Cell size is a determinant of stem cell potential during aging

Lengefeld, Jette

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**INTRODUCTION**

Adult stem cells are critical for the maintenance of many tissues in our body. For example, hematopoietic stem cells (HSCs) build the blood system throughout life. Their magnificent ability to proliferate and differentiate into the blood lineages is illustrated by the observation that a single HSC can repopulate the hematopoietic compartment of a lethally irradiated mouse when coinjected with radioprotective bone marrow (BM) (1).

As in almost every cell type, HSC division is coupled to cell growth. An increase in cell volume and mass through macromolecular biosynthesis ensures that stem cells retain a constant size after division. Growth control is mediated by the mTOR (mammalian target of rapamycin) pathway, which regulates macromolecule biosynthesis in response to amino acid availability and growth signals (2). Cell growth ultimately controls cell cycle progression. Cdk4/6–cyclin D complexes drive the decision of HSCs to exit the quiescent state and to divide. They promote cell cycle entry by inactivating the retinoblastoma (Rb) protein. Rb inhibits the G1/S transition by repressing expression of genes required for S phase entry (3).

After damage and during aging, stem cell function declines. For example, old HSCs are less competitive in transplantation assays compared to younger ones (4). How stem cell fitness declines during aging is only beginning to be understood. In culture, mammalian cells undergo replicative senescence—an irreversible cell cycle arrest (5). With age, senescent cells accumulate in mice and humans (6–8). Whether processes leading to replicative senescence in cultured cells also mediate stem cell aging in vivo is not clear.

A key characteristic of senescent cells is their large size (9, 10). Recent work in budding yeast and cultured human cells has provided an explanation for this observation. Senescent cells are large because cell growth and division are only loosely coupled. If cell division is blocked by damage-induced cell cycle checkpoints, then macromolecule biosynthesis continues to drive cell growth. As a consequence, cells increase in size without a corresponding increase in DNA content. Once the cell cycle arrest has been lifted, cells resume division at a larger size and decreased DNA:cytoplasm ratio (11, 12). It follows that the more divisions a cell undergoes, the more frequently it encounters cell cycle arrest–inducing damage. Hence, cell size increases and DNA:cytoplasm ratio decreases during regenerative aging of yeast and cultured mammalian cells (9, 13–15). Cellular enlargement affects cell physiology in vitro. Young cells manipulated to grow to a large size without a corresponding increase in DNA content exhibit a number of phenotypes observed in senescent cells—foremost, proliferation defects (12, 16). Whether large cell size is a cause of senescence and fitness loss during cellular aging in vivo is not known.

We show here that cell size affects the function of HSCs in vivo. Conditions known to induce stem cell dysfunction—DNA damage, cell cycle arrest, increased frequency of cell division, and aging—cause HSCs to increase in size. Preventing HSC enlargement by interfering with macromolecule biosynthesis or reducing their large size by accelerating progression through G1 prevents the loss of stem cell potential. We conclude that cell size is a critical determinant of stem cell potential and propose that stem cell enlargement contributes to the functional decline of HSCs during DNA damage and aging.

**RESULTS**

**Large cell size contributes to radiation-induced loss of stem cell fitness**

Previous studies showed that growing primary human cells to a large size in vitro decreases their proliferation potential (12). Whether
large cell size interferes with proliferation in vivo has not yet been determined. We chose HSCs to address this question because of their small size. To address whether large HSC size is associated with decreased fitness, we first asked whether an insult known to reduce HSC fitness and to induce senescence—DNA damage [17]—also causes an increase in HSC size. To induce DNA damage, we sublethally irradiated young mice with 3 gray (Gy). After 2 weeks, we isolated live HSCs (Lin−, Sca1/Ly6c, CD117/cKit+, CD150/Slamf1+, CD48/Slamf2−, and 7-ADD−; fig. S1A) and examined their size by Coulter counter and microscopy. With both methods, we found that irradiated HSCs were enlarged compared to control HSCs (Fig. 1A and fig. S1B). Our analysis further showed that only a fraction of HSCs that irradiated HSCs were enlarged compared to control HSCs (Fig. 1A).

We did not detect high SA-β-gal activity 2 weeks after either 3- or 6-Gy irradiation [17]. Enlargement was also observed when specifically analyzing G0/G1 HSCs (Fig. 1A). To determine whether large HSC size was associated with irradiation-induced senescence, we correlated cell size with senescence-associated beta-galactosidase (SA-β-gal) activity. In contrast, SA-β-gal high HSCs were readily observed in 6-Gy-irradiated animals. Next, we sorted HSCs on the basis of SA-β-gal activity levels and found that SA-β-gal high HSCs were larger than SA-β-gal low HSCs from the same animal (fig. S1, E to G). Thus, low doses of irradiation (3 Gy) cause HSC enlargement without detectable induction of SA-β-gal activity, whereas a higher dose (6 Gy) leads to enlarged HSCs that harbor high levels of SA-β-gal activity. These observations indicate that limited DNA damage enlarges HSCs before inducing a bona fide senescence program and that large HSCs are more likely to be senescent.

To determine whether increased HSC size contributes to their irradiation-induced dysfunction, we prevented HSC enlargement during irradiation. We treated mice with rapamycin (mTOR inhibitor) or vehicle for 2 weeks and irradiated them with 3 Gy or left the mice untreated (control), followed by a rapamycin or vehicle treatment for another 2 weeks. Rapamycin treatment prevented HSCs from increasing in size in response to irradiation (3 Gy + RAP; Fig. 1A and fig. S1B) without changing the cell cycle state of HSCs as measured by DNA content and 5-ethynyl-2′-deoxyuridine (EdU) incorporation (fig. S1, H and I). Rapamycin treatment neither decreased the level of DNA damage after 3-Gy irradiation as evaluated by alkaline comet assays (Fig. 1B and fig. S1I) nor altered the differentiation potential of HSCs as demonstrated by blood lineage analysis after reconstitution (fig. S1K). We conclude that rapamycin prevents HSC enlargement after irradiation.

Having established that rapamycin prevents HSC enlargement without affecting the degree of DNA damage, we assessed the effects of rapamycin treatment on HSC function. We isolated HSCs from donor mice expressing the pan-hematopoietic lineage allele CD45.2 that were treated with rapamycin or vehicle during 3-Gy irradiation. We then lethally irradiated recipient mice carrying the CD45.1 allele to eliminate the preexisting blood system. The recipient mice were reconstituted with CD45.2 donor HSCs and supporting CD45.1 BM cells to allow for donor-driven reconstruction of the blood system (fitness). Donor HSC fitness was determined by the fraction of peripheral CD45.2 white blood cells in CD45.1 recipients over time. Rapamycin had a marked effect on the fitness of irradiated HSCs: Donor HSCs from mice that were 3 Gy irradiated and received rapamycin treatment exhibited a significantly increased reconstitution potential compared to HSCs from 3 Gy–irradiated mice (Fig. 1C and fig. S1I). The degree of chimerism changed over time. The contribution to the blood system of 3 Gy–irradiated HSCs treated with rapamycin increased over the course of the reconstitution, whereas the fitness of vehicle-treated 3 Gy–irradiated HSCs decreased (slope analysis; Fig. 1C). This observation indicates that HSC proliferation, rather than homing to the BM, is affected by rapamycin. We note that rapamycin was not universally radioprotective. The drug failed to confer radioprotection at higher radiation doses (5 Gy; fig. S1M) despite suppressing SA-β-gal activity levels (fig. S1D). We conclude that rapamycin prevents radiation-induced HSC exhaustion. We interpret this result to suggest that when cellular enlargement is prevented by rapamycin during DNA damage, HSCs retain their fitness.

Fig. 1. Cellular enlargement contributes to DNA damage–induced fitness decline in HSCs. (A) Mean volume (fl) of HSCs obtained from vehicle (n = 6), sublethally irradiated (3 Gy, n = 4), Rapamycin-treated (RAP, n = 4), and RAP + 3 Gy–treated (n = 7) mice 2 weeks after irradiation (Δ = difference). (B) Measurement of DNA damage using CometChip: percentage tail DNA of HSCs (%) isolated from mice 2 weeks after treatment with vehicle, 3 Gy, RAP, or 3 Gy + RAP (n ≥ 166). (C) Reconstitution assay: Donor (CD45.2) mice were pretreated with RAP or vehicle for 2 weeks, sublethally irradiated (3 Gy), and treated with RAP (n; donors = 12, recipients = 8) or vehicle (n; donors = 12, recipients = 15) for another 2 weeks before 1000 CD45.2 HSCs were isolated and transplanted into lethally irradiated recipient mice. Control donor HSCs were not treated (control, n; donors = 6, recipients = 9) or treated with RAP without irradiation (control, n; donors = 3, recipients = 5). Recipient mice were not treated with RAP after reconstitution. Percentage of donor-derived white blood cells in recipients and slope of reconstitution kinetics over time were determined.

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The Cdk4/6 inhibitor palbociclib enlarges HSCs causing their decline in reconstitution potential

How does irradiation lead to HSC enlargement? Directly after irradiation, HSCs experience DNA damage and arrest in G2 to repair this damage (18). This arrest is, however, transient. HSC populations return to their preirradiation cell cycle state 2 weeks after sublethal irradiation (fig. S1, H and I). Despite the return of HSCs to the G0/1 state, their size increased (Fig. 1A). In vitro studies with budding yeast and primary human cells provide a potential explanation for this finding. During cell cycle arrest, mTOR continues to promote macromolecule biosynthesis and cells increase in size (11, 12).

To determine whether cell cycle arrest causes HSCs to enlarge, we examined HSC size in response to treating animals with the Cdk4/6 inhibitor palbociclib (PD), which arrests cells in G1 phase (19). Because HSCs rarely divide under physiological conditions (20, 21), we injected PD every other day for 120 days (fig. S2A). This treatment regimen increased G0/1 length as judged by cell cycle analysis and changes in blood composition of donor animals (fig. S2, B to E). Analysis of HSC size after various lengths of PD treatment showed that HSCs increased in size in a time-dependent manner (fig. S2A). After 85 days of PD treatment, the mean volume of HSCs was 263 fl as measured by Coulter counter, which reflects an increase in size of 15.5% compared to control HSCs (Fig. 2A). These data indicate that delaying cells in G0/1 by PD treatment causes HSC enlargement in vivo.

Characterization of PD-enlarged HSCs revealed increased DNA damage (Fig. 2B), which was not associated with the production of SA-β-gal activity (fig. S2F). The finding that a PD arrest is associated with DNA damage, causal or consequential, afforded us another opportunity to assess whether large HSCs that harbor DNA damage exhibit decreased reconstitution potential. A previous study showed that short-term inhibition of Cdk4/6 (12 hours, trilaciclib) did not reduce HSC reconstitution potential (19). Cell size, however, is not expected to increase within the treatment time frame of this study.

**Fig. 2. The Cdk4/6 inhibitor PD enlarges HSCs, causing their decline in reconstitution potential.** (A) Mean volume (fl) of HSCs isolated from mice treated with vehicle (n = 6), Cdk4/6 inhibitor (PD, n = 10), RAP (n = 4), or Cdk4/6 inhibitor + RAP (n = 5) for 85 days (∆ = difference). Same control as in Fig. 1A. (B) DNA damage in CometChip: percentage tail DNA of HSCs (%) isolated from mice treated with vehicle, Cdk4/6 inhibitor (PD), RAP, or Cdk4/6 inhibitor + RAP (n ≥ 552). (C) Reconstitution assay: CD45.2 mice were treated with vehicle (n; donors = 5, recipients = 8), Cdk4/6 inhibitor (PD, n; donors = 5, recipients = 7), RAP (n; donors = 5, recipients = 8), or Cdk4/6 inhibitor + RAP (n; donors = 5, recipients = 5) for 85 days before their HSCs were isolated for transplantation into lethally irradiated CD45.1 recipient mice. No drug treatment was performed after the reconstitution. Percentage (%) of donor-derived white blood cells in recipients and slope of reconstitution kinetics were determined over time. (D) Experimental strategy to determine the role of cell size for HSC fitness: If size determinates fitness, then similarly sized HSCs are expected to exhibit a similar reconstitution potential, irrespective of whether HSCs were treated with vehicle or Cdk4/6 inhibitor (PD). (E) Reconstitution assay: 600 M- or XL-sized HSCs of CD45.2 donor mice treated with vehicle (n; donors = 6, recipients ≥7) or Cdk4/6 inhibitor (PD, n; donors = 9, recipients = 7) were transplanted into lethally irradiated recipient mice (CD45.1), which were not treated with drugs after the reconstitution. Percentage (%) of donor-derived white blood cells in recipients and slope of reconstitution kinetics were determined over time.
We found that prolonged PD treatment enlarged HSCs and impaired their reconstitution potential (Fig. 2C and fig. S2G). To determine whether the large size of PD-treated HSCs contributed to their reduced reconstitution potential, we prevented size increase during PD treatment by simultaneously treating animals with rapamycin. When treated with PD and rapamycin, HSCs displayed DNA damage but they did not increase in size (Fig. 2, A and B). Their reconstitution potential was preserved (Fig. 2C). Thus, rapamycin prevents PD-induced enlargement of HSCs and preserves their fitness.

We hypothesized that if PD treatment indeed decreases fitness because it enlarges HSC size, then HSCs of PD-treated animals that did not grow to a large size should exhibit a reconstitution potential similar to that of untreated animals. In other words, medium (M)–sized HSCs from PD-treated mice should exhibit a greater reconstitution potential than large (XL)–sized HSCs from PD– or vehicle-treated mice (Fig. 2D). We found this to be the case. To obtain M-sized and XL-sized HSCs from PD-arrested or vehicle-treated mice, we used the forward scatter during cytometric sorting. We isolated the largest 10% of HSCs (XL) and HSCs of a mean size ± 10% (M) (22). Cell volume analysis confirmed that we isolated PD– or vehicle-treated HSCs of the same absolute size using the M (246 fl) or XL gate (305 fl, 24% larger; fig. S2H). M-sized PD-treated HSCs were more effective in reconstituting lethally irradiated mice than XL-sized PD– or vehicle-treated HSCs (Fig. 2E). These results indicate that PD-induced enlargement rather than PD-treatment per se causes HSCs to be less fit. We note that M-sized PD-treated HSCs appear less fit than vehicle-treated, M-sized HSCs when comparing reconstitution kinetics (slope). This difference is however not statistically significant. It is nevertheless possible that PD treatment also affects HSC potential in a cell size–independent manner. We conclude that PD reduces HSC fitness largely by increasing their cell size.

**Cellular growth enlarges HSCs and reduces their reconstitution potential**

Large size contributes to the decreased reconstitution potential of HSCs with DNA damage. To determine whether enlargement alone decreases HSC fitness in vivo, we analyzed HSCs that were large but lacked DNA damage. To create large undamaged HSCs, we manipulated mTOR pathway activity. The lack of TSC1 causes constitutive activation of mTOR signaling, which increases cell growth and enlarges the size of blood cells (23). Cre-driven excision of TSC1 in TSC1<sup>fl/fl</sup>;R26-creERT2 mice (henceforth TSC1<sup>−/−</sup>) enlarged HSCs by 27 to 60% without causing increased DNA damage (Fig. 3, A and B). Next, we isolated HSCs from TSC1<sup>fl/fl</sup>;R26-creERT2 mice and reconstituted lethally irradiated recipients (Fig. 3C). We allowed HSCs to home to the BM in recipients for 3 days, then induced TSC1 excision using tamoxifen, and assessed donor TSC1<sup>−/−</sup> HSC fitness. TSC1<sup>−/−</sup> HSCs were impaired in repopulating the blood system of recipient mice (Fig. 3D). We conclude that constitutive mTOR-driven growth enlarges HSCs without causing DNA damage and yet reduces their ability to reconstitute lethally irradiated recipients. These data support the conclusion that increased cell growth enlarges HSCs and decreases their fitness.

**Consecutive cell divisions cause HSCs to enlarge, which drives their exhaustion**

We hypothesized that if cellular enlargement contributes to HSC dysfunction, then any condition causing loss of stem cell potential ought to be accompanied by HSC enlargement. Successive cell divisions cause stem cell exhaustion. With each cell division, HSCs lose their cell division potential, such that each daughter cell is less potent than its mother (20, 24). We determined whether HSCs enlarge during two conditions known to cause higher levels of cell divisions in vivo: pregnancy (25) and transplantation into irradiated mice (4). G0/1 HSCs of breeding females and HSCs obtained after transplantation were enlarged (Fig. 4, A, C, and D). As in response to radiation, not all HSCs enlarged during serial transplantation, as judged by a broadening of the size distribution (fig. S3A). This was not due to changes in cell cycle distribution. Eighty days after transplantation (the time cell size was analyzed), HSCs had returned to the same cell cycle profile as before transplantation (fig. S3, B and C). In secondary transplants, donor HSCs did not increase further in size (Fig. 4D), suggesting that an upper size threshold exists for HSCs.

The two methods of increasing the rate of HSC division also caused a decrease in reconstitution potential (Fig. 4B and fig. S3D). This decreased fitness was not due to transplanting actively proliferating...
HSCs (26) because we only transplanted HSCs in G_0/1. We conclude that, similar to budding yeast and primary mammalian cell in vitro (9, 13), successive divisions of HSCs are accompanied by an increase in HSC size and decrease in fitness.

The reconstitution experiment afforded us the opportunity to determine whether cell division–driven enlargement promotes HSC exhaustion. We conducted transplantation experiments, in which recipients received prolonged rapamycin treatment to prevent HSC enlargement during the many divisions needed to reconstitute the hematopoietic compartment (Fig. 4C). This experimental regime indeed prevented donor HSCs from enlarging (Fig. 4D). Preventing enlargement of donor HSCs in the host via rapamycin treatment improved their fitness during the reconstitution (Fig. 4E). We conclude that successive divisions cause HSCs to enlarge, which reduces their stem cell potential.

To directly test whether HSCs that divided more often are larger, we took advantage of the inducible histone 2B (H2B)–green fluorescent protein (GFP) mouse model (24, 27) to simultaneously analyze division history and cell size. We induced H2B-GFP expression (pulse) and then transplanted GFP high HSCs into lethally irradiated recipients to induce HSC division (chase; Fig. 4F). Four weeks after the transplantation, HSCs from recipients treated with vehicle or rapamycin (chase-vehicle, RAP) lost their GFP intensity, indicating that the divisions needed to rebuild the recipients’ blood system diluted H2B-GFP in HSCs (Fig. 4G). In comparison, HSCs maintained high GFP intensity in donor animals 4 weeks after the pulse (chase-control). HSCs from vehicle-treated recipient mice were enlarged, while rapamycin prevented this increase in size (Fig. 4H). We conclude that HSCs increase in size after successive division.
Why does an increased cell division frequency cause HSC enlargement? Stochastic damage can occur during every cell division (28, 29). When cells are damaged, cell cycle checkpoints are activated to facilitate repair (18, 30). During this arrest, mTOR continues to promote macromolecule biosynthesis driving cell growth and enlargement (11, 12, 16). Hence, the more divisions a cell undergoes, the more likely it encounters damage that causes cell cycle arrest and therefore enlargement. Our data indicate that, in HSCs too, successive divisions cause enlargement, which, in turn, leads to HSC dysfunction. We note that this hypothesis also explains why only a fraction of HSCs enlarge during serial transplantations.

**Naturally large HSCs display decreased reconstitution potential**

Our data show that DNA damage, increased cellular growth, proliferation challenge, or artificially increasing cell size decreases HSC fitness. To determine the broader physiological relevance of this observation, we assessed the fitness of naturally large HSCs. We isolated the smallest 10% of HSCs (XS), the largest 10% of HSCs (XL), and HSCs of a mean size ± 10% (M; Fig. 5A) from young wild-type (WT) mice by flow cytometry using forward scatter. Cell volume analysis by Coulter counter confirmed that this method can differentiate HSCs on the basis of their size when size differences are large (Fig. 5, B and C). XS HSCs (mean = 209 fl) were 14% smaller than M HSCs (mean = 240 fl), which were 30% smaller than XL HSCs (mean = 312 fl).

We next investigated why XL HSCs are large. During cell division, cells increase in size to maintain constant volumes of the two daughter cells. To determine whether XL HSCs were large because they were in the process of dividing, we analyzed their DNA content. While most differently sized HSCs were in G₀, XL HSCs were less in G₁ and more often in S phase or mitosis (S/G₂-M; fig. S4, A to C). As XL HSCs are not polyploid (31), these data indicate that the XL HSC population is composed of large G₀/₁ HSCs and HSCs that are larger because they are in S/G₂-M.

**Fig. 5. Naturally large HSCs are impaired in reconstituting the hematopoietic compartment.** (A) Size distribution of HSCs as determined by forward scatter (FSC-A). Gates used to isolate small (XS), medium (M), and large (XL) HSCs are indicated. SSC-A, side scatter. (B) HSCs (%) per volume (fl) isolated using the XS, M, or XL gates shown in (A). Gaussian fit was used to determine mean cell volume. Dotted line marks the mean of M-sized HSCs. (C) Mean volume (fl) of HSCs isolated using the XS (n = 6), M (n = 8), XL (n = 6), or G₀/₁ XL (n = 3) gates (∆ = difference). (D) CometChip assay to measure DNA damage: Percentage tail DNA of XS-, M- and XL-, G₀/₁ XL-sized HSCs (n > 323 cells measured per condition). (E) Schematic of reconstitution experiments in (F) to (H): A total of 600 differently sized donor-derived HSCs were transplanted into lethally irradiated recipients. (F) Reconstitution assay: Donor-derived (CD45.2) white blood cells (%) in recipients after transplantation of XS (n = 6, recipients = 6), M (n = 8, recipients = 6), or XL (n = 6, recipients = 6) donor HSCs. Slope of reconstitution kinetics is shown. (G) Reconstitution assay: Donor-derived (CD45.2) white blood cells (%) in recipients after transplantation of XS/M donor HSCs (n = 6, recipients = 6) or XL donor HSCs (n = 6, recipients = 6). (H) Reconstitution assay: Donor-derived (CD45.2) white blood cells (%) in recipients after transplantation of XS/M donor HSCs (n = 6, recipients = 6) from Ki67-RFP mice. (I) Mean volume (fl) of XS- or G₀/₁ XL-sized CD45.2 HSCs before transplantation and their volume at 80 days after transplantation (n ≥ 3). Before data as in (C) and after as in Fig. 7G.
revealed that G₀/₁ XL HSC nuclei displayed a higher percentage of damage, we performed an alkaline CometChip assay. This analysis revealed that HSC DNA of XS and M-sized HSCs compared to small WT HSCs.

To determine whether naturally large G₀/₁ HSCs harbor DNA damage, we performed an alkaline CometChip assay. This analysis revealed that G₀/₁ XL HSC nuclei displayed a higher percentage of tail DNA compared to XS- and M-sized HSCs and higher levels of γH2AX phosphorylation (Fig. 5D and fig. S4D). We conclude that WT mice harbor large G₀/₁ HSCs, which have more DNA damage compared to small WT HSCs.

To assess the fitness of naturally XL HSCs in vivo, we isolated XS, M, and XL HSCs and reconstituted lethally irradiated recipient mice (Fig. 5E). Because HSCs in S/G₂-M are impaired in providing long-term multilineage reconstitution (26, 32), we specifically isolated G₀/₁ HSCs using a DNA stain. The reconstitution potential differed with respect to HSC size, XS- and M-sized G₀/₁ HSCs effectively contributed to the peripheral blood of recipient mice, whereas XL G₀/₁ HSCs exhibited a significantly reduced reconstitution potential (Fig. 5F and fig. S4, E and F). We observed that same result when we isolated G₀/₁ CD34-negative XS-, M-, and XL-sized HSCs or HSCs of different sizes in the G₀ cell cycle state (Fig. 5, G and H). DNA staining can alter HSCs fitness, but reconstitution without staining the DNA of HSCs revealed similar results (fig. S4G). XL HSCs enlarged during reconstitutions, while G₀/₁ XL HSCs remained large by the end of the reconstitution experiment (Fig. 5I). This indicates that XL HSCs do not shrink back to their original size during the divisions necessary to rebuild the recipients’ blood system.

In summary, we have examined six different experimentally induced or physiological conditions, under which HSCs exhaustion occurs: irradiation-induced DNA damage, Cdk4/6 inhibition, hyperactivation of mTOR, high division rate during transplantation, repeated pregnancy, and naturally large HSCs. We observe that HSCs enlarge under all these conditions. In all experimental settings, in which this could be investigated, preventing HSC enlargement with rapamycin preserved HSC fitness.

**Large HSCs exhibit decreased proliferation potential and changed metabolism**

Why are large HSCs less fit than small HSCs? Large size could affect (i) proliferation potential, (ii) stem cell identity and differentiation potential, (iii) the metabolic state of HSCs, and/or (iv) protein synthesis capacity. We chose naturally large and PD-enlarged HSCs to test these possibilities.

**(i) Proliferation potential**

The observation that PD-enlarged and XL-donor HSCs contribute less to the blood lineages of recipient animals over time (reconstitution slopes) indicated that cell size affects HSC proliferation. The analysis of HSC proliferation in vitro confirmed this conclusion. We found that PD-enlarged HSCs formed fewer colonies than control HSCs (fig. S5A). Rapamycin treatment partially restored colony formation of PD-treated HSCS. A decrease in proliferation was also observed in naturally large HSCs, although the effect was less notable. We also investigated whether large size affected homing of HSCs to the BM niche, which is essential for hematopoiesis. We injected XL- or PD-enlarged donor HSCs into CD45.1 recipient mice and examined the fraction of CD45.2 donor cells in the BM 21 hours thereafter. This analysis suggested that HSC size did not affect homing potential (fig. S5B). We conclude that cellular enlargement interferes with the ability of HSCs to proliferate.

**(ii) Stem cell identity and differentiation potential**

To determine whether cell size affects HSC identity or their ability to differentiate into the various haematopoietic lineages, we first conducted a comparison of gene expression profiles between differently sized HSCs using gene set enrichment analysis (GSEA). This analysis revealed that the expression pattern of several Gene Ontology (GO) gene sets changed in G₀/₁ XL HSCs compared to smaller control HSCs (M and XS). To identify transcriptional changes in XL HSCs that underlie the decline in fitness in vivo, we focused our analysis on GO sets that specifically changed in XL HSCs relative to XS and M HSCs but not between XS and M HSCs. A total of 2.4% of all GO gene sets passed this filter (table S1). Using a cutoff that required that >20% of GO gene sets associated with a given biological process to be differentially regulated between XL HSCs versus XS and M HSCs, we identified the following pathways (fig. S5C): DNA damage (21% of associated GO gene sets were differentially regulated in XL- versus XS/M-sized HSCs), proteasome (30%), excision/mismatch repair (50%), RNA processing (32%), transfer RNA modification (23%).
and nucleases (27%). The up-regulation of genes involved in DNA damage response and repair was biologically relevant. Naturally large HSCs harbored more DNA damage than smaller control HSCs (Fig. 5D). In the comparison between PD-enlarged HSCs to control HSCs, only 0.3% of the GO gene sets passed the functional filter and no enrichment for particular biological processes was observed (table S1).

To specifically determine whether size affected the self-renewal or differentiation ability of HSCs, we used published lists of genes related to HSC identity and differentiation (table S2) (33–40) and analyzed whether their expression changed in XL- and PD-enlarged HSCs. We found that only a few genes rose to the level of significant differential expression (table S3). A principle components analysis confirmed that size had little or no effect on the expression of genes sets associated with stem cell identity and differentiation (fig. S5D).

To evaluate the biological relevance of these results, we used functional assays to assess differentiation potential of large-sized HSCs in vitro and in vivo. The ability to form cells of the myeloid, B cell, and T cell lineages did not significantly differ between mice reconstituted with differently sized HSCs (fig. S5E). Differentiation was also not significantly affected in vitro. The types of colonies formed by HSCs in methylcellulose cultures were similar between HSCs of different sizes (fig. S5F). Last, the concentration of stem cell surface markers was similar between differently sized HSCs (fig. S5G). We conclude that cell size does not significantly affect stem cell identity or differentiation potential of HSCs.

(iii) Metabolic state
Prior studies suggested that stem cells can enter a metabolically activated state, which is characterized by an increase in cell size, high mitochondrial activity, high adenosine 5′-triphosphate (ATP) levels, and up-regulation of the interferon-γ (IFN-γ) response (41, 42). We determined whether HSC enlargement could reflect HSCs in such an activated state. In contrast to activated stem cells, mitochondrial function was decreased in large G0/1 HSCs as judged by...

Fig. 7. Reducing cellular size restores HSC fitness. (A) RB+/+;R26-cre or RB+/−;R26-cre mice were DNA-damaged (2.8 to 3 Gy) to measure HSC volume (B) and treated with tamoxifen reducing HSC size. Afterward, HSC volume was measured (B) and 700 G0/1 donor HSCs were transplanted into lethally irradiated recipients to measure their fitness (C) and volume (D) in recipients. (B) Mean volume (fl) of G0/1 HSCs from RB+/+;R26-cre or RB+/−;R26-cre mice after 2.8 to 3 Gy (n = 4) and tamoxifen treatment (n = 5 to 11) as described in (A). Day −1 = before irradiation. Same control and 2.8- to 3-Gy sample as in Fig. 1A. (C) Reconstitution assay: White blood cells (%) derived from donor RB+/+;R26-cre (n = 4) or RB+/−;R26-cre (n = 3) 2.8- to 3-Gy G0/1 HSCs that were treated before transplantation with tamoxifen as described in (A). Slope of reconstitution kinetics was determined. (D) Mean volume (fl) of recipient-derived donor RB+/+;R26-cre (n = 3) and RB+/−;R26-cre (n = 3) 2.8- to 3-Gy G0/1 HSCs that were treated before transplantation with tamoxifen as described in (A). (E) Experiment schematic: A total of 600 XS- or XL-sized G0/1 HSCs from RB+/+;R26-cre or RB+/−;R26-cre mice were transplanted into lethally irradiated recipients. Afterward, recipients were treated with tamoxifen to reduce HSC size and to measure fitness and volume of donor G0/1 HSCs in recipients. (F) Reconstitution assay: Percentage (%) of donor-derived white blood cells in recipients and slope of reconstitution as described in (E) (n; donors = 4, recipients XS-RB+/+ = 6, XS-RB+/− = 5, XL-WT = 9, XS-WT = 5). Red arrows indicate tamoxifen treatment. (G) Mean volume (fl) of donor G0/1 HSCs after treatment with tamoxifen from recipients that were reconstituted with XS- or XL-sized G0/1 donor HSCs from RB+/+;R26-cre or RB+/−;R26-cre mice (n ≥ 3).
mitochondrial concentration (Fig. 6A), reactive oxygen species (ROS) concentration (Fig. 6B), and transcript concentration of mitochondrial genes (fig. S6C), while mitochondrial fission (43) was not affected (fig. S6A). Liquid chromatography–mass spectrometry (LC-MS) revealed that Go/1 XL HSCs harbored significantly lower levels of ATP than XS-sized HSCs (Fig. 6D). Last, we found that 40% of GO gene sets associated with the IFN response were lower in XL HSCs compared to smaller HSCs but not significantly different between smaller HSCs (XS and M) using a relaxed functional filter (q value = 0.5; fig. S6B). Thus, when evaluating the concentration of energy-related factors, our data suggest that large HSCs do not exhibit characteristics of an activated state.

(iv) Protein synthesis capacity

Enlarged cultured primary human cells experience decreased protein synthesis rates and ribosome loss that leads to cytoplasm dilution (12, 44). To assess protein synthesis capacity in naturally large HSCs, we measured nucleolar size as this often correlates with ribosomal RNA synthesis and ribosome biogenesis (45, 46). Nucleolar size scaled with HSC size (fig. S6, C and D), suggesting that ribosome biogenesis does not decline in large HSCs. Consistent with this conclusion, cell density, to which ribosomes are a contributor (44), was not affected in large HSCs either (fig. S6E). Furthermore, mTOR activity (phosphorylated S6 levels) and protein synthesis in vivo (47) were not affected by cell size (fig. S6, F and G). Last, we measured the nucleus:cytoplasm ratio (C/V) of differently sized HSCs. We found that larger HSCs tended to display a lower C/V (fig. S6H). In summary, our characterization of naturally large and PD-enlarged HSCs indicates that large size primarily interferes with the ability of HSCs to proliferate and to maintain a functional metabolic state.

Large size decreases the colony-forming potential of intestinal stem cells

Does cell size also affect the proliferation potential of other adult stem cell types? To address this question, we used Lgr5-GFP knock-in mice to isolate intestinal stem cells (ISCs), which can be distinguished from transient amplifying cells by a twofold or higher intensity of Lgr5-GFP (fig. S7, A and B). We isolated the smallest 15% of ISCs, the largest 15%, and the mean-sized population ± 15% using the forward scatter as a measure of cell size (fig. S7C). Cell volume measurements confirmed that this method distinguished ISCs by their size (fig. S7D). Furthermore, like naturally large HSCs, XL ISCs harbored more DNA damage than smaller ones (fig. S7E). They also shared other characteristics with XL HSCs. They exhibited a reduced ability to form intestinal organoids (fig. S7F), a colony formation assay for ISCs. Among all the differently sized ISCs, XL ISCs displayed the highest intensity of Lgr5-GFP (fig. S7G), suggesting that the colony-forming defect observed in XL ISCs was not due to them having differentiated into Lgr5low progenitors. We conclude that, like in HSCs, DNA damage is associated with an increase in ISC size and a decrease in colony-forming potential.

Reducing the size of large HSCs restores their reconstitution potential

Our results indicate that preventing HSC enlargement with rapamycin during DNA damage or during high frequency of cell division preserves HSC fitness. To robustly test whether HSC size and fitness are causally connected, we modulated HSC size by means other than rapamycin treatment. We shortened G1.

Inactivation of the S-phase entry inhibitor Rb accelerates progression through G1 and reduces cell size (48). We hypothesized that reducing the size of large HSCs by reducing Rb levels improves HSC fitness. To reduce Rb levels in HSCs, we used mice that were heterozygous for an excisable Rb allele (Rb+/−;R26-creERT2). We first sublethally irradiated mice and allowed HSCs to enlarge for 7 days (fig. 7, A and B). We then excised one Rb allele by administering tamoxifen for another 7 days. Loss of one copy of Rb indeed led to decreased cell size after irradiation (fig. 7B). To determine whether reducing the size of previously enlarged HSCs improved their reconstitution potential, we transplanted these irradiated HSCs into recipients (fig. 7C). This analysis revealed that the lack of one Rb copy affected the fitness of previously irradiated, large HSCs: Irradiated Rb+/− HSCs built 15% of the blood cells of reconstituted animals, whereas irradiated Rb+/+ HSCs contributed only 5%, which is consistent with our hypothesis that DNA-damaged and Rb-deficient HSCs divide more (fig. S8A) (49). During the reconstitution, these irradiated Rb+/− HSCs were smaller in size than irradiated Rb+/+ HSCs (fig. 7D). We conclude that reducing cell size improves the reconstitution potential of irradiated HSCs.

Does reducing the size of naturally large HSCs also restore their reconstitution potential? To address this, we transplanted XL-sized Rb+/−;R26-creERT2 HSCs. Fourteen days after transplantation, we treated animals with tamoxifen to excise one copy of the Rb gene (Fig. 7E). This not only reduced the size of XL HSCs but also significantly increased the ability of XL HSCs to build the hematopoietic compartment of recipients. RB+/− HSCs formed 47% of blood cells in recipients, whereas RB+/+ HSCs contributed only 23% (Fig. 7, F and G). Tamoxifen itself had no significant effect on HSC fitness (fig. S8B). Consistent with increased reconstitution potential, RB-excised XL HSCs more readily entered the cell cycle (fig. S8C). RB removal did not improve HSC fitness of small or control HSCs (Fig. 7F) (50), indicating that lack of Rb does not improve HSC function per se but restores fitness of large HSCs by reducing their size. We conclude that the reduced fitness of naturally large HSCs can be improved by reducing their size. Our data demonstrate that HSC size is an important determinant of their in vivo fitness.

HSC enlargement contributes to their functional decline during aging

Like many other stem cells, the function of HSCs declines with organismal age with HSCs losing their ability to regenerate the hematopoietic system (51). Large HSCs share many of the characteristics of cellular aging: loss of stem cell potential, loss of proliferative abilities, up-regulated expression of genes associated with aging (fig. S9A), increased DNA damage, and enlarged nucleoli (42, 52). On the basis of these observations, we hypothesized that HSCs enlarge in vivo as mice age. We analyzed HSC size in a mouse strain that experiences cellular aging: loss of stem cell potential, loss of proliferative abilities, up-regulated expression of genes associated with aging (fig. S9A), increased DNA damage, and enlarged nucleoli (42, 52). On the basis of these observations, we hypothesized that HSCs enlarge in vivo as mice age. We analyzed HSC size in a mouse strain that experiences HSC decline at a younger age (D2) and in the BL/6 strain, in which HSC decline occurs later in life. HSCs were larger in old D2 (32 weeks), BL/6 middle-aged (56 to 65 weeks), and BL/6 old (86 to 102 weeks) animals compared to younger mice (8 weeks; Fig. 8, A and B). This size difference was neither due to changes in cell cycle distribution (fig. S9, B and C) nor associated with changes in SA-β-gal activity (fig. S9D). As in response to irradiation, only a fraction of HSCs became enlarged, as judged by a broadening of the size distribution (D2 and BL/6; fig. S9E). One interpretation of this observation is that this change in cell size distribution is due to stochastic cellular damage that occurs naturally as some HSCs divide during aging.
while most other HSCs stay quiescent or do not experience damage during cell division (53).

To determine whether cellular enlargement contributed to the fitness decline of HSCs from aged mice, we prevented HSC enlargement during organismal aging. We treated young D2 and BL/6 mice from week 8 with rapamycin and found that aging-induced HSC enlargement was prevented (Fig. 8, A and B). These small-old D2 HSCs proliferated more and formed more colonies in vitro compared to large-old D2 HSCs (Fig. 8C and fig. S9F). Rapamycin also preserved the reconstitution potential of old BL/6 HSCs. HSCs obtained from middle-aged or old BL/6 mice that were kept small by rapamycin treatment (Fig. 8B) were more effective in reconstituting lethally irradiated recipients than old-enlarged HSCs (Fig. 8, D and E, and fig. S9G). Rapamycin had no effect on the fitness of HSC from young mice (Figs. 1C and 2C) or on in vivo differentiation (fig. S9H). In secondary transplantations, this result remained as a trend (fig. S9I). These data indicate that HSC enlargement contributes to the fitness decline of HSCs during aging. However, rapamycin was not able to reverse HSC enlargement and age-induced loss of stem cell fitness. When we treated old animals (week 77 onward) for 2 to 3 months with rapamycin, we did not observe a reduction in HSC size (fig. S9J) or recovery in HSC reconstitution potential (fig. S9K). This observation further indicates that rapamycin does not improve HSC fitness per se but that its long-term effects on cell growth and size mediate preservation of HSC fitness. Our data suggest that HSC enlargement contributes to their functional decline during aging.

Last, we observed a similar relationship between cell size and aging in human HSCs (Lin−, CD34+, CD90+, CD38−, CD45RA−,
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and ±CD49f). HSCs were larger in 51- to 62-year-old individuals compared to 21- to 25-year-old individuals (Fig. 9, A and B). Old-large human HSCs also exhibited a decreased ability to form colonies in vitro and to form multicellular lineages upon differentiation (Fig. 9, C and D). We conclude that HSC enlargement during aging contributes to their functional decline in mice and humans.

**DISCUSSION**

**Large cell size causes a decline in stem cell function**

Stem cells are innately small in size. Here, we show that size maintenance is important for the function of HSCs and probably also for other stem cell types. Conditions known to reduce stem cell potential—DNA damage and successive cell proliferation—cause an increase in HSC size. Two lines of evidence indicate that cell size affects HSC function: (i) Preventing HSC enlargement during insults such as DNA damage, aging, and consecutive divisions protects HSCs from losing their stem cell potential and (ii) reducing the size of large HSCs improves their fitness.

Our data provide an explanation for why HSCs and ISCs are small. While this has been largely unexplored for other stem cell types, there are some reports showing that cell types displaying characteristics of stem cells are small in size (54–56). Thus, it is likely that mechanisms connecting cellular size with function are conserved in other stem cell types as well.

A key question regarding our findings is whether large HSCs are truly stem cells that have lost their stem cell potential or whether enlargement reflects a partially differentiated cellular state, in which multipotency had become restricted. We find that naturally and artificially enlarged HSCs are indistinguishable from smaller HSCs in their ability to home to the BM niche and to differentiate into the various hematopoietic lineages in vitro and in vivo. The perhaps most compelling evidence that large HSCs are true stem cells is the observation that reducing the size of naturally large or irradiated HSCs improved their reconstitution potential.

It is important to note that, in response to DNA damage, proliferation challenge, and aging, not all HSCs increase in size, but the size distribution of HSCs widens. This indicates that only a subpopulation of HSCs enlarges during these challenges. We propose that this subpopulation is composed of HSCs that experienced DNA damage during irradiation and have divided more often during proliferation challenge and aging. A history of divisions increases the likelihood of HSCs to have experienced DNA damage that caused cell cycle arrest and hence cellular enlargement. Most other HSCs are quiescent. Their size will not be affected by insults such as DNA damage because mTOR activity is low during quiescence (57).

Our analysis of naturally large HSCs also revealed that they do not return to a smaller cell size when induced to proliferate during reconstitution assays. At first glance, this result appears unanticipated. Several studies suggest that within their physiological size range, cells enter the cell cycle when they have reached a cell type–specific cell size, known as the critical size. When cells enlarge during cell cycle arrest, the subsequent G1 is shortened and two smaller daughter cells are born (58–64). We hypothesize that this return to a smaller cell size only occurs when enlargement during cell cycle arrest does not exceed the critical size. When HSCs enlarge during prolonged cell cycle arrest beyond their critical cell size, restoration of the physiological size is no longer possible. In other words, they cannot shrink back to their natural size. This is consistent with studies observing a size increase over successive divisions (9, 13, 14, 65). Our data also indicate that HSCs do not grow in size indefinitely. Perhaps HSCs have an upper size limit, beyond which they die or faithful size homeostasis occurs at a different size set point. However, it is clear from earlier studies that once cells become exceedingly large as occurs in cultured cells during senescence, multiple cellular processes, foremost cell division, fail (12, 16). Our results suggest that the size window, in which HSCs function physiologically, is small. Increasing HSC size by as little as 5 to 15% leads to a decline in fitness.

**Causes of fitness decline in large HSCs**

Our results indicate that in vitro proliferation capacity of HSCs is affected by large size. Given that cell proliferation is crucial for HSCs to rebuild the hematopoietic system of lethally irradiated mice, it is likely that reduced proliferative capacity is, at least in part, responsible for reduced fitness of large HSCs in vivo. We note the option that an underlying cause of cell size, rather than cell size itself, is...
responsible for reduced HSC fitness. Our previous work indicates that it is not the physical size of large cells that causes their reduced fitness, but rather the ensuing change in ratio of DNA to cytoplasm. Cellular enlargement in the absence of a corresponding increase in DNA content leads to a decrease in DNA:cytoplasm ratio. The concentration of unstable proteins decreases when this occurs in budding yeast (12). In naturally large HSCs, protein synthesis capacity and cell density of the whole cell are not changed, yet their fitness is decreased. HSCs have a very small cytoplasmic volume compared to their nuclear volume and, with enlargement, their DNA:cytoplasm ratio slightly decreases. As a result, loss of unstable proteins specifically in the cytoplasm might contribute to some degree to impaired fitness upon enlargement. This is consistent with the observation that protein synthesis rates in HSCs must be tightly controlled (66). The observation that rapamycin treatment suppresses the fitness decline of HSCs during DNA damage further raises the possibility that mTOR-regulated processes besides cell growth, such as autophagy, or mitochondrial and lysosome function (2) influence HSC fitness during aging. Last, while HSCs are able to scale mitochondrial and potentially other stem cells from aging. However, rapamycin prevents the enlargement of HSCs and thereby protects them and potentially other stem cells from aging. However, rapamycin does not restore HSC function once they are large. We predict that compounds that revert cellular enlargement and hence reduce the size of already enlarged stem cells warrant further exploration as potential antiaging therapies.

MATERIALS AND METHODS
Please find detailed description of materials and methods in the Supplementary Materials.

Mice
All work was performed in accordance with the Massachusetts Institute of Technology (MIT) Institutional Animal Care Facility and with guidelines at MIT (Institutional Animal Care and use committee) (protocol numbers 0715-073-18 and 0718-053-21). Mice were purchased from Jax Laboratories or as indicated: B6.SJL-Ptprc<sup>Pepec</sup>/B6j (#002014), C57BL/6J (#006664), DBA/2 J (D2) (JAX #00671, Charles River Laboratories #026), Lgr5-EGFP-IRES-CreERT2 (#008875), K67<sup>RE</sup> knock-in; (#029802) Rosa26CreERT2;Tg<sup>Ly-6a</sup> (#005680 and #008463), Rosa26CreERT2;Rosa26Ly-6a (#026563 and #008463), and R26-tTA tetO-H2B-GFP (#005104 and #006965).

HSC isolation and measurements
Murine BM-derived HSCs were isolated as described previously (69). The following antibodies from were used: Rat monoclonal phycoerhthrin (PE) (phycoerythrin)/Cy7 anti-mouse CD150, BioLegend, catalog no. 115913 [RRID (Research Resource Identifiers): AB_439796]; Rat monoclonal PE anti-mouse CD150, BioLegend, catalog no. 115904 [RRID (Research Resource Identifiers): AB_313683]; Armenian hamster monoclonal BV421 anti-mouse CD48, BioLegend, catalog no. 103427; (RRID (Research Resource Identifiers): AB_10895922); Armenian hamster monoclonal Allophycocyanin (APC)/Cy7 anti-mouse CD48, BioLegend, catalog no. 103431 [RRID (Research Resource Identifiers): AB_2516462]; Rat monoclonal PE/Cy7 anti-mouse Ly-6A/E, BioLegend, catalog no. 108114 [RRID (Research Resource Identifiers): AB_493596]; Rat monoclonal APC anti-mouse CD117, BioLegend, catalog no. 105812 [RRID (Research Resource Identifiers): AB_313221]; Rat monoclonal PE anti-mouse CD150, BD Biosciences, catalog no. 562651 [RRID (Research Resource Identifiers): AB_2737705]; Rat monoclonal fluorescein isothiocyanate (FITC) anti-mouse Ly-6A/E, BD Biosciences, catalog no. 562058 [RRID (Research Resource Identifiers): AB_10898185]; Rat monoclonal PE/Cy7 anti-mouse Ly-6A/E, BioLegend, catalog no. 108114 [RRID (Research Resource Identifiers): AB_493596]; Rat monoclonal PE/Cy5 anti-mouse CD150, BioLegend, catalog no. 115911 [RRID (Research Resource Identifiers): AB_493599]; Armenian hamster monoclonal FITC anti-mouse CD48, BioLegend, catalog no. 103404 [RRID (Research Resource Identifiers): AB_313019]; and Rat monoclonal APC anti-mouse CD117, BD Biosciences, catalog no. 561074 [RRID (Research Resource Identifiers): AB_10563203].

Human BM samples were purchased from AllCells, whose guidelines follow strictly the need for informed consent. HSCs were purified as described previously (70). The following antibodies were used: Mouse APC anti-human Lineage Cocktail (CD3, CD14, CD16, CD19, CD20, and CD56), BioLegend, catalog no. 348803; Mouse monoclonal FITC anti-human CD90, BD Biosciences, catalog no. 561969 [RRID (Research Resource Identifiers): AB_10895382]; Rat monoclonal PE-Cy5 anti-human CD49f, BD Biosciences, catalog no. 551279 [RRID (Research Resource Identifiers): AB_394062]; Mouse monoclonal PE-Cy7 anti-human CD45RA, BD Biosciences, catalog no. 560675 [RRID (Research Resource Identifiers): AB_1727498]; and Mouse monoclonal PE anti-human CD38, BD Biosciences, catalog no. 342371 [RRID (Research Resource Identifiers): AB_400453].

Cell cycle stage analysis
A total of 10<sup>6</sup> BM cells/ml in prewarmed Iscove's modified Dulbecco's medium (IMDM) with 2% fetal bovine serum and Hoechst-33342 (6.6 μg/ml) were incubated at 37°C in a water bath. To distinguish...
between G₀ and G₁ HSCs, we took advantage of transgenic Kit67-RFP mice and analyzed HSCs that were stained with Hoechst-33342 as described above using flow cytometry. Vybrant DyeCycle Violet Stain (Thermo Fisher Scientific, #V350003) was used at 5 µM per 10⁶ cells/ml incubating cells at room temperature for 30 min. For in vivo proliferation studies, 1.25 mg of EdU was injected intraperitoneally into mice 24 hours before sacrifice. EdU incorporation into the DNA of HSCs was evaluated according to the manufacturer’s instructions with the Click-it EdU Alexa Fluor 488 Imaging Kit.

**HSC volume measurements**

Size of HSCs was determined using a Multisizer-3 Coulter Counter (Beckman Coulter) or as indicated. The forward scatter (FSC-A) was used to isolate HSCs of a specific size (XS, M, and XL).

**Reconstitution and homing assays**

Reconstitution and homing assays were performed as described previously (69) using live HSCs (C57BL/6 J and CD45.2) combined with 420,000 B6.SJL (CD45.1) supporting white blood cells per mouse. Peripheral blood from recipient mice was depleted of red blood cells using Ammonium-Chloride-Potassium (ACK) buffer then incubated with the following: Mouse monoclonal PE anti-mouse CD45.1, BioLegend, catalog no. 109806 (RRID: AB_313443); Rat monoclonal FITC anti-mouse CD45.2, BioLegend, catalog no. 109806 (RRID: AB_313443); Rat monoclonal BV421 anti-mouse Ly-6G and Ly-6C, BD Biosciences, catalog no. 562709 (RRID: AB_2737736); Rat monoclonal BV421 anti-mouse CD11b, BD Biosciences, catalog no. 562605; (RRID: AB_11152949); Rat monoclonal BV421 anti-mouse CD45RB220, BD Biosciences, catalog no. 562922 (RRID: AB_2737894); Hamster monoclonal BV421 anti-mouse CD3e, BD Biosciences, catalog no. 562600 (RRID: AB_11153670).

Homing assays were performed as reconstitution experiments, except that 6000 to 8000 donor HSCs were injected. The percentages of donor HSCs in the bone in relation to recipient BM cells were determined 21 hours after reconstitution.

**RNA isolation**

HSCs were sorted into 750 µl of TRIzol LS. To extract RNA, 200 µl of chloroform was added to the sample and briefly vortexed at medium speed. The sample was centrifuged at 12,000 × g for 15 min. Four hundred microliters of the aqueous phase was re-
mixed and put into 1400 µl of diethyl pyrocarbonate water. Then, the Clontech v4 Low-Input RNA Kit was used for the PolyA library prep. RNA-seq data were aligned to the mm10 mouse genome assembly and the ensemble version 88 annotation with STAR version 2.5.3a and gene expression was summarized with RSEM version 1.3.0 (71).

**RNA-seq analysis**

Expression data were analyzed using two different data sets: (i) all human GO gene sets MSigDB version 7.1 and (ii) mouse gene categories of HSCs based on previous studies (33–40).

Differentially expressed genes were defined as those having an absolute log₂ fold change greater than 1 and a false discovery rate–adjusted P value of less than 0.05 (q value). DESeq2 and edgeR version 3.4.4 programs were used to perform principle components analysis. Data parsing and clustering were performed using TIBCO Spotfire Analyst 7.6.1. Mouse genes were mapped to human orthologs using Preranked. GSEA analysis was performed using javaGSEA version 2.3.0. Preranked GSEA (version 4.0.3) was run using the DESeq2 Wald statistic as ranking metric and human gene symbols with the MSigDB of the C5 GO gene sets.

**In vitro cultivation of murine and human HSCs**

Murine or human HSCs were resuspended in complete MethoCult GF M3434 medium or MethoCult H4435 Enriched (STEMCELL Technologies), grown at 37°C in a 5% CO₂ chamber, was monitored until colonies were visible (7 and 21 days, respectively). Number of colonies and colony type were quantified manually.

**Measurements of single-cell density and volume using a suspended microchannel resonator**

HSCs were isolated as detailed above and cultured ex vivo for 2 days in expansion medium (StemSpan SFEM, #09600 supplemented with cytokines). Single-cell density and volume measurements were carried out using the suspended microchannel resonator, as detailed previously (72, 73).

**Intestinal crypt isolation and organoid formation assay of ISCs**

Isolation of ISCs was previously reported (74). ISCs were sorted by flow cytometry into crypt culture medium, a modified form of medium as described previously (74). Isolated ISCs and Paneth cells were then mixed (1:1 ratio, 200 cells each) and seeded onto Matrigel (Corning, 356231 growth factor reduced) containing 1 µM JAG-1 protein (AnaSpec, AS-61298). Organoid-forming capacity of the sorted ISCs was quantified after 3 to 5 days of culture. Each frequency was quantified by n > 100 cells per view and n = 3 views per sample.

**Drug and irradiation treatments**

PD (30.4 mg/kg body weight), rapamycin (6.4 mg/kg body weight), or vehicle was intraperitoneally injected every 48 hours for the indicated treatment time. Mice were treated from week 8 with rapamycin every 3 days until week 102. The Cre-recombinase was activated via tamoxifen intraperitoneal injection of 2 mg/100 µl per dose.

**Fluorescence assays**

For immunofluorescence analyses, slides were primed with 0.1% polylysine and HSCs incubated for 1 hour. HSCs were fixed, permeabilized, and blocked using 10% donkey serum. Cells were incubated with primary antibody: anti–phospho-S6 ribosomal protein (Ser240/244) rabbit monoclonal antibody (Cell Signaling Technology, catalog no. 5364; RRID: AB_10694233), anti–P-Ser 139 H2AX (1:100; Cell Signaling Technology, catalog no. 2577; RRID: AB_211801), or anti–Drp1 (1:100; Abcam, catalog no. ab56788, RRID: AB_941306). The secondary antibody solution (1:500; goat anti-rabbit Alexa Fluor 488, Cell Signaling Technology, 4412S and 1:500 goat anti-mouse Alexa Fluor 488, Invitrogen, A-10680) was added for 1 hour. Coverslips were mounted with ProLong Gold Antifade Reagent (Invitrogen, Molecular Probes). Images were acquired using a DeltaVision Elite microscope (Applied Precision) platform.
Asterisks indicate $P$ values: $**P < 0.0001$, $***P < 0.001$, $**P < 0.01$, and $*P < 0.05$; NS, not significant. For all panels, statistical significance was calculated using unpaired $t$ test to compare two samples, one-way analysis of variance (ANOVA), multiple comparison, and Tukey’s post hoc test to compare multiple (three or more) samples or otherwise specified. Values were only excluded if the most extreme value in the dataset was a significant outlier from the rest ($P < 0.05$) according to Grubbs’ test. No statistical method was used to predetermine sample size. The RNA-seq data are available from the Gene Expression Omnibus under accession number GSE154335. All other data supporting the findings of the study are available from the corresponding author upon request.

**SUPPLEMENTARY MATERIALS**

Supplementary material for this article is available at https://science.org/doi/10.1126/sciadv.abk0271

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Cell size is a determinant of stem cell potential during aging

Jette LengefeldChia-Wei ChengPema MaretichMarguerite BlairHannah HagenMelanie R. McReynoldsEmily SullivanKyra MajorsChristina RobertsJoon Ho KangJoachim D. SteinerTeemu MiettinenScott R. ManalisAdam AntebiSean J. MorrisonJacqueline A. LeesLaurie A. BoyerÖmer H. YilmazAngelika Amon

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