

Rig-I^{-/-} mice develop colitis associated with downregulation of *Gai2*

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RIG-I (retinoid acid-inducible gene-I), a putative RNA helicase with a cytoplasmic caspase-recruitment domain (CARD), was identified as a pattern-recognition receptor (PRR) that mediates antiviral immunity by inducing type I interferon production. To further study the biological function of RIG-I, we generated *Rig-I*^{-/-} mice through homologous recombination, taking a different strategy to the previously reported strategy. Our *Rig-I*^{-/-} mice are viable and fertile. Histological analysis shows that *Rig-I*^{-/-} mice develop a colitis-like phenotype and increased susceptibility to dextran sulfate sodium-induced colitis. Accordingly, the size and number of Peyer's patches dramatically decreased in mutant mice. The peripheral T-cell subsets in mutant mice are characterized by an increase in effector T cells and a decrease in naïve T cells, indicating an important role for Rig-I in the regulation of T-cell activation. It was further found that *Rig-I* deficiency leads to the downregulation of G protein $\alpha 2$ subunit (*Gai2*) in various tissues, including T and B lymphocytes. By contrast, upregulation of *Rig-I* in NB4 cells that are treated with ATRA is accompanied by elevated *Gai2* expression. Moreover, *Gai2* promoter activity is increased in co-transfected NIH3T3 cells in a Rig-I dose-dependent manner. All these findings suggest that Rig-I has crucial roles in the regulation of *Gai2* expression and T-cell activation. The development of colitis may be, at least in part, associated with downregulation of *Gai2* and disturbed T-cell homeostasis.

Keywords: *Rig-I* knockout mice, colitis, Peyer's patches, T-cell homeostasis, *Gai2* expression

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Introduction

RIG-I (retinoid acid-inducible gene-I) was originally found to be upregulated in differentiating NB4 cells that are induced by all-trans retinoic acid (ATRA) [1, 2]. It is a member of the DEXD/H box protein family containing a C-terminal helicase domain and two tandem caspase-

recruitment domains (CARDs) [3]. Recent studies have shown that RIG-I plays a crucial part in guarding against viral invasion as an intracellular molecular sensor. RIG-I binds to synthetic dsRNA or viral dsRNA through its helicase domain, inducing a conformational change that allows the N-terminal CARD domains to recruit the downstream signaling protein MAVS (also called IPS-1, VISA, and Cardif). The interaction between RIG-I and MAVS triggers both NF- κ B and IRF3 signaling pathways, leading to the activation of the IKK and TBK-1/IKK ϵ kinase complexes, and, subsequently, the induction of IFN- β . Hepatitis C virus (HCV) can interrupt RIG-I signaling to IRF-3 and NF- κ B through the cleavage of MAVS by its NS3/4 protease [4-11]. The RIG-I-mediated antiviral activity is negatively

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regulated by the A20 protein [12]. It has been shown that RIG-I, but not the TLR system, has an essential role in the antiviral response *in vivo* in various cells except pDCs [13]. Thus, RIG-I is thought to be the third pattern-recognition receptor in addition to TLRs and NLRs. Moreover, RIG-I can also regulate the transcription of many genes including interferon- γ stimulated gene 15 in MCF-7 cells and *COX-2* in endothelial cells [14,15].

Human inflammatory bowel disease (IBD), including Crohn's disease and ulcerative colitis, is a multifactor disease that is manifested by cellular inflammation and intestinal tissue damage. It is also characterized by the dysfunction of mucosal immunity, including the malfunction of T cells and aberrant cytokine production. However, the precise mechanism that underlies colitis remains unclear. Studies on mice with targeted disruption of the genes that regulate the T-cell immune responses have shed light on the development of colitis. For example, mice with targeted disruption of *Gai2* develop colitis with 100% penetrance [16, 17]. *Gai2* is regarded as one of the candidate genes for IBD in human, because genetic linkage studies have mapped the *Gai2* gene within an IBD susceptible locus at chromosome 3p21 [18]. Heterotrimeric G proteins consist of α , β and γ subunits. *Gai2* is one of the *G α* subunits, which has a role in a large variety of cellular and metabolic processes [19-23]. Furthermore, a decreased number of Peyer's patches was also observed in *Gai2*^{-/-} mice [16,17,19]. It is important to emphasize that Peyer's patches provide the first line of defense against pathogen invasion in the intestine. Mice with *Gai2* ablation exhibit an accelerated transition from double-positive to single-positive thymocytes, leading to selective CD4⁺ T-cell disorders. Increases in effector T cells and decreases in naïve T cells were also observed in the spleen of *Gai2*^{-/-} mice [24,25]. These data suggest that *Gai2* is associated with the induction of colitis and that it is a negative regulator of the T-cell response.

To further investigate the biological function of RIG-I, we generated *Rig-I*-deficient (*Rig-I*^{-/-}) mice through homologous recombination, taking a different strategy to the previously reported strategy [13]. We found that *Rig-I*^{-/-} mice are viable and fertile. They develop a colitis-like phenotype and increased susceptibility to dextran sulfate sodium (DSS)-induced colitis, which is accompanied by a decrease in the size and number of Peyer's patches, abnormal activation of peripheral T cells and downregulation of *Gai2*. These findings reveal a novel role for RIG-I in the regulation of intestinal mucosal immunity and *Gai2* expression.

Materials and Methods

Generation of *Rig-I* knockout mice

A *Rig-I* targeting vector was designed to delete the 6.4-kb fragment that contains exons 4 to 8, which encodes part of the CARD

domain 2, and that contains the A and B motifs of the RNA helicase domain. The targeting construct was electroporated into ES cells. After double selection with G418 and GANC, the resistant clones were genotyped using Southern blotting. Two correctly recombined ES cell clones were used to create *Rig-I* mutant mice through blastocyst microinjection. The *Rig-I*^{-/-} mice were generated by crossing chimeras with wild-type 129S1 mice. They were genotyped by PCR using two primer pairs in one reaction, which allows the amplification of wild type and targeted alleles. The primers used for genotyping were 5'-GCCTAGCTAGCCAAAGTAACAC-3' and 5'-GCAGCGCATCGCCTTCTATC-3' for the targeted allele, and 5'-CACAGTTGCCTGCTGCTCAT-3' and 5'-CAGGAAGAGC-CAGAGTGTCAAGAT-3' for the wild-type allele. PCR was run for 30 cycles at 94 °C for 30 s, 58 °C for 90 s, 72 °C for 90 s, and a final extension at 72 °C for 10 min after an initial denaturation at 94 °C for 5 min. The *Rig-I* mutant mice were bred in specific pathogen-free conditions and maintained in a 129S1 background.

Northern blot analysis

Mouse primary embryonic fibroblasts (MEFs) were isolated from 13.5 dpc embryos and plated at a concentration of 2×10⁶ cells in 10-cm dishes. The cells were treated with 1000 U/ml murine IFN- β for 24 h. Total RNA was extracted using the TRIZOL reagent (Invitrogen, Carlsbad, CA, USA) and analyzed with northern blotting, using a 477-bp *Rig-I* cDNA fragment (477 bp, composed of exons 11 to 14) as a probe.

Western blot analysis

Cell suspensions from the spleen were prepared by passing tissues through a cell strainer. 10⁶ splenocytes were stimulated by LPS (20 μ g/ml) for 72 h. Cell lysates were prepared by adding 0.6 ml of RIPA buffer (1% Nonidet P-40, 0.5% sodium deoxycholate, 0.1% SDS in PBS) with freshly supplemented protease inhibitors (100 μ g/ml PMSF, 50 KIU/ml aprotinin, 1 mM sodium orthovanadate). In addition, cell lysates were also prepared from the colons and intestines of mice at 8 weeks of age as described above. Cell lysates (50 μ g) from cells or tissues were electrophoresed and transferred to PVDF membrane (BioRad, Hercules, CA, USA) according to the manufacturer's protocol. The protein blots were blocked with 5% non-fat milk in TBS, then incubated overnight with antibodies to RIG-I (1:2000 dilution in the blocking buffer), to *Gai2* (1:1000) (Santa Cruz Biotechnology, Inc. CA, USA), or to α -tubulin (1:10 000) (KPL, Gaithersburg, MD, USA). After washing, the membrane was incubated with horseradish peroxidase (HRP) conjugated anti-rabbit IgG (1:10 000, Sigma Chemical Co., St Louis, MO, USA). The blots were immersed in chemiluminescence luminol reagent (Pierce Chemical Co., Rockford, IL, USA) and exposed to X-ray film (Eastman Kodak, Rochester, NY, USA).

Histological assessment of colitis

Colons of wild type and *Rig-I*^{-/-} mice at 8 weeks of age were collected and fixed with 10% formalin for sectioning, followed by hematoxylin-and-eosin staining. Histological assessment was performed in a double-blind fashion. In brief, scores were determined as follows [26-28]: 0, normal morphology; 1, focal inflammatory cell infiltrate around the crypt base; 2, diffuse infiltration of inflammatory cells around the crypts or erosion/destruction of the lower one-third of the glands; 3, erosion/destruction of the lower two-thirds of the glands or loss of all the glands but with the surface epithelium

remaining; and 4, loss of all the glands and epithelium. Each field was assigned a grade of 0 to 4.

Induction and assessment of DSS-induced colitis

Wild type and *Rig-I*^{-/-} mice at 8 weeks of age were divided into two groups, receiving either water alone (control) or 3% (w/v) DSS (40 000–50 000 MW; Sigma Chemical Co., St Louis, MO, USA) in water for 5 days. The mice were checked each day for the development of colitis by monitoring their body weight and diarrhea. The degree of diarrhea was scored as follows: 0, normal; 2, loose stool; and 4, watery diarrhea [29, 30]. All mice were sacrificed after the experiment and the colons were taken for histological analysis. The methods and histological scores used were same as described above.

Analysis of apoptosis

Peyer's patches were collected from wild type and *Rig-I*^{-/-} mice and fixed in 10% neutral buffered formalin. Paraffin-embedded Peyer's patches were sectioned at 5 μm and apoptosis was investigated using the *in situ* TUNEL assay kit (Promega Co., Madison, WI, USA) according to the manufacturer's instructions. Apoptosis was also analyzed by flow cytometry. Peyer's patches were washed three times in cold PBS, and cell suspensions were obtained by passing tissue through a 200-μm nylon mesh. The Peyer's patch lymphocytes (1×10⁶) were stained with Annexin-V-FITC (Becton Dickinson, San Jose, CA, USA), PI and B220-APC (Becton Dickinson Immunocytometry, San Jose, CA, USA) antibodies for 30 min at 4°C. The analysis was performed on a FACSCalibur machine (Becton Dickinson, Franklin Lakes, NJ, USA) and the data obtained were processed with CellQuest software (Becton Dickinson, San Jose, CA, USA).

Analysis of T-cell subsets

Splenic lymphocytes from wild type and *Rig-I*^{-/-} mice were obtained by passing tissue through a 200-μm nylon mesh. Erythrocytes were lysed using a lysis buffer. Cells were counted and stained with fluorochrome-conjugated antibodies specific for CD4, CD8, CD44 and CD62L (eBioscience, San Diego, CA, USA) for 30 min. Flow cytometry analysis was performed as described above.

Semi-quantitative RT-PCR and real-time PCR

Total RNA was extracted with the Trizol reagent (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's protocol. For semi-quantitative RT-PCR and real-time PCR, RNA was treated with RNase-free DNase, and then 1 μg total RNA was reverse-transcribed according to the standard protocol (TaKaRa Shuzo, Ltd, Kyoto). The primers used were as follows: 5'-TTGGCCGCTCACGAGAATA-3' and 5'-GCTGACCACCCACATCAAACA-3' for *Gai2*; 5'-TCTTTGCTGACCTGCTGGATT-3' and 5'-TTCGAGAGGTCCTTTTCCACA-3' for *HPRT*; and 5'-AACGAGCGGTTCCGATGCCCTGAG-3' and 5'-TGTCGCCTTACCGTTCCAGTT-3' for β -*actin*. Semi-quantitative RT-PCR consists of 25–30 cycles at 94 °C for 30 s, 58 °C for 30 s, 72 °C for 30 s and a final extension at 72 °C for 10 min after an initial denaturation at 94°C for 5 min. Real-time PCR was performed using an ABI9700 PCR machine (Applied Biosystems, Foster City, CA, USA) for 40 cycles at 94 °C for 15 s, 58 °C for 15 s, 72 °C for 30 s and a final extension at 72 °C for 10 min after an initial denaturation at 94 °C for 5 min.

Purification of T cells and B cells from the spleen

Splenocytes of wild type and *Rig-I*^{-/-} mice were collected as described above. Splenic T cells labeled with CD3-PE were sorted out with a MoFlo high-speed cell sorter (DakoCytomation, Denmark). Splenic B cells were isolated using a Dynabeads[®] Mouse pan B (B220) (DynaL Biotech, Lake Success, NY, USA).

NB4 cell culture and treatment with ATRA

Retinoid acid-sensitive NB4 cells were cultured in RPMI 1640 medium (GIBCO, Grand Island, NY, USA), containing 10% FCS, 100 μg/ml streptomycin and 100 U/ml penicillin in an incubator at 37 °C. The cells were treated with 1 μM ATRA for 0, 24, 48 and 72 h, then the cells were lysed and total RNA was extracted for semi-quantitative RT-PCR.

Construction of pGL3-*Gai2* and pcDNA3.1-*Rig-I*

A 1.2-kb fragment of mouse *Gai2* promoter was isolated from mouse genomic DNA by PCR using 5'-AGCCATCCCTCCC-GCCCCCATTT-3' as the forward primer and 5'-TCTCAGGTCC-GCAGTTCCGAGCGA-3' as the reverse primer. The PCR product obtained was cloned into pGL3-Basic (Promega Co., Madison, WI, USA), using the *XhoI* and *SacI* sites. Full-length *Rig-I* cDNA was also amplified by PCR using the forward primer 5'-ACTGCG-GCCGCCCCACTTCGTTTCATCTCTG-3' and the reverse primer 5'-ACTGGGTACCACGGACATTTCTGCAGGATC-3'. The PCR product was sequenced and cloned to pcDNA3.1 at the *NotI* and *KpnI* sites. PCR amplification conditions consisted of 30 cycles at 94 °C for 30 s, 60 °C for 90 s, 68 °C for 180 s and a final extension at 72 °C for 10 min after an initial denaturation at 94 °C for 5 min. The construction was sequenced to verify that the proper sequence was amplified.

Luciferase assay

NIH3T3 cells were seeded at a concentration of 8 × 10⁴/ml in 12-well plates. The cells were co-transfected with the *Gai2* luciferase reporter construct (300 ng), *Renilla* luciferase and pcDNA3.1-*Rig-I* with increasing amounts (0, 300, 500 and 700 ng), or pcDNA3.1 (to keep the total amount of plasmids constant) using the SuperFect Transfection Reagent (Qiagen GmbH, Germany). In a standard assay, each transfection was tested in duplicate according to the protocol of the dual-luciferase reporter assay system kit (Promega Co., Madison, WI, USA).

Statistical analysis

In vivo experiments were performed using 5–10 mice per group. Each *in vitro* experiment was performed in triplicate and repeated three times. All values were expressed as the mean ± SD. Student's two-tailed *t*-test was used to analyze the significance among different groups. A *p*-value of less than 0.05 was considered to be significant and is shown by an asterisk.

Results

Targeted disruption of *Rig-I*

Intracellular viral infection is detected by the cytoplasmic RNA helicase RIG-I, which highlights a novel role for CARD-containing proteins in coordinating immune and apoptotic responses [31–34]. To further investigate the func-

tion of RIG-I, we disrupted 5 (4 to 8 exons) out of 18 exons of the *Rig-I* gene. In the mutant allele, exons 4 to 8 were replaced by the neo cassette (Figure 1A). G418 and GANC double resistant ES clones were examined for recombination by PCR. The correctly recombined ES clones were further confirmed by Southern blotting (Figure 1B). Two targeted ES clones were identified. Mice with wild type and the targeted allele were identified using PCR, which exhibited different bands of 1.58 kb (wild-type allele) and

2.84 kb (knockout allele) (Figure 1C). The disruption of Rig-I was confirmed by northern blotting with a *Rig-I* probe (Figure 1D) and western blotting using a polyclonal antibody to Rig-I (Figure 1E), respectively. It was found that Rig-I can be induced by IFN β and LPS in various tissues and cell types [15,35], as shown in wild-type MEFs treated with IFN β and splenocytes treated with LPS (Figure 1D and 1E). By contrast, no signals were detected by northern and western blotting in *Rig-I*^{-/-} MEFs and splenocytes even

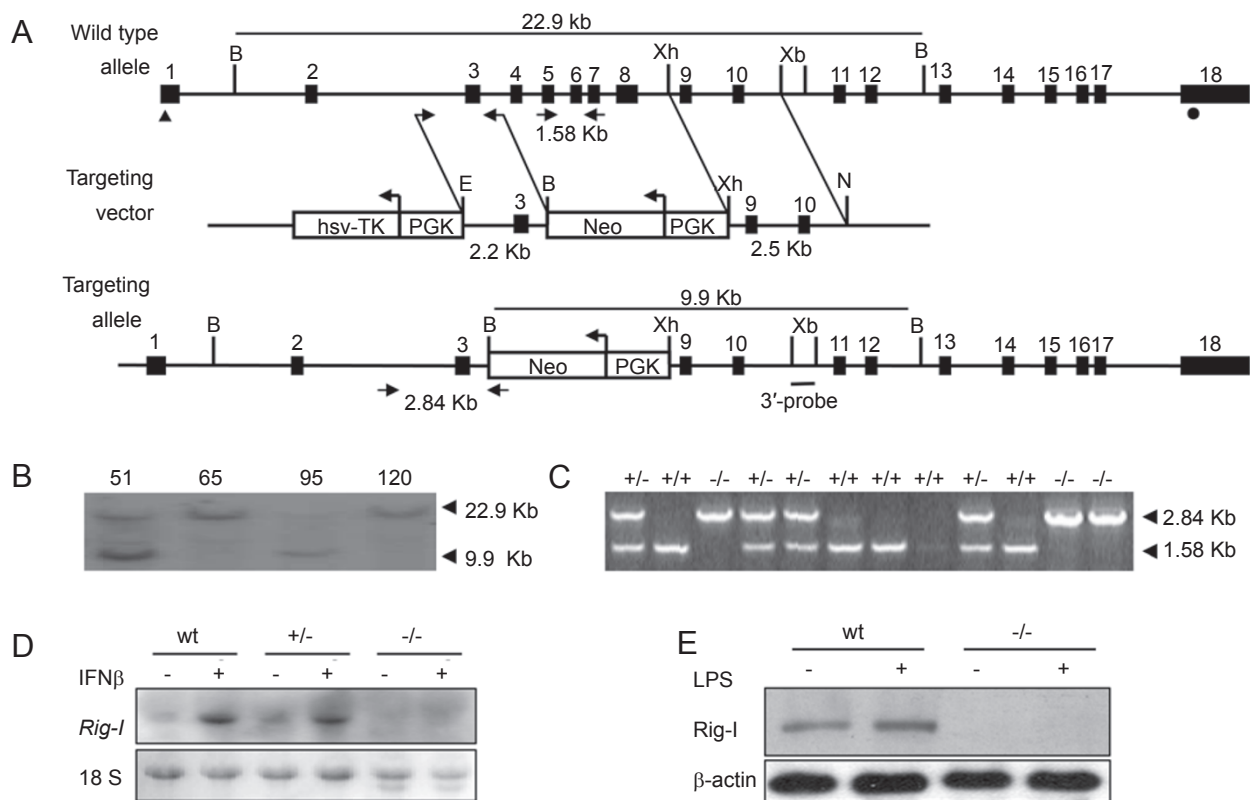


Figure 1 Targeted disruption of *Rig-I*. **(A)** *Rig-I* targeting strategy. Mouse genomic *Rig-I* contains 18 exons. The start codon and stop codon are indicated as \blacktriangle and \bullet , respectively. The targeting vector was designed to delete a 6.4-kb fragment containing exons 4 to 8, which encode part of CARD domain 2, and containing the A and B motifs of the RNA helicase domain. The 3' probe used for southern blotting (—) and two primer pairs (arrows) for PCR genotyping are indicated. The respective sizes of the wild type and targeted bands hybridized with the 3' probe in southern blotting upon *Bam*HI (shown as **B**) digestion, and of the PCR fragments amplified from wild type and mutant alleles are indicated. **(B)** Two recombined ES cell clones show the expected bands as detected by Southern blot analysis. **(C)** PCR using mouse tail DNA as a template and two primer pairs in one reaction shows three different genotypes. **(D)** Northern blot analysis of *Rig-I* in MEFs. Total RNA from wild type, *Rig-I*^{+/-} and *Rig-I*^{-/-} MEFs treated with or without 1000 U/ml IFN- β for 6 h was extracted and subjected to northern blot analysis using an *Hind*III fragment of *Rig-I* cDNA (477 bp, composed of exons 11 to 14). The same membrane was re-hybridized with an 18S probe as a control. Note that no signal was detected in *Rig-I*^{-/-} MEFs with or without treatment with IFN- β . **(E)** Western blot analysis of Rig-I expression in wild type and *Rig-I*^{-/-} splenocytes with or without treatment with LPS (20 μ g/ml) was performed using the polyclonal antibody raised in mice by immunizing mice with a glutathione S-transferase (GST)-RIG-I fusion protein encompassing the full-length human RIG-I. The same membrane was blotted again with antibody to β -actin. As reported by others, Rig-I can be induced by LPS in various tissues as well as splenocytes, while no bands were visualized in *Rig-I*^{-/-} splenocytes even after treatment with LPS.

after IFN β and LPS treatment, respectively. The mutant mice develop normally and they are fertile.

Rig-I^{-/-} mice develop colitis with increased susceptibility to DSS-induced colitis

It was observed that the body weight of *Rig-I*^{-/-} mice progressively decreased from 3 months of age on compared with that of the wild type (data not shown). *Rig-I*^{-/-} mice at 8 weeks of age displayed a colitis-like phenotype (Figure 2A); the incidence was around 70% (data not shown). After treatment with DSS, *Rig-I*^{-/-} mice exhibited more severe damage and inflammatory infiltration in the mucosa of the colon than was observed in wild-type mice (Figure 2A). The histological scores were significantly increased in *Rig-I*^{-/-} mice (Figure 2B). More body weight loss and higher

faecal scores were also observed in *Rig-I*^{-/-} mice after DSS treatment (Figure 2C and 2D). These findings indicate that *Rig-I*^{-/-} mice are much more susceptible to DSS-induced colitis than wild-type mice.

Decrease in number and size of Peyer's patches in *Rig-I*^{-/-} mice

Since the disruption of Rig-I in mice leads to the development of a colitis-like phenotype and increased susceptibility to DSS-induced colitis, and the development of colitis in *Gai2*^{-/-} mice is accompanied by fewer Peyer's patches, we also checked the number and size of Peyer's patches in *Rig-I*^{-/-} mice. It was found that the number and size of Peyer's patches were significantly reduced in *Rig-I*^{-/-} mice compared with wild-type mice (Figure 3A and 3B). The

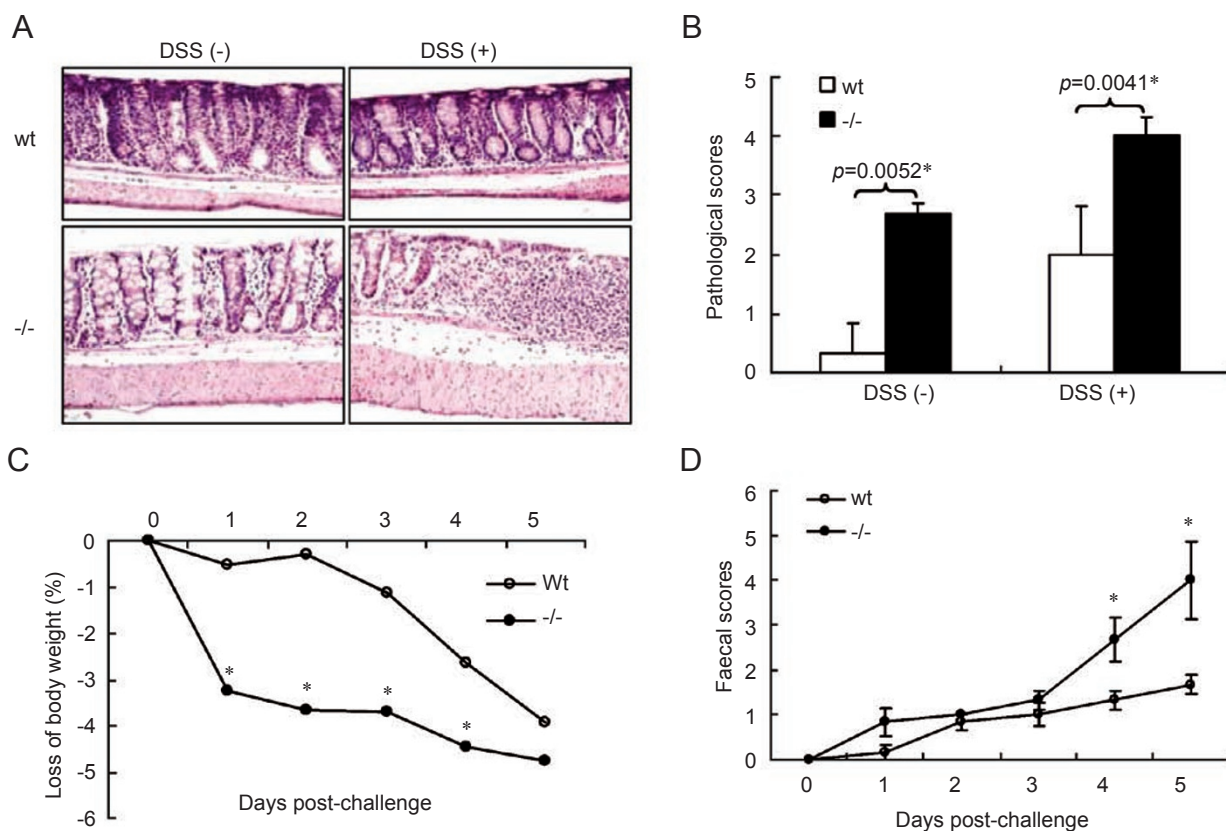


Figure 2 *Rig-I*^{-/-} mice exhibit colitis and are susceptible to DSS-induced colitis. (A) Histological analysis of colons from wild type and *Rig-I*^{-/-} mice with or without treatment with DSS (200 \times). Wild type and *Rig-I*^{-/-} mice of 8 weeks of age were administered with 3% DSS in drinking water. The mice were sacrificed on day 5 and the colons were analyzed. More severe damage and inflammatory infiltration can be observed in the colon mucosa of *Rig-I*^{-/-} mice compared with wild-type mice. (B) Histological score of colitis in wild type and *Rig-I*^{-/-} mice. (C) The body weights of the wild type and *Rig-I*^{-/-} mice were monitored everyday. The values for body weight are expressed as a percentage of body weight on day 0. Asterisks indicate significant differences between groups ($p < 0.05$). (D) Diarrhea in wild type and *Rig-I*^{-/-} mice upon treatment with DSS was monitored everyday. Asterisks indicate significant differences between groups ($p < 0.05$). Five mice were used for each group.

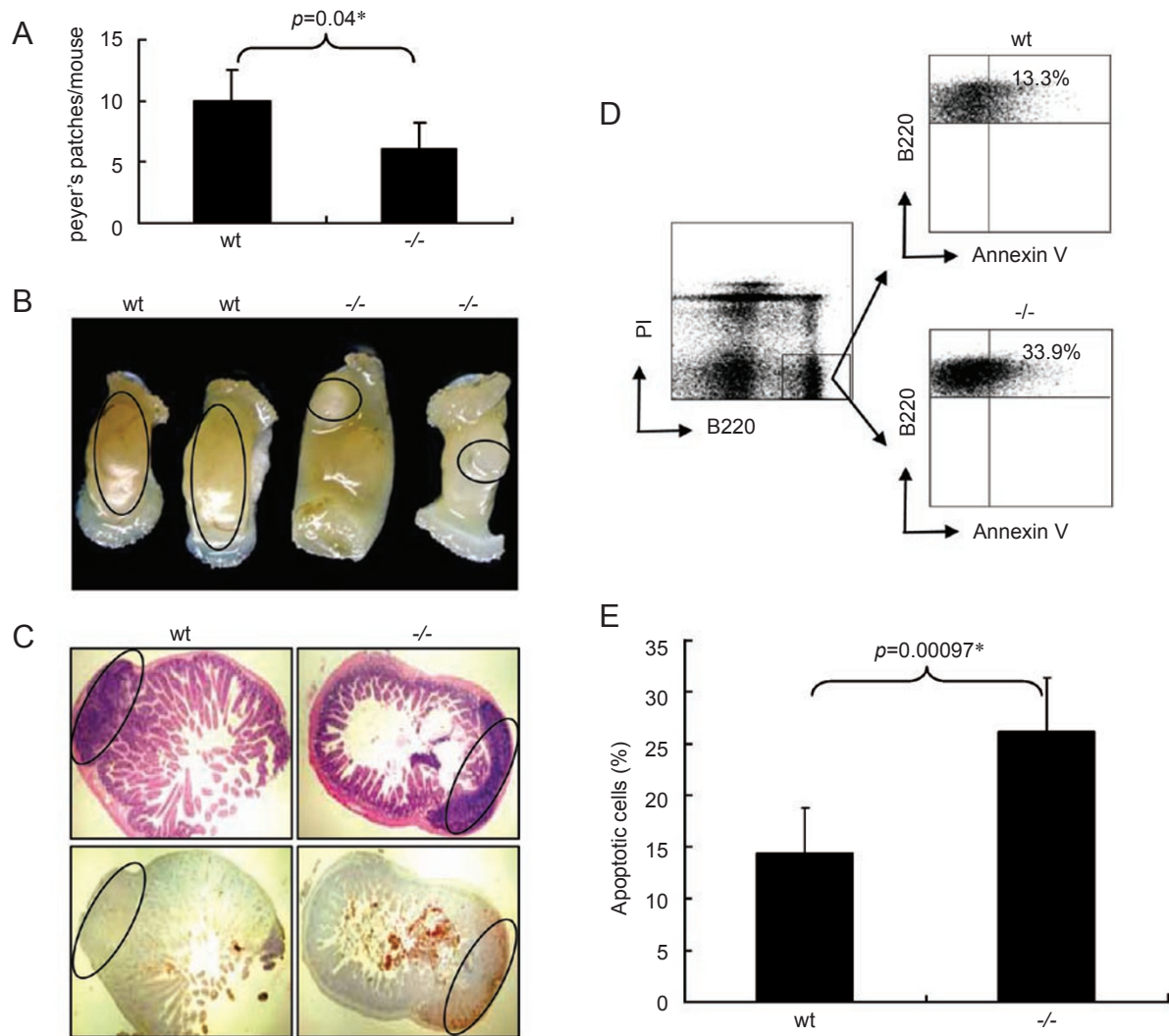


Figure 3 Regression of Peyer's patches in *Rig-I*^{-/-} mice. **(A)** The number of Peyer's patches decreased sharply in *Rig-I*^{-/-} mice compared with wild-type mice (10 mice per each group). **(B)** The size of Peyer's patches (as indicated by circles) in the intestines of *Rig-I*^{-/-} mice decreased significantly (6×, $n = 10$). **(C)** *In situ* TUNNEL analysis shows increased apoptotic cells in Peyer's patches of *Rig-I*^{-/-} mice (400×). Circles indicate the site of Peyer's patches in the transverse section of intestines. **(D)** Apoptotic cells were analyzed by flow cytometry after annexin V staining. As shown in **(D)** and **(E)**, a dramatic increase in apoptotic cells among the B220⁺ population derived from *Rig-I*^{-/-} Peyer's patches can be observed ($n = 5$).

reduced size and number of Peyer's patches raise the possibility of increased apoptosis in *Rig-I*^{-/-} Peyer's patches. As expected, a significant increase in apoptotic cells was detected by *in situ* TUNNEL (Figure 3C), and was further confirmed by Annexin-V flow cytometry in B220⁺ cells in the Peyer's patches deficient for Rig-I (Figure 3D and 3E).

Abnormal splenic T-cell subsets in *Rig-I*^{-/-} mice

It is known that the development of colitis is associated with abnormal T-cell activation [36,37]. For this

reason, we compared the proportion and total number of peripheral T-cell subsets in adult (6–8 weeks of age) *Rig-I*^{-/-} mice with wild-type mice. The total numbers of splenic CD4⁺ and CD8⁺ T cells were found to be similar between wild type and *Rig-I*^{-/-} mice (data not shown). However, the naïve T cells defined as CD44^{low}CD62L^{high} were markedly decreased ($p = 0.001$), whereas the percentages of CD44^{high}CD62L^{low} effector T cells ($p = 0.008$) and CD44^{high}CD62L^{high} memory T cells ($p = 0.019$) were significantly increased in the CD4⁺ splenic compartment of

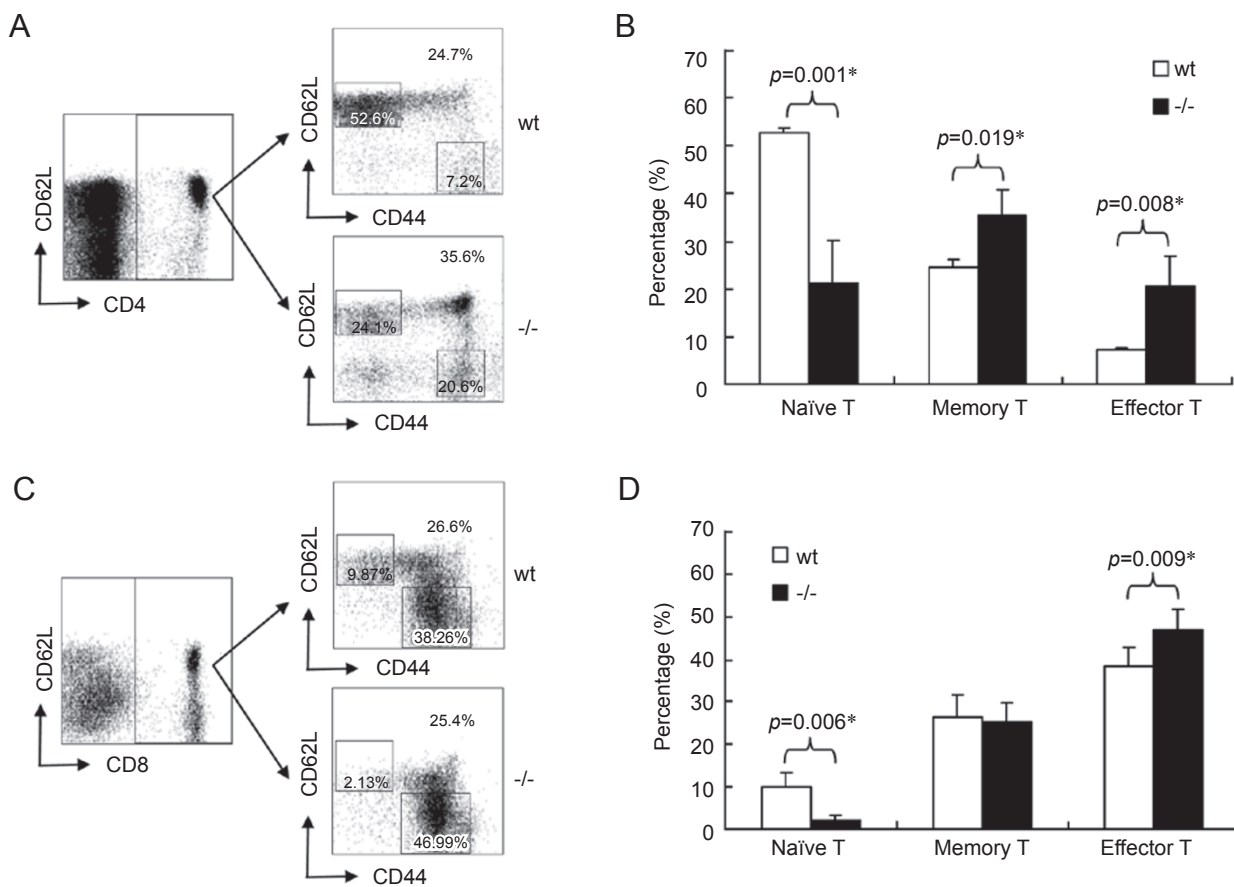


Figure 4 Hyperactivation of peripheral T cells in *Rig-I*^{-/-} mice. Splenocytes from wild type and *Rig-I*^{-/-} mice were stained with CD4, CD8, CD62L and CD44 antibodies conjugated with fluorescence, and the results were analyzed by flow cytometry. To identify naïve T cells (defined as CD44^{low}CD62L^{high}), memory T cells (defined as CD44^{high}CD62L^{high}) and effector T cells (CD44^{high}CD62L^{low}), three-color flow cytometry was performed. (A, B) In CD4⁺ cells, the percentages of memory T cells and effector T cells significantly increased in the absence of Rig-I, while naïve T cells decreased by more than 50% compared with the wild type. The *p*-values that are labeled indicate there are significant differences between groups (*n* = 5). (C, D) In CD8⁺ cells, and in the CD4⁺ cohort, a marked decrease in naïve T cells and an increase in effector T cells were found. However, memory T cells in CD8⁺ cells remained unchanged. The data shown are representative of three independent experiments.

Rig-I^{-/-} mice (Figure 4A and 4B). For CD8⁺ splenic compartments, the percentage of CD44^{low}CD62L^{high} naïve T cells was decreased (*p* = 0.006), accompanied by an increased percentage of CD44^{high}CD62L^{low} effector T cells (*p* = 0.009), while CD44^{high}CD62L^{high} memory T cells remained unchanged (Figure 4C and 4D). These findings suggest that the deletion of Rig-I in mice leads to the abnormal activation of peripheral T cells.

Reduced expression of *Gai2* in *Rig-I*^{-/-} mice

Previous data have shown that the induction of colitis in *Gai2*^{-/-} mice is associated with the regression of Peyer's patches and disorder of T-cell subsets [16]. The phenotype observed in *Rig-I*^{-/-} mice is to some degree similar to that

observed in *Gai2*^{-/-} mice, suggesting that *Gai2* and Rig-I may function in the same signaling pathway in the development of colitis. To address this hypothesis, we first compared *Gai2* expression levels between wild type and *Rig-I*^{-/-} mice. Interestingly, we found that the expression of *Gai2* was significantly reduced in the various tissues tested by real-time PCR (Figure 5A) and western blotting (Figure 5B) in *Rig-I*^{-/-} mice. We then isolated T and B cells from the spleen and checked the difference of *Gai2* expression between wild type and *Rig-I*^{-/-} cells. At the transcriptional level, it was found that *Gai2* expression was repressed in both B and T lymphocytes in the absence of Rig-I (Figure 5C and 5D). These data suggest that Rig-I may play a part in the regulation of *Gai2* expression, and that the develop-

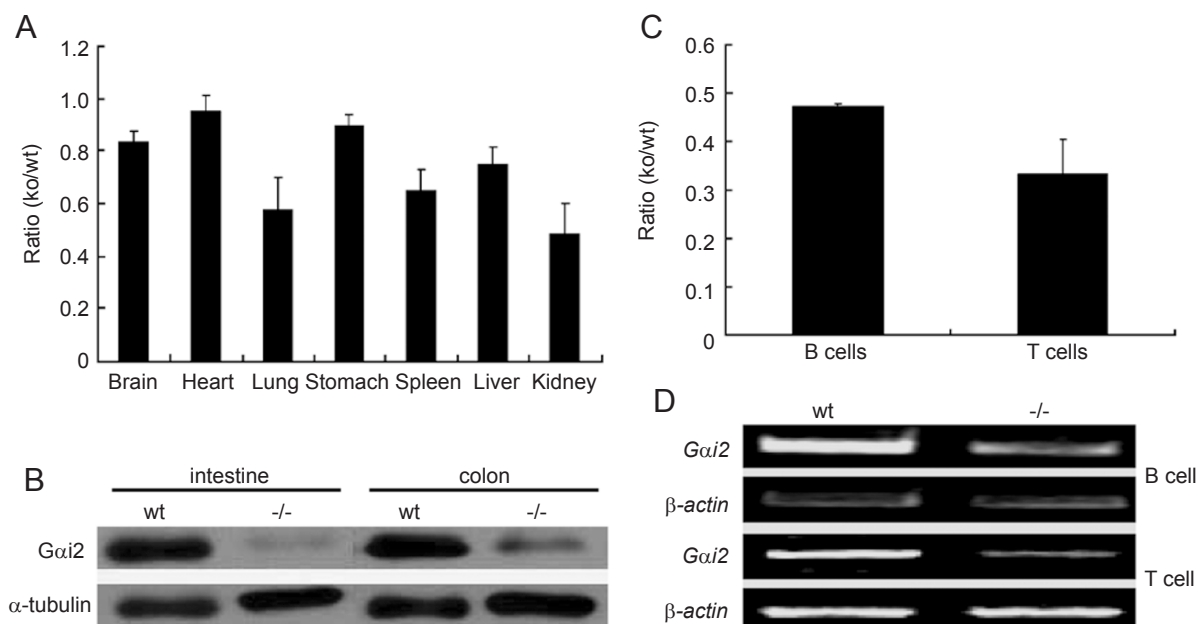


Figure 5 Expression of *Gai2* is reduced in *Rig-I*^{-/-} tissues or cells. **(A)** Total RNA from the tissues of wild type and *Rig-I*^{-/-} mice was extracted and reversely transcribed to cDNA. The expression of *Gai2* was analyzed by real-time PCR. The data from real-time PCR were normalized to an internal control and plotted relative to the level of *Gai2* in the tissues of wild-type mice. Among the tissues tested, *Gai2* expression was reduced by 30 to 50% in the spleen, lung and kidney, while a mild reduction in the other tissues is shown. **(B)** Western blot analysis shows that *Gai2* is highly expressed in wild-type intestines and colons. However, *Gai2* is dramatically reduced in *Rig-I* deficient intestines and colons. α -Tubulin was blotted as a loading control. **(C, D)** The expression of *Gai2* in sorted T and B lymphocytes was analyzed at the transcriptional level. Splenic T cells were enriched by sorting CD3-PE staining cells. B cells were purified by Dynabeads[®] Mouse pan B (B220) (DynaL Biotech, Lake Success, NY, USA). Both real-time PCR **(C)** and semi-quantitative RT-PCR **(D)** show decreased expression of *Gai2* in splenic B and T lymphocytes. β -actin in **(D)** serves as an internal control.

ment of colitis and regression of Peyer's patches in *Rig-I*^{-/-} mice may be caused by the downregulation of *Gai2*.

Rig-I regulates the transcriptional activity of the *Gai2* promoter

It is well known that *Rig-I* is induced in NB4 cells by treatment with ATRA [1]. But can the upregulation of endogenous *Rig-I* by ATRA increase *Gai2* expression? To this end, we tested the *Gai2* expression in NB4 cells treated with ATRA. As expected, the induction of *Rig-I* was paralleled with increased expression of *Gai2* (Figure 6A), further demonstrating an important role for *Rig-I* in the regulation of *Gai2* transcription. To further test the possibility of whether *Rig-I* regulates *Gai2* promoter activity, we constructed a *Gai2* promoter/luciferase reporter construct and co-transfected NIH3T3 cells with increasing doses of the *Rig-I* expression vector. As shown in Figure 6B, *Rig-I* indeed activates *Gai2* promoter activity in a dose-dependent manner. Thus, we may conclude that *Rig-I* has a crucial role in the normal transcription of *Gai2*.

Discussion

DExD/H box proteins are putative RNA helicases that are characterized by their ability to unwind dsRNA with intrinsic ATPase activity [38]. They have been implicated in a number of cellular processes that involve the alteration of secondary RNA structures such as translation initiation, nuclear and mitochondrial splicing, and ribosome and spliceosome assembly [39]. *RIG-I* encodes a member of the DExD/H box family proteins. Human *RIG-I* is located on chromosome 9p12 and encodes a 925-amino-acid protein that contains the RNA helicase-DEAD box motif. It is highly conserved from *Caenorhabditis elegans* to mammals and is expressed ubiquitously in the human and mouse. Originally, *RIG-I* was found to be induced in the acute promyelocytic leukemia cell line NB4 during ATRA-induced cell differentiation, suggesting that *RIG-I* might be an important mediator in the ATRA-signaling pathway [1]. Most importantly, *RIG-I* was recently identified as an essential regulator for virus-induced antiviral

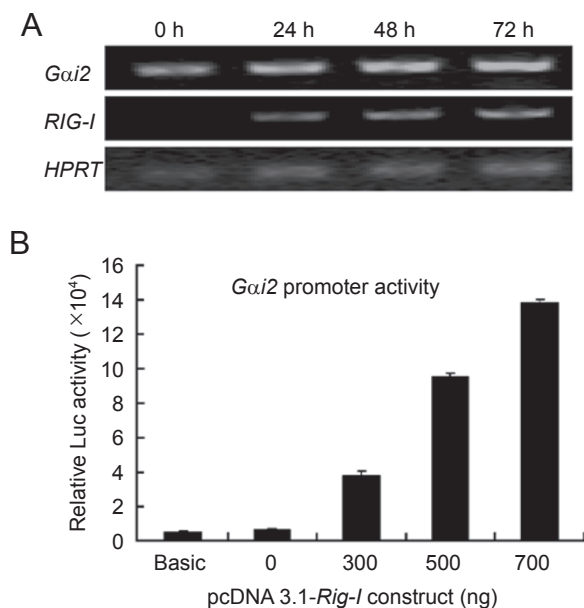


Figure 6 Induction of *Gai2* promoter activity by Rig-I. **(A)** NB4 cells were treated with 1 μ M ATRA for the time indicated, and total RNA was extracted. Induction of *RIG-I* and *Gai2* expression was analyzed by semi-quantitative RT-PCR. *HPRT* served as a control. The data shown represent one of the three independent experiments. **(B)** NIH3T3 cells were co-transfected with the *Gai2* promoter luciferase reporter construct, *Renilla* luciferase and pcDNA3.1-*Rig-I* with increasing amounts (0, 300, 500 and 700 ng), or pcDNA3.1. Forty-eight hours after transfection, *Gai2* promoter-driven luciferase activity was highly activated with increasing amounts of *Rig-I*-expressing vector present. The results shown represent one of three independent experiments.

immunity, capable of sensing intracellular viral dsRNA, which transduces signals through an adaptor protein (MAVS/IPS-1/VISA/Cardif), leading to the activation of IRF-3 and NF- κ B, and augmenting interferon production in response to viral infection [4-11]. The *in vivo* importance of Rig-I in antiviral defense was further demonstrated in *Rig-I*-deficient mice, in which exons 8 to 10 of *Rig-I* were deleted, by showing the cell-type-specific requirements for Rig-I in the antiviral response [13]. Unfortunately, *Rig-I* knockout mice generated by Akira's group mostly died during embryogenesis, and a few newborn mice died within 3 weeks after birth owing to extensive apoptosis in the fetal liver. In this study, we also generated *Rig-I* knockout mice, in which 5 exons (exons 4 to 8) encoding part of CARD domain 2, and the A and B motifs of the RNA helicase domain (aa141-405) were replaced with a *Neo* cassette by homologous recombination. Disruption of Rig-I was demonstrated by northern blot analysis using

the 3'-end fragment of *Rig-I* cDNA (477 bp, composed of exons 11 to 14) as a probe, and by western blot analysis using the polyclonal antibody specific to RIG-I. Unlike the previous study [13], our homozygous *Rig-I* knockout mice were viable and fertile. The genotype distribution in the littermates obtained from crossing heterozygote mice follows a Mendelian pattern of inheritance. MEFs derived from our *Rig-I*^{-/-} mice also showed a compromised antiviral response, similar to the previous report (unpublished data). However, the *Rig-I*^{-/-} mice displayed significant age-dependent loss of body weight. Extensive pathological analysis showed that 70% of adult *Rig-I*^{-/-} mice spontaneously developed a colitis-like phenotype with increased susceptibility to DSS-induced colitis. The different outcomes between our mutant mice and that reported by Kato *et al.* [13] likely result from the disruption of different regions of the *Rig-I* gene. In fact, this kind of phenomenon is not uncommon in mouse mutagenesis studies. A typical example emerged from the comparison of the phenotypes represented by three different *Prnp*^{-/-} mice [40]. This could be explained by the different truncated proteins that are expressed after genomic modification, although they may be expressed at very low levels. In our case, this possibility could not be excluded, but northern or western blotting detected no signals that correspond to truncated Rig-I messages or proteins. The *Rig-I*^{-/-} mice we generated survived and displayed a colitis-like phenotype, providing us an alternative model for studying the mechanisms that underlie inflammatory bowel disease, including colitis.

Inflammatory bowel disease is considered to be associated with a breakdown of tolerance to the resident intestinal flora [41, 42] and immune activation in the gut-associated lymphatic tissue (GALT). The GALT consists of Peyer's patches and mesenteric lymph nodes as organized intestinal lymphoid follicles. Previous studies have shown that a deficiency of Peyer's patches and mesenteric lymph nodes may be in part responsible for the development of colitis in mice. It is known that intraluminal and intestinal wall antigens have the capacity to induce tolerance toward inflammatory intestinal immune responses. A reduction in the number of Peyer's patches and mesenteric lymph nodes, especially the loss of normally present regulatory cells (such as dendritic cells) in these organs, may result in the failure of tolerance induction in the gut [43]. Therefore, the decrease in Peyer's patches that is due to increased apoptosis is, to some degree, related to the induction of colitis in *Rig-I*^{-/-} mice.

It has been shown that the disruption of several genes in mice leads to chronic inflammation of the bowel [17, 44-46]. Among them, *Gai2*-deficient mice display growth retardation and develop lethal diffuse colitis with clinical and histopathological features that closely resemble ulcerative colitis in humans [17]. It has also been shown that

Gai2^{-/-} mice exhibit a local increase in memory CD4⁺ and CD8⁺ cells that are characterized by increased levels of CD44 and decreased levels of CD45RB and CD62L, an increase in pro-inflammatory Th1-type cytokines and an increase in the infiltration of activated CD4⁺ T cells in the intestinal mucosa [47, 48]. All of these findings strongly suggest that *Gai2*-deficiency leads to a hyperimmune response and that the *Gai2* protein may negatively regulate T-cell immunity [17, 24, 47].

The regression of Peyer's patches and development of colitis in *Rig-I*^{-/-} mice raise the possibility that Rig-I may play a part in the regulation of T-cell homeostasis. As expected, we found that Rig-I deficiency leads to an increase in splenic CD4⁺ and CD8⁺ effector T cells with a decrease of naïve T cells, indicating the hyper-activation of effector T cells in *Rig-I*^{-/-} mice. These data also suggest an important role for Rig-I in the regulation of T-cell activation.

Gai2^{-/-} mice display colitis with 100% penetrance with smaller Peyer's patches and *Gai2*^{-/-} mice also exhibit disorders of the T-cell subsets [16]. These observations suggest that there may be a link between Rig-I and *Gai2*. Therefore, we examined *Gai2* expression in various tissues of wild type and *Rig-I*^{-/-} mice. As expected, *Gai2* expression decreased distinctly in many tissues of *Rig-I*^{-/-} mice, especially in the colons and intestines. On the contrary, up-regulation of Rig-I in NB4 cells upon treatment with ATRA is accompanied by elevated *Gai2* expression. Luciferase assay further demonstrated that Rig-I can markedly activate *Gai2* promoter activity in a dose-dependent manner. Based on these findings, we propose that Rig-I may function as a positive regulator for *Gai2* transcription.

In this report, we identified a novel role of Rig-I in T-cell activation and *Gai2* expression by showing the distinct phenotypes of *Rig-I*^{-/-} mice. The development of colitis in *Rig-I*^{-/-} mice might be in part associated with the downregulation of *Gai2* and disturbed T-cell homeostasis.

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