Mast Cells Recruited to Mesenteric Lymph Nodes during Helminth Infection Remain Hypogranular and Produce IL-4 and IL-6

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Mast Cells Recruited to Mesenteric Lymph Nodes during Helminth Infection Remain Hypogranular and Produce IL-4 and IL-6


Mast cells (MC) and basophils (Ba) express the high-affinity receptor for IgE (FcεRI) but can be distinguished by their divergent expression of KIT and CD49b. In BALB/c mice, MC lineage cells expressing high levels of FcεRI by flow cytometry were seen only in bone marrow whereas those expressing intermediate levels of FcεRI were present in bone marrow and spleen of naive mice and in mesenteric lymph nodes (mLN) of Trichinella spiralis–infected mice. These FcεRI⁺CD49b⁺KIT⁺ cells had a membrane phenotype similar to i.p. connective tissue-type MC, but were smaller and hypogranular by flow cytometry forward and side scatter profiles, respectively. Consistent with this, they lacked the prominent secretory granules identified by histochemistry and immunodetection for the MC-specific granule proteases that are readily seen in mature jejunal mucosal MC that also are induced by the infection and present at the same time. The concentration of these MC lineage cells in mLN determined by flow cytometry was comparable to that of MC progenitors (MCp) measured by limiting dilution and clonal expansion with maturation. We observed upregulation of IL-4 transcription by MCp in mLN and spleens of helminth-infected 4get mice, and we demonstrated by intracellular cytokine staining production of IL-4 and IL-6 by the mLN MCp in helminth-infected mice. Furthermore, treatment of helminth-infected mice with anti-FcεRI mAb, a protocol known to deplete basophils, also depleted mLN MCp. Thus, this study identifies a hypogranular subset of MCp recruited to mLN by helminth infection that may be an important unrecognized source of cytokines. The Journal of Immunology, 2013, 190: 000–000.
populations. These studies included mice in the naive state as well as mice injected locally with papain or infected systemically with the helminth *Trichinella spiralis*. MC lineage cells and mature Ba resided in BM and spleen of naive BALB/c mice. Ba could be recruited to local LN with both papain and *T. spiralis* infection whereas only the infection elicited a LN MC lineage population. Forward scatter (FSC) and side scatter (SSC) analysis by flow cytometry of these FcRε+KIT+CD49b+ MC revealed that they were small hypogranular cells. The parallel assessment of their numbers by LDA, which requires maturation, indicated that they were MCp at days 6 and 13 of infection. The hypogranular phenotype of these local nodal MCp at day 6 of infection was dramatically different from the appearance of fully granulated intestinal MMC in the same mice at the same time. Moreover, the hypogranular MCp in LN and spleen exhibited IL-4 mRNA that increased during *T. spiralis* infection in 4get reporter mice. Furthermore, in infected BALB/c mice, this population of MCp could produce IL-4 and IL-6 as determined by flow cytometric detection. Our findings suggest that MCp are not simply a developmental stage, but rather may be a tissue population with independent functions in locations where granulation is not needed or desirable.

**Materials and Methods**

**Mice**

Seven- to 18-wk-old BALB/c mice and 4get (C.129-H2m^m12a/J) mice were obtained from Taconic Farms or The Jackson Laboratory. IL-3^−/− mice are maintained in-house at the Dana Farber Cancer Institute (23). The use of mice for these studies was in accordance with institutional guidelines with review and approval by the Animal Care and Use Committee of the Dana Farber Cancer Institute.

**Abs**

Fluorescently labeled mAb directed against FcεRs (MAR-1, mouse IgE (23G3), CD49b (DX5), B220 (RA3-6B2), CD3 (145-2C11), CD19 (6D5), CD4 (RM4-5), Ly-6G/Ly-6C (Gr-1) (RB6-8C5), TCRβ (H57-597), IL-4 (1B11), IFN-γ (MP5-20F3), and TNF-α (MP6-XT22) were obtained from BioLegend (San Diego, CA). Anti-FcγRI/II (3.12G2), anti-KIT (2B8), and anti-β^+^ integrin (M293) mAb were obtained from BD Biosciences (San Diego, CA). Monoclonal anti-mouse MC protease (mMCPr)-1 was obtained from R&D Systems (Minneapolis, MN). Anti-mMCPr-5 is a rabbit anti-peptide preparation made against a specific peptide (24).

**Papain administration**

Fifty micrograms of papain (Sigma-Aldrich, St. Louis, MO) in HBSS was administered by gavage as previously described (11). *T. spiralis* was used to identify FcεRI expression. The LDA was performed as previously described with inclusion of SCF (MAR-1) and IL-3 to improve viability and maturation (9, 11). Mononuclear cells (MNC) were obtained by Percoll (Sigma-Aldrich) gradient fractionation of harvested cells by using the 44/67% Percoll interface. After LDA, the original MC progenitor concentration is expressed as the number of MCp per 10^6 MNC isolated from the tissue.

**Identification of MCp by limiting dilution and clonal expansion**

The LDA was performed as previously described with inclusion of SCF with IL-3 to improve viability and maturation (9, 11). Mononuclear cells (MNC) were obtained by Percoll (Sigma-Aldrich) gradient fractionation of harvested cells by using the 44/67% Percoll interface. After LDA, the original MC progenitor concentration is expressed as the number of MCp per 10^6 MNC isolated from the tissue.

**Histochemical and immunohistochemical evaluation of MC**

Tissues and isolated cells were evaluated for mature MC numbers by chloroacetate esterase (CAE) reactivity and immunohistochemistry for the mMCPr (21). After harvesting of popliteal LN (3), T. spiralis infection was performed by flow cytometry and for Ba lineage clonal expansion or flow cytometry and for Ba lineage cells by clonal expansion or flow cytometry, respectively.

**Statistical analysis**

Data are expressed as the means ± SEM when derived from three or more values. Significance was determined with a two-tailed Student *t* test where three or more values were available for analysis. Significance was determined with the Mann–Whitney *U* test when values did not follow a normal distribution. A value of *p* < 0.05 was considered significant.

**Results**

**Identification of two Ba and two MC lineage populations in BALB/c BM and a single phenotype for each lineage in peripheral tissues**

Earlier studies by our group and others with BM-derived cells cultured in vitro demonstrated that commitment to the MC and Ba lineages was closely followed by de novo expression of the high-affinity IgE receptor detected either by mAb to the α-chain or the
ability to bind IgE (26–29). Differentiation along the MC lineage was associated with the continued expression of KIT, the receptor for SCF, whereas this receptor was downregulated with Ba lineage development (29). To follow the parallel lineage development of MC and Ba in vivo, we analyzed the non–B, non–T cells (by excluding cells expressing CD19 or CD3) in BALB/c BM for expression of FcεRI and KIT (CD117), as well as CD49b as a Ba marker (30–32). Within the non–B, non–T population there were two contiguous populations of cells positive for both FcεRI and CD49b expression (pentagonal and ovoid gates in Fig. 1A). These cells showed a 10-fold range in the fluorescence intensities of FcεRI expression, and the population of cells expressing the highest levels of FcεRI (ovoid gate in Fig. 1A) had a 10-fold range in expression of CD49b. A third population of cells was negative for CD49b expression and intermediate in FcεRI expression (rectangular gate in Fig. 1A) and was predominantly KIT+ (Fig. 1A, top histogram), suggesting a committed MC lineage identity. The CD49b+ population that expressed intermediate levels of FcεRI (pentagonal gate in Fig. 1A) uniformly lacked KIT expression (Fig. 1A, bottom histogram), suggesting a committed Ba identity. The cells expressing high levels of FcεRI (ovoid gate) with a range of CD49b expression were heterogeneous in their KIT expression (Fig. 1A, middle histogram), suggesting at least two different precursor populations. To further classify these BM cell populations, we reanalyzed the non–B, non–T cells for FcεRI and KIT expression and then assessed CD49b expression (Fig. 1B). We identified a KIT– population (rectangle gate in Fig. 1B) that was predominantly CD49b+ (Fig. 1B, top dot plot), suggesting it is mostly composed of Ba lineage cells also identified in the oval and pentagonal gates in Fig. 1A. The population of cells expressing high levels of KIT and intermediate levels of FcεRI (Fig. 1B, pentagon) was largely CD49b+ (Fig. 1B, bottom dot plot), compatible with MC commitment. The population of cells with intermediate KIT and high FcεRI expression (Fig. 1B, ovoid gate) was heterogeneous for CD49b, suggesting two different precursor populations (Fig. 1B, middle dot plot) similar to the cells in the oval gate identified in Fig. 1A. Taken together, the FcεRI+ populations make up ~0.9% of non–B, non–T cells in BALB/c BM.

Using the same three cell surface markers, we compared the phenotypes of MC (FcεRI+KIT+CD49b+) and Ba (FcεRI+KIT+ CD49b−) within the non–B, non–T cells of BALB/c spleen, blood, and popliteal LN with those in the BM, using injection of papain in the footpads to elicit Ba in popliteal LN (3). In the spleen, there was only a single population of FcεRI+KIT+ cells expressing intermediate levels of FcεRI in both naive and papain-treated mice (Fig. 2A, top panel; rectangular gate). Few or no FcεRI+KIT+ cells were detected in blood or popliteal LN of naive and papain-injected mice (Fig. 2A, middle and bottom panels). There also was only a single population of FcεRI+CD49b+ cells expressing intermediate levels of FcεRI in the spleen and blood of both naive and papain-injected mice (Fig. 2B, top and middle panels). This CD49b+ population corresponds to the unmarked population of FcεRI+KIT+ cells seen in Fig. 2A. There were very few LN Ba in naive mice, but papain administration induced an influx of Ba into LN (Fig. 2B, bottom panels) as previously noted (3). The KIT+ FcεRI+ and KIT–FcεRI− populations seen in BM were notably undetectable in these peripheral tissues.

**Infection with T. spiralis expands MC and Ba lineage populations and recruits them to mLN**

To directly study recruitment of MC lineage progenitors to LN as predicted by LDA (12–15), we employed a *T. spiralis* infection in which tissues were harvested in the middle of (days 6–7) and toward the end of (days 12–14) the acute phase of intestinal infection. In contrast to the studies with papain, we used anti-IgE rather than anti-FcεRI to monitor FcεRI expression during *T. spiralis* infection to avoid any competing effects of host IgE on the assessment of FcεRI+ cells (33). IgE*ε*KIT+ MC lineage populations in naive mice were present in BM and spleen but were rare in mLN (Fig. 3A, top). The unmarked IgE*ε*KIT+ Ba population can be seen directly to the left of the gated MCp (Fig. 3A). After *T. spiralis* infection, there were significant increases in the frequency of BM IgE*ε*KIT+CD49b+ MC at days 6 and 12 (Fig. 3A, 3B). Furthermore, distinct IgE*ε*KIT+ MC lineage populations of similar phenotype appeared in spleen and mLN (Fig. 3A). There were concurrent significant rises in these splenic and LN populations on days 6 and 12 (Fig. 3B). Ba populations identified as IgE*ε*CD49b+ cells also significantly expanded in BM on days 6 and 12 (Fig. 3C). Splenic Ba numbers lagged at day 6 but had

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**FIGURE 1.** BM Ba and MC lineage populations in BALB/c mice defined by flow cytometric analysis of FcεRI, CD49b, and KIT expression. BALB/c BM cells were analyzed for expression of FcεRI, CD49b, and KIT after exclusion of CD3+ and CD19+ (non–T, non–B) cells. (A) Three populations are defined (polygons) by FcεRI and CD49b expression. The frequencies of the populations are shown as a percentage of non–T, non–B cells. Each of the three populations is further analyzed for KIT expression (black histograms) compared with isotype control (gray histograms). (B) Analysis of FcεRI and KIT expression within the non–T, non–B cells as in (A). Indicated populations are further analyzed for FcεRI and CD49b expression (right panels). Data are representative of six to nine mice in three experiments. Isotype control values were <5% of the indicated values.
A significant increase at day 12. The number of Ba in the mLN was significantly increased at days 6 and 12. In the mLN, MC lineage cells constituted a larger (~2-fold) fraction of the population than Ba at each time point.

LN MCp assessed by flow cytometry are highly immature and correspond in number to MCp assessed by limiting dilution and clonal expansion

To determine whether the numbers of lineage-committed MCp in mLN detected directly by their distinct cell surface phenotype in flow cytometry are comparable to the numbers of MCp assayed indirectly ex vivo by LDA, we compared these numbers in naive mice and in mice 13 d after T. spiralis infection by both assays using the MNC fraction. There were very few MCp in naive mLN with either assay (55.8 and 56.4 MCp/10⁶ MNC, mean from two experiments, five mice). At 13 d postinfection there were significant increases in the number of MCp detected by flow cytometry (6.2-fold, *p < 0.001) and by LDA (8.7-fold, *p < 0.01) (Fig. 4A). There was no significant difference between the measurements of MCp per million MNC obtained by the two methods in either

**FIGURE 2.** Identification of MC and Ba lineage populations in spleen, blood, and LN of naive and papain-injected BALB/c mice. (A) Three days after papain or PBS injection, MC lineage cells were identified as FcεRI⁺KIT⁺ cells in spleen, blood, and popliteal LN. (B) Three days after papain or PBS injection, Ba lineage cells were identified as non–T, non–B, FcεRI⁺CD49b⁺KIT⁺ cells in spleen, blood, and popliteal LNs. Data are representative of 9–12 mice in three experiments. Numbers indicate the frequency of MCp and Ba as a percentage of the non–T, non–B cells isolated from the indicated tissues. Isotype control values were <5% of the indicated values.

**FIGURE 3.** T. spiralis–infected BALB/c mice recruit MC and Ba to mLN and expand spleen and BM lineage pools. (A) Dot plots of BM, spleen, and LN cells from naive and day 12 infected BALB/c mice show the IgE⁺KIT⁺ MC lineage populations (square gate). Dot plots are representative of data from four experiments. (B) Frequencies of MC lineage populations from naive, day 6, and day 12 postinfection mice are shown as a percentage of total cells isolated from BM, spleen, and LN. (C) Frequencies of Ba lineage populations (IgE⁺CD49b⁺) in the BM, spleen, and LN as in (B). Data in (B) and (C) represent means ± SEM, n = 13 mice per group, four experiments. *p < 0.05, **p < 0.001, ***p < 0.0001.
naive or infected mice. The trend toward higher numbers obtained by LDA may reflect the lower specificity of this assay attributable to participation by myeloid lineage cells that differentiate into MC colonies in the presence of IL-3 and SCF (34).

To assess the maturity of LN MCp detected by flow cytometry, we analyzed the numbers of MCp in the LN obtained by cytometry before and after density gradient fractionation and compared them to the numbers of granulated MC detected by histochemistry. It had been established previously using peritoneal cells obtained by lavage that density gradient isolation of MNC yields a cell preparation enriched for MCp and depleted of mature MC, which by CAE reactivity as well as immunohistochemistry to mMCP-1 and mMCP-5, we used CAE reactivity as well as immunohistochemistry to mMCP-1 and mMCP-5 to detect mature MC and evaluate their protease phenotype. In the intestine after T. spiralis infection, these induced MCp were lower in both assessments than were immature BMMC derived with IL-3 and SCF, emphasizing their relative agranularity (Supplemental Fig. 1). Thus, although the recruited LN MCp, splenic MCp, BMMC, and peritoneal MC exhibit the same surface marker phenotype, when identified by flow cytometry, they are different in regard to size (FSC) and granularity (SSC).

In a histological examination of the parenchyma of mLN for MC we used CAE reactivity as well as immunohistochemistry to mMCP-1 and mMCP-5 to detect mature MC and evaluate their protease phenotype. In the intestine after T. spiralis infection, there was little CAE reactivity in the parenchyma of mLN (Fig. 4C, bottom panels) whereas the intraepithelial MMC from the jejunum of the same mice expressed mMCP-1 and the submucosal MC expressed mMCP-5 (Fig. 4C, bottom panels). These observations support the findings with the low density of helminth-induced LN MCp reported by Jarboe et al. (14). When we compared mLN and splenic MCp populations from day 6 after T. spiralis infection, these induced MCp were virtually identical in size (FSC profile) and granularity (SSC profile) and greater than the lymphocyte population in these parameters. Of note, these induced MCp were lower in both assessments than were immature BMMC derived with IL-3 and SCF, emphasizing their relative agranularity (Supplemental Fig. 1). Thus, although the recruited LN MCp, splenic MCp, BMMC, and peritoneal MC exhibit the same surface marker phenotype, when identified by flow cytometry, they are different in regard to size (FSC) and granularity (SSC).
by flow cytometry that with *T. spiralis* infection, dispersed mLN parenchymal cells harbor very few mature MC in concert with a dominant hypogranular subset of MC.

To directly visualize the morphology of this recruited subset, we sorted them from the mesenteric nodes of *T. spiralis*-infected mice at day 6 based on their distinct phenotype. After depleting the CD3<sup>+</sup>CD19<sup>+</sup> cells, the sorted KIT<sup>+</sup>FceRI<sup>+</sup>CD49b<sup>+</sup> cells were stained with Diff-Quick or toluidine blue. The LN MCp are small cells with a prominent nucleus and a cytosol that contains numerous empty vesicles after staining with Diff-Quick and reveals a few toluidine blue-positive granules (Fig. 4D). In comparison, CTMC from the peritoneal cavity are large and heavily granulated cells by either Diff-Quick or toluidine blue staining.

**Depletion of MCp by administration of anti–FceRI mAb with *T. spiralis* infection**

Depletion of Ba by systemic administration of anti–FceRI mAb (MAR-1) to assess their role in mouse models of inflammation (3, 4, 25, 32) is based on a protocol by Denzel et al. (33) in which Ba depletion is not accompanied by a change in the number of mature peritoneal MC. To assess the effect of this treatment on MCp, we administered anti–FceRI mAb i.p. to BALB/c mice prior to infection with *T. spiralis* and then enumerated the numbers of MCp in mLN, spleen, and BM. MCp were identified as β<sub>7</sub> integrin<sup>+</sup>KIT<sup>+</sup> cells, a combination that was equivalent to anti-IgE<sup>+</sup>KIT<sup>+</sup> identification of MCp in isotype-treated infected mice (data not shown). Six days after infection, the β<sub>7</sub> integrin<sup>+</sup>KIT<sup>+</sup> MCp were significantly reduced by ~70% (from 471 to 141 MCp per 10<sup>6</sup> nucleated LN cells) as compared with isotype control–injected mice (Fig. 5A). The fold reduction was similar when assessed by LDA in which cell numbers were reduced from 860 to 260 MCp per 10<sup>6</sup> LN MNC (Fig. 5B). In contrast, the numbers of MCp in the BM and spleen at day 6 postinfection were not reduced by this treatment when assessed by flow cytometry or by LDA. The number of β<sub>7</sub> integrin<sup>+</sup>KIT<sup>+</sup> MCp in isotype control mAb versus MAR-1–injected mice in the BM and spleen was 2020 ± 638 versus 2058 ± 157 MCp per 10<sup>6</sup> BM cells (mean ± SEM, n = 3) and 534 ± 48 versus 837 ± 227 MCp per 10<sup>6</sup> splenic MNC, respectively (mean ± SEM, n = 3). By LDA, we found 624 ± 63 MCp per 10<sup>6</sup> MNC in the spleens of isotype control–injected mice versus 750 ± 128 MCp per 10<sup>6</sup> MNC in the spleens of MAR-1–injected mice (mean ± SEM, n = 6, two experiments).

To address the possibility that the influx of Ba influenced the recruitment of MCp to draining nodes, we evaluated the response in the IL-3<sup>−/−</sup> strain, which had been reported to lack Ba in their mLN by FACS analysis after *Nippostrongylus brasiliensis* infection (35). The number of LN MCp in the IL-3<sup>−/−</sup> versus the BALB/c mice 6 d postinfection with *T. spiralis* was not different (0.70 ± 0.15 versus 0.68 ± 0.05% of non–B, non–T LN cells, respectively; n = 4 mice per genotype in a single experiment) whereas the increase in the number of Ba in these same mice was reduced by 77% (0.03 ± 0.01 versus 0.15 ± 0.05%, respectively). We obtained similar results in a second experiment indicating the independence of MCp recruitment to the draining LN.

**T. spiralis infection increases IL-4 mRNA in mLN MCp of 4get mice**

The infection-driven expansion of hypogranular MCp in the draining LN without the appearance of MMC that are so prominent in the intestine suggests that LN MCp might have a granule-independent function. Because many helminth infections generate a substantial Th2 type inflammation with an increased IgE response implicating IL-4, we examined IL-4 mRNA levels in MCp using IL-4/enhanced GFP (4get) reporter mice. In these mice, an enhanced GFP gene is inserted in the 3′ untranslated region of the endogenous IL-4 locus such that enhanced GFP is transcribed in parallel with IL-4 and thus serves as a marker of IL-4 mRNA levels. In naive 4get mice, BM MCp express very little GFP as measured by MFI (184 ± 10.6), consistent with the findings of Gessner et al. (36), whereas splenic MCp express moderate levels of GFP (761.4 ± 50.6), and peritoneal MC express uniformly high levels of GFP (1789 ± 85.3) (Fig. 6A, 6B, left panels). Very few naive LN MCp were detectable but those seen expressed low GFP levels comparable to naive splenic MCp (Fig. 6A, black histograms). Six days after *T. spiralis* infection, GFP expression increased in MCp in all tissues (Fig. 6A, red histograms). The increase in MFI with infection was significant for the MCp in BM, spleen, and mLN as well as for peritoneal MC (Fig. 6B, left panel). The Ba lineage demonstrated initial baseline GFP expression in BM, spleen, and LN, and with *T. spiralis* infection it significantly increased in the BM and splenic Ba. (Fig. 6A, 6B, right panels). Of note, the hypogranular MCp of spleen and LN increased expression of GFP by 2.5- and 3.6-fold, respectively, whereas the mature granular peritoneal MC increased GFP expression by only 1.3-fold with infection.

**Discussion**

We have addressed the parallel in vivo responses of MC and Ba from BM to blood, spleen, and regional LN using flow cytometry in mice subjected to local or systemic inflammation as compared with naive controls. Unlike other myeloid lineage cells, MC are released from BM as a progenitor, which is devoid of the secretory granules that define the mature tissue-resident cells. Thus, we first established that their cytometric detection and enumeration as FceRI<sup>+</sup>KIT<sup>+</sup>CD49b<sup>+</sup> MCp corresponded in numbers with their classical assay in tissues by limiting dilution and clonal expansion with maturation to granulated immature MC (34, 37). We then ob-

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**FIGURE 5.** Administration of anti–FceRI mAb depletes LN MCp. BALB/c mice were injected i.p. with anti–FceRI mAb (MAR-1) daily for 3 d before being infected with *T. spiralis*. mLN were harvested after 6 d and MCp were assayed. (A) In a flow cytometric assay, MCp were identified as β<sub>7</sub> integrin<sup>+</sup>KIT<sup>+</sup> cells and enumerated per million live nucleated nodal cells. Data represent means ± SEM, n = 10–11 mice per group, three experiments. (B) In the LDA, MCp were assayed after Percoll gradient isolation of MNC and expressed per million MNC. Data represent means ± SEM, n = 5–6 mice per group, two experiments. ***p < 0.0001.
served that the size (FSC) and granularity (SSC) of MCp by cytometric assay were more than those observed for lymphocytes and demonstrably less than these parameters for culture-derived immature BMMC. These findings were also confirmed by histochemistry in which MC in the jejunum were readily observed using either CAE reactivity or immunohistochemistry for the secretory granule proteases whereas those in the LN were not detectable by either measure. Turning to a positive definition of the nodal MCp, we sorted this subset by their lineage phenotype and assessed their morphology on cytospins. As expected, nodal MCp are small cells with a prominent nucleus and empty cytoplasmic vesicles by Diff-Quik stain. Toluidine blue staining showed a few granules. The contrast to peritoneal MC by size and granularity was marked, again as expected from the FACS study. Thus, even though the nodal MCp had the same membrane phenotype as mature granulated MC such as those in the peritoneal cavity, they are a novel MC subset with small size and little granularity.

Because the MCp recruited to parenchymal tissue of mLN or expanded in spleen with \( T. \) spiralis infection are granule deficient by cytometric presentation or direct histochemistry, they would not have been directly recognized in prior studies of MC biology. However, their phenotypic definition allows for a dynamic real-time assessment of their accumulation with cytometry. Whereas the jejunum was enriched with nMCP-1* MMC likely derived from MCp recruited by the \( T. \) spiralis infection (12, 13), the nodal MCp were hypogranular and remained as such even as they declined in numbers by day 13 when the infection is subsiding and the jejunal MMC are at their peak. Thus, we sought evidence of function in vivo for the hypogranular nodal subset. Exocytosis of preformed secretory granule mediators seemed excluded based on the lack of granules, so we turned to the production of cytokines, which is a well-recognized function for BMMC in response to various agonists (38). Using 4gt reporter mice, we found up-regulation of IL-4 mRNA during helminth infection that increased to a greater degree in mLN MCp than in granulated mature peritoneal CTMC or in the recruited Ba. Importantly, intracellular cytokine staining demonstrated that MCp of WT BALB/c mice had cytokine-generating function as shown by IL-4 and IL-6 production in most mice at day 6 after \( T. \) spiralis infection. We did not need to further activate these LN ex vivo to obtain cytokine generation but did provide IL-3 to maintain their viability during their exposure to brefeldin. We have not yet sought to optimize the postinfection time course for MCp cytokine production or surveyed for other cytokines. Rather, our current goal was to demonstrate function for this essentially agranular MC subset prominent in draining LN after \( T. \) spiralis infection. We appreciate that there is a longer term need to address the role of the MC lineage in afferent as well as the traditional effferent components of adaptive immunity.

Ginsburg and Lagunoff (16) first extrapolated the appearance of MC lineage progenitors in LN of BALB/c mice, using repeated injections of horse serum or hen albumin for systemic sensitization. In their study, LN cells cultured on embryonic fibroblast monolayers differentiated into histochemically defined MC at higher rates from immunized mice, and the dependence of this outcome on Ag restimulation during the culture suggested cytokine-dependent maturation. Subsequently, Crapper and Schrader (9) used a conditioned media to grow immature MC from putative MCp and used a limiting dilution analysis with clonal expansion to define the levels of MCp in BM, spleen, and LN of naive CBA mice as well to show an increase in their number following a local immunization. Guy-Grand et al. (10) used such an assay to indirectly recognize MCp in both the thoracic duct lymph and in the mLN during \( N. \) brasiliensis infection in BALB/c mice. Jarboe et al. (14) extended these findings to show that putative MCp harvested from mLN were of low density and could be expanded and matured with cytokine culture alone or on a fibroblast monolayer with the latter inducing a histochemical positivity for heparin. Similarly, Remnick et al. (15) demonstrated that IL-4 and IL-10 promoted expansion.

**FIGURE 6.** Increased IL-4 transcription in 4get mice and production of IL-4 and IL-6 by LN MCp after \( T. \) spiralis infection of BALB/c mice. (A) BM, spleen, mLN, and peritoneal lavage (PL) fluid were harvested from naive BALB/c and 4gt mice, and from 4gt mice on day 6 after \( T. \) spiralis (Ts) infection. The single-cell suspensions were assessed for GFP expression within the MC and Ba lineage populations. Histograms of GFP expression are shown for MC (left) and Ba (right) from each tissue as indicated. Histogram colors represent: gray, naive BALB/c mice; black, naive 4gt mice; red, \( T. \) spiralis–infected 4gt mice. Naive LN data are based on very few events. (B) MFI of GFP in the indicated MC (left) or Ba (right) lineage populations from 4gt mice represent mean ± SEM, \( n = 13–14 \) mice, three experiments. **\( p < 0.0005 \), calculated by the Mann–Whitney \( U \) test. (C) Intracellular cytokine staining for the indicated cytokines in mLN MCp day 6 after infection in a representative BALB/c mouse. The gray lines are the isotype control, and black lines are the indicated cytokine. Histograms are from one mouse whose response was close to the mean shown in (D). (D) MFI index of intracellular cytokine staining for IL-4 and IL-6 in mLN MCp, showing individual values and mean values ± SEM (bars), day 6 postinfection, 13 mice per group, five experiments.

TABLE 4. Intracellular Cytokine Staining of LN MCp and Ba Following \( T. \) spiralis Infection

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<th>Cytokine</th>
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<td>IL-6</td>
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*Data represent mean ± SEM, \( n = 13–14 \) mice, three experiments. **\( p < 0.0005 \), calculated by the Mann–Whitney \( U \) test.*
and maturation, respectively, of MCp recruited to the draining LN with helminth infection are committed MCp. However, our findings also point out that the assays of MCp by ex vivo expansion with maturation do not define their hypogranular in vivo phenotype and apparent failure to mature to MMC within the LN parenchyma. The number of MC subsets is of course not limited to agranular and granular. For example, within the granular subset, the MMC in the intestine induced by helminth infection express mMCP-1, whereas MMC induced to accumulate in the treachea by OVA sensitization and challenge express not only mMCP-1, a chymase, but also another chymase, mMCP-4, an elastase, mMCP-5, two tryptases, mMCP-6 and mMCP-7, and carboxypeptidase A3 (6, 21). There are also differences in the protease profile of the innate CTMC in intestine and treachea. Taken together, it begins to appear that the particular tissue and its microenvironment to which MCp are recruited can determine whether there is granulation as well as the protease profile of those that become granulated (21, 37). This heterogeneity along with the added contexts of cytokine and eosinomaid generation for a lineage with major innate and adaptive immune-induced members suggest that subset recognition is a step toward clarifying the complexities of overall MC lineage function. Because the MCp recruited to parenchymal tissue of LN and spleen with T. spiralis infection were granule deficient by cytometric presentation or histochemistry on cytospins, they would not have been recognized in studies in which MCp to FcεRI was used to deplete and thereby recognize a Ba function. Germaine to this, Giacomin et al. (39) recently evaluated this treatment in C57BL/6 mice infected with T. spiralis, and noted a decrease in the mucosal MC response in the small intestine, which they attributed to attenuation of the Th2 response, although they did not evaluate MCp. We observed an -70% reduction in accumulation of LN MCp with administration of mAb to FcεRI to mice prior to T. spiralis infection. This blocking was selective, as there was no significant concomitant reduction of MCp in BM or spleen assessed by either FACS or LDA. We have not yet addressed the kinetics of LN Ba and MCp depletion with mAb to FcεRI. Nonetheless, our findings with administration of anti-FcεRI are noteworthy because the contributions of IL-4 and/or IL-6 production by Ba have been implicated in host Th2 cell and B cell responses (3, 4, 25, 32, 33, 39, 40), whereas our new findings reveal a previously unrecognized possible contribution from LN MCp.

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Disclosures
The authors have no financial conflicts of interest.

References


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Supplemental Data

SUPPLEMENTAL FIGURE 1. Comparison of the forward and side scatter profiles of mesenteric LN and splenic MCp with cultured BMMC. Mesenteric LN and spleen MCp populations from d6 *T. spiralis*-infected mice and 6 wk old BMMC were assessed for forward and side scatter profiles by flow cytometry. The left panel shows LN and spleen MCp and BMMC size as assessed by forward scatter. The right panel shows the granularity as assessed by side scatter from the same 3 populations. The black line is LN MCp, the gray line is spleen MCp and the filled histogram is BMMC.