

発表者氏名	論文タイトル名	発表雑誌名	巻	頁	出版年
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<u>松本功</u>	薫風吹く膠原病診療—臨床を駆ける進歩の風—シェーグレン症候群	内科	in press		
<u>松本功</u>	K/BxNマウス—血清移入関節炎—	Clinical Calcium	in press		
<u>松本功</u>	関節リウマチにおける自己抗体の病態への関与	リウマチ科	in press		
井上明日香、 <u>松本功</u> 、住田孝之	TIARPによる炎症性サイトカインの産生抑制	臨床免疫・アレルギー科	in press		
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		リウマチ・膠原病内科 クリニカルスタンダード	東京	30-34
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V 平成22年度班会議プログラム

プログラム

13 : 00～13 : 05 開会の辞

13 : 05～13 : 15 厚生労働省 挨拶

13 : 15～ 研究発表

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T細胞分化誘導分子の強発現による自己免疫疾患制御法の開発に関する研究
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住田 孝之

2. 13 : 35～13 : 55

免疫疾患における TH1/TH2 細胞の役割と制御に関する研究
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高橋 智

3. 13 : 55～14 : 15

Collagen induced arthritis (CIA)における樹状細胞の役割と機能の解析
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4. 14 : 15～14 : 35

TNF α 誘導性 TIARP の自己免疫性関節炎における役割と、RA 患者における
シトルリン化 GPI 抗体の同定に関する研究
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松本 功

5. 14 : 35～14 : 55

TREM1 及びそのリガンド修飾による免疫疾患制御法の開発
東京医科歯科大学大学院医歯学総合研究科膠原病・リウマチ内科学
上阪 等

… … … コーヒーブレイク 14:55～15:10 … … …

6. 15:10～15:30

自己免疫疾患における免疫担当細胞のシグナル異常とその制御
(関節リウマチにおける RasGRP4 の発現検討)

北海道大学大学院医学研究科 内科学講座・第二内科
小池 隆夫

7. 15:30～15:50

関節炎モデルにおける MR1 拘束性 MAIT 細胞の役割に関する研究

国立精神・神経センター神経研究所免疫研究部
山村 隆

8. 15:50～16:10

CD4 陽性 CD25 陰性 LAG3 陽性制御性 T 細胞の抗体産生抑制能に関する研究

東京大学医学部アレルギーリウマチ内科
藤尾 圭志

9. 16:10～16:30

自己免疫疾患におけるケモカイン・ケモカインレセプターの役割と制御戦略に関する研究：SLE モデルにおける抗 BLC 中和抗体の治療効果の検討

東京大学大学院医学系研究科
石川 昌

10. 16:30～16:50

SLE における自己抗体産生機構と B 細胞を分子標的とした治療戦略に関する研究

産業医科大学医学部第一内科学講座
田中良哉

16:50～16:55 閉会の辞

VI 研究成果刊行物・別刷



Contents lists available at ScienceDirect

Journal of Autoimmunity

journal homepage: www.elsevier.com/locate/jautimm

Pathogenic role of immune response to M3 muscarinic acetylcholine receptor in Sjögren's syndrome-like sialoadenitis

Mana Iizuka^{a,1}, Ei Wakamatsu^{a,b,1}, Hiroto Tsuboi^a, Yumi Nakamura^{a,c}, Taichi Hayashi^a, Minoru Matsui^d, Daisuke Goto^a, Satoshi Ito^a, Isao Matsumoto^a, Takayuki Sumida^{a,*}

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ARTICLE INFO

Article history:

Received 16 May 2010

Received in revised form

20 August 2010

Accepted 22 August 2010

Keywords:

Sjögren's syndrome

M3 muscarinic acetylcholine receptor

Autoimmune disease

Autoreactive T cells

ABSTRACT

The aim of this study was to clarify the role of the immune response to muscarinic type 3 receptor (M3R) in the pathogenesis of Sjögren's syndrome (SS). M3R^{-/-} mice were immunized with murine M3R peptides and their splenocytes were inoculated into Rag1^{-/-} (M3R^{-/-} → Rag1^{-/-}) mice. M3R^{-/-} → Rag1^{-/-} mice had high serum levels of anti-M3R antibodies and low saliva volume. Histological examination showed marked infiltration of mononuclear cells in the salivary glands and immunohistochemistry demonstrated that the majority of these cells were CD4⁺ T cells with a few B cells and several IFN-γ- and IL-17-producing cells. Apoptotic cells were present in the salivary glands of M3R^{-/-} → Rag1^{-/-} mice. Moreover, transfer of only CD3⁺ T cells from M3R^{-/-} immunized with M3R peptides into Rag1^{-/-} mice resulted in cell infiltration and destruction of epithelial cells in the salivary glands, suggesting that M3R reactive CD3⁺ T cells play a pathogenic role in the development of autoimmune sialoadenitis. Our findings support the notion that the immune response to M3R plays a crucial role in the pathogenesis of SS-like autoimmune sialoadenitis.

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1. Introduction

Sjögren's syndrome (SS) is a chronic autoimmune disease characterized by infiltration of lymphocytes into lacrimal and salivary glands, and clinically by dry eyes and dry mouth [1]. Immunohistochemical studies have shown that most infiltrating lymphocytes around the labial salivary and lacrimal glands are CD4-positive αβ T cells [2]. B cells are also detected in inflammatory lesions and act as antigen-presenting cells (APC) and produce autoantibodies such as anti-Ro/SSA and anti-La/SSB antibodies. Previous studies analyzed autoantigens recognized by T cells infiltrating the labial salivary glands of patients with SS and several candidate autoantigens such as Ro/SSA 52 kDa, [3] α-amylase, [4] heat shock protein, T cell receptor BV6 [5] and M3 muscarinic acetylcholine receptor (M3R) [6,7] have been identified.

M3R is the major muscarinic acetylcholine receptor in the salivary glands. Studies in M3R knockout (M3R^{-/-}) mice showed the

involvement of these receptors in saliva secretion [8], suggesting that dysfunction of the M3R signaling in salivary glands can lead to a decrease in salivary secretion. The presence and specificity of anti-M3R antibodies in SS have been investigated using enzyme-linked immunosorbent assay (ELISA) or flow cytometry assay [9,10]. Robinson et al. [11] demonstrated that human anti-M3R antibodies reduced salivary secretion in NOD Iγμ^{null} mice. We also reported previously the presence of M3R reactive T cells in some patients with SS [12]. At this stage, however, it is not clear whether the immune response to M3R plays a role in the onset and progression of SS.

Amagai et al. [13] described a mouse model of pemphigus vulgaris (PV) using the combination of desmoglein 3 knockout (Dsg3^{-/-}) mice without Dsg3 and adoptive splenocytes transfer to lymphocyte-free Dsg3-positive Rag2^{-/-} mice (Dsg3^{-/-} → Rag2^{-/-}). In the Dsg3^{-/-} → Rag2^{-/-} mice, the Dsg3 molecule induces a powerful immune response and the cells break self-tolerance and attack Dsg3 autoantigens. The same approach might be applicable to T cell-mediated autoimmune disease as well as antibody-mediated disease such as PV.

Our research interest is the pathogenic role of the immune response against M3R in patients with SS. In the present study, we

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immunized M3R^{-/-} mice with murine M3R peptides and transferred their splenocytes into Rag1^{-/-} mice (M3R^{-/-} → Rag1^{-/-}). We succeeded in establishing M3R-induced SS-like sialoadenitis in M3R^{-/-} → Rag1^{-/-} mice as a new murine model of SS. The results also showed that CD3⁺ T cells play a crucial role in the generation of autoimmune sialoadenitis. We also discuss the possible molecular mechanism of M3R-induced autoimmunity in SS.

2. Materials and methods

2.1. Mice

C57BL/6j (B6) mice (M3R^{+/+}) were purchased from Charles River Laboratory (Yokohama, Japan). Rag1^{-/-} mice were purchased from The Jackson Laboratory (Bar Harbor, ME). M3R^{-/-} mice, which were generated from B6 mice, were kindly supplied by Dr. Matsui (Tokyo-Nishi Tokushukai Hospital, Tokyo, Japan). Mice were maintained under specific pathogen-free conditions in the Laboratory Animal Resource Center. All experiments were performed according to the Guidelines for the Care and Use of Laboratory Animals at Tsukuba University.

2.2. Synthesized peptides encoding M3R extracellular regions

Six types of peptides encoding murine M3R extracellular domains: N-terminus 1 (MTLHNSNTTSPFPNIISSWVHSPSEAGLP, N1), N-terminus 2 (VHSPSEAGLPLGTVSQDLSYNISGTSNFS, N2), N-terminus 3 (NISQTSGNFSSNDTSSDPLGGHTIWQV, N3), 1st extracellular loop (FTTYIIMNRWALGNLACDLW, 1st), 2nd extracellular loop (QYFVGKRTVPPGECFIQFLSEP, 2nd) and 3rd extracellular loop (VLVNTFCDSICPKTYWNLGY, 3rd), were synthesized chemically by a solid-phase procedure and purified by high performance liquid chromatography (AnyGen, Korea).

2.3. Immunization of mice

M3R^{+/+} and M3R^{-/-} mice were immunized intradermally at the base of the tail with a mixture of free-form extracellular peptides (each 20 µg) in Incomplete Freund's Adjuvant (IFA, Difco, Detroit, MI) containing 250 µg of inactivated *Mycobacterium tuberculosis* (H37RA, Difco). Pertussis toxin (500 ng; Sigma–Aldrich, Tokyo, Japan) was injected intraperitoneally on the day of immunization. On day 10, each mouse received another intradermal injection of the same mixture of peptides (each 20 µg) emulsified with IFA containing 250 µg of H37RA (Fig. 1A).

2.4. Analysis of cytokine profiles

On day 20 after the first immunization, the spleen was isolated from each M3R^{+/+} and M3R^{-/-} mouse and homogenized. The red blood cells were removed from the splenocytes by treatment with 0.16 M NH₄Cl solution. Then, the homogenates were adjusted to 1 × 10⁶ cells/ml and incubated with RPMI-1640 supplemented with 10% fetal bovine serum (FBS), 1000 U/ml penicillin, 100 µg/ml streptomycin and 55 µM 2-mercaptoethanol, together with a mixture of extracellular peptides (each 5 µg/ml) for 72 h under 5% CO₂ at 37 °C. After collection of the supernatant, the levels of IFN-γ, IL-4 and IL-17 were measured by enzyme-linked immunosorbent assay (ELISA) (IFN-γ, IL-4, and IL-17; R&D Systems Minneapolis, MN).

2.5. Adoptive transfer and cell sorting

On day 20 after the first immunization, the spleens were isolated from M3R^{+/+} and M3R^{-/-} mice. The spleens from each group of mice (each *n* = 3) were pooled and homogenized. The red blood

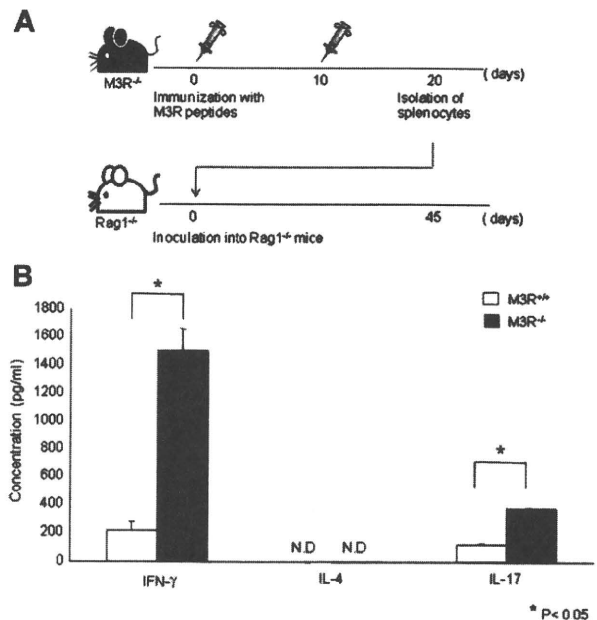


Fig. 1. Cytokine profile of M3R reactive T cells in M3R^{-/-} mice immunized with M3R peptides. (A) M3R^{-/-} and M3R^{+/+} mice were immunized with a murine M3R peptide mixture on days 0 and 10. On the day of immunization, 500 ng of pertussis toxin was injected intraperitoneally. Ten days after booster immunization, the spleens were isolated and transferred into Rag1^{-/-} mice. At day 45 after the transfer, the salivary glands of Rag1^{-/-} recipient mice were analyzed histologically. (B) M3R^{-/-} and M3R^{+/+} mice were immunized followed by a booster dose of M3R peptides mixture emulsified in IFA plus *M. tuberculosis*. Ten days later, the spleens were isolated from M3R^{+/+} and M3R^{-/-} mice and stimulated with the M3R peptides mixture. The concentrations of IFN-γ, IL-4 and IL-17 in the culture supernatants were measured by enzyme-linked immunosorbent assay. N.D.: not detected. Values are mean ± SD of three independent experiments (*n* = 3 mice per experiment). **P* < 0.05 (Mann–Whitney *U* test).

cells were removed from the splenocytes by treatment with 0.16 M NH₄Cl solution. After washing with phosphate buffered saline (PBS), the cells were resuspended in PBS.

CD3⁺ T cells were sorted from splenocytes of M3R^{+/+} and M3R^{-/-} by using the Pan T cell isolation kit (Miltenyi Biotec, Bergisch Gladbach, Germany). The high purity of CD3⁺ T cells (>93%) was confirmed by FACSCalibur (BD PharMingen, San Diego, CA). Cells were resuspended in PBS and 1 × 10⁷ cells were inoculated intravenously into Rag1^{-/-} mice (Fig. 1A).

2.6. Measurement of salivary volume

Mice were first anesthetized with intraperitoneal injection of pentobarbital (1.0 mg/kg), then injected subcutaneously with pilocarpine (25 mg/kg). This was followed 15 min later by collection of saliva from the oral cavity using a 200-µl micropipette. The volume of the sample was measured and expressed relative to body weight. Changes in saliva volume were calculated relative to the volume measured at baseline, using the formula [dayN saliva volume (ml)/weight (g)]/[day0 saliva volume (ml)/weight (g)].

2.7. Analysis of antibody levels by enzyme-linked immunosorbent assay

The peptide solution containing all types of extracellular peptides (each 5 µg/ml) was mixed with 0.1 M Na₂CO₃ buffer, pH 9.6, adsorbed onto a Nunc-Immunoplate (Nalge Nunc Int, Rochester, NY) at 4 °C overnight, then blocked with 1% bovine serum

albumin (Wako Pure Chemical Industries, Osaka, Japan) in PBS for 1 h at room temperature. Serum at 1:50 dilution in blocking buffer was incubated for 2 h at room temperature. The plates were then washed five times with 0.05% Tween 20 in PBS, and HRP-conjugated anti-mouse IgG antibody diluted 1:1000 in blocking buffer was added for 1 h at room temperature. After washing, 100 μ l of TMB solution (Kirkegaard & Perry Laboratories, Inc, Washington, DC) was added as a substrate and then the plates were incubated for 15 min at room temperature in the dark. After adding 50 μ l of 1 M phosphate buffer to stop the enzymatic reaction, the optical density was measured at 450 nm by plate spectrophotometry (Bio-Rad Laboratories, Hercules, CA).

2.8. Histological score

The inflammatory lesions were graded histologically (histological score) using the method proposed by Greenspan et al. [14] as follows: focus score was described as the number of a focus composed of >50 mononuclear cells per 4 mm² of tissue. Histological evaluation of the salivary glands was performed in a blind manner, and at least one tissue section from each salivary gland was examined.

2.9. Immunohistochemical analysis

Sections of the salivary glands were thawed, dried, and then fixed with acetone for 10 min. They were incubated with biotin-conjugated anti-mouse CD4, CD8, I-A^b, CD11c (Biolegend, San Diego, CA), rat anti-mouse Thy1 (Santa Cruz Biotechnology, Santa Cruz, CA), rat anti-mouse B220, CD86, F4/80 (Biolegend) or HRP-conjugated rabbit anti-mouse IgG antibodies (DAKO, Japan) for 2 h. To detect primary antibodies, horseradish peroxidase (HRP)-conjugated streptavidin or HRP-conjugated anti-rat IgG antibodies were added for 30 min. HRP activity was detected using 3,3'-diaminobenzidine (DAB; Nichirei, Tokyo) as a substrate. The stained sections were counterstained with Mayer's hematoxylin for 30 s, and mounted with aqueous medium. Control slides were incubated with a dilution buffer containing isotype-matched antibodies instead of the primary antibodies.

Double immunofluorescence staining was performed as follows: Sections of the salivary glands were thawed, dried, and then fixed with 4% paraformaldehyde PBS (Wako) for 10 min. The sections were incubated with rat anti-mouse IFN- γ (Biolegend) and rat anti-mouse IL-17 antibodies (Santa Cruz Biotechnology) for 30 min. To detect primary antibodies, Alexa Fluor 546 goat anti-rat IgG antibody was added for 30 min. The nuclear DNA was stained with DAPI (Sigma–Aldrich).

2.10. Terminal deoxynucleotidyl transferase-mediated nick and labeling staining

Apoptotic cells were detected by *in situ* apoptosis detection kit (Takara Biomedicals, Tokyo). Briefly, frozen sections were fixed with 4% paraformaldehyde for 30 min. Endogenous peroxidase activity was blocked with 0.3% hydrogen peroxidase/methanol. After washing in PBS, the sections were treated for 5 min on ice with the permeabilisation buffer and then incubated with TdT enzyme reaction for 90 min at 37 °C. An HRP-conjugated anti-FITC antibody was added for 30 min at 37 °C, and the HRP activity was detected using DAB as a substrate. Nuclei were counterstained with hematoxylin.

2.11. Statistical analysis

Data were expressed as mean \pm SD. Differences between groups were examined for statistical significance using the Mann–Whitney *U* test. *P* values less than 0.05 were considered significant.

3. Results

3.1. High production of IL-17 and IFN- γ by splenocytes of M3R^{-/-} mice

To compare the immune response to M3R between in M3R^{-/-} and M3R^{+/+} mice, both groups of mice were immunized with the M3R peptide mixture and their splenocytes were cultured with M3R *in vitro* at 20 days after first immunization (Fig. 1A). As shown in Fig. 1B, the production of IL-17 and IFN- γ by splenocytes of immunized M3R^{-/-} mice far exceeded that of M3R^{+/+} mice. On the other hand, IL-4 production was below the detection level in both groups. These results suggest a higher immune response to M3R in M3R^{-/-} than M3R^{+/+} mice.

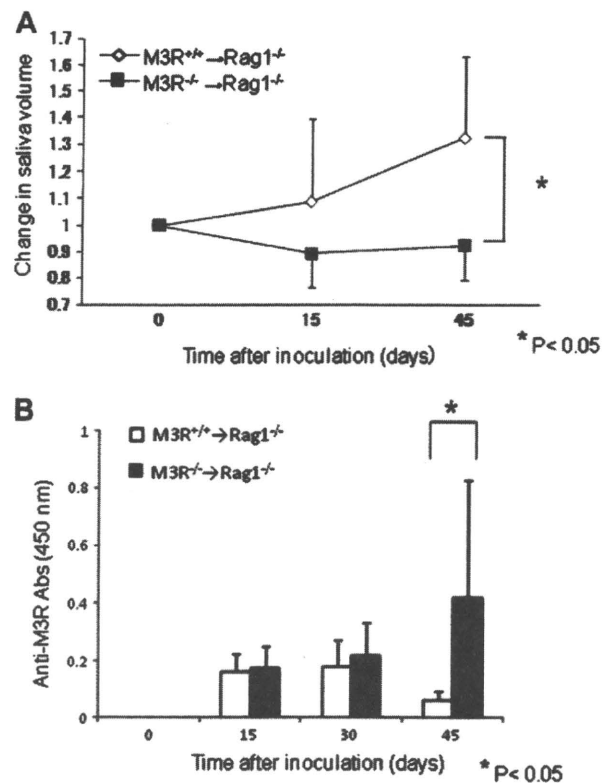


Fig. 2. Reduced salivary secretion and increased levels of anti-M3R antibodies in M3R^{-/-} → Rag1^{-/-} mice. Rag1^{-/-} mice inoculated with splenocytes from immunized M3R^{+/+} and M3R^{-/-} mice by intravenous injection into the tail vein. (A) Saliva was collected from Rag1^{-/-} mice at 0, 15, 45 days after the adoptive transfer. The saliva samples were collected from each mouse 15 min after stimulation with pilocarpine. The volume of each saliva sample was measured and adjusted for body weight, and calculated relative to the volume measured at baseline, using the formula [dayN saliva volume (μ l)/weight (g)]/[day0 saliva volume (μ l)/weight (g)]. (B) Titer of anti-M3R antibodies in sera of Rag1^{-/-} mice obtained at days 0, 15, 30, and 45 after adoptive transfer, determined by ELISA. **P* < 0.05 versus saliva volume and M3R antibodies derived from Rag1^{-/-} mice inoculated with splenocytes of immunized M3R^{+/+} mice at the same time point, by Mann–Whitney *U* test. Values are mean \pm SD of two independent experiments (*n* = 6 mice per experiment).

3.2. Development of sialoadenitis in $Rag1^{-/-}$ mice inoculated with splenocytes from immunized $M3R^{-/-}$ mice

To expose M3R reactive cells to the antigen, we isolated splenocytes from the immunized $M3R^{-/-}$ and $M3R^{+/+}$ mice and inoculated them into M3R-positive $Rag1^{-/-}$ mice (Fig. 1A). First, we examined saliva volume at days 0, 15, and 45 to determine the effect of inoculation of splenocytes of immunized $M3R^{-/-}$ or $M3R^{+/+}$ mice in $Rag1^{-/-}$ mice. The saliva volume decreased gradually from day 15–45 in $Rag1^{-/-}$ mice inoculated with splenocytes of $M3R^{-/-}$ mice compared with those inoculated with splenocytes of $M3R^{+/+}$ mice (Fig. 2A). At day 45 after the cell transfer, serum anti-M3R antibodies were significantly higher in $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice than $M3R^{+/+} \rightarrow Rag1^{-/-}$ mice (Fig. 2B).

To examine the influence of transferred splenocyte from $M3R^{-/-}$ or $M3R^{+/+}$ immunized with the M3R peptides on salivary glands of $Rag1^{-/-}$ mice, $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice and $M3R^{+/+} \rightarrow Rag1^{-/-}$ mice were analyzed histologically. Histological examination of mice at day 45 after inoculation showed marked mononuclear infiltration in the salivary glands and lacrimal glands of $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice but not in $M3R^{+/+} \rightarrow Rag1^{-/-}$ mice (Fig. 3A). However, no inflammatory lesions were observed in the intestine or liver (Fig. 3C). Quantitative analysis of the inflammatory lesions of the salivary glands indicated a higher histological score for $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice than $M3R^{+/+} \rightarrow Rag1^{-/-}$ mice (Fig. 3B). These results suggested that autoimmune response against M3R-induced infiltration of mononuclear cells in the salivary glands and salivary dysfunction.

To characterize the infiltrating cells in the inflammatory lesions of salivary glands, the frozen sections were analyzed immunohistochemically. The majority of infiltrating cells in $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice were $Thy1^+ CD4^+$ T cells, with only few $CD8^+$ T cells. Other cells such as $B220^+$, $CD11c^+$ cells and macrophage formed a minor population and were localized around T cells (Fig. 4A). Furthermore, deposition of IgGs was sometimes noted in the salivary glands of $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice (Fig. 4A). MHC class II and CD86 were expressed in ductal epithelial cells of the inflammatory lesions of salivary glands from $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice, suggesting that activated epithelial cells acted as APC.

We also examined cytokine production in the salivary glands of $M3R^{-/-} \rightarrow Rag1^{-/-}$ by immunofluorescence staining. The salivary glands of $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice, but not those of $M3R^{+/+} \rightarrow Rag1^{-/-}$ mice, showed differential expression of $IFN-\gamma$ and IL-17 (Fig. 4B). A few apoptotic cells were noted in the lesions of salivary glands isolated from $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice on TUNEL staining (Fig. 4D), which might explain the salivary destruction and dysfunction.

3.3. M3R reactive T cells and development of sialoadenitis

The above findings indicated that the infiltrated cells in the salivary glands of $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice were mainly T cells. To confirm that M3R reactive T cells play a role in the development of sialoadenitis in $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice, we transferred purified splenic $CD3^+$ T cells or $CD3^+$ T cells-free splenocytes ($CD3^-$ cells) from $M3R^{-/-}$ mice immunized with M3R peptides mix into $Rag1^{-/-}$ mice ($M3R^{-/-} CD3^+$

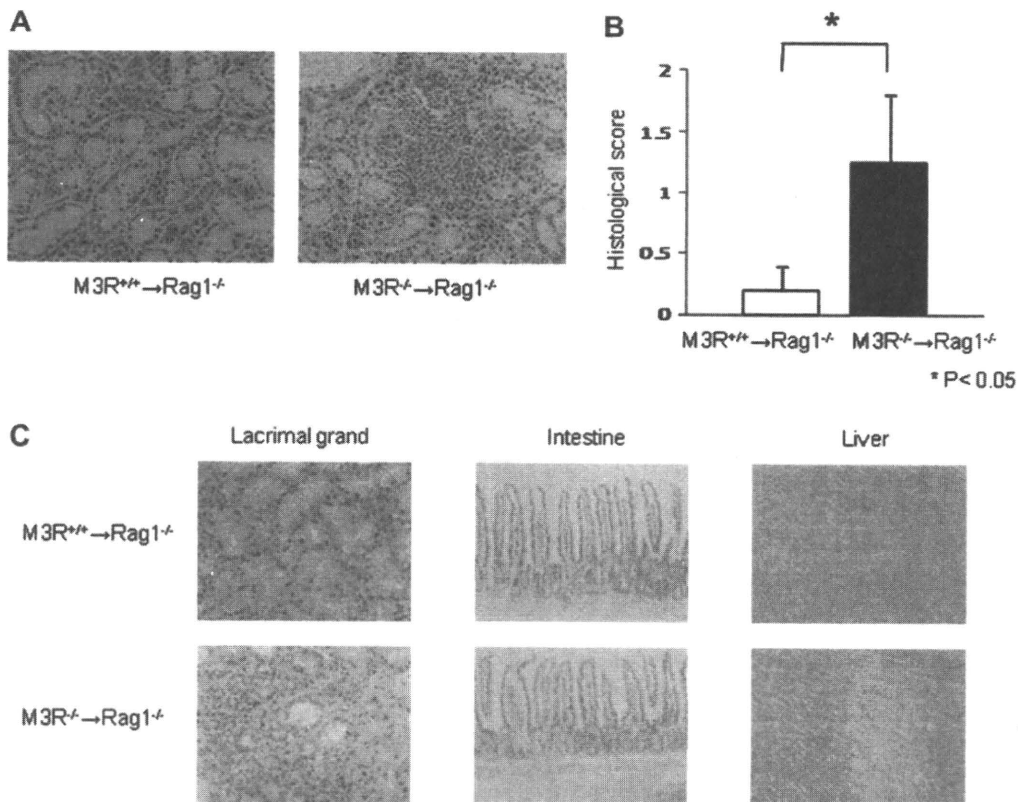


Fig. 3. Infiltration of salivary glands in $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice. Salivary glands isolated from $Rag1^{-/-}$ mice at day 45 after inoculation of splenocytes from immunized $M3R^{-/-}$ and $M3R^{+/+}$ mice. (A) Salivary glands were prepared into 4- μ m thick sections, and each section was stained with Mayer's hematoxylin and eosin (H&E). Representative images of five to seven mice in each group. (B) Mean grade (histological score) of inflammatory lesions in salivary glands of $M3R^{+/+} \rightarrow Rag1^{-/-}$ and $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice. Values are mean \pm SD of five mice. (C) H&E-stained sections of the lacrimal glands, intestine and liver isolated from $M3R^{+/+} \rightarrow Rag1^{-/-}$ mice and $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice. (Original magnification 100 \times).

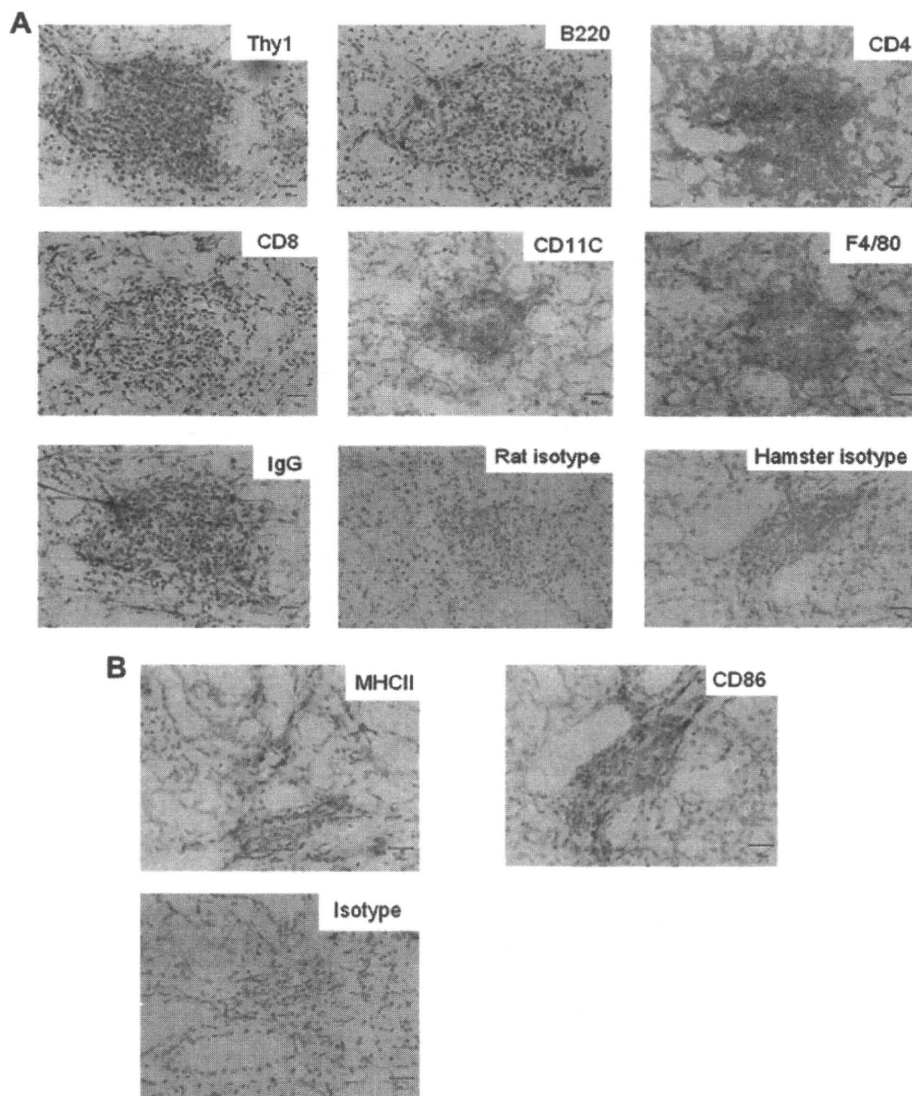


Fig. 4. Histological analysis of salivary glands isolated from $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice. (A) Inflammatory lesions in salivary glands of $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice stained with anti-Thy1, B220, CD4, CD8, CD11c, F4/80 as macrophage specific marker, IgG antibodies and control antibodies. Representative images of five to seven mice. (B) Expression of MHC class II and CD86 detected by immunohistochemistry using anti-I-A^b, CD86 and control antibodies. Representative images of three to five mice. (C) Immunofluorescence analysis of IFN- γ and IL-17 in salivary glands of $M3R^{+/+} \rightarrow Rag1^{-/-}$ and $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice. The stained sections were counterstained with H&E, and mounted with aqueous medium. Stained sections were observed at 100 \times original magnification. Representative images of three to five mice from each group. (D) Apoptotic cells in sections of salivary glands of $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice detected by the TUNEL method. Note the presence of a few apoptotic cells in the salivary glands of $M3R^{+/+} \rightarrow Rag1^{-/-}$ mice. Representative images of three to five mice from each group. Bars = 30 μ m.

cells $\rightarrow Rag1^{-/-}$ mice or $M3R^{-/-} CD3^{-}$ cells $\rightarrow Rag1^{-/-}$ mice). The purity of $CD3^{+}$ T cells was 93.6% and $CD3^{-}$ T cell included only 1.6% of $CD3^{+}$ T cells (Fig. 5A). Histological analysis showed marked cell infiltration in the salivary glands of $M3R^{-/-} CD3^{+}$ cells $\rightarrow Rag1^{-/-}$ mice, but not in $M3R^{-/-} CD3^{-}$ cells $\rightarrow Rag1^{-/-}$ mice (Fig. 5A). The majority of infiltrating cells in the salivary glands of $M3R^{-/-} CD3^{+}$ cells $\rightarrow Rag1^{-/-}$ mice were $Thy1^{+} CD4^{+}$ T cells, compared with only a few $CD8^{+}$ T cells (Fig. 5B). These findings suggest that M3R reactive T cells play a crucial role in the pathogenesis of sialoadenitis in the $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice.

4. Discussion

Our previous results (6) demonstrated that 14% of patients with SS harbor autoantibodies against M3R in their sera. In another study, we also reported that peripheral lymphocytes of 4 out of 9 patients

with SS included M3R-reactive T cells (12). These results suggested that the underlying pathomechanism of sialoadenitis in patients with SS could perhaps involve the immune response to M3R. The present study is an extension to our previous investigation and was designed to clarify the role of the M3R reactive immune response in the development of SS. For this purpose, $M3R^{-/-}$ mice were immunized with M3R peptides, their splenocytes were transferred into $Rag1^{-/-}$ mice, and the development of SS-like sialoadenitis was examined. Our results showed the development of mild to severe sialoadenitis in the salivary glands of $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice, indicating the involvement of the M3R reactive immune response in the development of sialoadenitis. The infiltrating cells in the salivary glands of $M3R^{-/-} \rightarrow Rag1^{-/-}$ mice were mainly $CD4^{+}$ T cells with a few surrounding B cells. The histological findings resemble those of infiltration of lymphocyte subset in the labial salivary glands of

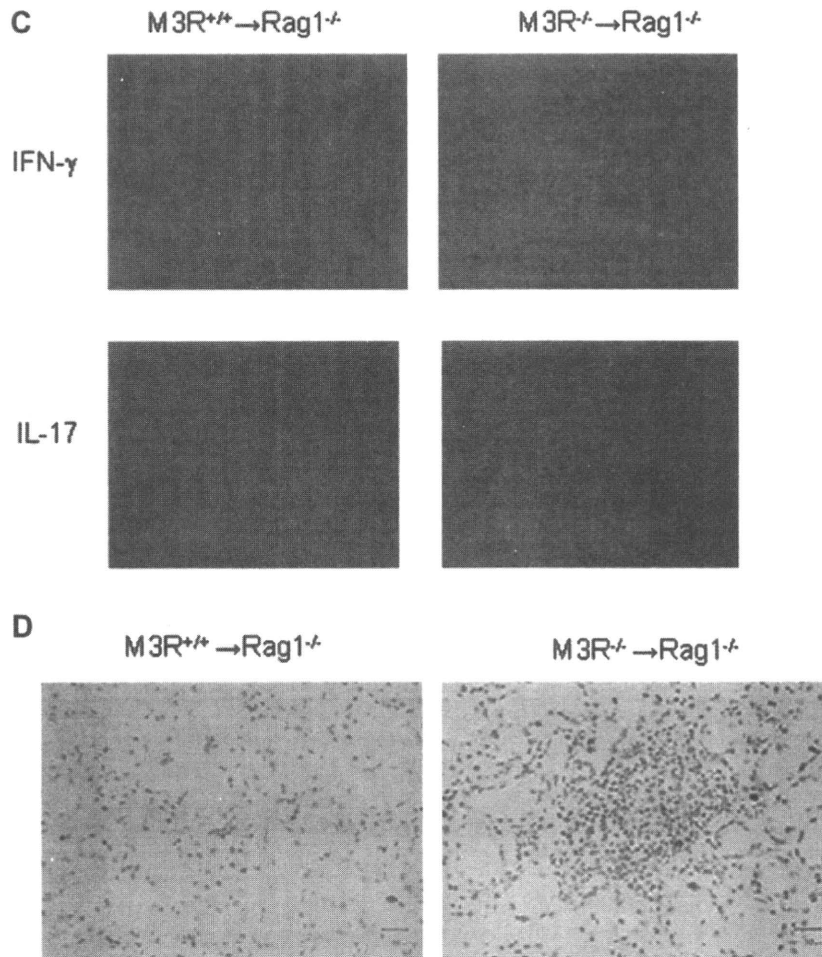


Fig. 4. (continued).

patients with SS [15]. Moreover, the M3R^{-/-} \rightarrow Rag1^{-/-} mice had high levels of anti-M3R antibodies and low saliva volume, similar to patients with SS. Previous studies analyzed the levels of anti-M3R antibodies in patients with SS by three methods including peptide-based ELISA, flow cytometry assay and western blot analysis [9,16,17]. Previously, we established peptide-based ELISA for detection of anti-M3R antibodies in SS patients [10,12] and thus applied this method in our mouse model in this study. The results suggest that the M3R molecule acts as an autoantigen to induce an autoimmune reaction in some patients with SS as well as experimental M3R-induced sialoadenitis.

What is the mechanism of M3R-induced sialoadenitis in our mouse model? In M3R^{-/-} \rightarrow Rag1^{-/-} mice, anti-M3R autoantibodies were detected in the serum. IFN- γ - and IL-17-producing cells were also detected in the salivary glands of M3R^{-/-} \rightarrow Rag1^{-/-} mice. Moreover, the adoptive CD3⁺ T cell transfer experiments showed that CD3⁺ T cells are essential for the development of sialoadenitis in M3R^{-/-} \rightarrow Rag1^{-/-} mice. Thus, M3R reactive T cells are important in the development of antigen-induced sialoadenitis in our mouse model. Although we have no direct evidence in support of a pathogenic role for IFN- γ -producing Th1 cells or IL-17-producing Th17 cells, the latter type of cells might be important in the pathogenesis of M3R-induced sialoadenitis, because none of the IFN- γ dominant T-bet transgenic mice immunized with M3R peptides developed sialoadenitis (data not shown). In this regard,

recent studies reported the expression of IL-17 in the salivary glands of patients with SS [18,19]. Thus, further studies using IFN- γ ^{-/-} mice or IL-17^{-/-} mice are necessary.

Why does the combination of M3R^{-/-} mice immunized with M3R peptides and Rag1^{-/-} mice enhance the generation of antigen-driven sialoadenitis? It is possible that immunization using a mixture of M3R peptides that includes the N region, and the 1st, 2nd, and 3rd extracellular domains of the M3R molecule, could have induced the immune response against exogenous antigens such as M3R in M3R^{-/-} mice. In fact, M3R reactive T cells and anti-M3R antibodies appeared in M3R^{-/-} mice immunized with M3R peptides. It is possible that these M3R reactive lymphocytes proliferate in Rag1^{-/-} mice and attack the M3R molecule expressed in their own salivary glands, resulting in sialoadenitis.

Why is tolerance to M3R autoantigens broken down in patients with SS? While there is no evidence for the expansion of M3R reactive T cells and B cells in the salivary glands of patients with SS, it is possible that overexpression of M3R autoantigen on APC present in the salivary glands plays a role in the induction of M3R lymphocytes in the peripheral blood with subsequent infiltration of these cells into the tissues [20,21]. The high expression of M3R in the salivary glands may be triggered by previous bacterial or viral infections in the local tissues [22–24].

Based on the results of the present study, we propose that the pathogenesis of sialoadenitis in patients with SS might involve

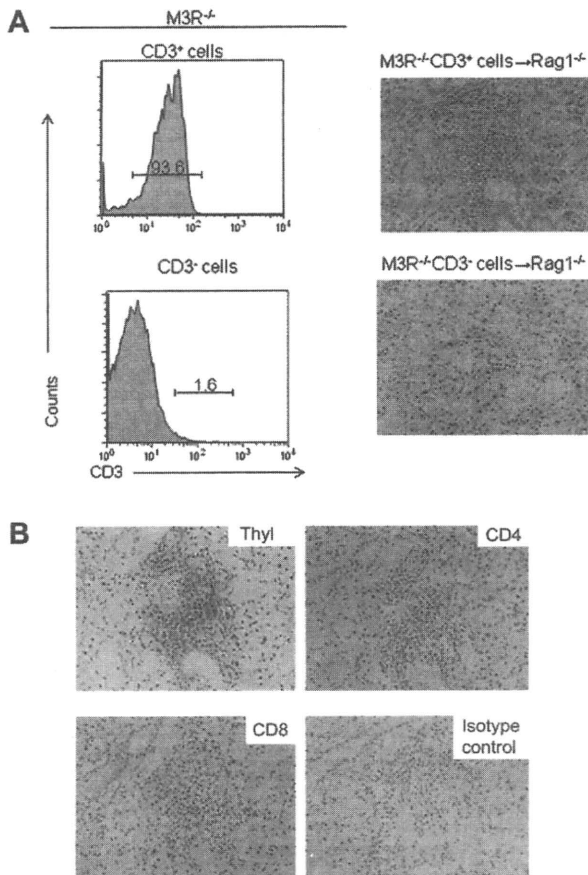


Fig. 5. Role of M3R reactive T cells in the development of sialoadenitis. CD3⁺ or CD3⁻ splenocytes of M3R^{+/+} and M3R^{-/-} mice immunized with M3R peptide mix obtained on day 20 after immunization were inoculated into Rag1^{-/-} mice. (A) Salivary glands isolated from Rag1^{-/-} mice at day 45 after transfer of CD3⁺ or CD3⁻ cells. Salivary glands were prepared into 4- μ m thick sections, and each section was stained with H&E. Representative images of five to seven mice. (B) Sections of salivary glands of M3R^{-/-}CD3⁺ cells \rightarrow Rag1^{-/-} mice stained with anti-CD4, CD8, Thy1 and isotype control. Representative images of three to five mice from each group. Magnification 40 \times .

induction of M3R reactive T cells and B cells in the salivary glands. Importantly, the altered peptide ligands (APL) for M3R binding to the HLA-DR molecule are known to suppress the M3R reactive T cells *in vitro* [25,26]. Therefore, the antigen-induced sialoadenitis in patients with SS could be regulated by APL of M3R. Targeting this antigen-specific modification of autoimmunity in SS could be a potentially useful therapeutic strategy.

In conclusion, we established a new model mouse of sialoadenitis in SS using M3R immunized M3R^{-/-} \rightarrow Rag1^{-/-} mice. Experiments using the new model suggest that the M3R reactive immune response, especially M3R reactive T cells, play a crucial role in the pathogenesis of SS. Targeting this antigen-specific modification of autoimmunity could be a potentially suitable therapeutic strategy in autoimmune diseases such as SS.

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Sex-specific association of X-linked Toll-like receptor 7 (TLR7) with male systemic lupus erythematosus

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Edited by Kenneth G. C. Smith, University of Cambridge, Cambridge, United Kingdom, and accepted by the Editorial Board July 28, 2010 (received for review February 2, 2010)

Systemic lupus erythematosus (SLE) is a multisystem, autoimmune disease that predominantly affects women. Previous findings that duplicated Toll-like receptor 7 (*Tlr7*) promotes lupus-like disease in male BXSB mice prompted us to evaluate *TLR7* in human SLE. By using a candidate gene approach, we identified and replicated association of a *TLR7* 3'UTR SNP, rs3853839 (G/C), with SLE in 9,274 Eastern Asians ($P_{\text{combined}} = 6.5 \times 10^{-10}$), with a stronger effect in male than female subjects [odds ratio, male vs. female = 2.33 (95% CI = 1.64–3.30) vs. 1.24 (95% CI = 1.14–1.34); $P = 4.1 \times 10^{-4}$]. G-allele carriers had increased *TLR7* transcripts and more pronounced IFN signature than C-allele carriers; heterozygotes had 2.7-fold higher transcripts of G-allele than C-allele. These data established a functional polymorphism in type I IFN pathway gene *TLR7* predisposing to SLE, especially in Chinese and Japanese male subjects.

functional polymorphism | disease susceptibility | autoimmunity | type I interferon

Systemic lupus erythematosus [SLE; Online Mendelian Inheritance in Man (OMIM) no. 152700] is a multisystem, autoimmune disease with strong genetic and environmental components (1). SLE predominantly affects women, with a female-to-male ratio of approximately 9:1. Male patients with SLE, although rare, tend to have more severe disease and poorer outcome (2), suggesting potential sex dimorphism in the disease development. Although the sex effect has often been attributed to sex hormones, the fact that XXY male subjects have approximately a 14-fold higher risk of developing SLE than 46 XY men indicates that X-linked genes may be risk factors for human SLE (3).

Located at Xp22.2, Toll-like receptor 7 (*TLR7*; OMIM no. 300365) and its functionally related gene *TLR8* (OMIM no. 300366) encode proteins that play critical roles in pathogen recognition and activation of innate immunity (4). They recognize endogenous RNA-containing autoantigens and induce the expression of type I IFN, a pivotal cytokine in the pathogenesis of SLE (5). In lupus-prone BXSB mice, the translocation of a segmental duplication of X chromosome to Y chromosome creates the Y-linked autoimmune accelerator (Yaa) locus, which was associated with autoreactive B cell responses to RNA-related antigens and exacerbation of glomerulonephritis in male mice (6). Although translocated X chromosome segment in Yaa may contain as many as 16 genes, the major gene for causation of the autoimmune phenotypes was identified to be *TLR7* (7), making it

a potential susceptibility gene for SLE. By using a candidate gene approach, we report herein that a functional polymorphism in 3'UTR of *TLR7* is associated with SLE in Chinese and Japanese populations, with a stronger effect in male than female subjects.

Results

Discovery and Replication of the Association of a *TLR7* 3'UTR SNP with SLE in Eastern Asian Population. We genotyped 27 SNPs from the *TLR7*–*TLR8* region (12 in *TLR7* and 15 in *TLR8*) in 1,434 SLE cases and 1,591 control subjects of Eastern Asian ancestry using the Beadstation Infinium II platform (Illumina). Eleven SNPs in *TLR7* and 12 SNPs in *TLR8* that showed a minor allele frequency greater than 0.01 were included in association analysis (Fig. 1B and Table S1). We observed evidence of association with SLE in 2 *TLR7* SNPs (rs5935436 and rs3853839) and 2 *TLR8* SNPs (rs3764880 and rs4830805; Fig. 1B). Only rs5935436 and rs3853839 in *TLR7* remained significant after Bonferroni correction ($P = 0.041$ and $P = 0.016$, respectively). The strongest association signal was detected at rs3853839 among Chinese subjects [cases vs. controls, 563 vs. 522; $P = 6.3 \times 10^{-6}$; odds ratio (OR) = 1.67 (95% CI = 1.33–2.08)], but not in Korean subjects [$P = 0.32$; OR = 0.92 (95% CI = 0.79–1.08); Fig. 1B], suggesting potential genetic heterogeneity of SLE between the two populations.

We next performed a haplotype-based association test using Haploview 4.03 software. The "GAACAC" haplotype formed by rs2897827, rs5935436, rs2302267, rs179019, rs5743740, and rs179016 had a frequency of 3.1% in SLE cases and 4.8% in con-

Author contributions: N.S. and B.P.T. designed research; Q.F., Y.D., X.Q., K.M.K., Y.L.W., Y.C.Y., Y.-J.T., J.-Y.C., W.Y., M.W., A.K., T.S., Y.K., H.S.H., Y.M.M., S.-Y.B., F.-L.L., D.-M.C., Y.T., H.H., J. M. Grossman, Y.W.S., S.-C.B., S.C., B.H.H., and L.Y.L. performed research; N.S., Y.C.Y., J.-Y.C., W.Y., M.W., N.T., T.S., Y.K., H.S.H., Y.M.M., S.-Y.B., D.-M.C., Y.T., H.H., J. M. Grossman, Y.W.S., S.-C.B., S.C., B.H.H., L.Y.L., and B.P.T. contributed new reagents/analytic tools; N.S., Q.F., Y.D., J.Z., Y.L.W., A.K., N.T., J.B.H., J. M. Guthridge, R.M.C., and B.P.T. analyzed data; and N.S., Q.F., Y.D., and B.P.T. wrote the paper.

The authors declare no conflict of interest.

This article is a PNAS Direct Submission. K.G.S. is a guest editor invited by the Editorial Board.

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This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1001337107/-DCSupplemental.

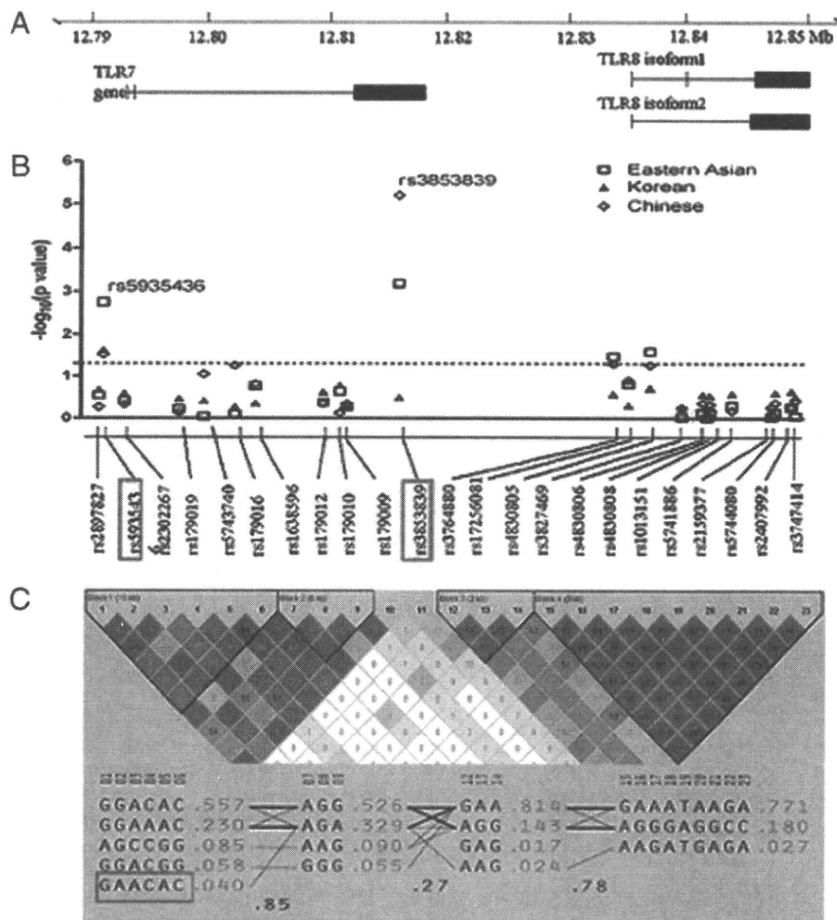


Fig. 1. A functional SNP rs3853839 in 3'UTR of *TLR7* is associated with SLE in a Chinese population. (A) *TLR7* and *TLR8* gene structure. (B) Eleven *TLR7* SNPs and 12 *TLR8* SNPs were genotyped in 1,434 SLE cases and 1,591 healthy controls of Eastern Asian descent. The two SNPs (rs5935436, rs3853839) that showed significant association after Bonferroni correction are highlighted. (C) Two haplotype blocks were constructed based on the strength of LD in each gene region. The R^2 values of each SNP pair are depicted. The protective haplotype GAACAC is highlighted.

controls ($P = 0.0017$; Fig. 1C). Given that only this *TLR7* protective haplotype carries the minor allele of rs5935436, we genotyped rs5935436 in replication studies to represent the SLE-associated haplotype. Rs3853839 was in low linkage disequilibrium (LD) with other SNPs in the region. To minimize missing any other common polymorphisms, we sequenced 5' promoter region (2 kb upstream) as well as three exons (including 3'UTR) of *TLR7* in 48 Chinese female patients with SLE, which revealed no additional polymorphism and raised the possibility that rs3853839 might be causal.

To verify the association of rs3853839 and rs5935436 with SLE, we then conducted a replication study in two independent case-control Chinese and Japanese panels. Whereas rs5935436 was not replicated in these studies ($P = 0.97$ and $P = 0.25$, respectively), rs3853839 showed a consistent association with SLE in both replication panels [Chinese, 2,340 vs. 2,436; $P = 9.0 \times 10^{-4}$; OR = 1.21 (95% CI = 1.08–1.35); and Japanese, 560 vs. 913; $P = 0.007$; OR = 1.28 (95% CI = 1.07–1.53); Table 1]. A combined analysis of discovery and replication panels showed compelling evidence supporting that G allele of *TLR7* SNP rs3853839 conferred risk for SLE [$P_{\text{combined}} = 6.5 \times 10^{-10}$, OR_{combined} = 1.27 (95% CI = 1.17–1.36)]. Furthermore, G allele showed an additive effect in female subjects, as the OR for female homozygous GG versus CC was 1.45 (95% CI = 1.17–1.79) and OR for heterozygous GC versus CC was 1.15 (95% CI = 0.93–1.43), which reinforced a role of rs3853839 in developing SLE. Stratification by

clinical subsets including age of disease onset, presence of mucocutaneous manifestations, lupus nephritis, dsDNA, or anti-RNA binding protein antibodies (presence of one or more autoantibodies to Ro/SSA, La/SSB, RNP, and Sm) (8) revealed a weak association of G allele with the presence of anti-RNA binding protein [$P = 0.049$, OR = 1.16 (95% CI = 1.00–1.35); missing data, 45%], suggesting that *TLR7* binding of RNA containing immune complexes might play a role in the initiation and perpetuation of autoimmunity.

Significant Male Effect of rs3853839 in the Risk of Developing SLE. Of interest, we observed a stronger association of rs3853839 with male SLE. In the discovery panel, G allele showed higher OR in male patients compared with female patients [OR = 1.79 (95% CI = 1.03–3.13) vs. 1.22 (95% CI = 1.06–1.39); Table 1], especially in Chinese subjects [OR = 5.56 (95% CI = 1.85–16.7) vs. 1.54 (95% CI = 1.22–1.96)]. This notable male effect was verified in both replication panels: Chinese male patients with SLE had a significantly higher frequency of G allele than controls [92% vs. 81%; OR = 2.73 (95% CI = 1.57–4.74)]; in contrast, female cases only showed a modest increase of G allele versus controls [83% vs. 80%; OR = 1.19 (95% CI = 1.06–1.35)]. A similar finding was also observed in the Japanese subject replication panel. In the combined analysis, G allele occurred in 89% of male cases ($n = 358$), but only 77% of male controls ($n = 1,550$),

Table 1. Association of rs3853839 with SLE in Eastern Asian populations

Ethnicity and panel	Case/control	G risk allele frequency		P value	OR (95% CI)
		Case	Control		
Eastern Asian*:					
Discovery					
Male	126/229	0.83	0.73	0.038	1.79 (1.03–3.13)
Female	1,308/1,362	0.79	0.76	3.00E-03	1.22 (1.06–1.39)
All	1,434/1,591	0.80	0.76	6.70E-04	1.24 (1.1–1.41)
Chinese: Replication 1					
Male	196/931	0.92	0.81	2.31E-04	2.73 (1.57–4.74)
Female	2,144/1,505	0.83	0.80	4.24E-03	1.19 (1.06–1.34)
All	2,340/2,436	0.83	0.80	9.02E-04	1.21 (1.08–1.35)
Japanese: Replication 2					
Male	36/390	0.89	0.69	0.014	3.51 (1.22–10.2)
Female	524/523	0.75	0.71	0.037	1.23 (1.01–1.49)
All	560/913	0.75	0.70	7.00E-03	1.28 (1.07–1.53)
Eastern Asian*: Combined					
Male	358/1,550	0.89	0.77	1.33E-06	2.33 (1.64–3.30)
Female	3,976/3,390	0.80	0.77	1.19E-07	1.24 (1.14–1.34)
All	4,334/4,940	0.81	0.77	6.50E-10	1.27 (1.17–1.36)

*Includes subjects of Chinese, Korean, or Japanese descent.

showing a strong association with SLE ($P = 1.33 \times 10^{-6}$) and significantly higher OR in male versus female subjects [2.33 (95% CI = 1.64–3.30) vs. 1.24 (95% CI = 1.14–1.34); $P = 4.1 \times 10^{-4}$]. The significant male sex effect of rs3853839 in SLE was confirmed by a higher G allele frequency in male cases than female cases ($P = 1.1 \times 10^{-4}$; OR = 1.90 (95% CI = 1.36–2.64)] and by a higher OR in male subjects than the OR calculated by using only female homozygotes [GG vs. CC, OR = 1.45 (95% CI = 1.17–1.79); $P = 0.02$].

TLR7 SNP rs3853839 Confers Elevated Expression of TLR7 in Vivo. The consistent association of rs3853839 with SLE led us to investigate the potential functional consequences of the G risk allele. We first examined whether the 3'UTR polymorphism affected the expression level of *TLR7* transcripts. We isolated peripheral blood mononuclear cells (PBMCs) from selected Chinese individuals carrying various genotypes and measured the mRNA expression levels of *TLR7* by using real-time PCR. As shown in Fig. 2A, male controls carrying G allele had significantly higher *TLR7* transcripts than those carrying C allele ($P = 0.02$). Similarly, female cases and controls homozygous for G allele showed notably higher *TLR7* mRNA expression than those carrying homozygous C allele ($P = 7.4 \times 10^{-6}$ and $P = 0.03$, respectively). No sex differences in *TLR7* mRNA expression levels were observed between normal controls carrying the same allelic genotype of rs3853839 ($P = 0.07$ or $P = 0.55$ for GG females vs. G males or CC females vs. C males, respectively; Fig. 2A). The sex comparison was not replicated in patients with SLE because of insufficient sample size of blood collected from male patients with SLE.

To exclude potential bias between individuals, we next assessed the allelic specific transcriptional expression of *TLR7* in Chinese female G/C heterozygotes by pyrosequencing. We extracted genomic DNA (gDNA) and cDNA from PBMCs of heterozygous SLE patients and controls and determined the exact ratios of G/C in gDNA and cDNA for each individual. As shown in Fig. 2B, the mean G/C ratio in gDNA of all individuals was 1.05, which was consistent with the theoretical value. However, SLE and control female heterozygotes showed a 2.7-fold higher G/C ratio in *TLR7* transcripts than that in gDNA ($P = 2 \times 10^{-4}$ and $P = 2 \times 10^{-3}$, respectively; $P_{\text{overall}} = 1.2 \times 10^{-6}$), meaning that there was significantly higher level of G allele-containing *TLR7* transcripts than C allele-containing transcripts in PBMCs, even though there was same amount of gDNA that contains either allele.

To investigate whether the disparity observed between transcript and gDNA was a result of imbalanced X chromosome inactivation (XCI) in female subjects, we analyzed the XCI pattern in these individuals by measuring the degree of methylated CAG alleles in androgen receptor (*AR*) gene as previously described (9). Fig. 2C showed no significant skewed XCI in either SLE or controls ($P = 0.8$), suggesting that skewed XCI or somatic selection might not account for the current finding. Taken together, these data suggested rs3853839 polymorphism could play a functional role in the regulation of *TLR7* transcript levels in vivo.

To investigate whether allelic differences of rs3853839 corresponded to *TLR7* protein levels, we isolated proteins from PBMCs of healthy Chinese male subjects carrying the G or C allele for Western blot analysis. Fig. S1 showed that five of the six male G allele carriers had higher expression levels of *TLR7* protein than the two C allele carriers after normalization of the amount of protein loading using β -actin. Although the result was not statistically significant ($P = 0.21$, probably because of the very small sample size), the finding of higher *TLR7* protein expression of the G risk allele carriers was consistent with what we observed at mRNA levels of *TLR7*.

We next investigated that whether the functional SNP rs3853839 might influence the IFN reaction downstream of *TLR7*. A prominent feature of patients with SLE is an increased expression of type I IFN-regulated genes (i.e., IFN signature) in PBMCs compared with unaffected controls (10, 11). We measured expression levels of four type I IFN-regulated genes, including lymphocyte antigen 6 complex, locus E (*LY6E*), myxovirus resistance 1 (*MX1*), IFN-inducible protein with tetratricopeptide repeats 1 (*IFIT1*), and *IFIT3* by real-time PCR in PBMCs from clinically inactive female SLE patients carrying various rs3853839 genotypes and calculated an IFN score for each individual. As shown in Fig. 2D, female SLE patients carrying GG genotype showed a more pronounced IFN signature in PBMCs compared with those carrying GC and CC genotypes, indicating rs3853839 might modulate expression levels of *TLR7*, affecting IFN response in vivo.

Discussion

There is compelling evidence supporting the contribution of *TLR7* to the development of autoimmunity. Transgenic mice with a twofold overexpression of *TLR7* would have increased production of RNA-related autoantibodies and develop spontaneous