CSF-1–dependent donor-derived macrophages mediate chronic graft-versus-host disease

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Chronic GVHD (cGVHD) is the major cause of late, nonrelapse death following stem cell transplantation and characteristically develops in organs such as skin and lung. Here, we used multiple murine models of cGVHD to investigate the contribution of macrophage populations in the development of cGVHD. Using an established IL-17–dependent sclerodermatous cGVHD model, we confirmed that macrophages infiltrating the skin are derived from donor bone marrow (F4/80+ CSF-1R+ CD206+ iNOS–). Cutaneous cGVHD developed in a CSF-1/CSF-1R–dependent manner, as treatment of recipients after transplantation with CSF-1 exacerbated macrophage infiltration and cutaneous pathology. Additionally, recipients of grafts from Csf1r–/– mice had substantially less macrophage infiltration and cutaneous pathology as compared with those receiving wild-type grafts. Neither CCL2/CCR2 nor GM-CSF/GM-CSFR signaling pathways were required for macrophage infiltration or development of cGVHD. In a different cGVHD model, in which bronchiolitis obliterans is a prominent manifestation, F4/80+ macrophage infiltration was similarly noted in the lungs of recipients after transplantation, and lung cGVHD was also IL-17 and CSF-1/CSF-1R dependent. Importantly, depletion of macrophages using an anti–CSF-1R mAb markedly reduced cutaneous and pulmonary cGVHD. Taken together, these data indicate that donor macrophages mediate the development of cGVHD and suggest that targeting CSF-1 signaling after transplantation may prevent and treat cGVHD.

Introduction

Graft-versus-host disease (GVHD) remains a major complication of allogeneic stem cell transplantation (SCT). GVHD can present in acute and chronic forms, which differ in their time of onset and symptoms. Acute GVHD (aGVHD) occurs early after transplantation, with target organ damage characterized by apoptosis. In contrast, chronic GVHD (cGVHD) is a late complication of SCT and is characterized by fibrosis. Indeed, cGVHD presents with many features that overlap with certain autoimmune diseases. While skin is the primary organ involved in cGVHD, both lung and liver fibrosis can also occur, and these manifestations are all associated with significant morbidity and mortality. Our understanding of the pathophysiology of aGVHD is far more advanced than that of cGVHD, and it is clear that these forms are mediated by different immunological subsets and cytokine networks. Currently, the majority of clinical allogeneic transplants use granulocyte colony-stimulating factor–mobilized (G-CSF–mobilized) peripheral blood (PB) stem cells, which has led to rapid hematopoietic reconstitution, improved leukemic eradication, and similar levels of aGVHD, but increased levels of cGVHD (1). Therapeutically, there are limited options available for the treatment of cGVHD, with corticosteroids representing the mainstay of treatment. Unfortunately, this is often ineffective and is associated with significant morbidity, thus cGVHD represents an increasing burden in the clinic.

Macrophages play an essential role in both homeostasis and pathology and are characterized by high functional heterogeneity (2). The differentiation, proliferation, and survival of the majority of macrophage populations are dependent on colony-stimulating factor 1 (CSF-1) (3, 4). Macrophages acquire diverse phenotypic and functional forms in response to local cytokines and microbial signals, which has resulted in the “M1” and “M2” macrophage classifications (5, 6). Classically activated macrophages (M1) mediate defense of the host from a variety of bacteria, protozoa, and viruses and have roles in antitumor immunity. Activation of proinflammatory M1 macrophages is typically induced by IFN-γ, lipopolysaccharide, and cytokines such as granulocyte-macrophage colony-stimulating factor (GM-CSF) (5–7). Alternatively activated macrophages (M2) have antiinflammatory functions and regulate tissue repair and remodeling. M2 macrophage activation is induced by IL-4 and IL-13 (8) as well as immune complexes, glucocorticoids, and the
cytokine CSF-1 (6, 7). Although the M1 and M2 classification system is widely used, it is increasingly clear that these macrophage populations represent the extreme ends of a wide spectrum of phenotypes associated with macrophage activation.

Recent preclinical and clinical data from our group established a highly reproducible and informative model of cGVHD that supports a role for IL-17 as a central mediator of pathology, particularly within the skin (9). Cutaneous cGVHD was shown to be exacerbated by G-CSF mobilization in an IL-17–dependent manner, and late after transplantation, scleroderma was absent in recipients of Il17a–/– grafts compared with wild-type (WT) grafts. Our initial studies also identified neutrophils and T cells within the mononuclear infiltrate in skin during GVHD (9), however, they were far less dominant than the F4/80+ macrophage infiltrate illustrated in Figure 1, and only the macrophages were IL-17 dependent. Although not examined here, our initial studies also identified neutrophils and T cells within the mononuclear infiltrate in skin during GVHD (9), however, they were far less dominant than the F4/80+ macrophage infiltrate illustrated in Figure 1, and only the macrophages were IL-17 dependent.

Skin-infiltrating macrophages are donor M2-like CSF-1R-expressing macrophages. To examine the phenotype of these F4/80+ macrophages, IHC was performed using markers for both classically activated and alternatively activated macrophages (inducible nitric oxide synthase [iNOS] and mannose receptor CD206, respectively). Additionally, IHC for the congenic marker CD45.1 was used to mark donor cells. IHC in serial sections was performed 21 days after transplantation in lethally irradiated mice receiving either G-CSF–mobilized T cell–depleted (TCD) grafts (Figure 1D). In mice receiving nonmobilized grafts, we noted F4/80+ macrophage infiltration in the dermis by day 21 after transplantation (Figure 1E), and by day 28 after transplantation, F4/80+ macrophages were predominantly located within the s.c. fat layer (Figure 1, F and G), with minimal macrophage infiltration noted in mice that received TCD grafts (Figure 1H). Although not examined here, the vast majority of infiltrating F4/80+ cells in mice receiving G-CSF–mobilized grafts were donor (CD45.1+) alternatively activated (CD206+) macrophages, with minimal iNOS expression (F4/80+CD45.1+CD206–iNOS−) (Figure 2A and Supplementary Figure 1A; supplemental material available online with this article; doi:10.1172/JCI75935DS1). We noted minimal donor macrophage infiltration in mice that received G-CSF–mobilized...
CD11b\(^+\)F4/80\(^+\)Ly6C\(_{hi}\) classical monocytes and CD11b\(^+\)F4/80\(^+\)Ly6C\(_{lo}\) inflammatory monocytes in naive B6.WT, B6.Ccr2\(^{-/-}\), and B6 common \(\beta\) chain\(^{-/-}\) mice to examine the requirement of chemokine (C-C motif) ligand 2 (CCL2) and GM-CSF, respectively. To examine the requirement of CSF-1, we used fetal liver chimeras (FLCs) on a B6 background, since CSF-1R deficiency is neonatally lethal. We examined monocyte populations using a gating strategy (Figure 3A) that removed Ly6G\(^+\)CD3\(^+\) and high side-scatter cells (SSCs). As expected, compared with B6.WT mice, we observed a significant reduction in the frequency and absolute numbers of circulating CD11b\(^+\)F4/80\(^+\)Ly6C\(^{lo}\) classical monocytes in the Ccr2\(^{-/-}\) mice (Figure 3, B and C; \(P = 0.004, \ *)\) and B6.Ccr2\(^{-/-}\) FLCs exhibited a significant reduction in Ly6C\(^{lo}\) subset frequencies and absolute numbers (Figure 3, B and C; \(***P = 0.002, *P = 0.0286\)). The contribution of GM-CSF to circulating monocyte populations was minimal, since the frequencies and absolute numbers of both Ly6C\(^{lo}\) and Ly6C\(^{lo}\) cell populations were not significantly altered in the common \(\beta\) chain-deficient mice.

**CSF-1 treatment after SCT exacerbates cutaneous cGVHD.** We had previously confirmed in Figure 3 that CSF-1 was required for the development of the Ly6C\(^{lo}\) PB monocyte/macrophage population, which is suggested to be a tissue macrophage precursor. Therefore, we further examined the contribution of CSF-1 to macrophage infiltration and cutaneous cGVHD after transplantation. Lethally irradiated B6 mice received G-CSF-mobilized BALB/c whole spleen or TCD spleen and were treated with either saline or CSF-1 for 5 days from day 14 after transplantation. Compared with saline-treated recipients, we found that CSF-1 treatment significantly increased F4/80\(^+\) macrophages in the skin 19 days after transplantation (Figure 4A), quantified as positive pixels/mm\(^2\) (Figure 4B; \(**P = 0.0017\)). CSF-1 treatment preferentially expanded donor alternatively activated macrophages, as confirmed via IHC (F4/80\(^+\)CD45.1\(^+\)CD206\(^+\)iNOS\(^-\)) (Figure 4C). Semiquantitative histopathology confirmed that recipients treated with CSF-1 had significantly higher cutaneous pathology scores than did those treated with saline (Figure 4D; \(**P = 0.0087\)).

Further analysis of PB monocyte populations 19 days after transplantation illustrated a trend toward an increase in the frequency of Ly6C\(^{lo}\) cells after 5 days of CSF-1 treatment (Figure 5A). Therefore, we carried out further monocyte/macrophage analysis of cells isolated 19 days after transplantation from the skin (ears) of mice treated with either saline or CSF-1 (gating...
CSF1R–/– grafts had a significantly lower clinical GVHD score throughout the time course examined compared with that of WT graft recipients (Figure 6A). IHC performed 21 days after transplantation illustrated that mice receiving WT grafts (Figure 6B) had significantly higher F4/80+ macrophage infiltration compared with that seen in mice receiving CSF1R–/– grafts (Figure 6B), quantified as positive pixels/mm² (Figure 6C; **P = 0.003). Masson’s trichrome staining (collagen fibers are stained blue) and semiquantitative histopathology scores assessed 48 days after transplantation confirmed that mice receiving CSF1R–/– grafts had significantly lower cutaneous pathology and fibrosis than did those receiving WT grafts (Figure 6D; *P = 0.045, **P = 0.008). Masson’s trichrome staining confirmed a pathogenic role for CSF-1/CSF-1R signaling in the development of cutaneous pathology after transplantation. Analysis of PB monocyte populations 21 days after transplantation illustrated that recipients of CSF1R–/– FLCs exhibited a significant increase in the frequency of Ly6Clo cells and a significant reduction in the Ly6Chi cell population (Figure 6E; *P = 0.0286). Other CSF-1R–dependent cells reside within the skin apart from macrophages, most notably langerin-expressing Langerhans cells, which reside in the epidermis. In contrast to macrophages, CSF1R–/– grafts had a significantly lower clinical GVHD score throughout the time course examined compared with that of WT graft recipients (Figure 6A). IHC performed 21 days after transplantation illustrated that mice receiving WT grafts (Figure 6B) had significantly higher F4/80+ macrophage infiltration compared with that seen in mice receiving CSF1R–/– grafts (Figure 6B), quantified as positive pixels/mm² (Figure 6C; **P = 0.003). Masson’s trichrome staining (collagen fibers are stained blue) and semiquantitative histopathology scores assessed 48 days after transplantation confirmed that mice receiving CSF1R–/– grafts had significantly lower cutaneous pathology and fibrosis than did those receiving WT grafts (Figure 6D; *P = 0.045, **P = 0.008). Masson’s trichrome staining confirmed a pathogenic role for CSF-1/CSF-1R signaling in the development of cutaneous pathology after transplantation. Analysis of PB monocyte populations 21 days after transplantation illustrated that recipients of CSF1R–/– FLCs exhibited a significant increase in the frequency of Ly6Clo cells and a significant reduction in the Ly6Chi cell population (Figure 6E; *P = 0.0286). Other CSF-1R–dependent cells reside within the skin apart from macrophages, most notably langerin-expressing Langerhans cells, which reside in the epidermis. In contrast to macrophages,
however, Langerhans cells are instructed by the alternative CSF-1R ligand IL-34 (23). To investigate the contribution of Langerhans cells to the development of CSF-1R-dependent sclerodermatous cGVHD, mice received BM and T cell grafts from langerin-diphtheria toxin receptor–transgenic (langerin-DTR–transgenic) mice in which DTR administration nor the development of cutaneous pathology was altered (Supplemental Figure 3A), but neither F4/80+ macrophage infiltration nor the development of cutaneous pathology was altered (Supplemental Figure 3, B and C), thus establishing that Langerhans cells do not contribute to cutaneous GVHD.

F4/80+ macrophage infiltration and cutaneous fibrosis after transplantation is GM-CSFR independent. Both CSF-1/CSF-1R and GM-CSF/GM-CSFR signaling pathways are involved in regulating the number and function of macrophage lineage populations, and both signaling pathways have been shown to contribute to macrophage heterogeneity (7). Therefore, we examined the contribution of GM-CSF signaling to macrophage infiltration and cutaneous GVHD. Serum GM-CSF was only detected 7 days after transplantation (Figure 7A; \( *P = 0.01 \)), with no difference in serum GM-CSF levels between mice receiving either allogeneic or TCD grafts from day 14 after transplantation. F4/80+ macrophages were still noted 21 days after transplantation in the skin of lethally irradiated mice that received WT or common \( \beta \) chain–/– BM plus T cell grafts (Figure 7B). The common \( \beta \) chain–/– mouse has defective signaling for IL-3 and IL-5 as well as for GM-CSFR signaling (24), therefore, we specifically blocked GM-CSFR signaling with an anti–GM-CSF Ab (M250 mAb; Amgen). Treatment with M250 starting 7 days after transplantation had no effect on F4/80+ macrophage infiltration (Figure 7C), quantified as positive pixels/mm\(^2\) (Figure 7D). PB monocyte analysis 21 days after transplantation showed no change in the frequencies of Ly6C\(^+\) and Ly6C\(^{−}\) cell populations in mice receiving either B6 WT or B6 common \( \beta \) chain–/– grafts (Figure 7E). Thus, GM-CSF is not required for the infiltration of F4/80+ macrophages and the subsequent development of cutaneous pathology after transplantation.

Development of cutaneous pathology is CCR2 independent. Monocyte chemoattractant protein 1 (MCP-1/CCL2), a multifunctional chemokine belonging to the C-C chemokine superfamily, has been shown to be upregulated in a variety of fibrotic conditions (25–27). Furthermore, patients with scleroderma exhibit elevated levels of CCL2 in both serum and skin (28, 29). Similarly, we found elevated levels of CCL2 in the serum from 7 to 28 days after transplantation in lethally irradiated mice receiving BM plus T cell grafts (Allo) compared with levels detected in TCD non-GVHD controls (Figure 8A). To investigate the contribution of donor CCL2/CCR2 signaling to the development of cutaneous GVHD, lethally irradiated mice received BM from B6 WT or B6 Ccr2–/– mice with B6 WT T cells. IHC demonstrated that F4/80+ macrophages were still present in the skin 28 days after transplan-
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Figure 5. Analysis of PB and cutaneous monocyte and macrophage populations after transplantation and CSF-1 treatment. (A) Representative dot plots of PB monocyte and macrophage analysis of recipients 19 days after transplantation. Numbers in each dot plot indicate the percentage of Ly6C<sup>+</sup> cells (top 2 quadrants) and Ly6C<sup>−</sup> cells (bottom 2 quadrants) and their expression of CCR2. Results illustrate a trend toward increased frequencies of Ly6C<sup>+</sup> cells after CSF-1 treatment. Representative dot plot shows frequency of Ly6C<sup>+</sup> cells (saline, 96.4% and CSF-1, 89.4%) and Ly6C<sup>−</sup> cells (saline, 3.57% and CSF-1, 10.66%). (B) Representative dot plots illustrate the gating strategy for cutaneous monocyte and macrophage analysis of recipients 19 days after transplantation. Numbers in each dot plot indicate the percentage of positive cells in each gate. Results illustrate a significant increase in the absolute numbers of CD45<sup>+</sup> monocytes (Ly6C<sup>−</sup>CD11b<sup>+</sup>F4/80<sup>+</sup>) and CD45<sup>+</sup> macrophages (Ly6C<sup>−</sup>F4/80<sup>−</sup>). CD45<sup>+</sup>Ly6C<sup>−</sup>CD11b<sup>+</sup>F4/80<sup>+</sup> monocyte absolute numbers: ***P = 0.0087; CD45<sup>+</sup>Ly6C<sup>−</sup>F4/80<sup>−</sup> macrophage absolute numbers: *P = 0.026 (n = 6/group, from 3 mice/group; 2 ears/mouse). Statistically significant differences were calculated using 2-tailed Mann-Whitney U tests. Data represent the mean ± SEM.

We have previously demonstrated that M279 specifically depletes tissue-resident macrophages (30). Lethally irradiated B6 recipients of G-CSF–mobilized BALB/c grafts were treated with either rat IgG control or M279 mAb beginning 7 days after transplantation. IHC staining demonstrated that M279 mAb treatment significantly reduced cutaneous GVHD (Figure 9, C and D; *P = 0.012), and similar to mice receiving Csf1r<sup>−/−</sup> grafts (Figure 6D), M279-treated mice showed no evidence of cutaneous fibrosis.
Development of cutaneous GVHD is TGF-β dependent. We have previously reported that in the B10.BR → BALB/c model of scleroderma, skin-infiltrating CD11b+ mononuclear cells produce high levels of TGF-β, and neutralization of this cytokine attenuated cGVHD (31). We therefore speculated that TGF-β is a mediator of fibrotic skin pathology invoked by macrophages in the current study. Thus, we examined the expression of TGF-β in the CD11b+ F4/80-Ly6C+ macrophages in the skin of mice receiving FLCs or Csf1r−/− FLCs. We found that recipients of KO FLC grafts had significantly lower fibrosis compared with those that received WT FLC grafts (*P = 0.045; **P = 0.008). These results suggest that TGF-β is a key player in the development of cutaneous fibrosis in cGVHD.

Figure 6. F4/80+ macrophage infiltration and cutaneous fibrosis following BMT are CSF-1/CSF-1R dependent. Lethally irradiated B6D2F1 mice received BM plus T cells from WT FLCs or Csf1r−/− FLCs (KO FLCs). (A) Mice that received KO FLC grafts had significantly lower GVHD clinical scores (day 7, ***P ≤ 0.0001; day 14, **P = 0.007; day 21, ***P = 0.0001; day 28, ***P = 0.0003; day 35, *P = 0.043). (B) IHC for F4/80 expression from skin 21 days after transplantation illustrates that recipients of KO FLC grafts had less F4/80+ macrophage infiltration than did mice that received WT FLC grafts. Minimal F4/80+ macrophage infiltrate was noted in mice that received TCD grafts. (C) Quantification of F4/80+ staining as positive/pixels/mm2 (**P = 0.003). (D) Masson’s trichome images and semiquantitative histopathology (n = 19 WT, n = 23 KO, n = 6 TCD) scores for cutaneous pathology and total cutaneous fibrosis on day 48 after transplantation confirmed that recipients of KO FLC grafts had significantly lower fibrosis compared with those that received WT FLC grafts (*P = 0.045; **P = 0.008). (E) Representative dot plots of PB monocyte/macrophage analysis of recipients 21 days after transplantation. Numbers in each dot plot indicate the percentage of Ly6C+ cells (top 2 quadrants) and Ly6C− cells (bottom 2 quadrants) and their expression of CCR2. Results illustrate a significant increase in the frequency of Ly6C+ cells and a significant decrease in Ly6C− cell frequency in recipients of KO FLC grafts (*P = 0.0286, *P = 0.0286). n = 4/group. Statistically significant differences were calculated using 2-tailed Mann-Whitney U tests. Data represent the mean ± SEM. Original magnification, ×5. (Figure 9D; ***P = 0.0006). PB analysis on day 48 after transplantation also confirmed that M279 mAb treatment resulted in a significant increase in the frequency of Ly6C+ monocytes and a significant decrease in Ly6C− monocytes (Figure 9E; **P = 0.0012, *P = 0.0262). Thus, CSF-1R Ab–mediated depletion of donor macrophages after transplantation may be an effective therapeutic strategy to prevent and/or treat cutaneous cGVHD.
PB monocyte precursor population after transplantation. Our results confirmed that the PB monocyte precursors to the pathogenic tissue macrophages rapidly produced TGF-β in response to TLR4 ligation with LPS (Supplemental Figure 4A). Furthermore, Ab blockade of TGF-β from days 14 to 46 after transplantation significantly reduced GVHD clinical scores and, importantly, significantly decreased cutaneous pathology compared with the control mAb–treated group (Supplemental Figure 4, B and C). Taken together, the data suggest that donor CSF-1R–dependent macrophages contribute to cGVHD via the expression of TGF-β.

**Development of lung GVHD is IL-17 and CSF-1R dependent.** Both transplantation models used above (G-CSF–mobilized BALB/c → B6 and B6 BM plus T cell → B6D2F1) resulted in the development of scleroderma after transplantation, but neither model elicited fibrotic manifestations in other cGVHD target organs. Therefore, we next investigated the contribution of CSF-1/CSF-1R–dependent macrophages to cGVHD using the recently described multiorgan system cGVHD model (B6 → B10.BR) (32), in which lung injury is associated with obstructive lung disease and fibrosis, with increased collagen deposition surrounding bronchioles (bronchiolitis obliterans

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**Figure 7.** F4/80+ macrophage infiltration and cutaneous fibrosis after BMT is GM-CSF/GM-CSFR independent. (A) GM-CSF serum levels (pg/ml) in lethally irradiated B6D2F1 mice that received either B6 BM plus T cell (Allo) or TCD grafts 7, 14, 21, and 28 days after transplantation. (B) Representative images of IHC to detect F4/80 expression illustrate that recipients of common β chain−/− grafts still acquired F4/80+ macrophage infiltration after transplantation (n = 6 WT, n = 4 KO, n = 3 TCD). (C) Lethally irradiated B6 mice received either G-CSF–mobilized BALB/c grafts or TCD grafts and were treated with anti–GM-CSF (400 μg every 2 weeks) from days 7 to 33 after transplantation. Representative IHC images of F4/80 expression at day 34 after transplantation (n = 4/group for all groups, except 3/TCD group), confirming that M250 treatment did not reduce F4/80+ macrophage infiltration, quantified in D as positive/pixels/mm². (E) Representative dot plots of PB monocyte/macrophage analysis of recipients 21 days after transplantation. Numbers in each dot plot indicate the percentage of Ly6C+ cells (top 2 quadrants) and Ly6C− cells (bottom 2 quadrants) and their expression of CCR2. Results illustrate no significant changes in either Ly6C+ or Ly6C− cell frequencies between groups (n = 4/group). Statistically significant differences were calculated using 2-tailed Mann-Whitney U tests. Data represent the mean ± SEM. Original magnification, ×5.
plus splenocyte (Sp) grafts that developed cGVHD also had elevated airway resistance, which correlated with lung constriction (Resistance), and elevated elastance, which signifies increased stiffness or rigidity of the lungs (Elastance), and decreased total lung capacity (BO) but without scleroderma manifestations. BO is characterized by airway blockage, peribronchiolar fibroproliferation, and obliteration of bronchioles and is a late-stage complication of GVHD. Pulmonary function tests (PFTs) demonstrated that recipients of BM plus Sp grafts had elevated airway resistance, which correlated with lung constriction (Resistance), and elevated elastance, which signifies increased stiffness or rigidity of the lungs (Elastance), and decreased total lung capacity.

Figure 8. F4/80+ macrophage infiltration and cutaneous fibrosis post BMT is CCL2/CCR2 independent. (A) Serum CCL2 (MCP-1; pg/ml) in lethally irradiated B6D2F1 mice that received B6 BM plus T cell (Allo) or TCD grafts 7, 14, 21, and 28 days after transplantation (days 7 and 14, *P = 0.015; day 21, *P = 0.035; day 28, **P = 0.009), n = 4–6/group. (B) Lethally irradiated B6D2F1 mice received BM plus T cell grafts from B6 or Ccr2−/− donors. IHC to detect F4/80 expression at day 28 shows that recipients of Ccr2−/− grafts had F4/80+ macrophage infiltration levels similar to those in mice that received WT grafts, quantified in C as positive/pixels/mm² (P = 0.207) (n = 9 WT, n = 8 KO, n = 5 TCD). (D and E) H&E-stained images and semiquantitative histopathology (n = 15 WT, n = 14 KO, n = 6 TCD) illustrating that recipients of Ccr2−/− grafts had cutaneous pathology similar to that of recipients of WT grafts (P = 0.720). (F and G) Lethally irradiated B6 mice received G-CSF–mobilized BALB/c or TCD grafts and were treated with hamster IgG or anti-CCL2 from days 7 to 33 (n = 15 hamster IgG, n = 14 anti-CCL2, n = 3 TCD). Similar levels of F4/80+ infiltration were noted in both groups, quantified in G as positive/pixels/mm² (P = 0.2727). (H) Semi-quantitative histopathology score illustrating that anti-CCL2 administration had no effect on cutaneous pathology (P = 0.922). (I) Representative dot plots of recipient PB monocyte and macrophage analysis at day 21. Numbers in each dot plot indicate the percentage of Ly6Chi cells (top 2 quadrants) and Ly6Clo cells (bottom 2 quadrants) and their expression of CCR2. Results show no significant changes in Ly6Chi or Ly6Clo cell frequencies (n = 4/group). Statistically significant differences were calculated using 2-tailed Mann-Whitney U tests. Data represent the mean ± SEM. Original magnification, ×5.
and compliance (Compliance) (32). As with cutaneous GVHD (9), lung GVHD developed in an IL-17–dependent manner, since mice receiving grafts deficient in the retinoid-related orphan receptor γ (Rorc−/−), which is required for lineage commitment in IL-17–producing cells, exhibited significantly better pulmonary function relative to that of mice receiving WT grafts (Figure 10A). We acknowledge that we cannot discriminate the cellular sources of IL-17 by this approach and that effects may be mediated by T cells, innate lymphoid cells, or another as-yet uncharacterized cytokine-producing cell population.

Development of lung pathology was also confirmed to be CSF-1R dependent, as recipients of Csf1r−/− grafts had significantly better pulmonary function compared with that of mice receiving WT grafts or those receiving WT BM with Csf1r−/− splenocytes (Figure 10B). Recipients of Csf1r−/− BM plus splenocyte grafts also displayed a significant

Figure 9. Anti–CSF-1R Ab treatment after transplantation attenuates cutaneous GVHD. Lethally irradiated B6 mice received G-CSF–mobilized WT BALB/c grafts and were treated with rat IgG control or anti–CSF-1R mAb (M279; 400 μg/3 times week) from days 7 to 33 after transplantation. (A) IHC to detect F4/80 expression 34 days after transplantation (n = 8-10/group for all groups; n = 3/group for TCD), confirming that M279 treatment resulted in a significant depletion of F4/80+ cells, quantified in B as positive/pixels/mm² (***P = 0.002). (C and D) Lethally irradiated B6D2F1 mice received B6 BM and T cell grafts and were treated with either rat IgG or M279 from days 7 to 48 after transplantation (n = 7-8/group; n = 3/group for TCD). (C and D) H&E-stained images and semiquantitative histopathology confirmed that M279 treatment resulted in a significant reduction in cutaneous pathology and cutaneous fibrosis (*P = 0.01; ***P = 0.0006). (E) Representative dot plots of PB monocyte and macrophage analysis of recipients 48 days after transplantation. Numbers in each dot plot indicate the percentage of Ly6C+ cells (top 2 quadrants) and Ly6C− cells (bottom 2 quadrants) and their expression of CCR2. Results show a significant increase in the frequency of Ly6C+ cells and a significant decrease in Ly6C− cell frequencies in M279-treated recipients (***P = 0.0012; *P = 0.026). n = 7/group. Statistically significant differences were calculated using 2-tailed Mann-Whitney U tests. Data represent the mean ± SEM. Original magnification, ×5.
Figure 10. Lung GVHD develops in an IL-17– and CSF-1R–dependent manner. (A) B10.BR recipients treated with 120 mg/kg/day cyclophosphamide (days –3 and –2) and lethally irradiated (day –1; 850 cGy) were transplanted with B6 BM with either B6 or Rorc–/– Sp (n = 4/all groups). On day 60 after transplantation, pulmonary function measures were performed. R, resistance; E, elastance; C, compliance. Recipients of Rorc–/– grafts exhibited significantly improved pulmonary function compared with that of WT graft recipients (R: *P = 0.02, *P = 0.03; E: *P = 0.01, *P = 0.03; C: **P = 0.005, *P = 0.01). (B) Similarly, recipients of Csf1r–/– BM plus Csf1r–/– Sp grafts had significantly improved pulmonary function compared with that of mice receiving WT BM plus Csf1r–/– Sp. (R: *P = 0.024, *P = 0.042, *P = 0.043; E: *P = 0.013, *P = 0.031, *P = 0.01; C: **P = 0.001, **P = 0.0031, *P = 0.033). n = 4. (C) Trichrome staining illustrates reduced collagen deposition in mice that received Csf1r–/– grafts compared with those that received WT grafts, quantified in D as trichrome area/total area (**P = 0.0037, ***P = 0.0005; **P = 0.0023). (E) IHC for F4/80 expression in recipients of WT B6 plus Sp or BM-only grafts that were given control IgG or M279 mAb after transplantation from days 0 to 28 after transplantation. Minimal F4/80+ cells were noted in recipients treated with M279 mAb compared with those detected in control IgG-treated recipients. (F) Lung function parameters confirmed an improvement in lung function after M279 mAb treatment (R: **P = 0.001, **P = 0.008; E: **P = 0.003, *P = 0.034; C: **P = 0.004, *P = 0.02). n = 4. (G) Trichrome staining confirmed that M279 mAb treatment significantly reduced collagen deposition, quantified in H (**P = 0.017; ***P = 0.0003). Statistically significant differences were calculated using unpaired t tests. Data represent the mean ± SEM. Original magnification, ×20.
reduction in collagen deposition around the bronchioles compared with recipients of WT grafts (Figure 10C), quantified as trichrome area/total area (Figure 10D). These data suggest that donor BM is the source of CSF-1R+ tissue-resident macrophages that are essential for cGVHD-induced BO.

Last, we investigated whether M279 mAb treatment resulted in a reduction in lung cGVHD. Recipients were administered control IgG or M279 mAb after transplantation from days 0 to 28. IHC to detect F4/80 expression confirmed that macrophages infiltrated the lungs of mice that received BM plus Sp grafts and rat IgG (Figure 10E), with reduced F4/80+ cell infiltration in recipients treated with M279 mAb. We noted minimal macrophage infiltration in mice that received BM-only grafts (Figure 10E). Furthermore, we found that M279 mAb treatment significantly improved all lung PFT parameters (Figure 10F) and resulted in a significant reduction in collagen deposition (Figure 10G), quantified as trichrome area/total area (Figure 10H). Overall, these data confirm that cutaneous and pulmonary GVHD develop in a CSF-1/CSF-1R–dependent manner, and depletion of this population after transplantation represents a novel therapeutic strategy to prevent and treat cGVHD.

Discussion

Macrophages have been shown to play crucial roles in tissue repair as well in the resolution and/or progression of tissue fibrosis (10–13). This study provides new insight into the pathogenic role of donor macrophages in the progression of fibrosis, the cardinal feature of cGVHD. We specifically demonstrate that CSF-1/CSF-1R–dependent donor BM–derived macrophages infiltrate GVHD target organs as early as 7 days after transplantation, which precedes the development of cutaneous and pulmonary GVHD. The infiltration of these macrophages was demonstrated to be both CCR2 and GM-CSF independent. Most importantly, blocking the action of CSF-1/CSF-1R using either Csf1r−/− mice or an anti–CSF-1R Ab depleted these donor macrophages from the skin and lung, resulting in a dramatic reduction in cGVHD.

The origin of tissue-resident macrophages remains controversial. During development, yolk sac and liver embryonic macrophage precursors seed the resident macrophage populations of most tissues including the skin, liver, and lung. During the neonatal period, these tissue-resident macrophage populations are expanded by local proliferation and maintained during adulthood by self-renewal (33). In the gut, however, the resident macrophage population is derived from BM (34, 35). During injury or infection, PB monocytes can be recruited to tissues and sites of inflammation and give rise to a variety of tissue-resident macrophages. In mice, circulating monocyte populations can be divided into 2 distinct groups (22). The classical/inflammatory monocytes, which are classified as Ly6C+CCR2+ and Cx3CR1−, constitute the monocyte subset most likely to be recruited to sites of inflammation. The nonclassical/patrolling monocytes are Ly6CloCCR2lo and Cx3CR1+ and are thought to contribute to tissue-resident macrophage populations (22, 36). Whether the patrolling monocytes give rise to tissue macrophages under steady state has recently come into question (37, 38). Importantly, during fibrosis, at least in the liver, macrophages are suggested to be derived from either tissue-resident cell populations, such as Kupffer cells, or from BM immigrants (39, 40). Although SCT induces a highly inflammatory environment including an early systemic release of MCP-1 and GM-CSF, our data surprisingly illustrate that neither CCR2 nor GM-CSF signaling is required for the development of cutaneous GVHD and that, instead, fibrosis in both skin and lung models of GVHD is CSF-1 dependent. Blocking the action of CSF-1/CSF-1R using either Csf1r−/− mice or an anti–CSF-1R Ab resulted in a significant decrease in Ly6C+ cell populations in both the blood and skin. As previously observed (30), the reduction in the Ly6C+ cell population was balanced by an increase in the Ly6Clo cell population, supporting the proposed model that suggests a precursor relationship between the immature inflammatory monocytes and mature resident monocytes in vivo (36, 41). Therefore, we propose that the precursor to the pathogenic tissue macrophages that sequester in the GVHD target organs is a nonclassical/patrolling F4/80+CD11b+Ly6C+ donor BM–derived monocyte subset.

Macrophages and CSF-1/CSF-1R signaling have already been shown to contribute to engraftment and the development of aGVHD following transplantation (42). CSF-1 levels are substantially elevated in the circulation in mice with aGVHD, which could function to extend the survival of host macrophages after transplantation (43). We previously demonstrated that pretreatment of recipients with the anti–CSF-1R mAb M279 prior to allogeneic BMT significantly ablated macrophages in GVHD target organs, resulting in exaggerated donor T cell activation and accelerated GVHD pathology after transplantation (30). Furthermore, host intestinal macrophages were also shown to engulf and clear donor T cells, thus contributing to the attenuation of alloreactive T cell responses (44). Therefore, donor and host macrophages appear to exert opposing effects on GVHD outcomes, with host macrophages being protective for aGVHD, while donor macrophages are pathogenic for cGVHD. Thus, in contrast to the attenuation of cGVHD that CSF-1 blockade provided, interrupting this pathway in the early peritransplantation period could exacerbate aGVHD. These observations are reminiscent of our earlier findings, in which TGF-β neutralization early after transplantation resulted in a significant exacerbation of aGVHD, whereas delayed neutralization attenuated sclerodermatous cGVHD (31). In that study, a skin-infiltrating donor CD11b+ mononuclear cell population expressed the highest levels of TGF-β. Here, we confirm and extend these findings, demonstrating that blockade of TGF-β after transplantation in the B6 → B6D2F1 model significantly reduced cutaneous pathology and further demonstrating TGF-β expression by the F4/80+CD11b+Ly6C+ blood monocyte precursor to the pathogenic skin macrophages. Taken together, the data support the notion that donor CSF-1–dependent skin-infiltrating macrophages contribute to cutaneous GVHD in a TGF-β–dependent manner.

These studies highlight Ly6C+ monocyte precursors, macrophages, and their effector molecules (e.g., TGF-β) as potential targets for the prevention and treatment of cGVHD. In the current study, we have used a mAb against mouse CSF-1R that blocks the actions of CSF-1 without inducing apoptosis or overt inflammation (30). While it is clear that blockage of CSF-1R signaling can have functional consequences on tissue-resident macrophages (45), treatment with the anti–CSF-1R mAb M279 following transplantation phenocopied the effects produced using a Csf1r−/− allograft (i.e., a dramatic reduction in skin-infiltrating macrophages and attendant pathology). While we can-
not completely exclude additional effects on function, the M279 mAb appears to be acting on monocytes and macrophages in more of a quantitative rather than a qualitative fashion when used after BMT. There are multiple agents that target the CSF-1R/CSF-1 pathway in clinical trials, predominantly to ablate tumor-associated macrophages as a means to limit tumor progression. These include a humanized version of the rodent CSF-1R mAb used here. In addition, many small-molecule tyrosine kinase inhibitors such as imatinib, sunitinib, and sorafenib are used in clinical practice to treat various malignancies. Interestingly, imatinib, at least, has significant off-target effects that interrupt the CSF-1R pathway (46), and this agent has demonstrated efficacy, albeit limited, in the treatment of cGVHD (47–49). Together, it appears that targeting the CSF-1 pathway may provide an effective means for treating chronic GVHD, and clinical trials to test this hypothesis could now be rapidly initiated.

Methods

Mice. Female C57BL/6 (B6) (H-2b, CD45.2), B6.Ptprc<sup>c</sup> (H-2<sup>c</sup>, CD45.1<sup>c</sup>), BALB/c (H-2d, CD45.2), and B6D2F1 (H-2b/d, CD45.2) mice were purchased from the Animal Resources Center. Mice were housed in sterilized microisolator cages and received acidified autoclaved water (pH 2.5) after transplantation. The mice ranged in age from 8 to 14 weeks. BALB/c CD45.1<sup>+</sup> (H-2<sup>b</sup>) mice were supplied by Mark Smyth (QIMR Berghofer Medical Research Institute, Queensland, Australia). Csf1<sup>r<sup>−/−</sup></sup> mice were provided by Richard E. Stanley (Albert Einstein College of Medicine, New York, New York, USA). C-C chemokine receptor 2 (Ccr2<sup>−/−</sup>) (50) mice were provided by Mark Smyth (QIMR Berghofer Medical Research Institute). Common β chain<sup>−/−</sup> (Csf2rb<sup>−/−</sup>) (24) mice were provided by Angel Lopez (Center for Cancer Biology, Adelaide, Australia). Langerin DTR-EGFP mice (Cd207<sup>tm3(DTR/GFP)Mal</sup>) were provided by Bernard Malissen (Centre d’Immunologie de Marseille, Luminy, France) (51). B10.BR (H-2k) mice were purchased from the Jackson Laboratory, and B6 (H<sup>2</sup>) mice were purchased from the National Cancer Institute.

Cytokine mobilization. Recombinant human G-CSF was administered s.c. at 10 μg/animal daily for 6 days.

Generation of Csf1<sup>r<sup>−/−</sup></sup> FLCs. To generate FLCs, mice heterozygous for Csf1<sup>r</sup> deficiency were time-mated, and at E18/19, pregnant mice were culled, pups removed, and the fetal liver harvested into a single-cell suspension. A portion of each pup’s tail was harvested. A single-cell suspension. A portion of each pup’s tail was harvested into QuickExtract DNA extraction solution (Epicentre Biotechnologies, Madison, Wisconsin, USA) (51). B10.BR (H-2k) mice were purchased from the Jackson Laboratory, and B6 (H2<sup>d</sup>) mice were purchased from the National Cancer Institute.

Cytokine mobilization. Recombinant human G-CSF was administered s.c. at 10 μg/animal daily for 6 days.

Generation of Csf<sup>1r</sup><sup>−/−</sup> FLCs. To generate FLCs, mice heterozygous for Csf1<sup>r</sup> deficiency were time-mated, and at E18/19, pregnant mice were culled, pups removed, and the fetal liver harvested into a single-cell suspension. A portion of each pup’s tail was harvested. A single-cell suspension. A portion of each pup’s tail was harvested into QuickExtract DNA extraction solution (Epicentre Biotechnologies, Madison, Wisconsin, USA) (51). B10.BR (H-2k) mice were purchased from the Jackson Laboratory, and B6 (H2<sup>d</sup>) mice were purchased from the National Cancer Institute.

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**PB in vitro stimulation.** Unfractionated red cell-lysed PB was cultured with 100 ng LPS for 2 hours in Iscove’s modified Dulbecco’s medium (IMDM) supplemented with 10% FBS (Gibco), 1 mM sodium pyruvate (Thermo Scientific), 1 mM Pen Strep (Gibco), and 1 mM gluta-
mime (HyClone), 1 mM nonessential amino acids (Gibco), and 23 mM β-mercaptoethanol (Sigma-Aldrich).

**Histopathology and immunostaining of GVHD target organs.** At various times after transplantation, GVHD target tissues were harvested, fixed in 10% formalin for 24 hours, embedded in paraffin, and pro-
cessed to generate 5-μm-thick sections. All lung tissue harvested was
embedded in optimal cutting-temperature compound, snap-frozen in
liquid nitrogen, and stored at −80°C. Lungs were inflated by infusion
of 1 ml of optimal cutting-temperature compound/PBS (3:1) intra-
tracheally before harvesting. H&E sections of skin were examined in a
blinded fashion (by A.D. Clouston) using a semiquantitative scoring
system for GVHD as previously published (54). Samples were scored
from 0 to 4 for epidermal and dermal inflammation, dermal fibrosis
and subcutaneous fibrosis (summed to give a total cutaneous fibrosis
score of 8), epidermal apoptosis (total score of 4), and loss of s.c. fat
(total score of 4). IHC was performed on deparaffinized and rehydrated
sections. Briefly, slides were incubated with antigen retrieval solution
(0.37% Carezyme Trypsin; Biocare Medical) for 10 minutes. Slides
were then incubated in serum block for 60 minutes (10% FBS, 10%
mouse serum) followed by HRP-conjugated streptavidin (Jackson
ImmunoResearch). DAB was developed according to the manu-
facturer’s instructions (Dako), and all slides were counterstained with
Mayer’s hematoxylin and mounted using permanent mounting media.

For trichrome staining, 6-μm sections were cut and incubated in
Bouin’s solution for 15 minutes at 55°C, washed, and stained for 5
minutes in Weigert’s iron hematoxylin solution. Slides were washed in tap
water, then distilled water for 5 minutes and stained for 5 minutes in
Biebrich Scarlet-Acid Fuchsin solution (Thermo Scientific). Slides were
subsequently washed in distilled water, stained in phosphotungstic/
phosphomolybdic acid solution for 5 minutes, aniline blue solution
for 5 minutes, and 1% acetic acid solution for 2 minutes, and washed in
distilled water to remove all residue. Slides were then dehydrated through
alcohol baths and xylene washes and coverslipped. Images were col-
lected using a BX51 light microscope (Olympus).

Frozen tissue samples were embedded in Tissue-Tek OCT compound
(Sakura Finetek) without prior fixation, and IHC was carried out on 7-μm
sections fixed with 75% acetone/35% ethanol. IHC was performed as
described above but with the addition of an endogenous avidin/biotin
blocking step (10 minutes with avidin, 10 minutes with biotin; Vector
Labs). Slides were then blocked in serum as described above (with an
additional F(ab′)2 fragment–blocking step for CD45.1 Ab IHC)(Jackson
ImmunoResearch) and incubated in one of the following primary anti-
bodies: rat anti-mouse F4/80 (BioLegend), rat anti-mouse CD206 (AbD
Serotec); rabbit anti-mouse iNOS (Abcam), or mouse anti-mouse CD45.1
(BioLegend) or matching isotype controls, and normal Rabbit IgG (Santa
Cruz Biotechnology Inc.) or mouse IgG (BioLegend). Endogenous per-
oxidase activity was blocked using 3% H2O2. Cells were subsequently
incubated with either goat anti-rat or goat anti-rabbit biotinylated F(ab′)2
fragment followed by HRP-conjugated streptavidin. Slides were devel-
oped as described above. Immunofluorescence (IF) of frozen tissues was
performed as described above, but using streptavidin-conjugated Alexa
Fluor 555 tertiary Ab. Slides were then stained with DAPI. All IHC slides
were viewed using an Aperio Scanscope XT microscope with Scanscope
software (version 10.2.2.2352). IF slides were viewed on an LSM 710
confocal microscope (Zeiss) with ImageJ 1.44p software (NIH).

**Cytokine analysis.** Serum cytokine concentrations were deter-
mined using the BD Cytometric Bead Array system (BD Biosciences —
Pharmingen) according to the manufacturer’s protocol.

**Statistics.** Survival curves were plotted using Kaplan-Meier esti-
mates and compared by log-rank analysis using PRISM 5 (GraphPad
Software). A P value of less than 0.05 was considered statistically
significant. A 2-tailed Mann-Whitney U test or an unpaired t test was
used to evaluate significant differences between groups, and all data
represent the mean ± SEM.

**Study approval.** All mouse experiments were performed in accord-
ance with and under the approval of the QIMR Berghofer Medical
Research Institute’s Animal Ethics Committee and the IACUC of the
University of Minnesota.

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