

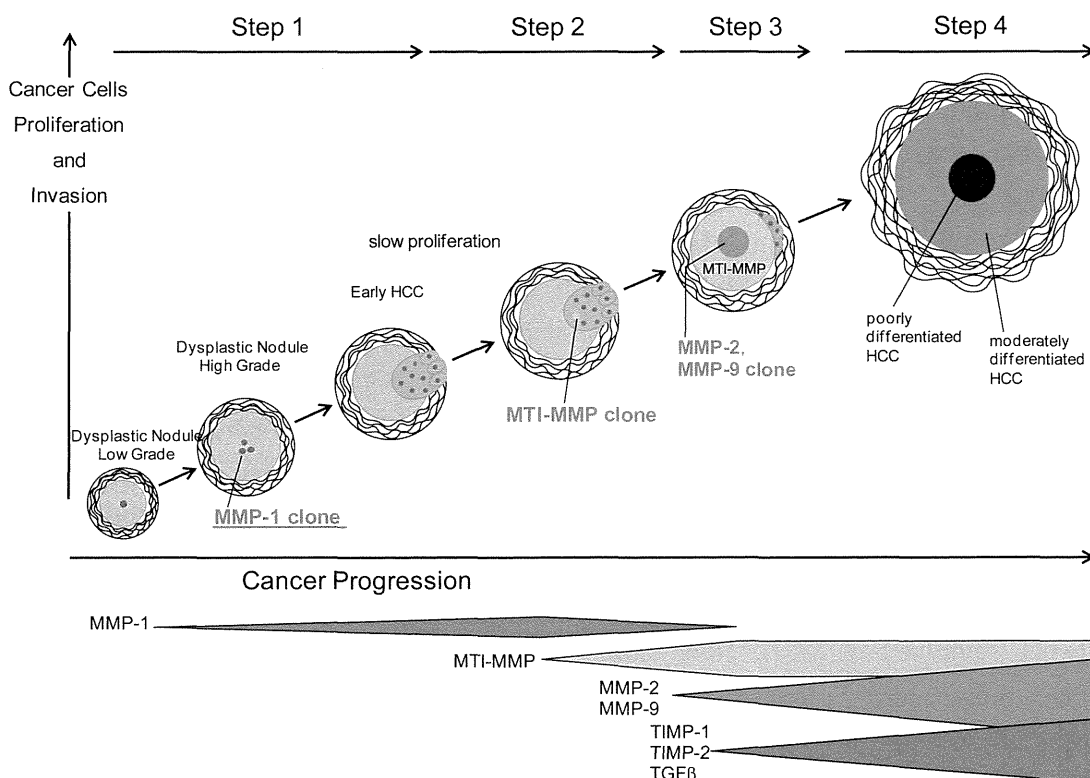
only well-differentiated HCC expressed MMP-1, two cases with both well-differentiated and moderately differentiated HCC showed positive staining, and one case with only moderately differentiated cells showed negative staining. No case of advanced HCC showed MMP-1 mRNA. The positive cells were well-differentiated cancer cells located at the invading front of the cancer. An interesting finding was that positive cells were scattered in a ratio of approximately 1% to 2% in cancer. This was very different from the findings of MMP-9 expression reported in other studies described above. Hepatocytes of non-cancerous liver did not express transcripts of MMP-1. Positive staining of MMP-1 protein was seen in early HCC with well-differentiated HCC cells and invaded portal tract. In another case with early HCC, well-differentiated HCC cells positive for MMP-1 protein were compressed by moderately differentiated cancer cells which were negative for MMP-1 staining. MMP-1 mRNA was seen in HCC cells infiltrated into the small portal tract left in tumor nodule as well as in the fibrous bands surrounding the cancer cell nodule. MMP-1 expression was associated with growth of small HCC in which well-differentiated cancer cells invade the portal tract and fibrous bands, and these fibrous tissues disappear upon participation of MMP-1 [32].

Nakatsukasa *et al.* [156] reported that TIMP-1 mRNA and TIMP-2 mRNA in cancerous tissue were homogeneously stained more intensively than in non-tumorous tissue of HCC by *in situ* hybridization. All HCC tissues contained transcripts of both TIMP-1 and TIMP-2 with stronger expression in HCC cells than in the surrounding tissue. The expression and distribution of the transcripts for TIMP-1 and TIMP-2 did not differ among the various cancer differentiation stages. The intensity of TIMPs mRNA expression varied from nodule to nodule. Stromal cells in and surrounding the HCC expressed both TIMP-1 and TIMP-2 mRNA, and their expression in stromal cells present in the capsule was especially strong. On the other hand, Musso *et al.* [145] did not observe either mRNA of MMP-2 or TIMP-2 in HCC cells, but observed them in  $\alpha$ SMA-positive cells at the invasive front. The MMP-2(+)/TIMP-2(+)/ $\alpha$ SMA(+) cells in the perisinusoidal space adjacent to liver tumors are considered to be HSC. This discrepancy is probably due to the histological differences in HCC used in the study above. TIMPs act to modulate the matrix/tumor interaction [138–140,142]. Furthermore, TIMPs may play an important role in cell growth, and pro-MMP-2 may be activated by MT1-MMP and TIMP-2 on the cell surface of HCC cells, stromal cells and stellate cells resulting in stromal invasion. TIMP-1 and TIMP-2 expression by stromal cells was associated with a poorer prognosis of HCC as revealed by an immunohistochemical study using tissue microarrays [153,154].

The above observations on MMP-1, -2, -9, MT-1 MMP and TIMP-2 lead to the following hypothesis, as shown in Figure 2 [35]. The conversion from low-grade dysplastic nodule to high-grade dysplastic nodule within liver cirrhosis results in a phenotype that expresses MMP-1, resulting in the formation of a new clone. Well-differentiated HCC cells proliferate slowly with the ability of stromal invasion ([32], reviewed in [35]). New clones can proliferate and invade portal tracts destroying fibrous tissue. Subsequently other clones arise to degrade effectively not only fibrous tissue but also basement membrane. These next generation clones express MT1-MMP in the process of cancer development. Several well-differentiated HCC cells express MT1-MMP and gradually small amounts of MMP-2 and MMP-9, probably stimulated by inflammatory cytokines or TGF- $\beta$ , which may participate in the stromal invasion or the formation of the thick capsule of cancer nodules. Pro-MMP-9 is activated by MMP-2, or well- to moderately differentiated HCC cells to obtain a phenotype expressing MMP-9. TIMP-1 and TIMP-2 gene transcripts in HCC cells appeared with increased

expression of MMP-2 and/or MMP-9. MMP-1-positive clones (well-differentiated cancer cells) are compressed by new clones (moderately differentiated cancer cells) and subsequently disappear.

**Figure 2.** MMPs and TIMPs expression related with HCC progression based on the reported results in HCV-derived HCC [35]. The terminology of nodular hepatocellular lesions in this figure is modified by the report of the International Working Party [157]. Step 1: A conversion from low-grade dysplastic nodule to high-grade dysplastic nodule within liver cirrhosis obtains a phenotype to express MMP-1, resulting in the formation of a new clone. Early HCC cells proliferate slowly with the ability of stromal invasion. Step 2: New clones can proliferate and invade portal tracts and fibrous tissue. Subsequently other clones arise to degrade effectively not only fibrous tissue but also basement membrane. These clones of the next generation express MT1-MMP in the process of cancer development. Step 3: Several early HCC cells express MT1-MMP and gradually small amounts of MMP-2 and MMP-9, probably stimulated by inflammatory cytokines or TGF- $\beta$ , which may participate in the stromal invasion or the formation of the thick capsule of cancer nodules. Pro-MMP-9 is activated by MMP-2, or early HCC to moderately differentiated HCC cells obtain a phenotype expressing MMP-9. TIMP-1 and TIMP-2 gene transcripts in HCC cells increased with increased expression of MMP-2 and/or MMP-9. Step 4: MMP-1 positive clones (early HCC cells) are compressed by new clones (moderately differentiated hepatoma cells) and subsequently disappear [35].



There is no direct evidence for this hypothesis. However, we have previously reported that stem cells derived from bone marrow changed their phenotypes of MMP-13 (a major interstitial collagenase in rodents with homology to human MMP-1) to MMP-9 expression in the recovery phase from experimental liver fibrosis and cirrhosis [24]. A similar switch in MMP expression may occur in the dedifferentiation process of cancer stem cells (Figure 2). On the other hand, positive staining for both MMP-2 and MMP-9 proteins was observed in inflammatory cells, fibroblasts and endothelial cells. MMP-9 mRNA was detected in mesenchymal cells inside and outside cancer nodules, and in fibrous capsules around the necrosis of cancer nodules [128]. Mesenchymal cells and inflammatory cells positive for MMP-2 and MMP-9 were numerous and stained strongly for both mRNA and protein compared with cells positive for MMP-1 [32,145,147]. These positive cells may participate in the degradation of the fibrous tissue to allow HCC cells to invade easily or to form the thick capsule around the nodule.

Cancer-associated mesenchymal stem cells (MSC) could cross-talk with tumor cells and secreted many growth factors and chemokines, which play crucial roles in tumor progression [158,159]. A recent report by Yan *et al.* [160] clearly demonstrated the presence of liver cancer-associated MSCs (LC-MSCs) which promote the proliferation and metastasis of HCC cells. They indicated that S100A4 secreted from LC-MSCs can promote HCC cell proliferation and invasion, and the invasion-promoting effect of S100A4 was attenuated by a miR-155 inhibitor. MiR-155 induced by S100A4 increased MMP-9 expression; S100A4 facilitated the process by up-regulating MMP-9. S100A4 and miR-155 expression and down-regulating SOCS1 gene expression, which regulates p-STAT3, one of the mediators involved in regulating MMP-9 expression, stimulate HCC invasion. Moreover, Roderfeld *et al.*, demonstrated that MMP-9 expressing macrophages invade at the tumor front of HCC [161].

Expression of MMPs is controlled mainly at the transcriptional level. The promoter regions of MMPs contain several common elements where the common transcription factors such as AP-1, Ets, and/or NF- $\kappa$ B bind (reviewed in [35]). The present authors showed that the c-Jun NH2-terminal kinase (JNK) pathway is involved in constitutive MMP-1 expression in a well-differentiated cell line (HLE cells) among five HCC cell lines derived from various dedifferentiation stages. C-Jun is phosphorylated by JNK, one of the four distinctly regulated MAPK pathways; the other three pathways are extracellular signal-related kinases (ERK)-1/2, p38 proteins and ERK5. HLE cells constitutively expressed MMP-1 gene and protein as well as its enzymatic activity without the use of any stimulators such as phorbol ester. MMP-1 gene transcription was controlled by the activation of c-Jun through the JNK pathway [33].

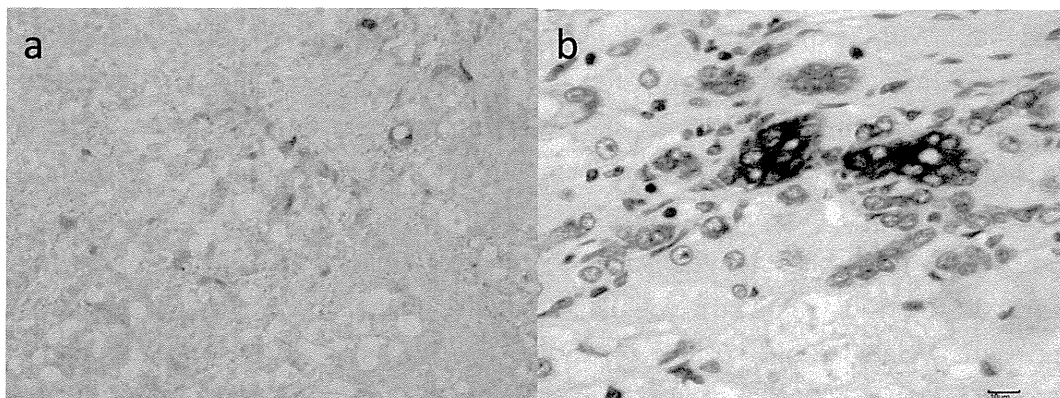
PTEN inhibits the migration and invasion of HCC by the down-regulation of MMP-2 and MMP-9 in a PI3K/Akt/MMP-dependent manner [162]. Lysophosphatidic acid (LPA) produced extracellularly by autotaxin (ATX), increases cell survival, angiogenesis, invasion and metastasis [35]. Park *et al.* [163] revealed that silencing or pharmacological inhibition of LPA1 inhibited LPA-induced MMP-9 expression and HCC cell invasion because ATX transcripts and LPA receptor type 1 (LPA1) protein levels were higher in HCC than in normal tissue. They also found that MMP-9 is downstream of LPA1. Moreover, LPA-induced MMP-9 expression with subsequent invasion was abrogated by inhibition of phosphoinositol-3 kinase (PI3K) signaling or dominant or negative mutants of protein kinase C and p38 mitogen-activated protein kinase (MAPK) [163]. Increased MMP-2, -9 and VEGF caused by

hypoxia (via ERK1/2) is suppressed with  $\text{Na}^+/\text{H}^+$  exchanger 1 (NHE1) inhibited by 5-(*N*-ethyl-*N*-isopropyl) amiloride [164].

### 7.2. MMPs and TIMPs in NASH-related Carcinogenesis

There are no reports on MMPs and TIMPs in NASH-derived HCC. Figure 3a is a MMP-9 staining microscopic finding of surgically resected NASH-derived HCC. Strong staining is seen in some of the HCC cells diffused in the nodule. MMP-1 and MMP-2 staining are also positive with different distribution (not shown). The tumor size in this case is less than 2 cm in diameter, and the pathological features of HCC cells are well differentiated. According to the hypothesis shown in Figure 2, there is negative staining for both MMP-9 and MMP-2 in small cancer. This discrepancy may be based in the etiology of HCC, because the hypothesis of Figure 2 is based on HBV- or HCV-related HCC while Figure 3a is NASH-related HCC. The involvement of HPCs in NASH appears to be very different from viral chronic liver diseases as discussed above. The present authors are currently investigating the involvement of MMP-positive cells in the dedifferentiation process of early HCC cells in NASH-derived HCC.

**Figure 3.** Immunostaining of NASH-derived HCC: (a) NASH-derived HCC cells with cytoplasmic reactivity to the MMP-9 antibody are scattered sparsely throughout the nodule (100× magnification); (b) NASH-derived HCC cells with cytoplasmic reactivity to the CK19 antibody are also seen (400× magnification).



MMPs can be influenced by reactive oxygen species (ROS), resulting in the activation of neutrophils and macrophages at the tumor site with inflammation. These oxidants initially activate MMPs via oxidation of the pro-domain cysteine or via modification of amino acids of the catalytic domain by hydrochlorous acid in combination with myeloperoxidase (reviewed in [165]) The methylation status of cytokines in CpG dinucleotides located in the MMP promoter also plays a role in controlling gene expression of MMPs, especially in cancer cells. Recent studies on DNA methylase inhibitors, such as 5-aza-2'-deoxycytidine, showed a possible induction of hypomethylation of MMPs genes at the promoter level in human HCC cells [166].

Stefanou *et al.* [167] reported that leptin up-regulated telomerase activity in HepG2 cells through the binding of STAT3 and Myc/Max/Mad network proteins to the promoter of human telomerase reversed transcriptase (hTERT). Leptin could affect the progression and invasion of HCC through its

interaction with cytokines and MMPs in the tumorigenic microenvironment. Leptin increased the levels of MMP-13 and MMP-9 in a dose- and time-dependent manner. Insulin receptor-mediated signaling promotes MMP-2 and MMP-9 expression [168]. On the other hand *Kiss-1* gene, a putative metastasis suppressor gene, is also reported in HCC related with decreased expression of MMP-9 [169].

HPCs derived from bile ducts and the canals in the liver or bone marrow seem to play an important role in the dedifferentiation process from injured hepatocytes ([32], reviewed in [35]). Figure 3b shows the cytoplasmic reactivity to the CK19 antibody in NASH-derived HCC cancer cells. As noted above, one of characteristic pathological findings in NASH is the infiltration of HPCs. Therefore, expression of MMP-1, MMP-2 and MMP-9 seems to be expected in NASH-derived HCC, and the expression is probably different from that found in viral-derived HCC. The regulatory mechanism of TIMPs in NASH-derived HCC also remains unknown [119,170]. Further regulatory research on MMPs and TIMPs should be conducted to prevent the progress of NASH to HCC.

## 8. Conclusions: Future Management of NASH Focusing on MMPs and TIMPs

Distinguishing between benign NAFLD patients and advanced NASH patients is very difficult. To counter this problem the author's research group has a short-admission program for NASH patients that includes liver biopsy, metabolic examination for glucose tolerance and diet education. We follow up the courses of NASH patients focusing on the complications of HCC. Patients should undergo abdominal echography or CT/MRI and serum markers. Liver tissue obtained by needle biopsy should be checked for stem/progenitor marker-positive cells. Our group is now investigating whether MMP-1 staining or MMP-9 staining is a predictable indicator of HCC. Finally, further investigation of signal transduction pathways in MMPs and TIMPs is essential because future prevention and treatment of NASH-related HCC will be based on gene regulation of MMPs and TIMPs.

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## Author Contributions

IO made a scheme of the manuscript and wrote the role of MMPs and TIMPs in fibrogenesis and carcinogenesis of NASH; TN, NT and EY wrote the mechanism of carcinogenesis in NASH from the viewpoint of surgical treatment; HK described the pathological findings of NASH cases including the immunohistochemical findings of MMPs; MN reviewed the description of HCC according to the report of the International Working Party; HY wrote the characteristics of HPC in NASH; YI reviewed the mechanism of fibrogenesis and carcinogenesis in NASH from the viewpoint of regenerating medicine.

## Conflicts of Interest

The authors declare no conflict of interest.

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# Lymph Node Stromal Cells Negatively Regulate Antigen-Specific CD4<sup>+</sup> T Cell Responses

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Lymph node (LN) stromal cells (LNSCs) form the functional structure of LNs and play an important role in lymphocyte survival and the maintenance of immune tolerance. Despite their broad spectrum of function, little is known about LNSC responses during microbial infection. In this study, we demonstrate that LNSC subsets display distinct kinetics following vaccinia virus infection. In particular, compared with the expansion of other LNSC subsets and the total LN cell population, the expansion of fibroblastic reticular cells (FRCs) was delayed and sustained by noncirculating progenitor cells. Notably, newly generated FRCs were preferentially located in perivascular areas. Viral clearance in reactive LNs preceded the onset of FRC expansion, raising the possibility that viral infection in LNs may have a negative impact on the differentiation of FRCs. We also found that MHC class II expression was upregulated in all LNSC subsets until day 10 postinfection. Genetic ablation of radioresistant stromal cell-mediated Ag presentation resulted in slower contraction of Ag-specific CD4<sup>+</sup> T cells. We propose that activated LNSCs acquire enhanced Ag-presentation capacity, serving as an extrinsic brake system for CD4<sup>+</sup> T cell responses. Disrupted function and homeostasis of LNSCs may contribute to immune deregulation in the context of chronic viral infection, autoimmunity, and graft-versus-host disease. *The Journal of Immunology*, 2014, 193: 1636–1644.

Lymph nodes (LNs) are the primary site of Ag encounter by lymphocytes. Circulating lymphocytes reside there for up to 24 h (1) and undergo multiple rounds of cell-to-cell contact with Ag-presenting dendritic cells (DCs) (2). The LN structure and microenvironment are designed to concentrate Ags transported from the periphery and to promote the migration and survival of lymphocytes and DCs (3–5).

LN stromal cells (LNSCs) play a critical role in the functional organization of the LNs (6). LNSCs consist of multiple types of fibroblastic cells, lymphatic endothelial cells (LECs), and blood vessel endothelial cells (BECs). One subset of fibroblastic LNSCs,

fibroblastic reticular cells (FRCs) in the T cell region, produce IL-7 and exist in close contact with T cells and DCs (7, 8). FRCs also express the homeostatic chemokines CCL19/CCL21 (9–11) and ICAM-1, which together act as the guiding cue and driving force for the intranodal migration of lymphocytes and DCs (4, 12). Moreover, FRCs regulate vascular growth in reactive LNs during inflammation (13), thereby ultimately controlling lymphocyte trafficking. Therefore, FRCs represent one of the key cellular components providing structural and microenvironmental support for adaptive immune responses in LNs.

Recently, a newly described role for LNSCs as APCs in adaptive immunity has attracted much attention. In the steady-state, LNSCs differentially express peripheral tissue-specific Ags and present them to CD8<sup>+</sup> T cells for the maintenance of self-tolerance (14–16). In contrast, LNSCs stimulated with LPS for 12 h in vivo upregulate MHC class II (17). Furthermore, *Pdpr*-Cre-driven expression of a model Ag in LECs and FRCs leads to the expansion of adoptively transferred Ag-specific CD4<sup>+</sup> T cells, even under noninflammatory conditions (16). These observations suggest that the outcome of Ag presentation to CD4<sup>+</sup> T cells by LNSCs could be either immunogenic or tolerogenic, depending on the inflammatory environment. However, because previous studies used sterile models of inflammation, it remains unclear how FRCs and other LNSCs adapt functionally during replicative cytopathic virus infections.

In the current study, we performed a detailed analysis of LNSC responses during vaccinia virus (VV) infection. BECs and LECs showed rapid expansion, peaking at day 14 postinfection (p.i.). In contrast, we observed a delayed, but sustained, expansion of terminally differentiated FRCs, which were replenished by noncirculating progenitor cells in a lymphotoxin- $\beta$ -dependent manner. Of note, FRCs and other LNSCs expressed MHC class II p.i., which contributed to the contraction of Ag-specific CD4<sup>+</sup> T cells at the later time points of the immune response. Taken together, our data elucidate the dynamics of LNSC expansion and function during antimicrobial immune responses.

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Abbreviations used in this article: B6, C57BL/6; bm12, B6.C-H2-Ab1<sup>bm12</sup>; Col1a2, type I collagen  $\alpha$ 2; DC, dendritic cell; DN, double negative; FRC, fibroblastic reticular cell; HEV, high endothelial venule; LN, lymph node; LNSC, LN stromal cell; LT $\beta$ R, lymphotoxin- $\beta$  receptor; LT $\beta$ R-Ig, rIg Fc region-fused soluble recombinant lymphotoxin- $\beta$  receptor protein; #639/#474 mice, FucciG<sub>1</sub>/#639×FucciS/G<sub>2</sub>/M-#474 double-transgenic mice; p.i., postinfection; popLN, popliteal lymph node; Tfh, T follicular helper; VV, vaccinia virus; VV-OVA, OVA expressing recombinant VV; WT, wild-type.

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## Materials and Methods

### Mice, viral infection, and immunization

C57BL/6 (B6) mice were purchased from Japan SLC. *Rag2*<sup>-/-</sup> OVA<sub>323-339</sub>-specific TCR-transgenic (OT-II) mice were purchased from Taconic. B6.C-H2-Ab1<sup>bm12</sup> (bm12) and B6.SJL (CD45.1) mice were purchased from The Jackson Laboratory. FucciG<sub>1</sub>-#639×FucciS/G<sub>2</sub>/M-#474 double-transgenic mice (#639/#474 mice) on a B6 background (18) were provided by Atsushi Miyawaki (RIKEN). *Colla2*-GFP mice were generated as described previously (19). Mice were 6–8 wk old at the commencement of experiments. Mice were either infected s.c. with  $1 \times 10^4$  PFU OVA-expressing recombinant VV (VV-OVA) (20) or were hock immunized (21) with 50  $\mu$ g OVA protein emulsified in CFA. In some experiments, mice were given an i.p. injection of 100  $\mu$ g rIg Fc region-fused soluble recombinant lymphotoxin- $\beta$  receptor (LT $\beta$ R) protein (LT $\beta$ R-Ig) 1 d before immunization and on a weekly basis thereafter. All animal experiments were conducted in accordance with the guidelines of the Animal Care and Use Committee of the University of Tokyo.

### Abs

mAbs against CD4 (RM4-5), CD8 $\alpha$  (53-6.7), CD11b (M1/70), CD11c (HL3), CD19 (6D5),  $\beta$ 1 integrin (Ha2/5), CD31 (390), CD44 (IM7), CD45 (30-F11), CD45.1 (A20), CD45.2 (104), B220 (RA3-6B2), CD80 (16-10A1), CD86 (GL1), VCAM-1 (429), CD138 (281-2), CD157 (BP-3), ICOS (7E.17G9), PD-1 (RMP1-30), CXCR5 (2G8), gp38 (8.1.1), Ly-6G/C (RB6-8C5), NK1.1 (PK136), Ter-119 (TER-119), BrdU (Bu20a), MHC class I (28-14-8), I-A/I-E (M5/114.15.2), TCR V $\alpha$ 2 (B20.1), and TCR $\gamma$  $\delta$  (UC7-13D5) were purchased from BioLegend, BD Biosciences, or eBioscience and used for flow cytometry. For the immunofluorescent staining of tissue sections, purified anti-pan-endothelial Ag (MECA-32) and biotinylated anti-gp38 (8.1.1) mAbs were purchased from BioLegend, anti-type IV collagen rabbit antiserum was purchased from LSL, and Alexa Fluor-labeled secondary Abs and streptavidin were purchased from Life Technologies.

### Flow cytometry

LN were either minced by filtering through a cell strainer (BD Biosciences) or digested in 0.1% crude collagenase (Wako; cat. #32-10534), 0.96 mg/ml Dispase II (Roche), and 20 kU/ml DNase I (Calbiochem) in DMEM supplemented with 2% FCS and 10 mM HEPES for 30 min at 37°C. Throughout the digestion process, the suspension was stirred gently using a small magnetic stirrer bar. Aliquots of the resulting single-cell suspension were stained with appropriate Ab mixtures. Data were collected on a Gallios flow cytometer (Beckman Coulter) and analyzed using FlowJo software (TreeStar).

### Measurement of viral load in tissues

Viral load in reactive LNs and infected footpads was measured by copy number assay. In brief, LNs and footpads were homogenized using a bead-based cell disruptor, and total DNA was isolated using a Tissue Genomic DNA Extraction Mini Kit (Favorgen). Copy numbers of *Ova* gene were measured by subjecting 45 ng total DNA/reaction to quantitative PCR with FastStart TaqMan Probe Master (Roche), a TaqMan Gene Expression Assay kit Gg03366808\_m1 (for *Ova*), and a TaqMan Copy Number Reference Assay kit (Applied Biosystems). The limit of detection of the assay was 10 copies.

### In vivo BrdU labeling

For short-term pulse labeling, mice were injected i.p. with 1 mg/mouse BrdU (Sigma-Aldrich) 16 h before sacrifice. For long-term continuous labeling, mice were provided with drinking water containing 0.8 mg/ml BrdU for the duration of the experiment, commencing immediately p.i. BrdU water was replaced every 2–3 d.

### Immunofluorescent staining of LN sections

Six-micron-thick cryosections of fresh LNs were prepared and fixed for 10 min in acetone. Fixed sections were rehydrated with PBS, blocked with Blocking One reagent (Nacalai Tesque), and stained with Ab mixtures (in PBS containing 2% BSA) for 1 h at room temperature. Sections were incubated further with appropriate secondary Abs. For BrdU staining, sections were fixed for 10 min with 4% paraformaldehyde in PBS after the staining of the other Ags. Fixed sections were treated with 2 M HCl for 1 h at 37°C before incubation with anti-BrdU Ab. After staining, sections were mounted with ProLong Gold reagent (Life Technologies). Immunofluorescently stained sections were observed

under a TCS SP5 confocal microscope (Leica Microsystems). The acquired images were processed and quantified using ImageJ software (National Institutes of Health).

### Parabiosis

Parabiosis surgery was performed on body weight-matched partners. A longitudinal incision was made through the skin and fascia of mice deeply anesthetized with pentobarbital. The incised skins and fascia of partner mice were joined by sutures. More than 6 wk after the surgery, mice were infected s.c. with VV-OVA via the footpad distal to the conjoined side of the body.

### Generation of bone marrow chimeric mice and adoptive transfer

CD45.1<sup>-</sup> CD45.2<sup>+</sup> bm12 and B6 recipient mice were exposed to 8.5 Gy irradiation before transplantation with  $5 \times 10^6$  CD45.1<sup>+</sup> CD45.2<sup>+</sup> whole bone marrow (BM) cells the following day. More than 6 wk after transplantation,  $2 \times 10^4$  CD45.1<sup>+</sup> CD45.2<sup>-</sup> *Rag2*<sup>-/-</sup> OT-II T cells were adoptively transferred into recipient mice via the tail vein 1 d before immunization. For OT-II T cell preparation, CD4<sup>+</sup> T cells were enriched from the spleen of OT-II mice by negative selection using streptavidin MicroBeads and an AutoMACS cell separator (Miltenyi Biotec). Before magnetic labeling with MicroBeads, cells were labeled with biotinylated Abs against CD8 $\alpha$ , CD11b, CD11c, CD19, CD138, Ly-6G/C, NK1.1, Ter-119, and TCR $\gamma$  $\delta$ . The purity of CD4<sup>+</sup> TCR V $\alpha$ 2<sup>+</sup> OT-II T cells was routinely >95%.

### Statistical analysis

Data were analyzed for statistical significance by Student *t* test (for comparison of two groups) or one-way ANOVA (for comparison of three or more groups); post hoc tests were performed as described in the figure legends). All statistical analyses were performed using GraphPad Prism software. The *p* values < 0.05 were considered statistically significant.

## Results

### LNSCs expand in a subset-specific manner during viral infection

In a recent study, immunization with protein Ag and CFA caused the number of FRCs and endothelial cells in the LNs to increase in parallel with the lymphocyte number (22). We confirmed this observation in a sterile OVA/CFA immunization model (Supplemental Fig. 1A–C). However, the expansion of LNSC subsets during antimicrobial immune responses remained to be investigated. Therefore, we developed a protocol for the flow cytometric analysis of stromal cells in reactive popliteal LNs (popLNs) following s.c. VV-OVA infection, using contralateral nonreactive popLNs as controls.

LNSCs were identified based on the differential expression of gp38 and CD31 among CD45<sup>-</sup> Ter-119<sup>-</sup> nonhematopoietic cells in the LNs (23) (Fig. 1A, Supplemental Fig. 1A). Using this approach, we observed a >10-fold increase in total popLN cell numbers, peaking on day 10 p.i. (Fig. 1B, 1C). LEC and BEC expansion peaked on day 14 p.i., with a 5-fold increase in their numbers. Strikingly, FRC expansion was significantly delayed (Fig. 1B, shaded area) but was sustained until day 28 p.i., whereas expansion of LECs and BECs began as early as day 4 p.i. (Fig. 1B, 1C). The numbers of LNSCs in the contralateral nonreactive popLNs were not affected by VV infection. The percentage of T cell region reticular cells (9) among total FRCs, identified by CD157 expression, remained essentially stable (data not shown). Of note, the onset of FRC expansion coincided with the decline of VV-OVA copy number in reactive popLNs (Fig. 1D). Viral gene was almost undetectable on day 10 p.i. in reactive popLNs, whereas virus persisted for longer at the infection site. Reactive popLNs harbored considerably less virus than the infection site throughout the time course of our analysis. Importantly, the delayed expansion of FRCs relative to that of lymphocytes and other LNSC subsets clearly demonstrates that reactive LN growth and increased FRC numbers are not synchronized in the VV-OVA infection model, unlike in sterile inflammation (22).