Inherited STING-activating mutation underlies a familial inflammatory syndrome with lupus-like manifestations

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Introduction

The type I IFN response is a key component of innate immunity to viral infection. A tight control of this pathway is required to avoid disease-causing inflammation. This is well illustrated by the elucidation of the genetic basis of Aicardi-Goutières syndrome (AGS), an inflammatory phenotype sometimes mimicking pathogenic viral infection, which is related to enhanced type I IFN signaling as a consequence of mutations in TREX1, RNASEH2A, RNASEH2B, RNASEH2C, SAMHD1, and ADAR (1–4). All of these proteins normally participate in regulating nucleic acid metabolism, and their dysfunction leads to an accumulation in the cytosol of nucleic acid, which is then detected to instigate a prototypic antiviral response.

Recently, gain-of-function mutations in IFIHI (also known as MDA-5), encoding a cytosolic viral RNA receptor, were reported in patients demonstrating a spectrum of inflammatory phenotypes, including classical AGS (5). Similarly, cytosolic DNA sensors have been described as leading to type I IFN and inflammatory cytokine induction (e.g., IL-1 and IL-18) (6, 7). In particular, stimulator of type I IFN gene (STING) has been identified as a central mediator of responses to cytosolic DNA upon induced dimerization (8–11) and as the receptor of cyclic GMP-AMP (cGAMP) produced by the cGAMP synthase in response to cytosolic DNA. Structural modeling supported constitutive activation of the mutant STING protein based on stabilized dimerization. In agreement with the model predictions, we found that the STING mutant spontaneously localizes in the Golgi of patient fibroblasts and is constitutively active in the absence of exogenous 2′,3′-cGAMP in vitro. Accordingly, we observed elevated serum IFN activity and a type I IFN signature in peripheral blood from affected family members. These findings highlight the key role of STING in activating both the innate and adaptive immune responses and implicate aberrant STING activation in features of human lupus.

Results and Discussion

Clinical presentation and familial history. We report 4 members of a single kindred (Figure 1, A and B) exhibiting a complex systemic inflammatory syndrome associated with pulmonary fibrosis (Figure 1, B and C) and autoimmunity (Table 1, Supplemental Methods, and Supplemental Table 1; supplemental material available online with this article; doi:10.1172/JCI91000DS1). The index case had early-onset febrile attacks, malar rash, lung disease, and failure to thrive. The clinical history suggested a familial syndrome, with variable clinical expression. The proband’s father (II-5) and paternal uncle (II-6) are monozygotic twins and presented with a sim-
ilhar inflammatory syndrome, with lung disease and arthritis (see Supplemental Methods for details). The paternal grandfather of the proband (I-4) is currently 65 years old, and no clinically relevant lung disease has been observed (Table 1).

**Genetic analysis reveals a TMEM173/STING mutation.** We undertook whole-exome sequencing on DNA from the 2 available patients (proband [III-2] and II-6) and the healthy mother of the proband (II-4) and looked for variants present in both patients and absent in the mother. After exclusion of common polymorphisms described in publically available libraries (dbSNP, 1000 genomes project, Exome Variant Server) and an in-house database of 4,047 exomes, we identified a rare variant c.463G>A (resulting in a p.V155M substitution) in *TMEM173*, encoding STING (Figure 1B). This variant was confirmed by Sanger sequencing (Supplemental Table 2). The 3 affected surviving members tested (III-2, II-6, I-4) all carried the same p.V155M variant (Figure 1B), which was considered as likely pathogenic on the basis of species conservation, in silico (sorting intolerant from tolerant and Polyphen2) predictions, and the previous observation that mutagenesis at this position (V155R) profoundly affects STING function by impairing its dimerization (14).

**3D modeling of the V155M mutant.** In order to gain further insight into the effect of the p.V155M substitution on protein activity, we examined the experimental 3D structure of the C-terminal cytosolic domain (CTD) of STING (14–16). The V155 residue is located in the first highly hydrophobic helix (α5) of the CTD of STING that forms intermolecular hydrophobic interactions also involving helix α7 (Supplemental Figure 1). Within the dimer, p.V155 is at the center of a hydrophobic network, in the vicinity of the closest contact between the 2 subunits (p.G158) (Supplemental Figure 1B). This network is similar whatever the conformational state of the protein (bound or not to cyclic dinucleotides). There is only one major possibility for accommodating the methionine side chain of the p.V155M substitution (Supplemental Figure 1C), which is predicted to lead to the establishment of a strikingly tighter network of interactions. The p.V155M substitution is likely to stabilize the position of p.M271 from the same subunit, which forms a strong sulfur-aromatic interaction with p.W161 from the other subunit. This should reinforce the stability of the dimer. It is thus possible that the p.V155M mutant mimics the effect of ligand binding.

**Constitutive activation of the V155M mutant in vitro.** To examine the activity of the p.V155M mutated STING protein, we used a luciferase reporter assay that includes the IFN-β gene promoter. In this assay, overexpression of wild-type STING protein activated the IFNB promoter 2-fold over control in the absence of ligand (Figure 2A). Stimulation with synthetic 2′3′-cGAMP enhanced promoter activation in a dose-dependent manner, and this induction was not observed in the absence of STING (Figure 2A). In contrast, the p.V155M mutant induced reporter activity in the absence of syn-
Table 1. Clinical features of family members carrying V155M

<table>
<thead>
<tr>
<th></th>
<th>I-4</th>
<th>II-5</th>
<th>II-6</th>
<th>III-2</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Age of onset</strong></td>
<td>Adulthood</td>
<td>Teenage years</td>
<td>Teenage years</td>
<td>Infancy</td>
</tr>
<tr>
<td><strong>Gender</strong></td>
<td>Male</td>
<td>Male</td>
<td>Male</td>
<td>Female</td>
</tr>
<tr>
<td><strong>Age at last fu (yr)</strong></td>
<td>65</td>
<td>29</td>
<td>33</td>
<td>4</td>
</tr>
<tr>
<td><strong>Status at last fu</strong></td>
<td>Alive</td>
<td>Died</td>
<td>Alive</td>
<td>Alive</td>
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<tr>
<td><strong>Febrile attacks</strong></td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td><strong>Failure to thrive</strong></td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td><strong>Sparse and thin hair</strong></td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td><strong>Relapsing malar rash</strong></td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td><strong>Intestinal lung disease</strong></td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td><strong>Lung biopsy</strong></td>
<td>Not done</td>
<td>MA, FH, and IF</td>
<td>MA, FH, and IF</td>
<td>MA, FH, and IF</td>
</tr>
<tr>
<td><strong>Arthralgia/arthritis</strong></td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
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<tr>
<td><strong>ESR</strong></td>
<td>Elevated</td>
<td>Elevated</td>
<td>Elevated</td>
<td>Elevated</td>
</tr>
<tr>
<td><strong>CRP</strong></td>
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<td>Elevated</td>
<td>Elevated</td>
<td>Elevated</td>
</tr>
<tr>
<td><strong>ANA</strong></td>
<td>Neg/1:340*</td>
<td>1:640</td>
<td>1:320</td>
<td>1:200–1:800</td>
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<tr>
<td><strong>RF (IU/l)</strong></td>
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<td>521</td>
<td>1030</td>
<td>512</td>
</tr>
<tr>
<td><strong>Native anti-DNA (IU/l)</strong></td>
<td>Neg</td>
<td>Neg</td>
<td>Neg</td>
<td>4.1–10.2</td>
</tr>
</tbody>
</table>

*The first test was negative; the second test was positive and resulted in the value shown. fu, follow-up; Neg, negative; MA, macrophage alveolitis; FH, follicular hyperplasia; IF, interstitial fibrosis; ESR, erythrocyte sedimentation rate; CRP, C-reactive protein; ANA, antinuclear antibody (n < 1:100); RF, rheumatoid factor (n < 20 IU/l). Native anti-DNA (n < 5.5 IU/l).

Functional consequences of the V155M STING mutant. Activation of STING is known to induce type I IFN production through TBK-1 phosphorylation and IRF3 phosphorylation (9). In order to study the functional consequences of the V155M STING variant, we assessed the expression of 6 gene transcripts known to be overexpressed in PBMCs of patients with AGS (IFI44L, SIGLEC1, RSAD2, IFI27, IFIT1, and ISG15) (17). Positive controls were generated by treatment of healthy control PBMCs with IFN-α (1,000 U/ml) for 6 hours (18). PBMCs from the patient (III-2) and her grandfather (I-4) exhibited an overexpression of all 6 tested genes as compared with control PBMCs and PBMCs from the healthy mother (II-4) (Supplemental Figure 2). Similar overexpression was also seen in vitro–activated T cells (Supplemental Figure 3). In contrast, a set of non–type I IFN–regulated genes remained normally expressed in peripheral blood compared with control samples (Supplemental Figure 4). These results suggest that cells with the V155M variant spontaneously express type I IFN. Accordingly, serum-type I IFN activity was found to be elevated in patient blood (III-2).

Collectively, the results reported here suggest a gain-of-function consequence of the V155M variant. The constitutively active mutant thus results in upregulated type I IFN production, as measured by serum IFN activity, and a type I IFN signature in whole blood. The very same mutation and 2 other mutations at neighboring residues have been recently reported to be associated with inflammation and severe vasculopathy in humans (19). The present work thus confirms the gain-of-function nature of the V155M mutation, provides a structural model accounting for constitutive mutant STING activity, and extends the spectrum of clinical phenotypic expression.
Our findings highlight the central role of STING in type I IFN production and demonstrate its causal role in inflammatory syndromes variably accompanied with small vessel vasculopathy, pulmonary fibrosis, and autoimmunity reminiscent of SLE. Hence, TMEM173 gain-of-function mutations should be screened for as a monogenic cause of this broad spectrum of diseases. STING could represent a new therapeutic target in these disorders as well as other more common inflammatory diseases triggered by cytosolic DNA stimulation of microbial or endogenous origin, resulting in dysregulated type I IFN production.

Methods

Further details are provided in the Supplemental Methods.

Statistics

Analyses were performed with PRISM software (version 4 for Macintosh, GraphPad Inc.). Statistical hypotheses were tested using 2-tailed t test. A P value of less than 0.05 was considered significant.

Study approval

Written informed consent (parental consent, in case of minors) was obtained from all participants of the study. The study and protocols conform to the 1975 Declaration of Helsinki and were approved by the comité de protection des personnes Ile de France II and the French advisory committee on data processing in medical research.

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