of an Arg by a Gln at position 319 (R319Q) (Fig. 1 D). The two mutations were detected in cDNAs, indicating that they corresponded to NEMO and not the nearby NEMO pseudogene (27). These mutations were not found in 800 unrelated healthy controls (1,200 X chromosomes) from 51 ethnic groups (HGDP-CEPH database). The familial segregation of NEMO in kindred A was consistent with linkage between the observed syndrome and this gene (unpublished data). The heterozygous grandmother (I.1), and three other women in kindred A (II.3, III.2, III.10), like the mother of P2 in kindred B (I.1) and the mother of P3 in kindred C (I.1), were obligate carriers, but displayed no signs of incontinentia pigmenti or EDA (unpublished data). These data suggest that these three unrelated families suffer from XR-MSMD as the result of missense mutations in NEMO.

Modeling of the molecular environment of the E315 and R319 residues

Amino acids E315 and R319 are both located within the leucine zipper (LZ) domain of NEMO (Fig. 1 D). Several studies have shown that NEMO self-assembles into trimers (28, 29). The minimal oligomerization domain of the protein consists of the CC2 and LZ coiled-coil motifs, and we recently suggested that these motifs interact to form a pseudo-six-helix bundle, in which the LZ \( \alpha \)-helices dock in the crevices defined by two of the helices of the central trimeric CC2 coiled-coil (Fig. 2 A) (30). A similar scaffold was described for the HIV-1 gp41 protein (31). We therefore modeled the NEMO trimeric CC2-LZ domain based on the X-ray structure of the gp41 ectodomain (Fig. 2 B). In our model, the E315 and R319 residues, located in the middle of the LZ domain, face the interior of the coiled coil assembly. The environment of the two residues is shown in greater detail in Fig. 2 C. E315 and R319 probably form an intramolecular salt bridge stabilizing the LZ \( \alpha \)-helix. Other amino acids located in the vicinity of these residues in the model are also shown, including K277, from the same NEMO subunit, and Q278 from the CC2 motif of an adjacent subunit, which probably interact via a hydrogen bond. The E315A and R319Q mutations found in XR-MSMD patients would break the predicted salt bridge and might induce local plasticity in the LZ helices of the NEMO trimer. Within the highly structured CC2-LZ trimer, this might also result in local modifications to interactions with the central CC2 domains. Our structural model therefore also provides a rationale for the remarkable similarity and narrowness of the clinical phenotypes of the patients described, with NEMO mutations disrupting a common salt bridge in the LZ domain.

Normal expression of NEMO protein in blood cells and fibroblasts

We assessed NEMO expression by Western blotting extracts of EBV-transformed B cells and SV40-transformed fibroblasts with p18 and 3328 antibodies, which recognize the N-terminal region of NEMO. The mutant proteins, E315A (P1) (not depicted) and R319Q (P2), were expressed in similar amounts to wild-type NEMO in EBV-transformed B cells (Fig. 3 A). The R319Q protein was also expressed in normal amounts in SV40-transformed fibroblasts from P2 (Fig. 3 B). Cell lines from P3 (R319Q) and fibroblasts from P1 (E315A) were not available. The NEMO X420W mutant, which causes the most severe form of EDA-ID (24), with osteopetrosis and lymphoedema (OL-EDA-ID), was detected only in trace amounts, at a higher molecular weight, on Western blots of EBV-transformed B cells and SV40-transformed fibroblasts (Fig. 3, A and B). As a negative control (C--), no NEMO was detected in SV40-transformed fibroblasts (Fig. 3, A and B). The NEMO X420W mutant, which causes the most severe form of EDA-ID (24), with osteopetrosis and lymphoedema (OL-EDA-ID), was detected only in trace amounts, at a higher molecular weight, on Western blots of EBV-transformed B cells and SV40-transformed fibroblasts (Fig. 3, A and B). As a negative control (C--), no NEMO was detected in SV40-transformed fibroblasts bearing a large amorphic deletion in NEMO (27). We assessed intracellular NEMO expression by flow cytometry, using antibody 278–396, which recognizes the C-terminal region of NEMO (32). NEMO was normally
expressed in EBV-transformed B cells (P1, P2) and SV40-transformed fibroblasts (P2) from the patients, taking seven and five control cell lines, respectively, as a reference, but not in fibroblasts bearing a large deletion in NEMO (Fig. 3, C and D). NEMO was barely detectable in EBV-transformed B cells and SV40-transformed fibroblasts from the patient with OL-EDA-ID. The intracellular expression of NEMO was also normal in freshly isolated monocytes and T cells from P2 (Fig. 3E). Thus, levels of NEMO expression were strictly normal in patients bearing the E315A and R319Q mutations as shown by Western blotting and flow cytometry in hematopoietic and nonhematopoietic cell lines and in freshly prepared blood cells.

**Response of blood cells and fibroblasts to LPS, R-848, TNF-α, and IL-1β**

NEMO mutations in patients with EDA-ID are usually associated with impaired cellular responses to multiple stimuli, including LPS (via TLR-4), TNF-α, and IL-1β (24, 25). We thus stimulated whole blood cells from the patients and
10 healthy controls with LPS, TNF-α, IL-1β, and PMA/ionomycin, and measured the induction of IL-6 (unpublished data), IL-10, and TNF-α. The three patients displayed normal levels of IL-10 (Fig. 4 A), IL-6, and TNF-α (not depicted) production upon stimulation with LPS, IL-1β, and PMA plus ionomycin. IL-10 was also induced by TNF-α in P2 and P3, although to lower levels (Fig. 4 A). EBV-transformed B cells from P2 responded normally to R-848, an agonist of TLR-7/8, in terms of TNF-α production (Fig. 4 B). We then assessed the impact of NEMO mutations in fibroblasts from P2, a NEMO-deficient fibroblastic cell line bearing a large NEMO deletion, and fibroblasts from nine healthy controls. Fibroblasts from P2 produced normal amounts of IL-6 and IL-8 in response to both IL-1β and TNF-α (Fig. 4 C). In contrast, fibroblasts from all EDA-ID patients tested, bearing other NEMO mutations, showed various levels of impairment of IL-6 and IL-8 production (unpublished data). We assessed IkBα cytoplasmic degradation by Western blotting and the IkB-binding activity of nuclear extracts by electrophoretic mobility shift assays. In contrast with what was observed in fibroblasts from the OL-EDA-ID patient bearing NEMO mutation X420W (24), both IkBα degradation and IkBα binding activity were completely normal in fibroblasts from P2 (Fig. 4 D). Thus, the NEMO–NF-κB signaling pathway in response to TLR-4, 7, and 8 agonists, IL-1β, and TNF-α, was normal in SV40-fibroblastic and EBV-transformed B cell lines from our patients.

**Impaired production of IL-12 and IFN-γ by peripheral blood mononuclear cells upon PHA activation**

We previously reported that PBMCs from P1 produced small amounts of IFN-γ upon stimulation with PHA (21, 22). PBMCs from P2 and P3 produced normal amounts of IFN-γ in response to PMA/ionomycin but not in response to PHA or CD3 stimulation, with normal levels determined as those in response to PMA/ionomycin and BCG. Overall, the cellular phenotype of impaired IL-12–dependent production of IFN-γ by PHA-stimulated PBMCs is suggestive of a common pathogenic mechanism of predisposition to mycobacterial disease associated with NEMO mutations E315A and R319Q.

**Impaired IL-12 secretion by PHA-stimulated monocytes and T cells**

We previously described a specific defect in IL-12 production by P1 monocytes upon PHA stimulation in the presence of control T cells (21, 22). We tested cells from P2 and P3 in a similar coculture assay and measured the production of IL-12p70, IL-12p40, and IFN-γ by ELISA (Fig. 6 A). These cytokines were produced in very small amounts or not at all in monocytes stimulated with PHA in the absence of T cells or in T cells in the absence of monocytes. P2 and P3 monocytes cocultured with autologous or healthy T cells produced much less IL-12p70, IL-12p40, and IFN-γ than control monocytes cocultured with autologous, P2, or P3 T cells. The T lymphocytes of these patients produced IFN-γ after costimulation with control monocytes and PHA. The low levels of IFN-γ secretion were the result of poor IL-12 production as indicated by (a) the complementation provided by recombinant IL-12 (but not IL-23) (unpublished data) and (b) the poor production of IFN-γ documented with IL-12p40–deficient monocytes or IL-12Rβ1–deficient monocytes.
cytokines secreted by T cells and monocytes (TNF-α, IL-12, and IFN-γ, respectively) were impaired in the PHA-activated system, and the result obtained was compared with the reference value (C/C). The production of *MCP-1 and *MIP-1β by monocytes was PHA-dependent but cell-independent, as monocytes responded to PHA by producing large amounts of these cytokines, whereas the addition of T cells did not increase cytokine production. The defects in the production of IL-6, IL-12p70, G-CSF, IFN-γ, and MCP-1 were confirmed in three independent experiments on blood cells from P2 and one experiment on blood from P3.

Figure 6. IL-12 and IFN-γ production by cocultured monocytes and T cells from the patients studied and healthy controls.
(A) IL-12p70, IL-12p40, and IFN-γ production, measured using classical sandwich ELISA, in a mixture of purified monocytes and T cells, as indicated upon stimulation with PHA. The results shown are representative of three independent experiments for P2 and one for P3. (B) The same coculture supernatants were analyzed for a multiplex of 16 cytokines, using the Bioplex array. Each column represents the data for one monocyte–T cell coculture system, and all four columns correspond to the same experiment. Each row corresponds to one cytokine. The gray-scale bar indicates the magnitude of cytokine expression, using the control/control (C/C) coculture system as a reference. For each data point, the amount of cytokine produced in the unstimulated system was subtracted from that produced in the PHA-activated system, and the result obtained was compared with the reference value (C/C). The production of *MCP-1 and *MIP-1β by monocytes was PHA-dependent but cell-independent, as monocytes responded to PHA by producing large amounts of these cytokines, whereas the addition of T cells did not increase cytokine production. The defects in the production of IL-6, IL-12p70, G-CSF, IFN-γ, and MCP-1 were confirmed in three independent experiments on blood cells from P2 and one experiment on blood from P3.

T cells (unpublished data). Certain monokines, such as IL-6, G-CSF, and MCP-1, were poorly induced, whereas others were induced in normal (IL-4, IL-10) or large (IL-5, IL-13) amounts by monocytes from P2 and P3, indicating that these cells were not globally unresponsive (Fig. 6 B and not depicted). Two other lymphokines (IL-2, IL-4) were not affected and the production of IL-17 was impaired. Finally, cytokines secreted by T cells and monocytes (TNF-α, IL-7, IL-10, and GM-CSF) were normally induced. All three probands had a specific immunological phenotype in which IL-12 production by monocytes in response to PHA and T cells was affected. Impaired IFN-γ production does not reflect an intrinsic T cell defect and is instead a consequence of impaired IL-12 production by monocytes.

PHA-activated T cell–dependent monocyte secretion of IL-12 is driven by CD40
The two NEMO mutations exerted their effects downstream from monocyte receptors triggering the induction of IL-12. The CD40 signaling pathway has been shown to be critical for the T cell–dependent induction of IL-12 in monocytes and dendritic cells (34–37). After PHA stimulation, PBMCs from CD40L- and CD40L-deficient patients (38) produced much lower levels of IL-12 and IFN-γ than did PBMCs from 10 healthy controls (unpublished data), consistent with previous data (39). The induction of IL-12 by LPS and that of IFN-γ by PMA/ ionomycin were normal (unpublished data). IL-12 induction was abolished if CD40L-deficient T cells were cocultured with healthy or CD40L-deficient monocytes, resulting in low levels but not the total absence of IFN-γ production (Fig. 7 A). Conversely, normal IL-12 induction was observed if control or CD40L-deficient monocytes were mixed with T lymphocytes from a healthy donor. Low levels of IFN-γ induction were associated with the presence of small amounts of IL-12 in this assay. IL-12 induction was abolished if CD40-deficient monocytes were incubated with CD40-deficient or normal T cells (Fig. 7 B). Paradoxically, IFN-γ secretion was not significantly impaired, perhaps reflecting the direct cross-linking of CD40L by PHA (40). In contrast, control monocytes produced normal amounts of IL-12 when cultured with control or CD40-deficient T cells. Our findings for the monocyte–T cell coculture assay unambiguously indicate that the engagement of the monocyte CD40 by CD40L-expressing T cells is required for the optimal induction of IL-12 production. These data suggest that the NEMO mutations in P1, P2, and P3 were pathogenic as a result of their impact on CD40 signaling within monocytes, leading to low levels of IL-12 secretion upon T cell stimulation.

NEMO mutation impairs CD40 signaling in dendritic cells but not B cells
We assessed the responses to CD40 stimulation of cells from our patients. We first incubated purified monocytes from P2 with mouse fibroblastic L cells (L-cells) and L-cells stably transfected with a construct encoding human CD40L (L-cells-hCD40L). Monocytes from P2 did not produce IL-12, IL-6, and TNF-α upon stimulation with L-cells-hCD40L (unpublished data). We then tested monocyte-derived dendritic cells (MDDCs) as DCs are major producers of IL-12 in vivo. MDDCs produce large amounts of IL-12 upon CD40 stimulation in vitro (36). MDDCs from P2 and P3 were activated with LPS plus IL-1β, L-cells, or L-cells-hCD40L with or without IL-1β. MDDCs from P2 and P3 displayed severely impaired cytokine production in response to L-cells-hCD40L but not in response to LPS plus IL-1β (Fig. 7 C), whereas induction of the costimulatory molecules
CD80 and CD86, unlike that of CD40, was maintained (Fig. 7 D). These data are consistent with our previous observations in a child with a severe NEMO mutation associated with OL-EDA-ID and severe mycobacterial infection (24). MDDCs from P2 and P3 expressed normal levels of NEMO (Fig. 7 E). B cells from P2 produced normal amounts of IgE in response to costimulation with IL-4 and CD40L, as shown by ELISA, with data from 20 healthy controls and a CD40-deficient patient used as a reference (Fig. 7 F). Moreover, B cell proliferation, as assessed by the measurement of [3H]thymidine incorporation, was also normal (unpublished data). These data suggest that the CD40 signaling pathway was not affected in B cells in vitro, consistent with the normal B cell switch and antibody response in vivo in our patients. Altogether, these findings suggest that the patients with XR-MSMD bearing the E315A and R319Q mutations in NEMO suffered from mycobacterial disease as a result of the impaired IL-12 production by monocytes and dendritic cells after stimulation with the CD40L on T cells.

Delayed nuclear accumulation of NF-κB/c-Rel in CD40-stimulated dendritic cells

We evaluated the impact of the NEMO mutations identified by confocal microscopy analysis of the subcellular distributions of NF-κB/c-Rel.
of the NF-κB subunits RelA (p65) and c-Rel in MDDCs from P2 and a healthy control, unstimulated and in response to LPS, IL-1β, TNF-α, mouse L-cells, or human L-cells expressing mouse L-cells. LPS treatment resulted in the nuclear accumulation of RelA and c-Rel in MDDCs from both the healthy control and P2 (Fig. 8 A). IL-1β induced the translocation of RelA, but not of c-Rel, in MDDCs from both the healthy donor and P2 (unpublished data). The nuclear translocation of RelA in response to TNF-α seemed to be less efficient in MDDCs from P2 (Fig. 8 A), possibly accounting for the weak induction of IL-10 in PBMCs (Fig. 4 A). The translocation of RelA in response to CD40 stimulation was normal in MDDCs from P2 up to 8 h after stimulation (Fig. 8 B). In contrast, the nuclear accumulation of c-Rel in response to CD40 was clearly impaired in MDDCs from P2, 2 (Fig. 8 B) and 5 h after stimulation (not depicted). Only after 8 h of stimulation was c-Rel accumulation detected in the nuclei of MDDCs from P2 (Fig. 8 B). These data strongly suggest that the NEMO mutation identified in P2 impairs CD40-triggered NF-κB activation by delaying the nuclear accumulation of c-Rel. They also suggest that CD40-driven, NEMO-dependent IL-12 production in human MDDCs depends on c-Rel, as previously shown in mice (41, 42). Furthermore, our data indicate that the R319Q and E315A mutations in the NEMO LZ domain are associated with XR-MSMD because they impair the T cell-dependent, CD40-triggered, NF-κB/c-Rel-mediated induction of IL-12 in monocytes and dendritic cells (Fig. 8 C).
DISCUSSION

We describe here the first genetic etiology of XR-MSMD, a syndrome clinically defined for the first time in 1994 in a multiplex American kindred (1, 21), after the publication of individual case reports (20). The four patients from this family carried the E315A mutation in NEMO. XR-MSMD is not limited to a single family, as a different, but related NEMO mutation, R319Q, was found in two unrelated European boys, from France and Germany. NEMO is the sixth MSMD-causing gene to be identified, after the identification of IFNGR1 in 1996 (6, 7), IFNGR2, IL12B, and IL12RB1 in 1998 (8–11), and STAT1 in 2001 (18) (Fig. 8 C). It is the sixth genetic defect associated with MSMD but the 13th genetic etiology of this syndrome, given the considerable allelic heterogeneity of previously reported defects of the IL-12–IFN-γ circuit (15) (unpublished data). One of our patients with EM disease (II.4 in kindred A) also suffered from miliary tuberculosis in childhood, and two of our probands (P2 and P3) probably suffered from tuberculosis, as the sole infectious phenotype suggested by consistent histological results and strongly positive tuberculin skin tests. Patients with BCG and EM diseases and otherwise healthy children with severe tuberculosis should therefore be investigated for NEMO mutations (5). The possibility of NEMO mutations cannot be excluded by the absence of developmental signs, as shown in four of our six patients and in two other recently reported patients (43).

We can now suggest a rationale for the pathogenesis of mycobacterial diseases in patients with XR-MSMD. The two causal NEMO mutations impair CD40 signaling in monocytes and dendritic cells, delaying the nuclear accumulation of NF-κB/c-Rel and impairing IL-12 secretion upon stimulation by CD40L-expressing T cells. In turn, impaired IL-12 production by antigen-presenting cells results in impaired IFN-γ production by T cells. X-linked NEMO is thus physiologically connected to the five autosomal IL-12/23–IFN-γ circuit genes known to cause MSMD (4). These data are consistent with the observation that CD40-deficient (44) and CD40L-depleted mice (45) are susceptible to Mycobacterium avium infections. CD40L-deficient mice are also susceptible to BCG and CD40-deficient mice are susceptible to Mycobacterium tuberculosis (46, 47). Moreover, CD40L-deficient patients frequently develop localized disease caused by BCG, and severe tuberculosis (5, 48). However, human CD40 and CD40L are not recognized as bona fide MSMD-causing genes, as CD40- and CD40L-deficient patients have never been reported to suffer from disseminated BCG or EM disease. This implies that pathways other than CD40–NEMO–IL-12, such as the TNF-α signaling pathway (Figs. 4 A and 8 A) (49), are probably involved in the pathogenesis of diseases caused by EM, at least, in patients with mutations in the NEMO LZ domain. In any event, human phagocytes and dendritic cells require T cell stimulation via CD40, NEMO, and c-Rel to produce the amounts of IL-12 necessary to control mycobacteria in natural conditions of infection (50).

Null mutations in NEMO are lethal in utero in male fetuses (27). Patients with hypomorphic mutations in NEMO suffer from XR-EDA-ID (23–26). To date, 36 patients bearing 28 different NEMO mutations have been described (23–27, 32, 43, 51–55) (unpublished data). 11 out of the known 36 XR-EDA-ID patients have developed severe mycobacterial infection, mostly caused by M. avium. However, these patients also suffered from infections caused by many other microorganisms. In contrast, five of our six patients presented mycobacterial disease as their sole invasive infection. The invasive Haemophilus influenzae b infection in one of our patients may not have occurred by chance. Similarly, two out of the six patients had conical incisors (decidual teeth in one and permanent teeth in the other), implying that the penetrance of these particular NEMO genotypes was low (but not null) for pyogenic infections and developmental defects, but high for mycobacterial disease. Our report stresses the heterogeneity of phenotypes associated with hypomorphic NEMO mutations. Two patients with XR-EDA-ID, both with the X420W genotype, presented XR-OL-EDA-ID (24, 53, 54). Most patients present the less severe clinical syndrome of XR-EDA-ID, with typical (23–25) or hidden (conical incisors) (26) developmental signs and multiple infections. Two other patients with severe infections but no developmental disorder were recently reported (43). Finally, we report here two novel NEMO mutations, responsible for MSMD in six patients. All six patients are selectively susceptible to mycobacteria and display selective impairment of the CD40-dependent induction of IL-12 in antigen-presenting cells. These findings provide the first link between a NEMO genotype and immunological and infectious phenotypes.

Why do these two mutations have selective effects? The E315A and R319Q mutations are located in the LZ domain of NEMO and do not affect protein expression. Residues E315 and R319 probably form a salt bridge that is disrupted by the two pathogenic mutations (Fig. 2 C). The two mutations may induce local plasticity in a region of the LZ domain critical for signaling via CD40, but less important for other signaling pathways. However, CD40 signaling was not totally abolished in dendritic cells from our patients, as the nuclear accumulation of RelA, and the induction of CD80 and CD86 were normal, whereas the induction of CD40 was not. These findings are consistent with the normal CD40-mediated induction of HLA-II and CD86 previously reported in dendritic cells from a patient with OL-EDA-ID (24). It is unknown whether the CD40–CD80/86 and CD40–HLA-II pathways are truly NEMO independent or whether they are unaffected by the NEMO mutations tested. The E315A and R319Q NEMO mutations impair at least one CD40 signaling pathway involving NF-κB–c-Rel in monocytes and dendritic cells, but they have no significant effect on B cells, in vivo and in vitro, unlike other previously reported NEMO mutations (24, 25, 52, 55). In conclusion, specific NEMO mutations may selectively target the CD40–NF-κB–c-Rel signaling pathway in monocytes and dendritic
cells, preventing the production of sufficient quantities of IL-12 after T cell stimulation. This results in impaired IFN-γ–mediated immunity and predisposition to mycobacterial diseases (Fig. 8 C).

MATERIALS AND METHODS

Case reports. The first family (kindred A) with XR-MSMD has been described elsewhere (1, 20–22). None of the family members were vaccinated with BCG. Severe M. avium infection was documented in four materially related male family members in two successive generations (Fig. 1 A; patients II.1, II.4, III.7, and III.8). The clinical features of patient 1 (P1, II.4), the index case, have been described elsewhere (1, 20). In brief, at the age of 13 yr, P1 presented granulomatous cutaneous lesions, thought to be sarcoid.

Extensive erosive lesions on the face and arm were subsequently found to be the result of M. avium complex infection. Treatment with rifampicin, ethambutol, clofazimine,isoniazid and streptomycin was initiated. After 2.5 yr of therapy, smears and cultures of skin from the patient’s face and arm remained positive for M. avium complex X cluster. Intensive antibiotic and IFN-γ therapy has led to periods in which the skin has healed and cultures have tested negative, but this patient has frequently displayed intermittent mycobacteremia over the last 10 yr. Three other family members also developed disseminated M. avium complex infection. Patient II.1 was cured of miliary tuberculosis at the age of 6 yr. Disseminated M. avium infection occurred in this patient at the age of 40 yr, and was never completely eradicated. The patient died of E. coli bacteraemia complicating parenteral nutrition at the age of 48 yr. Patient III.7 was successfully treated for disseminated M. avium infection at the age of 5 yr, but died in an automobile accident at the age of 10. His brother, patient III.8, had recurrent Haemophilus influenzae bacteraemia at the age of 6 yr. At the age of 14 yr, he presented disseminated M. avium complex infection involving abdominal lymph nodes and blood. Overt signs of eczematous dysplasia (conical teeth, hypodontia, hypotrichosis, abnormal hair whorl) were evaluated. This patient has remained mycobacteremic despite treatment with multiple antibiotics and IFN-γ. Sparse teeth were the only development abnormality on physical examination, and long went unrecognized in patient 1 (Fig. 1 B, left). Cells of the various blood lineages and lymphoid subsets (CD3, CD4, CD8, CD20, CD16, CD56) were present in normal numbers. T cells proliferated normally in vitro in response to mitogenic (PHA) and antigenic (recall antigens) stimulation. In P1, serum levels of Ig isotypes (IgG, IgM, IgA, IgE, IgD) were normal for age, and there was a normal Ab response to protein antigens. There were no allo-hemagglutinins (group A). The patient had detectable, but very low titers of antibodies against polyclonal antibodies at the age of 11 yr, before vaccination. After vaccination with 23-valent nonconjugated vaccine at the age of 11 yr, titers rose and reached normal levels.

Mutations in the five known MSMD-causing autosomal genes (IFNγR1, IFNγR2, STAT1, IL12B, IL12RB1) were excluded in the three kindreds by means of genetic and immunological assays (unpublished data). Other patients with well-defined genetic defects were enrolled in our study, including patients with IL-12p40 deficiency, IL-12Rβ1 deficiency, IFN-γR1 deficiency, CD40 deficiency, and CD40L deficiency. Their genetic lesions are available upon request. Our study was conducted according to the principles expressed in the Helsinki Declaration and was approved by our Institutional Review Boards. An informed consent was provided by all patients studied, or by their parents, in the case of children.

Blood cell culture and stimulation. Whole blood samples were diluted 1/2 in RPMI 1640 (GIBCO BRL) and infected by incubation with live M. bovis BCG (Pasteur strain), at a multiplicity of infection of 20:1, alone or with coinfectant IFN-γ (5,000 IU/ml; Innokin, Boehringer Ingelheim) or recombinant IL-12p70 (20 ng/ml; R&D Systems). LPS (from Salmonella minnesota, 1 μg/ml; Sigma-Aldrich), TNF-α (20 ng/ml; R&D Systems), IL-1β (10 ng/ml; R&D Systems), phorbol 12-myristate 13-acetate (PMA) (10−7 M; Sigma-Aldrich) with ionomycin (10−3 M; Sigma-Aldrich) and supernatants were recovered after 14 and 48 h. Cytokine production was normalized according to the number of PBMCs in the individual tested. PBMCs were obtained from patients and healthy donors by centrifuging heparin-treated blood diluted 1/2 in RPMI 1640 on Ficoll-Paque Plus (GE Healthcare), followed by isolation in mononuclear cell medium. PBMCs were cultured in
RPNI 1640 medium (GIBCO BRL) supplemented with 10% heat-inactivated pooled FBS (GIBCO BRL), referred to as complete RPMI 1640. Cells (106 PBMCs/ml-well) were activated by incubation with phytohemagglutinin-P 1/700 (PHA, Becto PHA-P; Becton Dickinson), alone or in combination with recombinant IFN-γ (5,000 IU/ml; Imukin, Boehringer Ingelheim) or recombinant IL-12p70 (20 ng/ml; R&D System) or IL-23 (20 ng/ml; R&D Systems), anti-CD3 antibody (10 ng/ml, OKT3, OrthoPharmaceutical) and LPS (from Salmonella minnesota, 1 μg/ml; Sigma-Aldrich) for 14 and 48 h.

Culture and stimulation of cell lines. Fibroblast cell lines were derived from dermal biopsy samples from patients and healthy donors and immortalized by transformation with a plasmid-containing SV40 large T antigen. We added 105 fibroblasts to DMEM (GIBCO BRL) supplemented with 10% (vol/vol) heat-inactivated FBS (GIBCO BRL) in each well of a 24-well plate. Fibroblasts were stimulated with TNF-α (20 ng/ml; R&D Systems), IL-1β (10 ng/ml; R&D Systems), or PMA (10−7 M; Sigma-Aldrich) plus ionomycin (10−9 M; Sigma-Aldrich) and supernatants were analyzed on a 3100 ABI Prism Genetic Anaizaler (Applied Biosystems). Sequencing products were purified on Sephadex G-50 Superfine resin (GE Healthcare) by centrifugation through Sephadex G-50 Superfine resin. Primer sequences for the amplification of exons and cDNA are available upon request. PCR products were purified using a Qiaquick PCR Purification kit (Qiagen). Genomic DNA was isolated by phenol/chloroform extraction from blood cells, which were washed in TE 10:1 buffer (10 mM Tris, 1 mM EDTA, pH 7.4) and lysed in extraction buffer (10 mM Tris, 0.1 M EDTA, 0.5% SDS, and 10 mg/ml proteinase K) overnight at 37°C. RNA was extracted from EBV-transformed B cell lines or SV40-transformed fibroblasts with TRIzol (Invitrogen), according to the kit manufacturer’s instructions. We used 1–5 μg total RNA for direct reverse transcription with Oligo-dT (Invitrogen). PCR was performed using Taq polymerase (Invitrogen), and the GeneAmp PCR System 9700 (Applied Biosystems). Primer sequences for the amplification of NEMO exons and cDNA are available upon request. PCR products were purified by centrifugation through Sephadex G-50 Superfine resin (GE Healthcare) and electrotransfered onto nitrocellulose membranes (Schleicher & Schuell). Membranes were blocked by incubation in 5% nonfat milk powder (Nestle USA) in 0.05% Tween-20 in PBS for 60 min at room temperature. NEMO was detected using rabbit polyclonal anti-NEMO antibodies (332B and p18, gifts from G. Courtois, INSERM, Saint Louis Hospital, Paris, France), rabbit antibodies against GAPDH (25778, Santa Cruz Biotechnology, Inc.), rabbit anti-IκBα (C-21, sc-37, Santa Cruz Biotechnology, Inc.), and mouse antibodies against Stat-3 (Santa Cruz Biotechnology, Inc.). Membranes were washed several times in 0.05% Tween-20 in PBS, and antibody binding was detected by incubation with horseradish peroxidase-conjugated anti-rabbit secondary antibodies (GE Healthcare), using the ECL system (GE Healthcare).

Purification of peripheral T cells and monocytes. For T cell isolation, we depleted peripheral PBMCs of adherent cells and performed negative immunomagnetic depletion using a cocktail of antibodies against CD14, CD16, CD19, CD36, CD56, CD123, and glycoherpin A (Macles; Miltenyi Biotec), according to the kit manufacturer’s instructions. The preparation was >95% pure, as assessed by flow cytometry with FITC-CD2 and PE-CD3 staining (BD Biosciences). Monocytes were isolated from peripheral PBMCs by negative immunomagnetic depletion, using a cocktail of antibodies against CD3, CD7, CD16, CD19, CD56, CD123, and glycoherpin A (Macles; Miltenyi Biotec), according to the kit manufacturer’s instructions. Monocytes were >80% pure, as assessed by flow cytometry with PE-CD14 (BD Biosciences) staining.

Coculture of monocytes and T cells. We plated 106 monocytes per well in complete RPMI 1640 medium in 24-well plates (Nunc) and incubated them for 3 h at 37°C in an atmosphere containing 5% CO₂. The nonadherent cells were washed off and the adherent cells were incubated overnight with 400 μl of complete RPMI 1640. The following day, T cells were purified as described in a previous paragraph and 5 × 105 T cells were added to the monocytes. Selected wells were stimulated with a 1/700 dilution of PHA (Becto PHA-P; Becton Dickinson), alone or in combination with recombinant IFN-γ (5,000 IU/ml; Imukin, Boehringer Ingelheim, France), recombinant IL-12p70 (20 ng/ml; R&D Systems), and recombinant IL-23 (20 ng/ml; R&D Systems). Supernatants were collected 14 and 48 h after activation.

Generation of dendritic cells from purified monocytes. MDDCs were obtained from purified monocytes as described in a previous paragraph. They were incubated for 2 h in complete RPMI 1640 medium at 37°C under an atmosphere containing 5% CO₂ to remove all nonadherent cells, thereby increasing purity. The adherent cells were cultured in complete RPMI 1640 in the presence of GM-CSF (50 ng/ml; R&D Systems) and IL-4 (10 ng/ml; R&D Systems). Optimal conditions were maintained by splitting these cultures every 2 d. Cells were collected on day 7, when the cultures contained >95% immature CD1a+ (BD Biosciences) dendritic cells.

CD40 activation. Mouse fibroblastic L-cells transfected with the human ligand of CD40 (L-cell-hCD40L) were used to induce CD40 activation on MDDCs. Nontransfected L-cells were used for control cultures. L-cells were first treated with 10 μg/ml mitomycin (Sigma-Aldrich) in sterile 1 × PBS for 2 h at 37°C in 5% CO₂. L-cells were washed five to seven times in 1 × PBS to remove all trace of mitomycin. We then plated 105 L-cells per well in 24-well plates and incubated them for 2 d in complete RPMI 1640 at 37°C in an atmosphere containing 5% CO₂. We incubated 2 × 106 MDDCs in complete RPMI 1640 with mitomycin-treated L-cells and recovered cell-free supernatants for cytokine analysis and MDDCs for cell surface phenotyping of CD40, CD80, and CD86 (BD Biosciences) by flow cytometry 24 h later. CD40 was activated on B cells with a mixture of soluble recombinant CD40L (500 ng/ml; Amgen) and IL-4 (100 IU/ml; R&D Systems). In brief, PBMCs were cultured for 5 d for proliferation (assayed by [3H]thymidine incorporation) assays and 12 d for the measurement of IgG production (assayed by ELISA) as previously described (43).

Flow cytometry. For the staining of NEMO in EBV-transformed B cells, fibroblastic cell lines, and highly purified monocytes and T cells isolated from PBMCs, we fixed 2 × 105 cells with 4% paraformaldehyde (PFA, Fluka) in 1 × PBS and permeabilized the cells by incubation in 0.1% saponin (Sigma-Aldrich) in PBS. The cells were incubated with anti-NEMO (611306; BD Biosciences) antibody and the corresponding mouse IgG1 isotype (BD Biosciences), and primary antibody binding was detected by incubation with Alexa Fluor 488-labeled anti-mouse antibodies (Invitrogen). Cell surface phenotyping was performed by flow cytometry, in MDDCs incubated with L-cell or L-cell-hCD40L, using directly labeled antibodies. Dual-color fluorescence assays were performed with PE-CD1a

Genetic analysis. Genomic DNA was isolated by phenol/chloroform extraction from blood cells, which were washed in TE 10:1 buffer (10 mM Tris, 1 mM EDTA, pH 7.6) and lysed in extraction buffer (10 mM Tris, 0.1 M EDTA, 0.5% SDS, and 10 mg/ml proteinase K) overnight at 37°C. RNA was extracted from EBV-transformed B cell lines or SV40-transformed fibroblasts with TRIzol (Invitrogen), according to the kit manufacturer’s instructions. We used 1–5 μg total RNA for direct reverse transcription with Oligo-dT (Invitrogen). PCR was performed using Taq polymerase (Invitrogen), and the GeneAmp PCR System 9700 (Applied Biosystems). Primer sequences for the amplification of NEMO exons and cDNA are available upon request. PCR products were purified by centrifugation through Sephadex G-50 Superfine resin (GE Healthcare) and electrotransfered onto nitrocellulose membranes (Schleicher & Schuell). Membranes were blocked by incubation in 5% nonfat milk powder (Nestle USA) in 0.05% Tween-20 in PBS for 60 min at room temperature. NEMO was detected using rabbit polyclonal anti-NEMO antibodies (332B and p18, gifts from G. Courtois, INSERM, Saint Louis Hospital, Paris, France), rabbit antibodies against GAPDH (SC-25778, Santa Cruz Biotechnology, Inc.), rabbit anti-IκBα (C-21, sc-37, Santa Cruz Biotechnology, Inc.), and mouse antibodies against Stat-3 (Santa Cruz Biotechnology, Inc.). Membranes were washed several times in 0.05% Tween-20 in PBS, and antibody binding was detected by incubation with horseradish peroxidase-conjugated anti-rabbit secondary antibodies (GE Healthcare), using the ECL system (GE Healthcare).
(BD Biosciences) in combination with FITC-CD40, FITC-CD80, and FITC-CD86 (all from BD Biosciences). The respective isotype controls were performed with mouse PE-IgG1 (BD Biosciences) and mouse FITC-IgG1 (BD Biosciences). Fluorescence was analyzed with a FACSscan apparatus (Becton Dickinson), using CELLQuest software.

Cytokine analysis. Cytokine concentrations in supernatants were measured by two-sided sandwich ELISA, according to the kit manufacturer's instructions: IL-12p40, IL-12p70, G-CSF (R&D Systems), and TNF-α. Cytokine analysis was performed on culture supernatants, using a cocktail of 17 cytokines: IL-1β, IL-2, IL-4, IL-5, IL-6, IL-8 (Sanquin). Multiplex cytokine assays were also performed on culture supernatants, using a cocktail of 17 cytokines: IL-1β, IL-2, IL-4, IL-5, IL-6, IL-7, IL-8, IL-10, IL-12p70, IL-13, IL-17, TNF-α, IFN-γ, GM-CSF, G-CSF, MCP-1, and MIP-1β (Bio-Plex Suspension Array System).

Structural modeling of the NEMO oligomerization domain. The NEMO sequence encompassing the CC2-LZ region is not >30% of identity to any reference protein in the Protein Data Bank. We therefore used experimental data to search for comparable structure references. The NEMO oligomerization domain forms a globular trimer by equilibrium sedimentation with a hydrodynamic radius of 26.1 Å, as shown by gel filtration (30) and dynamic light scattering (unpublished data), and the CC2 and LZ coiled-coil subdomains interact by fluorescence polarization (30). Limited proteolysis in combination with mass spectrometry identified a tryptic-sensitive site at residue Lys302, coinciding with the loop connecting the CC2 and LZ coiled-coils (unpublished data). Finally, the CD spectrum of the trimer showed it to contain 92% α-helix at 277 K (unpublished data). Based on these data, we used the HIV-1 gp120 ectodomain (PDB no. 1F23; reference 31) as a structure reference to provide atomic coordinates. The trimeric CC2-LZ domain of NEMO was modeled using the Insight II program (Accelrys, Inc.). The model was constructed by manually docking the Cα backbone of the CC2 coiled-coil (residues 260–292) with that of the LZ coiled-coil (residues 306–344) in an antiparallel manner. During docking, we looked for unfavorable and favorable contacts between the CC2 and LZ atoms, by calculating electrostatic and van der Waals interaction energies, using the Docking module of Insight II. The resulting energy-minimized model is shown in Fig. 2.

Immunofluorescence microscopy. MDDCs were allowed to differentiate and were activated by CD40L-expressing fibroblasts, as previously described. MDDCs were immediately fixed upon activation, by incubation in 4% formaldehyde/PBS at 4°C for 20 min, followed by surface staining with mouse anti-human CD1a (BD Biosciences) at 4°C for 15 min. Cells were washed in PBS and incubated with goat Cy3-conjugated anti-mouse IgG antibody (Zymed Laboratories). For intracellular staining, MDDCs were permeabilized by incubation in 0.2% Triton X-100 (Sigma-Aldrich) in PBS for 15 min. Cells were washed twice in PBS, blocked by incubation with FcR-blocking reagent (Macs; Miltenyi Biotec) for 20 min and washed once with PBS. MDDCs were incubated with 1 μg primary antibody/PBS, rabbit anti-p65 (C20, Santa Cruz Biotechnology, Inc.) and rabbit anti-κB Rel C (Santa Cruz Biotechnology, Inc.) at 4°C for 30 min and were washed with PBS. Cells were incubated with Alexa 488-conjugated goat anti-rabbit IgG antibody (1/300 dilution) (Invitrogen) and with 4,6-diamidino-2-phenylindole (DAPI) (1/10,000 dilution; Invitrogen) for 15 min. They were washed at least three times with PBS. MDDCs were resuspended in 100 μl of PBS and plated on lysine-coated slides (VWR), using the CytoSpin system. The coverslips were mounted on glass slides with Mowiol. Slides were viewed under an LSM 510 confocal microscope.

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