

Expression of the G-CSF receptor in monocytic cells is sufficient to mediate hematopoietic progenitor mobilization by G-CSF in mice

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Granulocyte colony-stimulating factor (G-CSF), the prototypical mobilizing cytokine, induces hematopoietic stem and progenitor cell (HSPC) mobilization from the bone marrow in a cell-nonautonomous fashion. This process is mediated, in part, through suppression of osteoblasts and disruption of CXCR4/CXCL12 signaling. The cellular targets of G-CSF that initiate the mobilization cascade have not been identified. We use mixed G-CSF receptor (G-CSFR)-deficient bone marrow chimeras to show that G-CSF-induced mobilization of HSPCs correlates poorly with the number of wild-type neutrophils. We generated transgenic mice in which expression of the G-CSFR is restricted to cells of the monocytic lineage. G-CSF-induced HSPC mobilization, osteoblast suppression, and inhibition of CXCL12 expression in the bone marrow of these transgenic mice are intact, demonstrating that G-CSFR signals in monocytic cells are sufficient to induce HSPC mobilization. Moreover, G-CSF treatment of wild-type mice is associated with marked loss of monocytic cells in the bone marrow. Finally, we show that bone marrow macrophages produce factors that support the growth and/or survival of osteoblasts in vitro. Together, these data suggest a model in which G-CSFR signals in bone marrow monocytic cells inhibit the production of trophic factors required for osteoblast lineage cell maintenance, ultimately leading to HSPC mobilization.

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Abbreviations used: G-CSFR, G-CSF receptor; HSPC, hematopoietic stem and progenitor cell; KLS, c-kit⁺lineage⁻Sca-1⁺.

In the adult human, the majority of hematopoietic stem and progenitor cells (HSPCs) reside in specialized environments within the bone marrow collectively referred to as the hematopoietic stem cell niche. The number of HSPCs in the circulation can be markedly increased in response to several stimuli, including hematopoietic growth factors, myeloablative agents, and environmental stresses such as infection. Recently, mobilized stem cells have become the preferred cellular source for reconstitution of the bone marrow after myeloablative therapy because of their potency, predictability, and safety. G-CSF, a hematopoietic growth factor, is the most commonly used mobilizing agent clinically. However, there is considerable variability in the magnitude of HSPCs mobilized by G-CSF, and in ~10% of cases, insufficient cells are mobilized for stem cell transplantation (Anderlini et al., 2001). An understanding of the mechanisms by which

G-CSF elicits mobilization of HSPCs is critical to the development of novel more effective mobilizing agents.

There is accumulating evidence that disruption of CXCR4/CXCL12 signaling is a key step in G-CSF-induced HSPC mobilization. CXCL12 (SDF-1) is a chemokine constitutively expressed at very high levels in the bone marrow and is a potent chemoattractant for HSPCs. In mice lacking CXCL12 (Nagasawa et al., 1996) or its major receptor CXCR4 (Zou et al., 1998), there is a failure of the migration of HSPCs from the fetal liver to the bone marrow. Moreover, CXCR4^{-/-} bone marrow chimeras exhibit constitutive mobilization and fail to mobilize HSPCs in response to G-CSF (Ma et al., 1999; Christopher et al., 2009). G-CSF treatment is associated with

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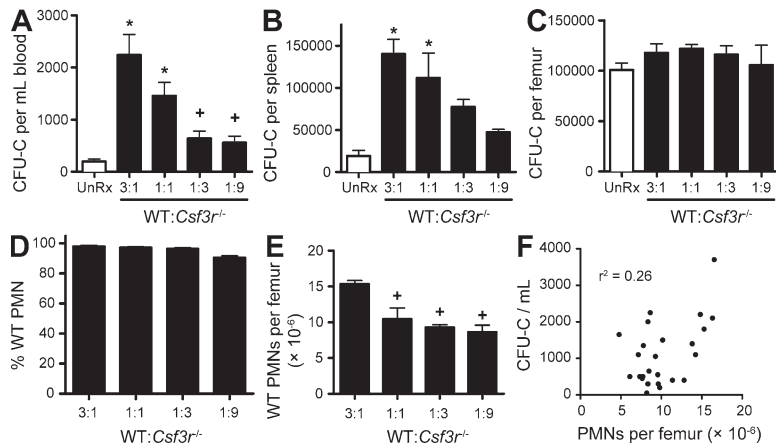


Figure 1. Neutrophil number in the bone marrow correlates poorly with G-CSF-induced HSPC mobilization. Wild-type and *Csf3r*^{-/-} bone marrow cells were mixed at the indicated ratios and transplanted into irradiated recipients. 6 wk later, the mixed bone marrow chimeras were treated with G-CSF (250 μ g/kg/d G-CSF for 7 d), and the number of CFU-C in the peripheral blood (A), spleen (B), or bone marrow (C) was measured. As a control, a cohort of mixed chimeras was analyzed without G-CSF treatment (UnRx). Because similar results were obtained with each type of chimera, the untreated data were pooled. The percentage of neutrophils in the bone marrow derived from wild-type cells (D) and the absolute number of wild-type neutrophils per femur (E) were determined after 7 d of G-CSF administration. (F) The number of CFU-C in the blood versus the number of wild-type neutrophils in bone marrow. The Pearson r^2 value is shown. Data represent the mean \pm SEM of six to nine mice and is pooled from two independent transplantation experiments. *, $P < 0.05$ compared with untreated chimeras; +, $P < 0.05$ compared with 3:1 chimeras.

decreased CXCL12 mRNA and protein expression in the bone marrow and decreased CXCR4 expression on HSPCs (Petit et al., 2002; Lévesque et al., 2003a; Semerad et al., 2005; Christopher et al., 2009). A potential mechanism for the decreased CXCL12 expression is provided by the observation that G-CSF treatment is associated with a marked suppression of osteoblasts (Semerad et al., 2005; Katayama et al., 2006; Christopher and Link, 2008; Christopher et al., 2009), which are an important source of CXCL12 in the bone marrow (Ponomaryov et al., 2000; Semerad et al., 2005; Jung et al., 2006; Christopher et al., 2009). The importance of the CXCL12–CXCR4 axis is illustrated by the success of the CXCR4 inhibitor plerixafor (AMD3100) to rapidly mobilize HSPCs in humans and mice (Liles et al., 2003; Broxmeyer et al., 2007).

Through the study of G-CSF receptor (G-CSFR; *Csf3r*)^{-/-} bone marrow chimeras, we previously showed that G-CSFR signaling in hematopoietic cells, but not stromal cells, is required for HSPC mobilization by G-CSF (Liu et al., 2000). Within the hematopoietic compartment, the G-CSFR is expressed on neutrophils, monocytes/macrophages, HSPCs, and a subset of B lymphocytes and NK cells. The simplest model suggests that G-CSF directly acts upon HSPCs to induce their mobilization. However, strongly arguing against this model, in mixed bone marrow chimeras containing wild-type and *Csf3r*^{-/-} HSPCs, both types of cells were mobilized equally after G-CSF treatment (Liu et al., 2000).

There is some evidence implicating neutrophils in G-CSF-induced HSPC mobilization. During G-CSF treatment, neutrophils release certain proteases into the bone marrow microenvironment (Lévesque et al., 2001, 2002, 2003a,b; Heissig et al., 2002; Petit et al., 2002; Christopherson et al., 2003). Although controversial, these proteases, through cleavage of CXCL12 (Christopherson et al., 2003; Lévesque et al., 2003a), c-kit (Lévesque et al., 2003b), and VCAM-1 (Lévesque et al., 2001), may contribute to HSPC mobilization. A previous study reported that depletion of neutrophils using an antibody against Gr-1 (Ly6C/G) results in reduced HSPC mobilization by G-CSF (Pelus et al., 2004). However, Gr-1 is expressed on both neutrophils and a subset of monocytes;

thus, a role for reduced monocytes in this phenotype is possible. In this study, we used a genetic approach to systematically examine the contribution of neutrophils and other hematopoietic cell populations to G-CSF-induced HSPC mobilization. We show that G-CSFR expression on monocytic cells in the bone marrow is sufficient to initiate HSPC mobilization by G-CSF.

RESULTS

The mobilization response to G-CSF correlates poorly with the number of wild-type neutrophils in the bone marrow

To evaluate the importance of neutrophils to G-CSF-induced mobilization, we generated a series of bone marrow chimeras by transplanting wild-type and *Csf3r*^{-/-} bone marrow cells in different ratios into lethally irradiated wild-type mice. Donor chimerism was assessed in peripheral blood leukocytes 6 wk after transplantation. As reported previously (Richards et al., 2003), the contribution of *Csf3r*^{-/-} cells to the B cell lineage was near that expected based on the input ratio (Fig. S1). However, because of the marked competitive advantage of *Csf3r*^{+/+} cells to the neutrophil lineage, virtually all of the neutrophils in the circulation and bone marrow were derived from *Csf3r*^{+/+} cells (Fig. 1, D and E; and not depicted). Moreover, the number of neutrophils in the blood was similar in all of the chimeras (Fig. S2).

We next assessed the mobilization response to G-CSF in these chimeras by quantifying CFUs (CFU-C) in the peripheral blood, bone marrow, and spleen. We predicted that an inverse correlation between *Csf3r*^{-/-} donor input and HSPC mobilization would be observed. Indeed, the number of CFU-Cs in blood and spleen after treatment with G-CSF was highest in the 3-to-1 (wild-type-to-*Csf3r*^{-/-}) chimeras and progressively decreased with increasing *Csf3r*^{-/-} donor input (Fig. 1, A–C). Analysis of donor chimerism in mature neutrophils (Gr-1^{hi} SSC^{hi}) in the bone marrow after G-CSF revealed that the great majority of neutrophils were derived

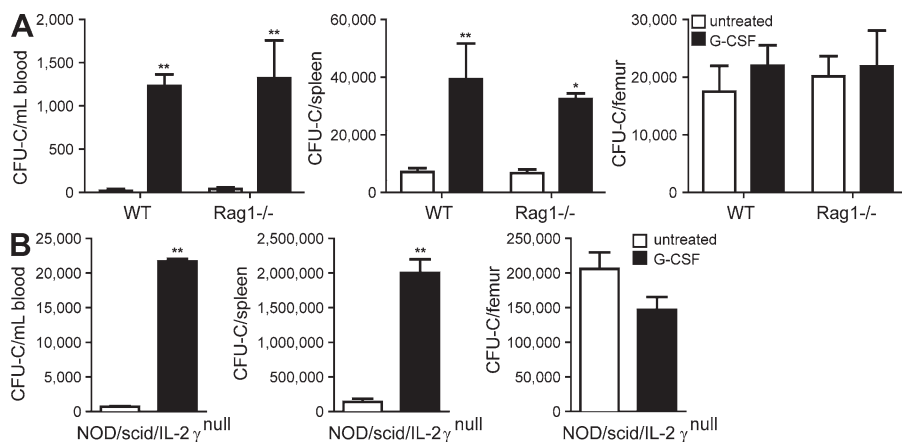


Figure 2. G-CSF-induced HSPC mobilization is normal in *Rag1*^{-/-} and *NOD/scid/IL-2γ*^{null} mice. Wild-type, *Rag1*^{-/-} (A), or *NOD/scid/IL-2γ*^{null} mice (B) were treated with G-CSF (250 μg/kg/d for 5 d) or left untreated. The number of CFU-C in the blood, bone marrow, and spleen was measured after 5 d of G-CSF. Data represent the mean ± SEM of four to five mice per genotype per treatment group and is pooled from four independent experiments. *, *P* < 0.01; **, *P* < 0.001.

from wild-type (*Csf3r*^{+/+}) cells in all of the chimeras (Fig. 1 D). In fact, the correlation between the number of wild-type neutrophils in the bone marrow and CFU-C in the blood was poor (Fig. 1, E and F).

G-CSF-induced HSPC mobilization is normal in lymphocyte-deficient mice

The contribution of B and T lymphocytes to G-CSF-induced HSPC mobilization is controversial. Reca et al. (2007) reported that G-CSF-induced mobilization is impaired in *Rag2*^{-/-}, SCID, and Jh mice. In contrast, Katayama et al. (2006) reported that *Rag1*^{-/-} mice and *IL-7R*^{-/-} mice exhibited a normal mobilization response to G-CSF. In this paper, we characterized HSPC mobilization by G-CSF in two lymphocyte-deficient mouse strains, *Rag1*^{-/-} and *NOD/scid/IL-2γ*^{null} mice. *Rag1*^{-/-} mice lack mature B and T cells, and *NOD/scid/IL-2γ*^{null} mice lack all B, T, and NK cells. Consistent with a previous paper (Katayama et al., 2006), HSPC mobilization in *Rag1*^{-/-} mice was comparable to that in wild-type mice (Fig. 2 A). In *NOD/scid/IL-2γ*^{null} mice, the baseline level of circulating HSPC was increased and marked mobilization in response to G-CSF was observed (Fig. 2 B). These data demonstrate that B, T, and NK cells are not required for G-CSF-induced mobilization.

Generation of transgenic mice with monocyte-restricted expression of the G-CSFR

To evaluate the role of monocytes in G-CSF-induced mobilization, we generated transgenic mice in which the CD68 (macrosialin) promoter drives expression of the G-CSFR (Fig. 3 A). A previous study established that regulatory elements of the CD68 gene are sufficient to direct transgene expression to the monocyte/macrophage lineage (Lang et al., 2002). Two transgenic founder lines were identified that expressed the GFP in circulating monocytes (unpublished data). The transgenic founder mice were crossed with *Csf3r*^{-/-} mice to obtain *CD68:mGCSFR;Csf3r*^{-/-} mice, hereafter referred to as CD68:G-CSFR mice. Because the phenotype of CD68 transgenic mice derived from the two founder lines was similar, the data have been pooled. It is of note that the

influence of strain effects on phenotype, littermate controls were used in all studies.

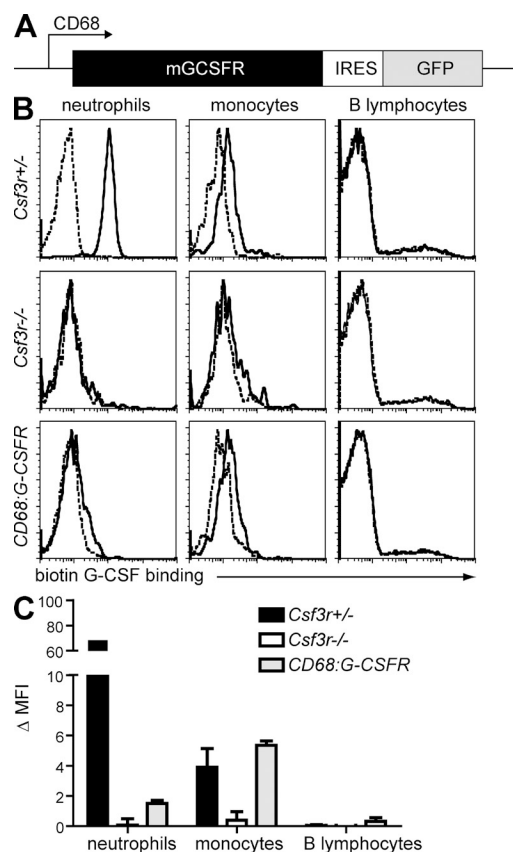


Figure 3. G-CSFR expression is mainly restricted to monocytic cells in CD68:G-CSFR mice. (A) Schematic of the CD68:G-CSFR transgene. IRES, internal ribosomal entry sequence. (B) Representative histograms showing biotinylated G-CSF binding in the absence (solid line) or presence (dashed line) of a 100-fold molar excess of unlabeled G-CSF in the indicated blood leukocyte population. G-CSFR surface expression is proportional to the difference in median fluorescence intensity (Δ MFI) between the two curves. (C) The mean Δ MFI in the indicated blood leukocyte population is shown. Data represent the mean ± SEM of four to five mice per genotype and is pooled from four independent experiments.

Table I. Peripheral blood counts

Parameter	Csf3r ^{+/-}	Csf3r ^{-/-}	CD68:G-CSFR	Csf3r ^{+/-} versus Csf3r ^{-/-}	Csf3r ^{+/-} versus CD68:G-CSFR
Hemoglobin (g/dL)	13.80 ± 1.01	15.57 ± 1.06	18.00 ± 2.83	NS	NS
Platelets (K/μL)	820 ± 147	701 ± 90	678 ± 188	NS	NS
Leukocytes (K/μL)	8.76 ± 1.82	8.51 ± 4.10	9.82 ± 2.56	NS	NS
Neutrophils (K/μL)	1.38 ± 0.62	0.16 ± 0.03	0.24 ± 0.05	P < 0.001	P < 0.001
Monocytes (K/μL)	0.24 ± 0.12	0.12 ± 0.08	0.25 ± 0.06	NS	NS
B cells (K/μL)	2.75 ± 0.57	3.53 ± 1.52	4.92 ± 1.53	NS	P < 0.05
T cells (K/μL)	1.95 ± 0.75	2.23 ± 0.82	1.78 ± 0.42	NS	NS

Values represent mean ± SD for two to five mice per genotype and is pooled from three independent experiments. Comparisons in the two right columns were made using a one-way ANOVA with Bonferroni's post test corrected for multiple comparisons

G-CSFR expression in CD68:G-CSFR mice is predicted to be restricted to cells of the monocyte lineage. To test this prediction, we measured surface expression of the G-CSFR on blood leukocytes using a biotinylated G-CSF binding assay (Liu et al., 1996). Consistent with previous results, in wild-type and *Csf3r*^{+/-} mice, expression of the G-CSFR was highest in neutrophils, detectable but lower in monocytes, and undetectable in B or T cells (Fig. 3, B and C; and not depicted). As expected, G-CSFR expression was not detected on any blood leukocytes in *Csf3r*^{-/-} mice. In CD68:G-CSFR mice, the highest expression of the G-CSFR was detected on

blood monocytes with levels similar to that seen in wild-type or *Csf3r*^{+/-} mice. G-CSFR expression was barely detectable on neutrophils, and no expression was detected on B or T lymphocytes. Similar data were observed using bone marrow cells (unpublished data). These data suggest that hematopoietic expression of the G-CSFR in CD68:G-CSFR mice is mainly limited to monocytic cells.

CD68:G-CSFR mice are neutropenic

G-CSFR signals on granulocytic precursors are required for normal cell proliferation and differentiation (Liu et al., 1996).

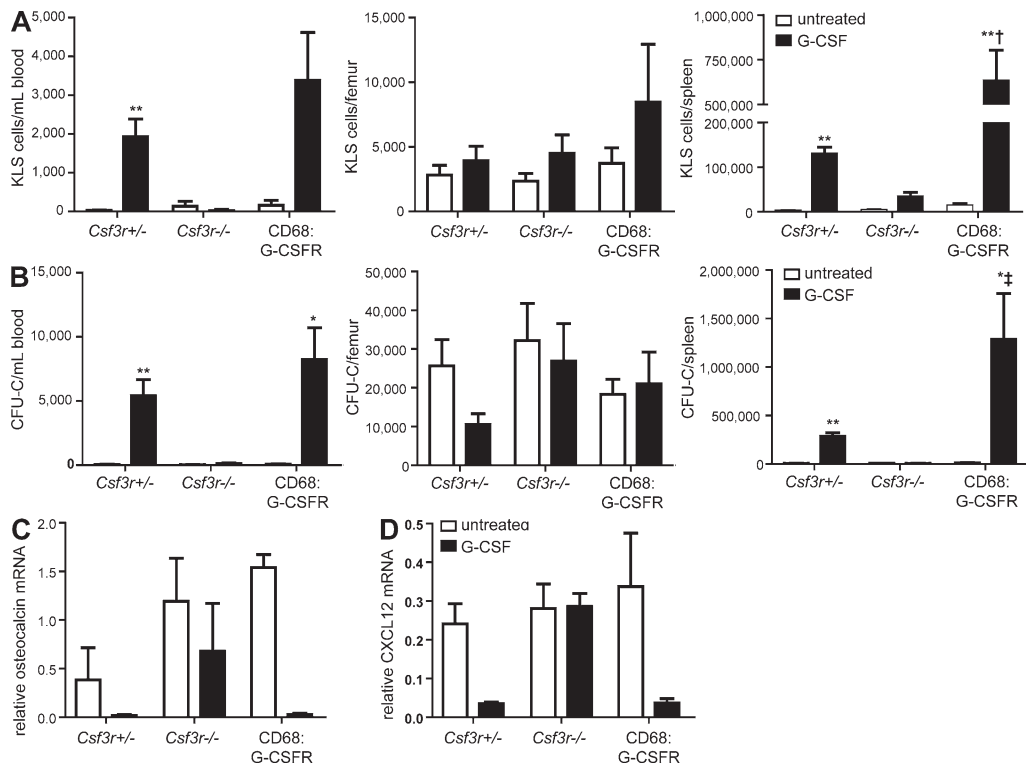


Figure 4. G-CSF-induced HSPC mobilization is normal in CD68:G-CSFR mice. Mice of the indicated genotype were treated with G-CSF for 7 d or left untreated. The number of KLS (A) or CFU-C (B) in the blood, bone marrow, and spleen on day 7 is shown. The mRNA expression in the bone marrow on day 7 of osteocalcin (C) or CXCL12 (D) relative to β-actin is shown. Data represent the mean ± SEM of three to five mice per genotype per treatment group and is pooled from three independent experiments. *, P < 0.01 compared with untreated mice of the same genotype; **, P < 0.05 compared with untreated mice of the same genotype; †, P = 0.07 compared with G-CSF-treated *Csf3r*^{+/-} mice.

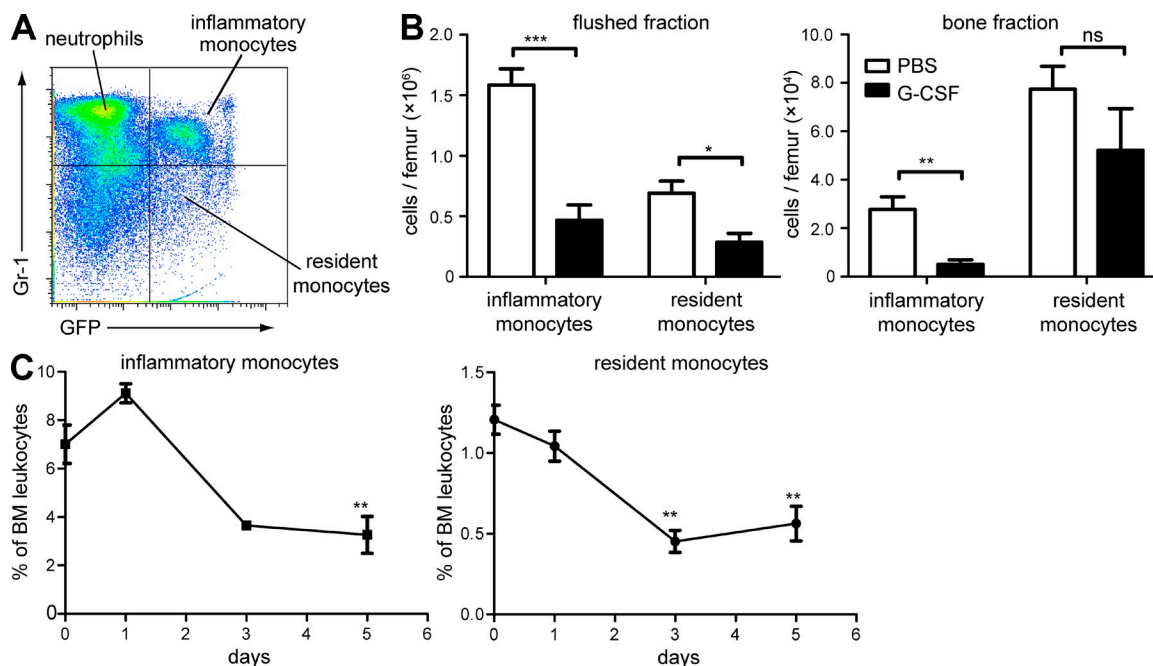


Figure 5. G-CSF treatment leads to a loss of monocytic cells from the bone marrow. *CX3CR1^{GFP/+}* mice were treated with PBS or G-CSF for 5–7 d and the flush and bone fractions harvested as described in Materials and methods. (A) Representative dot plot showing the gating strategy used to identify inflammatory ($Gr-1^{high} GFP^{+}$) and resident monocytes/macrophages ($Gr-1^{low} GFP^{+}$). (B) The absolute number of inflammatory and resident monocytes/macrophages in the flushed and bone fractions are shown. Data represent the mean \pm SEM of four mice per cohort pooled from two independent experiments. *, $P < 0.05$; **, $P < 0.005$; ***, $P < 0.001$. (C) The percentage of inflammatory and resident monocytes in the flush fraction of bone marrow was determined at the indicated time points. In these experiments, wild-type mice rather than *CX3CR1^{GFP/+}* mice were used, and CD115 was used to identify monocytic cells. Data represent mean \pm SEM of two to six mice per cohort pooled from four independent experiments. **, $P < 0.005$ compared with untreated mice as determined by one-way ANOVA with Dunnett's post-test to correct for multiple comparisons.

Thus, we predicted that the loss of G-CSFR expression on granulocytic cells in CD68:G-CSFR mice would result in neutropenia. Indeed, CD68:G-CSFR mice display basal neutropenia that is similar in magnitude to that seen in *Csf3r^{-/-}* mice (Table I). Interestingly, CD68:G-CSFR mice had a modest but significant increase in circulating B lymphocytes. A nonsignificant trend to increased B lymphocytes also was seen in the *Csf3r^{-/-}* mice (Liu et al., 1996). All other measured hematopoietic parameters were normal in the CD68:G-CSFR mice.

G-CSF–induced HSPC mobilization is normal in CD68:G-CSFR mice

We next evaluated the mobilization response of these mice to G-CSF. Specifically, we measured the number of $c-kit^{+}$ lineage⁻Sca-1⁺ (KLS) cells and CFU-C in the blood, bone marrow, and spleen after 7 d of G-CSF. Consistent with previous results (Liu et al., 1996), in *Csf3r^{+/-}* mice, G-CSF administration resulted in a significant increase in KLS cells and CFU-Cs in the blood and spleen (Fig. 4, A and B). As expected, no mobilization was observed in *Csf3r^{-/-}* mice. G-CSF treatment of CD68:G-CSFR mice induced HSPC mobilization that was at least as great as that observed in control mice. In fact, a significantly greater number of KLS cells were mobilized to the spleen in CD68:G-CSFR mice.

We have previously shown that G-CSF–induced HSPC mobilization is associated with osteoblast suppression and decreased CXCL12 expression in the bone marrow (Christopher et al., 2009). We assessed osteoblast suppression by measuring mRNA expression of osteocalcin, a specific marker of mature osteoblasts (Semerad et al., 2005). As reported previously (Semerad et al., 2005), G-CSF treatment resulted in a significant decrease in osteocalcin and CXCL12 mRNA expression in the bone marrow of control (*Csf3r^{+/-}*) mice (Figs. 4, C and D). A similar decrease was observed in CD68:G-CSFR but not *Csf3r^{-/-}* mice after G-CSF administration. Together, these data suggest that G-CSFR expression in monocyte lineage cells is sufficient to induce HSPC mobilization and osteoblast suppression.

G-CSF treatment of wild-type mice is associated with a loss of monocytic cells in the bone marrow

To assess the effect of G-CSF on monocytic cells in the bone marrow, we took advantage of *CX3CR1^{GFP/+}* transgenic mice in which monocytic cells express the GFP (Geissmann et al., 2003). Based on Gr-1 expression, bone marrow monocytes/macrophages can be divided into two distinct subsets: $Gr-1^{high} GFP^{+}$ inflammatory monocytes/macrophages and $Gr-1^{low} GFP^{+}$ resident monocytes/macrophages (Fig. 5 A; Geissmann et al., 2003). *CX3CR1^{GFP/+}* mice were treated

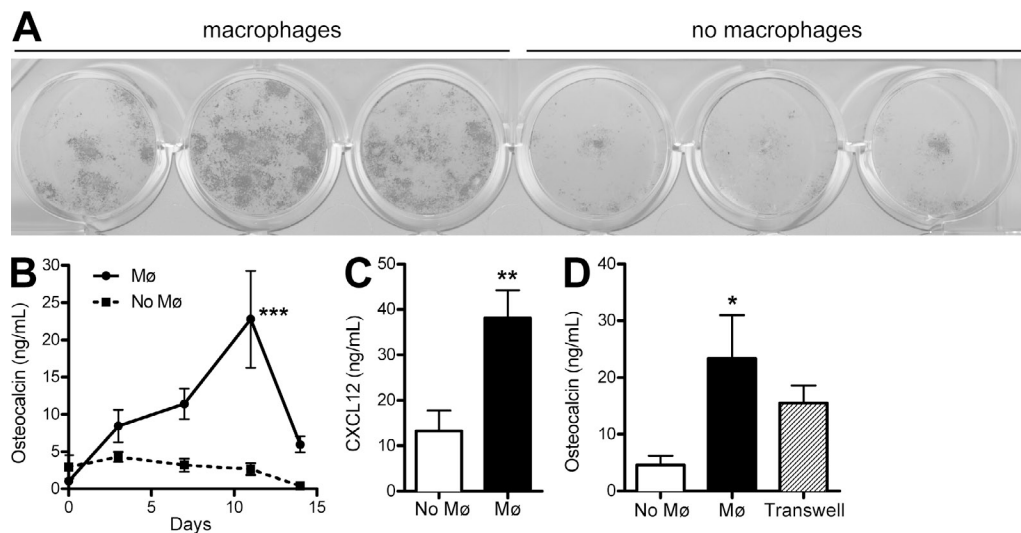


Figure 6. Macrophages support the growth of mature osteoblasts in vitro. Unfractionated bone marrow cells from wild-type mice were cultured for 10 d and then sorted by flow cytometry into stromal (CD45⁻ Ter119⁻) and macrophage (CD45⁺ CD115⁺) cell populations. Stromal cells were cultured for an additional 14 d in the absence (No Mø) or presence (Mø) of an equal number of macrophages. Ascorbic acid and calcium were included in all cultures to stimulate mature osteoblast development. (A) Representative photomicrographs of cultures on day 14 that were stained for alkaline phosphatase. (B) Osteocalcin protein concentration in conditioned media was measured by ELISA at the indicated time points. (C and D) CXCL12 protein (C) and Osteocalcin (D) concentrations in conditioned media were measured by ELISA on day 14 of culture. Where indicated, the macrophages were separated from the stromal cells by a semipermeable membrane (transwell). Data represent the mean \pm SEM of three independent experiments. *, $P < 0.05$; **, $P < 0.005$; ***, $P < 0.001$.

with G-CSF for 5 d and the number of inflammatory and resident monocytes/macrophages in the bone marrow determined by flow cytometry. A recent study suggested that collagenase treatment of murine long bones after flushing of bone marrow yields a cell population enriched for stromal cells and stromal macrophages (Crocker and Gordon, 1985; Morikawa et al., 2009). Thus, in addition to our standard bone marrow harvesting, we also analyzed cells in the bone fraction obtained after collagenase treatment of flushed femurs. In each fraction, the number of inflammatory monocytes/macrophages was significantly reduced (Fig. 5 B). A smaller decrease in resident monocytes/macrophages in the flushed, but not bone, fractions was also observed. We next examined the kinetics of monocyte/macrophage loss during G-CSF-induced mobilization (Fig. 5 C). Because *CX3CR1*^{GFP/+} mice were in limited supply, we performed these experiments using wild-type mice, using CD115 to identify monocytic cells. Importantly, the decrease in the number of inflammatory and resident monocytes/macrophages in the bone marrow was maximal by 3 d of G-CSF treatment, a time point at which osteoblast suppression first becomes evident (Christopher and Link, 2008).

Macrophages support the growth of osteoblasts in vitro

To further evaluate the role of monocytes/macrophages in osteoblast growth and survival, we cultured bone marrow stromal cells in the presence or absence of bone marrow macrophages. Stromal cells cultured in the presence of macrophages generated many more alkaline phosphatase-positive (osteoblast lineage) cells than those cultured in the absence of

macrophages (Fig. 6 A). Moreover, secretion of osteocalcin and CXCL12 into the conditioned media was significantly increased in cultures containing macrophages (Fig. 6, B and C). It is of note that no alkaline phosphatase colonies or osteocalcin or CXCL12 protein secretion were detected in cultures of macrophages alone (unpublished data). These data are consistent with a paper by Chang et al. (2008) showing that macrophages induced osteoblast mineralization in vitro. To determine whether macrophages produce a soluble factor that stimulates osteoblast development, we repeated these experiments, this time including transwell cultures in which the macrophages were separated from the stromal cells by a semipermeable membrane (Fig. 6 D). Mature osteoblast development, as measured by osteocalcin protein secretion into conditioned media, was partially induced in the transwell cultures. Collectively, these data suggest that bone marrow macrophages produce factors, at least some of which are secreted, that support the growth and/or survival of osteoblasts.

DISCUSSION

The contribution of neutrophils to HSPC mobilization by G-CSF is controversial. Neutrophils are a major source of proteases that have been implicated in HSPC mobilization, including neutrophil elastase, cathepsin G, and MMP-9 (Kjeldsen et al., 1994; Borregaard and Cowland, 1997). However, the importance of these proteases is controversial, as mice lacking these proteases exhibit a normal mobilization response to G-CSF (Robinson et al., 2003; Levesque et al., 2004; Pelus et al., 2004). There is strong evidence showing that HSPC mobilization by the chemokine IL-8 is dependent

on neutrophils. *Csf3r*^{-/-} mice, which are profoundly neutropenic, fail to mobilize in response to IL-8 (Liu et al., 1997). Moreover, antibody-mediated depletion of neutrophils (using anti-CD11a or anti-Gr-1 antibodies) abrogated IL-8-induced HSPC mobilization (Pruijt et al., 1998, 2002). With respect to G-CSF, Pelus et al. (2004) reported that neutrophil depletion using anti-Gr-1 antibodies attenuated G-CSF-induced HSPC mobilization. However, Gr-1 is expressed on both neutrophils and a subset of monocytes; thus, a role for reduced monocytes in this phenotype is possible. In the current study, we demonstrate, using G-CSFR-deficient bone marrow chimeras, that the mobilization response to G-CSF is poorly correlated with the number of wild-type neutrophils. Moreover, CD68:G-CSFR mice, which are neutropenic and have barely detectable expression of G-CSFR on neutrophils, exhibit a normal mobilization response to G-CSF. These data, although not excluding a role for neutrophils, strongly suggest that G-CSF signals in neutrophils are not sufficient to induce normal HSPC mobilization.

The contribution of lymphocytes to G-CSF-induced HSPC mobilization is also controversial. Reca et al. (2007) reported that G-CSF-induced mobilization is impaired in *Rag2*^{-/-}, SCID, and Jh mice and that this deficit can be reversed through administration of complement-inducing immunoglobulin. In contrast, Katayama et al. (2006) reported that *Rag1*^{-/-} mice and *IL-7R*^{-/-} mice exhibited a normal mobilization response to G-CSF. Consistent with the latter findings, we observed that *Rag1*^{-/-} and *NOD/scid/IL-2γ*^{null} mice exhibit a normal mobilization response to G-CSF. The basis for these discrepancies remains unclear. Although all of these mouse lines share deficits in B and T lymphopoiesis, there are subtle differences. For example, natural killer activity is normal in *Rag1*^{-/-} and *Rag2*^{-/-} mice but is absent in *NOD/scid/IL-2γ*^{null} mice. In any case, our data strongly suggest that neither B and T lymphocytes nor NK cells are required for a normal mobilization response to G-CSF.

There is accumulating evidence that monocyte lineage cells in the bone marrow contribute to osteoblast homeostasis and HSPC trafficking. Chang et al. (2008) demonstrated that macrophages are anatomically juxtaposed with endosteal osteoblasts, forming a canopy over the osteoblasts at sites of bone formation. Moreover, they showed that ablation of monocytic cells using the MAFIA transgenic mouse model resulted in a loss of osteoblasts (Chang et al., 2008). Similarly, Winkler et al. (2010) recently showed that macrophage ablation using the MAFIA transgenic mouse model or through administration of clodronate-loaded liposomes resulted in a loss of osteoblasts and HSPC mobilization. Finally, Chow et al. demonstrated in a companion paper in this issue that depletion of monocytic lineage cells using a variety of methods is sufficient to induce mobilization of HSPCs. Together, these data strongly suggest that monocytic cells produce trophic factors required for osteoblast maintenance and HSPC retention. Consistent with this conclusion, we show that macrophages support osteoblast growth in vitro, at least in part, through production of a soluble factor. The identity of these factors is currently unknown.

In this study, we provide novel evidence that G-CSFR signaling in monocytic cells is sufficient to induce HSPC mobilization. We generated transgenic mice in which expression of the G-CSFR is mainly limited to cells of the monocyte lineage and showed that G-CSF-induced HSPC mobilization, osteoblast suppression, and decrease in CXCL12 expression are similar to that control mice. In the bone marrow, there are at least four distinct monocytic cell populations: inflammatory monocytes/macrophages, resident monocytes/macrophages, myeloid dendritic cells, and osteoclasts. Because the CD68 transgene used in our study is expected to direct G-CSFR expression in each of these cell populations, all of them are candidates to mediate HSPC mobilization. There is considerable (though conflicting) data on the role of osteoclasts in HSPC mobilization. Kollet et al. (2006) reported that activation of osteoclasts by injection of RANKL (RANK ligand) was associated with moderate HSPC mobilization, and inhibition of osteoclasts, either genetically by knocking out *PTPε* or by injecting mice with calcitonin, blunts the mobilization response to G-CSF. It is of note that osteoclasts produce the protease cathepsin K, which can cleave CXCL12 in vitro (Drake et al., 1996; Kollet et al., 2006). In contrast, other studies indicate that osteoclasts may actually inhibit mobilization, as mice that were given pamidronate, an osteoclast-inhibiting bisphosphonate, exhibit increased mobilization in response to G-CSF (Takamatsu et al., 1998; Winkler et al., 2010). In contrast to osteoclasts (Takamatsu et al., 1998; Winkler et al., 2010), we show that inflammatory and resident monocytes/macrophages decrease after G-CSF treatment. It is of note that the timing of the decrease in these cell populations during G-CSF treatment is similar to that reported for the decrease in osteoblasts (Christopher and Link, 2008) and precedes HSPC mobilization. Definitive identification of the monocytic cell population that mediates G-CSF-induced HSPC mobilization will require further study.

In summary, we provide evidence that monocytic cells in the bone marrow are sufficient to elicit HSPC mobilization and osteoblast suppression by G-CSF. These data suggest a model in which monocyte lineage cells in the bone marrow produce trophic factors required for the maintenance of osteoblasts. G-CSF-induced suppression of monocytic cells and/or signaling in these cells results in decreased production of the putative trophic factors, suppression of osteoblast lineage cells (and CXCL12 expression), and ultimately HSPC mobilization. The precise monocytic cell population and factors produced by these cells that regulate osteoblast lineage cells are areas of active investigation.

MATERIALS AND METHODS

Mice. Sex- and age-matched wild-type, *Csf3r*^{-/-}, and *CX3CR1*^{GFP/+} mice on a C57BL/6 background were maintained under SPF conditions according to methods approved by the Washington University Animal Studies Committee (Saint Louis, MO). The *Csf3r*^{-/-} mice have been previously described (Liu et al., 1996). The *CX3CR1*^{GFP/+} mice were a gift from D. Littman (Skirball Institute of Biomolecular Medicine, New York School of Medicine, New York, NY).

Generation of mixed chimeras. Wild-type (Ly5.1) or *Csf3r*^{-/-} (Ly5.2) bone marrow cells were harvested. A total of two million bone marrow cells were mixed at a 3:1, 1:1, 1:3, or 1:9 ratio and injected retroorbitally into lethally irradiated wild-type mice (Ly5.1). Recipient mice were conditioned with 1,000 cGy from a ¹³⁷Cesium source at a rate of ~95 cGy/min before transplantation. Prophylactic antibiotics (trimethoprim-sulfamethoxazole; Alpharma) were given during the initial 2 wk after transplantation. Mice were analyzed 8–10 wk after transplantation.

Generation of CD68:G-CSFR mouse. To express G-CSF receptor under the control of the CD68 promoter, we made use of a variant of the CD68 promoter construct described by Lang et al. (2002), in which the 728 bp of sequence 5' to the ATG and the 83-bp first intron of the human CD68 gene were subcloned into the pUR19 backbone. A fragment containing bases 93–2694 of the murine G-CSF receptor cDNA, which includes the entire coding region of the murine G-CSF receptor, was subcloned into this backbone 3' of the first CD68 intron. An IRES-GFP cassette (derived from pIRES2-eGFP; Takara Bio Inc.) was subcloned into the backbone 3' of the G-CSF receptor fragment. For injection into male nuclei of B6CDF1 zygotes, the construct was digested with *Dra*I and purified according to standard procedures. Offspring derived from the injection were screened by PCR for GFP. A sample of peripheral blood was taken from those mice positive for GFP by PCR and analyzed for the presence of GFP⁺ neutrophils and monocytes. Transgene-bearing founder mice were mated with C57BL/6 mice with germline deletion of G-CSF receptor (*Csf3r*^{-/-}). Two founder lines produced viable offspring. Initial characterization of these mice revealed similar mobilization responses to G-CSF, so the data from the two founder lines were pooled and are collectively referred to as CD68:G-CSFR mice.

Macrophage/osteoblast co-culture. Bone marrow cells were recovered from the femurs of wild-type mice by flushing with PBS. The femurs were then infused with PBS containing 50 mg/ml of type II collagenase (Worthington Biochemical) and incubated at 37°C for 30 min. The collagenase-treated femurs were flushed again with PBS. The cells were pooled (containing both hematopoietic and stromal cells) and cultured for 7 d in base media (α -MEM with 10% fetal calf serum). On day 7 of culture, cells were trypsinized and stained with PE-conjugated anti-mouse CD115 and FITC-conjugated anti-mouse CD45. CD45⁺ CD115⁺ (macrophages) and CD45⁻ (stromal cells) were sorted separately using a MoFlo high-speed cell sorter (Dako). CD45⁻ cells were plated at 10,000 cells per well in a 24-well plate in the absence or presence of 20,000 CD115⁺ CD45⁺ cells. As a control, 20,000 CD115⁺ CD45⁺ were plated alone. In each case, after incubation for 1–2 d in base media, cells were cultured for an additional 14 d in base media supplemented with 10 mM β -glycerophosphate and 50 μ g/ml ascorbic acid. Alkaline phosphatase staining was performed on day 14 of culture, per the manufacturer's instructions (Vector Laboratories).

G-CSF mobilization protocol. Recombinant human G-CSF (Amgen) was diluted in phosphate-PBS with 0.1% low endotoxin BSA (Sigma-Aldrich) and administered at a dose of 250 μ g/kg/d either by daily subcutaneous injection for 5 d or by continuous infusion via subcutaneous osmotic pump for 7 d. Mice were analyzed 3–4 h after the final cytokine dose.

CFU-C assays. Blood, bone marrow, and spleen cells were harvested from mice using standard techniques, and the number of nucleated cells in these tissues was quantified using a Hemavet (Drew Scientific) automated cell counter. We plated 10 μ l of blood, 5 \times 10⁴ nucleated spleen cells, or 2.0 \times 10⁴ nucleated bone marrow cells in 2.5 ml methylcellulose media supplemented with a cocktail of recombinant cytokines (MethoCult 3434; STEMCELL Technologies Inc.). Cultures were plated in duplicate and placed in a humidified chamber with 5% CO₂ at 37°C. After 7 d of culture, the number of colonies per dish was counted. The frequency of colonies per femur or spleen was determined based on the number of cells present in the cell suspension immediately after harvest.

Real-time quantitative RT-PCR. Femurs were flushed with a total of 0.75 ml TRIzol reagent (Invitrogen). RNA was isolated according to the

manufacturer's instructions and resuspended in 150 μ l RNase/DNase-free water. Real-time RT-PCR was performed using the TaqMan One-Step RT-PCR Master Mix Reagents kit (Applied Biosystems) on a GeneAmp 5700 Sequence Detection System (Applied Biosystems). The reaction mix consisted of 5 μ l RNA, 12.5 μ l RT-PCR mix, 200 nM of forward primer, 200 nM of reverse primer, 280 nM of internal probe, and 0.625 μ l MultiScribe reverse transcription and RNase inhibitor in a total reaction volume of 25 μ l. Reactions were repeated in the absence of reverse transcription to confirm that DNA contamination was not present. RNA content was normalized to murine β -actin. PCR conditions were 48°C for 30 min and 95°C for 10 min, followed by 40 cycles of 95°C for 15 s and 60°C for 1 min. Primers were: CXCL12 forward, 5'-GAGCCAAAGTCAAGCATCTG-3'; CXCL12 reverse, 5'-CGGGTCAATGCACACTTGTC-3'; CXCL12 dT-FAM/TAMRA probe, 5'-TCCAAACTGTGCCCTTCAGATTGTTGC-3'; β -actin forward, 5'-ACCAACTGGGACGATATGGAGAAGA-3'; β -actin primer, 5'-TACGACCAGAGGCATACAGGGACAA-3'; β -actin dT-FAM/TAMRA probe, 5'-AGCCATGTACGTAGCCATCCAGGCTG-3'; osteocalcin forward, 5'-TCTCTCTGCTCACTCTGCTGGCC-3'; osteocalcin reverse, 5'-TTTGTGCACTCAGGGCCGC-3'; and osteocalcin dT-FAM/TAMRA probe, 5'-TGCGCTCTGTCTCTCTGACCTCACAGATGCCA-3'.

Flow cytometry. Red blood cells in peripheral blood and bone marrow mononuclear cell preparations were lysed in Tris-buffered ammonium chloride buffer, pH 7.2, and incubated with the indicated antibody at 4°C for 1 h in PBS containing 0.1% sodium azide, 1 mM EDTA, and 0.2% (wt/vol) BSA to block nonspecific binding. The following directly conjugated monoclonal antibodies were used: allophycocyanin-eFluor 780-conjugated rat anti-mouse Gr-1 (RB6-8C5, IgG2b; eBioscience); allophycocyanin-conjugated rat anti-mouse CD115 (AFS98, IgG2a; eBioscience); FITC-conjugated rat anti-mouse Gr-1 (RB6-8C5, IgG2b; eBioscience); allophycocyanin-conjugated rat anti-mouse CD3e (17A2, IgG2b; eBioscience); and allophycocyanin-eFluor 780-conjugated rat anti-mouse B220 (RA3-6B2, IgG2a; eBioscience). For KLS analysis, we used the following antibodies: PE-conjugated rat anti-mouse Gr-1 (RB6-8C5, IgG2b; eBioscience); PE-conjugated rat anti-mouse B220 (RA3-6B2, IgG2a; eBioscience); PE-conjugated Armenian hamster anti-mouse CD3e (145-2C11, IgG; eBioscience); PE-conjugated rat anti-mouse Ter-119 (TER-119, IgG2b; eBioscience); rat anti-mouse Sca-1 (D7, IgG2a; eBioscience); and rat anti-mouse c-kit (2B8, IgG2b; eBioscience). To assess surface G-CSFR expression, G-CSF was biotinylated using NHS-LC-biotin (Thermo Fisher Scientific) as previously described (Shimoda et al., 1992). Peripheral blood mononuclear cells were incubated at 4°C for 1 h with biotinylated G-CSF (25 ng/10⁶ cells) in the presence or absence of a 100-fold molar excess of nonlabeled G-CSF, followed by incubation with PE-conjugated streptavidin. All cells were analyzed on a FACScan flow cytometer.

In some cases, the bone fraction of the bone marrow was analyzed by flow cytometry. In brief, bone marrow was extracted from femurs either by flushing with PBS or by centrifugation at 3,300 *g* for 1 min at room temperature. The pellet was set aside for analysis as the flushed fraction. The flushed femurs were then pulverized with a mortar and pestle, and the bone chips were incubated with PBS containing 2 mg/ml of type II collagenase (Worthington Biochemical) at 37°C for 60 min with agitation. After allowing the bone chips to settle by gravity, the cell suspension was harvested and analyzed.

CXCL12 and osteocalcin ELISAs. For ELISAs, 96-well plates were coated with 100 μ l CXCL12 capture antibody (2 μ g/ml) diluted in PBS and incubated overnight at room temperature. After incubation for 1 h at room temperature with 300 μ l of blocking solution (1% BSA, 5% sucrose, and 0.05% NaN₃), a 100- μ l sample was added to each well and incubated for 2 h at room temperature. After washing, 100 μ l polyclonal biotinylated anti-human CXCL12 (250 ng/ml) in ELISA diluent (0.1% BSA, 0.05% Tween 20 in Tris [tris(hydroxymethyl)-aminomethane]-buffered saline, pH 7.3) was added to each well and incubated at room temperature for 2 h. The reaction was developed by successive incubations with 1 μ g/ml horseradish peroxidase streptavidin, substrate solution, and 50 μ l 2N H₂SO₄ to stop

the reaction. A microplate reader set at 450 nm was used to determine optical density with readings at 570 nm subtracted from the results. Recombinant human CXCL12 α was used to generate a standard curve. CXCL12 ELISA reagents were purchased from R&D Systems. Osteocalcin ELISA was performed using a kit according to the manufacturer's instructions (Human Osteocalcin Instant ELISA; eBioscience).

Statistics. Significance was determined using Prism software (GraphPad Software, Inc.). Statistical significance of differences was calculated using two-tailed Student's *t* tests (assuming equal variance) or, where indicated, one- or two-way ANOVA with Bonferroni's or Dunnett's post testing. *P*-values <0.05 were considered significant. All data are presented as mean \pm SEM except as noted.

Online supplemental material. Fig. S1 shows that the percentage of Csf3r^{-/-} B cells in the mixed chimeras are as predicted from the input ratios of wild-type to Csf3r^{-/-} cells. Fig. S2 shows the absolute numbers of circulating neutrophils in the mixed chimeric mice. Online supplemental material is available at <http://www.jem.org/cgi/content/full/jem.20101700/DC1>.

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