



Hepcidin as a therapeutic tool to limit iron overload and improve anemia in β -thalassemic mice

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Excessive iron absorption is one of the main features of β -thalassemia and can lead to severe morbidity and mortality. Serial analyses of β -thalassemic mice indicate that while hemoglobin levels decrease over time, the concentration of iron in the liver, spleen, and kidneys markedly increases. Iron overload is associated with low levels of hepcidin, a peptide that regulates iron metabolism by triggering degradation of ferroportin, an iron-transport protein localized on absorptive enterocytes as well as hepatocytes and macrophages. Patients with β -thalassemia also have low hepcidin levels. These observations led us to hypothesize that more iron is absorbed in β -thalassemia than is required for erythropoiesis and that increasing the concentration of hepcidin in the body of such patients might be therapeutic, limiting iron overload. Here we demonstrate that a moderate increase in expression of hepcidin in β -thalassemic mice limits iron overload, decreases formation of insoluble membrane-bound globins and reactive oxygen species, and improves anemia. Mice with increased hepcidin expression also demonstrated an increase in the lifespan of their red cells, reversal of ineffective erythropoiesis and splenomegaly, and an increase in total hemoglobin levels. These data led us to suggest that therapeutics that could increase hepcidin levels or act as hepcidin agonists might help treat the abnormal iron absorption in individuals with β -thalassemia and related disorders.

Introduction

β -thalassemia is one of the most common congenital anemias arising from partial or complete lack of β -globin synthesis. β -thalassemia major, also known as Cooley anemia, is the most severe form of this disease and is characterized by ineffective erythropoiesis (IE) and extramedullary hematopoiesis (EMH) in the liver and spleen. Patients require regular blood transfusions to sustain life (1). In the milder form, termed β -thalassemia intermedia, blood transfusions are not always necessary, yet iron overload still occurs due to progressive iron absorption from the gastrointestinal tract (2). In β -thalassemia intermedia patients, studies show that the rate of iron absorption from the gastrointestinal tract is approximately 3 to 4 times greater than normal, varying between 2 and 5 g per year depending on the severity of erythroid expansion (1). Regular transfusions may double the rate of iron accumulation. In these patients, IE often worsens over time, exacerbating anemia, iron absorption, and splenomegaly (3). Increased gastrointestinal iron absorption may also play a role in transfused β -thalassemia major patients, increasing when hemoglobin (Hb) levels decrease (4). Progressive iron overload affects multiple organs and is the primary cause of death in patients with β -thalassemia syndromes (1).

The *th3/+* mouse, a model of β -thalassemia, harbors a heterozygous deletion of β^{minor} and β^{major} genes (5, 6) and exhibits

features comparable to those of patients affected by β -thalassemia intermedia, including Hb levels between 7 and 9 g/dl (5–7), IE, EMH, increased production of immature erythroid cells, aberrant erythrocyte morphology, and hepatosplenomegaly. Serum iron, transferrin (Tf) saturation, and nontransferrin-bound iron (NTBI) levels are elevated in *th3/+* mice (8). Iron accumulates primarily in the spleen and in the Kupffer cells of the liver. The Hb levels in *th3/+* mice decrease with time, while the spleen size, the number of nucleated erythroid cells, and the ratio of liver to spleen iron all increase (8). Thus, over time these mice exhibit some of the features associated with the most severe forms of the disease.

Hepcidin (HAMP) (9, 10), a peptide produced in the liver, regulates iron metabolism by triggering the degradation of ferroportin (FPN1) (11), an iron-export protein localized on absorptive enterocytes, hepatocytes, and macrophages. Altered expression of hepcidin is responsible for the modifications of iron metabolism that characterize several diseases, including β -thalassemia (8, 12). *th3/+* mice have relatively low hepatic *Hamp1* expression, suggesting that insufficient hepcidin may be responsible for the high iron levels in these mice (8, 13, 14). Similarly, low HAMP levels have been measured in the urine of patients with β -thalassemia (15), further supporting this hypothesis.

The iron absorbed by patients with β -thalassemia intermedia or *th3/+* mice is excessive relative to the amount of iron needed to maintain a Hb of 9 g/dl (2, 3, 8). In this case, liver parenchymal cells store the surplus iron. Therefore, we postulate that (a) limiting the dietary

Conflict of interest: The authors have declared that no conflict of interest exists.

Citation for this article: *J Clin Invest.* 2010;120(12):4466–4477. doi:10.1172/JCI41717.

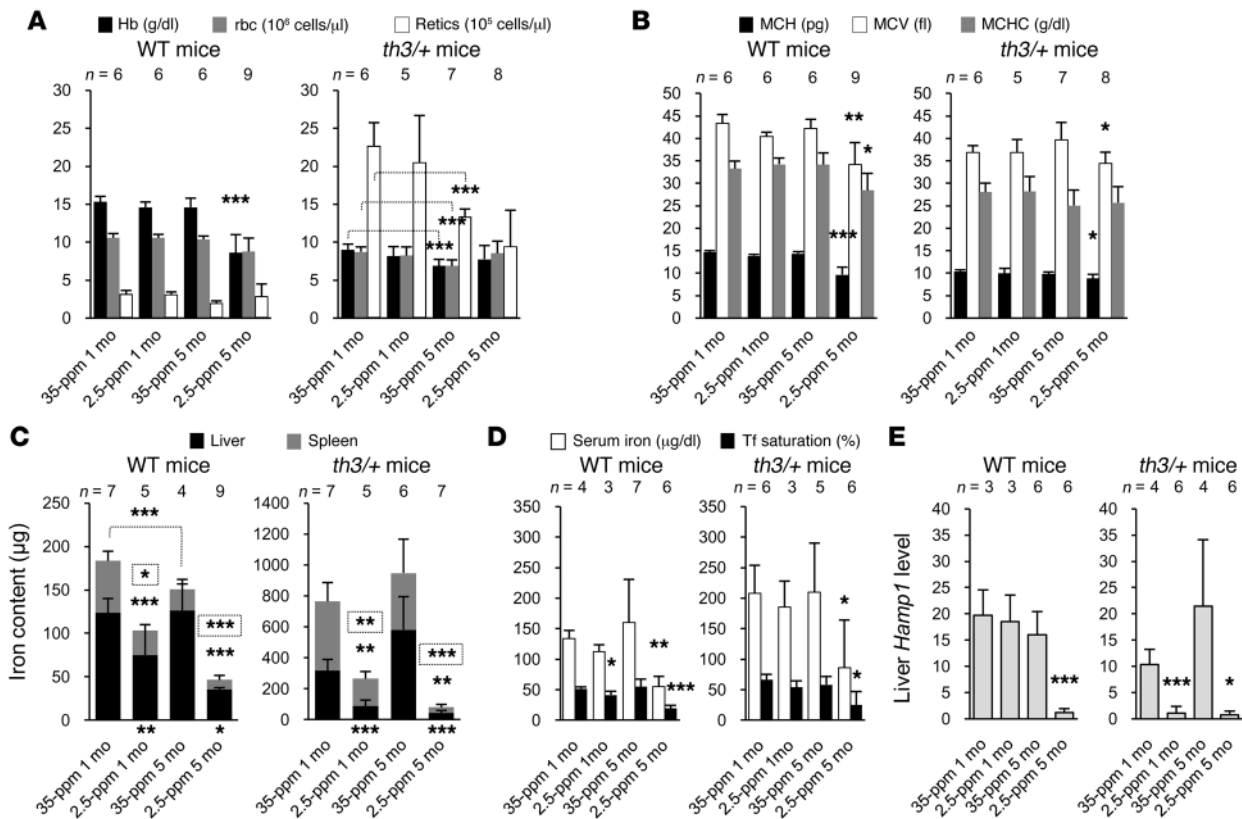


Figure 1

Hematological and iron-related parameters in groups of WT and *th3/+* mice fed diets with 35 and 2.5 ppm iron for 1 or 5 months. Complete blood counts show (A) the Hb, rbc, and reticulocyte values, and the (B) MCH, MCV, and MCHC values. The figure also shows (C) total iron content of liver and spleen as measured by atomic absorption, (D) serum iron concentration and Tf saturation, and (E) *Hamp1* mRNA expression levels relative to mouse *Gapdh*, obtained by Q-PCR of the liver using primers specific for mouse *Hamp1*. Error bars represent SD. *P* values were calculated using unpaired, 2-tailed Student's *t* test. **P* < 0.05; ***P* < 0.01; ****P* < 0.001. Groups of mice on the 2.5-ppm diet were compared with corresponding groups on the 35-ppm diet fed for the same length of time unless otherwise indicated by brackets. In C, *P* values relative to comparisons between spleens are above the columns, while those between the livers are under the x axis. *P* values in the small rectangles above the columns refer to the total iron content of liver and spleen.

iron intake of *th3/+* mice would decrease organ iron with no effect on erythropoiesis, and that (b) similar results could be achieved by limiting dietary iron intake via increased *Hamp1* expression.

Since Fpn1 is also localized on macrophages, upregulation of *Hamp1* in normal mice affects both dietary iron absorption and the recycling of iron, resulting in modified erythropoiesis (16). Therefore, the upregulation of *Hamp1* in *th3/+* mice could also affect iron recycling and its availability for erythropoiesis, ultimately worsening their anemia. Since endogenous hepcidin in *th3/+* mice is low relative to the amount of liver iron available for erythropoiesis (8), moderate hepcidin supplementation might limit iron absorption without interfering with the release of iron for erythropoiesis. Thus, the therapeutic benefit would depend upon the level of *Hamp1* achieved. To address these questions, we analyzed normal and *th3/+* mice overexpressing *Hamp1* at different levels and compared them with mice maintained on an iron-deficient diet (2.5 ppm). In the latter group of mice, egress of iron from macrophages was not expected to be altered since *Hamp1* is extremely low under conditions of iron deficiency (17).

Here we show that reducing iron intake in *th3/+* mice by feeding a low-iron diet supports our first hypothesis, indicating that they absorb far more iron than is required to sustain erythropoiesis. Our

second hypothesis is supported by the fact that *th3/+* mice overexpressing *Hamp1* exhibit not only reduced organ iron overload but also a remarkable amelioration of their anemia and IE. Thus, our study reveals a potential role for *Hamp1* or *Hamp1* agonists in the development of new pharmacological approaches to treating the abnormal iron absorption in β -thalassemia and related disorders.

Results

Low dietary iron intake markedly affects erythropoiesis in normal mice. WT and *th3/+* mice were generated by breeding and by engraftment of WT and *th3/+* HSCs into normal mice after complete myeloablation (8). Using the engraftment of HSCs instead of breeding, we were able to obtain a larger number of mice for analysis in a shorter time. Here we present the results obtained using transplanted mice, there being no major differences observed between *th3/+* mice on diets containing 35 and 2.5 ppm iron generated by the 2 methods (Supplemental Figure 1; supplemental material available online with this article; doi:10.1172/JCI41717DS1).

A commercial rodent diet contains 200 ppm iron, more than necessary for normal physiological requirements. Therefore, we investigated defined diets containing either 35 ppm iron (iron-suf-

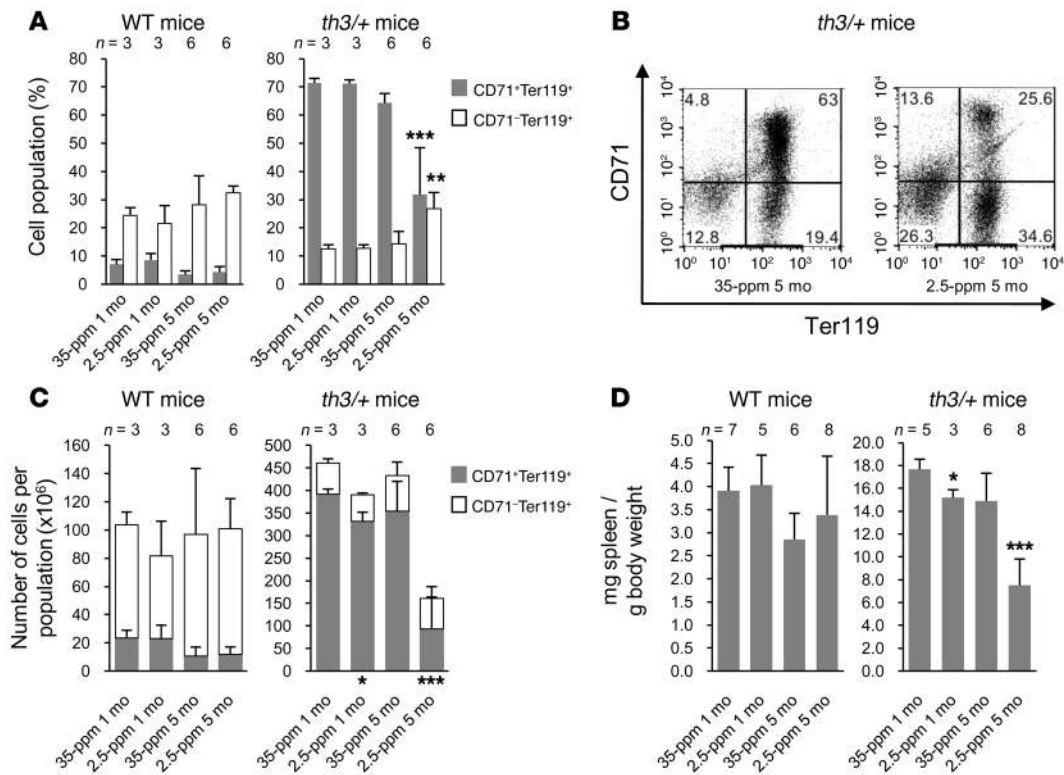


Figure 2

Effects of dietary iron on the size of the spleen (normalized to body weight) and the percentage of mature and immature erythroid cell populations in the spleens of WT and *th3/+* mice. (A) FACS analysis performed on splenic erythroid cells using CD71 (Tf receptor) and Ter119 (erythroid-specific) containing. The graphs indicate the percentages of early erythroid precursors (CD71⁺Ter119⁺), which correspond mainly to basophilic erythroblasts and late basophilic and chromatophilic erythroblasts, and those of mature erythroid cells (CD71⁻Ter119⁺), including both enucleated erythroid cells and orthochromatic erythroblasts. (B) FACS analysis of spleen cells from 2 representative *th3/+* mice fed the 35-ppm (left panel) and 2.5-ppm (right panel) diets. (C) Number of CD71⁺Ter119⁺ and CD71⁻Ter119⁺ cells in the spleen. (D) Spleen weights normalized to body weight. Groups of mice on the 2.5-ppm diet were compared with the corresponding groups on the 35-ppm diet fed for the same length of time. **P* < 0.05; ***P* < 0.01; ****P* < 0.001. Data are presented as mean ± SD.

cient diet) or 2.5 ppm iron (low-iron diet). No statistical differences were observed in tissue iron levels or parameters pertaining to erythropoiesis between WT and *th3/+* mice fed the 35-ppm diet or mice fed the commercial diet for up to 5 months. Thus, we used the 35-ppm diet as our control diet.

After 1 month, the hematological values of WT mice fed the 35- and 2.5-ppm iron diets were similar (Figure 1, A and B) and essentially identical to those of mice analyzed on standard commercial diet (not shown). However, the amount of iron in the livers and spleens of WT mice fed the 2.5-ppm diet was reduced compared with mice fed the 35-ppm diet (Figure 1C). The serum iron levels were not significantly different from those of controls, although the corresponding Tf saturations were reduced (Figure 1D) with increased serum erythropoietin (Epo) levels (Supplemental Figure 2A).

After 5 months, WT mice fed the 35-ppm diet did not show any hematological changes (Figure 1, A and B) and exhibited a decrease in the total amount of iron in the spleen (Figure 1C) compared with mice analyzed at 1 month. The iron in the kidneys and heart was reduced (Supplemental Figure 3, A and B). Mice fed the 2.5-ppm diet for 5 months, however, exhibited a dramatic decrease in Hb, mean cell Hb (MCH), mean corpuscular volume (MCV), and mean corpuscular Hb concentration (MCHC) levels (Figure 1, A and B).

Serum iron levels and Tf saturation were reduced (Figure 1D). In addition, *Hamp1* expression was extremely low (Figure 1E), while Epo levels were increased (Supplemental Figure 2A).

FACS analysis showed that there were no statistically significant differences in the percentages or absolute numbers of immature (CD71⁺Ter119⁺) and mature (CD71⁻Ter119⁺) erythroid progenitor cells in the spleen (Figure 2, A and C) or BM (not shown) of WT mice on either the 2.5- or 35-ppm diet for 1 and 5 months. In summary, this analysis indicated that WT mice on an iron-restricted diet exhibit reduced Hb and rbc synthesis.

Low dietary iron intake positively affects erythropoiesis while reducing tissue iron levels in th3/+ mice. As in the case of normal mice, the hematological values of *th3/+* mice fed the 35- and 2.5-ppm iron diets for 1 month were similar (Figure 1, A and B) and identical to those of mice analyzed on a standard commercial diet (not shown). As in WT mice, a reduction was seen in the amount of iron in the liver and spleen (Figure 1C) and also in the kidneys and heart (Supplemental Figure 3, A and B) of the mice fed the 2.5-ppm diet. The serum iron levels and Tf saturation of *th3/+* mice fed the 2.5-ppm iron diet were unchanged relative to controls (Figure 1D). Epo levels were increased (Supplemental Figure 2A) and *Hamp1* expression was reduced in the *th3/+* mice fed the 2.5-ppm diet (Figure 1E). This suggests that *Hamp1* expression is more sensitive to the sup-

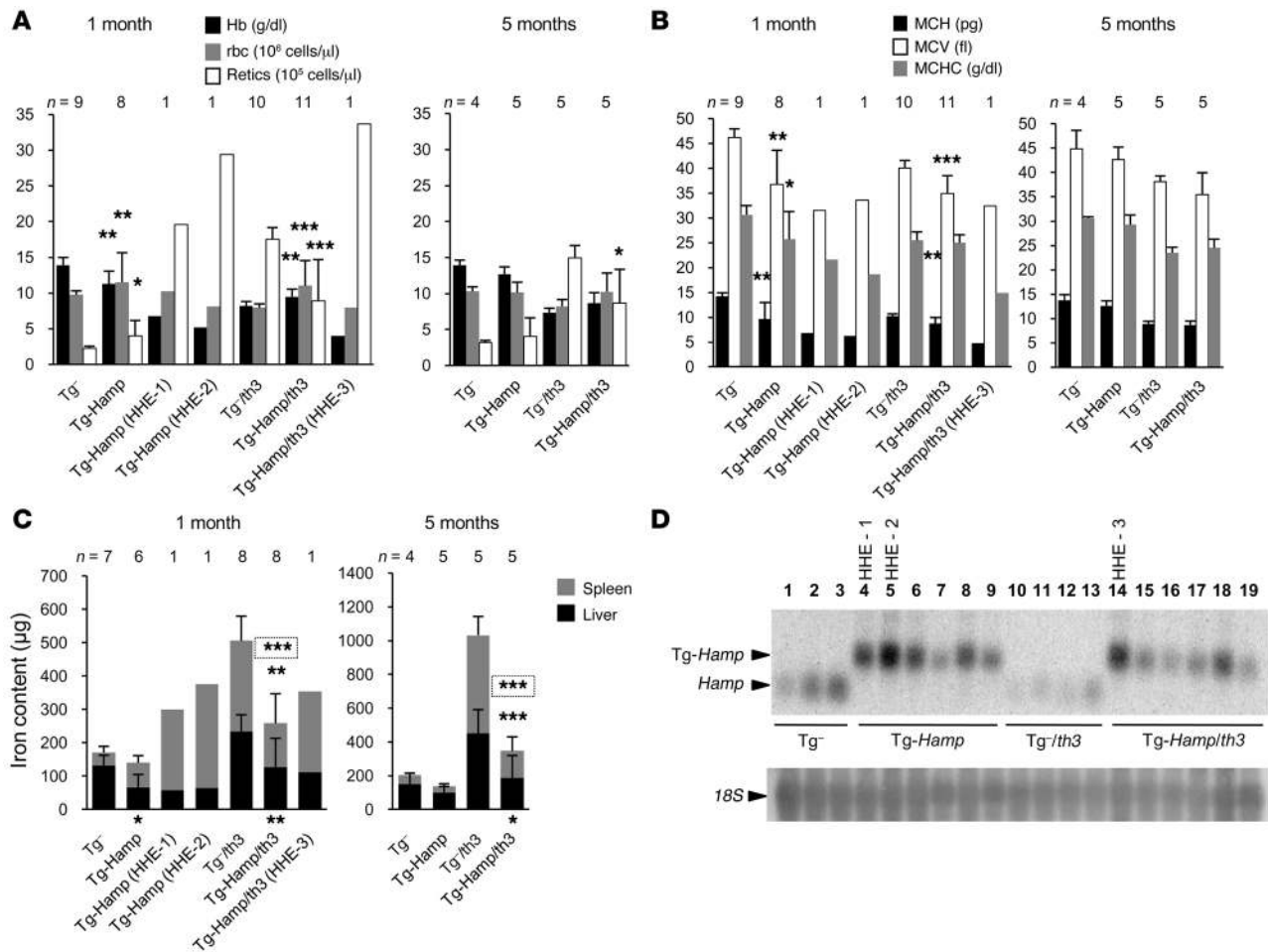


Figure 3

Hematological and iron-related parameters in Tg-Hamp and Tg-Hamp/th3 mice fed a diet containing 35 ppm iron for 1 and 5 months. (A) Hb, rbc, and reticulocyte values. (B) MCH, MCV, and MCHC values. (C) Total iron content of liver and spleen as measured by atomic absorption. Groups of Tg-Hamp mice were compared with Tg⁻ mice, and Tg-Hamp/th3 mice with Tg/th3 controls. (D) Northern blot analysis of the endogenous (bottom band) and transgenic (upper band) Hamp1 mRNA transcripts. 18S, ribosomal subunit 18S loading control. *P < 0.05; **P < 0.01; ***P < 0.001. Data are presented as mean \pm SD.

pressive effect of iron restriction in states of increased erythropoietic activity than in th3/+ mice. The size of the spleen in th3/+ mice fed the 2.5-ppm diet for 1 month was reduced (Figure 2D), while that of the liver was unchanged (Supplemental Figure 4A).

After 5 months on the 35-ppm diet, th3/+ mice exhibited decreases in Hb levels compared with th3/+ mice at 1 month (from 9.0 \pm 0.7 g/dl to 6.9 \pm 0.9 g/dl; Figure 1A). After the same length of time, th3/+ mice fed the 2.5-ppm diet exhibited low Hamp1 expression (Figure 1E) together with low serum iron levels and Tf saturations (Figure 1D), while Epo levels were not statistically different (Supplemental Figure 2A). Organ iron content was considerably reduced (Figure 1C and Supplemental Figure 3, A and B). Both the spleen and liver weights were reduced (Figure 2D and Supplemental Figure 4A, respectively). However, th3/+ mice on the 2.5-ppm iron diet did not experience a drop in their Hb concentrations (Figure 1, A and B). FACS analysis and measurement of organ cell numbers revealed that th3/+ mice fed the 2.5-ppm diet for 5 months exhibited a decrease in both the percentage and total number of immature erythroid progenitor cells (CD71⁺Ter119⁺) in

their spleens together with an increase in the population of mature cells (CD71-Ter119⁺; Figure 2, A-C). In conclusion, these findings demonstrate that th3/+ mice on a low iron diet, despite relative systemic iron deficiency, do not exhibit a worsening anemia although its secondary effects, such as hepatosplenomegaly, are mitigated.

Overexpression of transgenic Hamp1 leads to sequestration of iron in the spleen and erythropoietic effects in normal mice. We used mice that uniformly overexpress a transgenic form of Hamp1 in the liver (Tg-Hamp mice, C57BL/6 background) (16). We engrafted these mice with th3/+ HSCs (C57BL/6 background) generating Tg-Hamp/th3 mice. HSCs from WT mice were transplanted into Tg-Hamp mice to generate positive controls. Mice that did not overexpress the transgenic Hamp1 were designated Tg⁻. Tg⁻ mice were also transplanted with WT or th3/+ HSCs to generate Tg⁻ and Tg⁻/th3-negative controls, respectively. All mice were maintained on the 35-ppm diet.

After 1 month on this diet, most Tg-Hamp mice showed reduced Hb, MCH, MCV, and MCHC levels and increased rbc and reticulocyte counts (Figure 3, A and B) as well as an increased number of

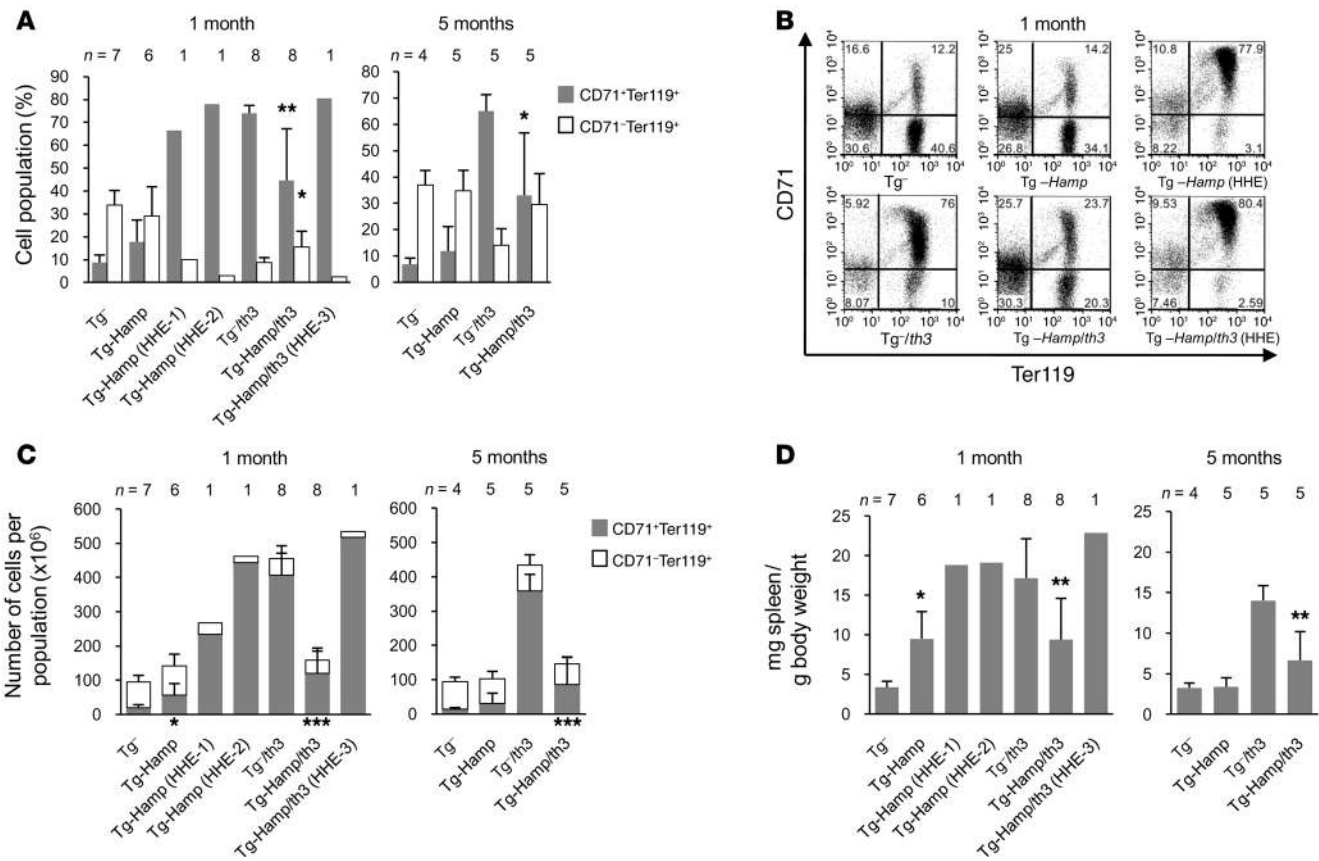


Figure 4

Effects due to overexpression of *Hamp1* on the percentage of mature and immature erythroid cell populations and on the spleen size (normalized to body weight) of Tg-*Hamp* and Tg-*Hamp/th3* mice fed a diet containing 35 ppm iron for 1 and 5 months. (A) FACS analysis of splenic erythroid cells using CD71 and Ter119 costaining. (B) FACS profiles from representative Tg⁻, Tg-*Hamp*, and Tg-*Hamp* (HHE) mice (upper panels) and Tg-*th3*, Tg-*Hamp/th3*, and Tg-*Hamp/th3* (HHE) mice (lower panels). (C) Number of CD71⁺Ter119⁺ and CD71⁻Ter119⁺ cells in the spleen. (D) Spleen weights normalized to body weight. **P* < 0.05; ***P* < 0.01; ****P* < 0.001. Data are presented as mean ± SD.

immature erythroid progenitor cells (CD71⁺Ter119⁺) in the spleen (Figure 4C). In addition, the serum iron levels and the Tf saturations were reduced, becoming nearly undetectable in Tg-*Hamp* mice compared with Tg⁻ controls (not shown). Epo values did not change significantly (Supplemental Figure 2B).

We employed both Northern blot and real-time quantitative PCR (Q-PCR) assays to quantify the total *Hamp1* transcribed (Figure 3D). Identification of the endogenous and transgenic mRNAs by Northern blot is possible because Tg-*Hamp* mRNA contains the β-globin poly(A) sequence instead of the endogenous *Hamp1* 3' UTR and poly(A) elements, resulting in an increased length of the transcript (16). The Northern blot assay indicated that both the Tg-*Hamp* and Tg-*Hamp/th3* mice expressed only the transgenic *Hamp1* (Figure 3D).

In Tg-*Hamp* mice, Northern blot analysis indicated that the level of transgenic *Hamp1* is increased approximately 2-fold compared with the mean expression of endogenous *Hamp1* in Tg⁻ mice. Consistently, the total amount of iron in the liver was reduced in Tg-*Hamp* mice compared with Tg⁻ mice. However, the total amount of iron in the spleen of Tg-*Hamp* mice was increased after 1 month on the diet (Figure 3C). In 2 mice, designated high *Hamp1* expressers (Figure 3D), we observed very low levels of Hb (6.8 and 5.2 g/dl, respectively; Figure 3A) compared with an average value of 11.2 g/dl

in control mice. This correlates with higher levels of *Hamp1* expression (approximately 4-fold when compared with the average expression in Tg⁻ mice). In these mice, the iron content of the liver was also reduced, but that in the spleen was more than 6.2-fold higher than that in Tg⁻ mice and 3.2-fold higher than in the other Tg-*Hamp* mice. These individual differences indicate that very high levels of hepcidin can markedly inhibit the release of iron from macrophages (Figure 3C and Supplemental Figure 5A), leading to a dramatic inhibition of rbc production. To confirm that the *Hamp1* transgenic mRNAs did not carry any mutation acquired during transgenesis that could modify or alter the correlation between *Hamp1* expression and the abnormal parameters observed in these mice, the mRNAs were isolated from the livers of the HHE-1 and HHE-2 mice, and the transgenic *Hamp1* was sequenced. No mutations were identified in any of these transcripts.

After 5 months, although the transgenic *Hamp1* remained elevated (not shown), no significant differences were observed in hematological parameters (Figure 3, A and B) or the iron content of the liver, spleen (Figure 3C), and heart (Supplemental Figure 3D), when comparing Tg-*Hamp* to Tg⁻ mice. The only significant reduction of the iron content was observed in the kidneys (Supplemental Figure 3C). The fact that no major differences were present indicates that, after a few months, a yet-undescribed feedback

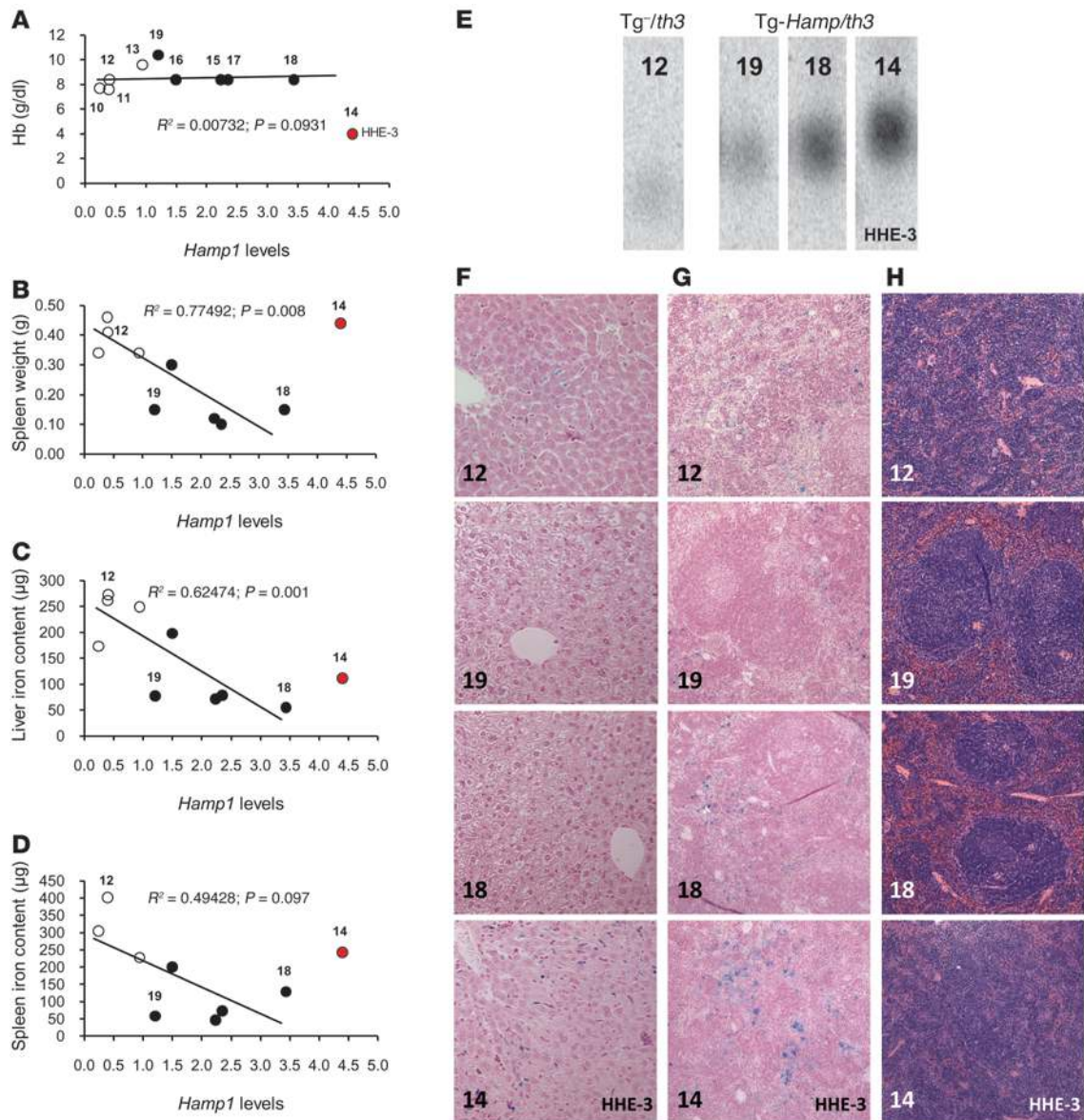


Figure 5

Effects of different levels of transgenic *Hamp1* expression on the distribution of iron in the liver and spleen, and on spleen size and morphology in *th3/+* mice. The numbers refer back to the Northern blot in Figure 3D. Correlations between transgenic *Hamp1* expression (as determined by the band intensity of the Northern blot in Figure 3D) in Tg-/th3 (white circles) and Tg-Hamp/th3 mice (black circles) and (A) Hb values, (B) spleen weight, (C) hepatic iron content, and (D) splenic iron content. The spleen specimen of a control mouse (number 11) was lost during the iron analysis. Histopathological examinations were performed on 1 Tg-/th3 mouse (number 12), 2 Tg-Hamp/th3 mice with intermediate levels of *Hamp1* expression (numbers 19 and 18), and the Tg-Hamp/th3 HHE mouse (number 14). (E) Northern blot from Figure 3D. Iron deposition in (F) the liver and (G) spleen. (H) Spleen morphology. Images were captured on a Nikon Eclipse E800 microscope, with a Retiga Exi camera (Qimaging), then acquired using the IPLab 3.65a software (Scanalytics Inc.). Brightness/contrast and color balance were adjusted using Adobe Photoshop 7.0.1 (Adobe System Inc.). Original magnification, $\times 200$ (F); $\times 100$ (G and H).

mechanism in Tg-Hamp mice compensated for the increased level of transgenic *Hamp1* expression, leading to normalization of organ iron contents and erythropoiesis.

Limited overexpression of transgenic *Hamp1* reduces tissue iron levels with a beneficial effect on erythropoiesis in *th3/+* mice. In the majority of Tg-Hamp/th3 mice, moderate overexpression of *Hamp1* (on average a 4-fold increase relative to endogenous *Hamp1*) led to a reduction of the organ iron contents to levels similar to those

observed in normal mice on the 35-ppm iron diet. Moreover, the hematological parameters in the majority of Tg-Hamp/th3 mice improved compared with those of Tg-/th3 mice after both 1 and 5 months. Specifically, Tg-Hamp/th3 mice exhibited higher Hb levels with lower MCH and MCV (Figure 3, A and B). Epo values did not change (Supplemental Figure 2B). Additionally, the reticulocyte counts (Figure 3A) and both the percentage and the absolute number of immature erythroid progenitor cells (CD71⁺Ter119⁺)

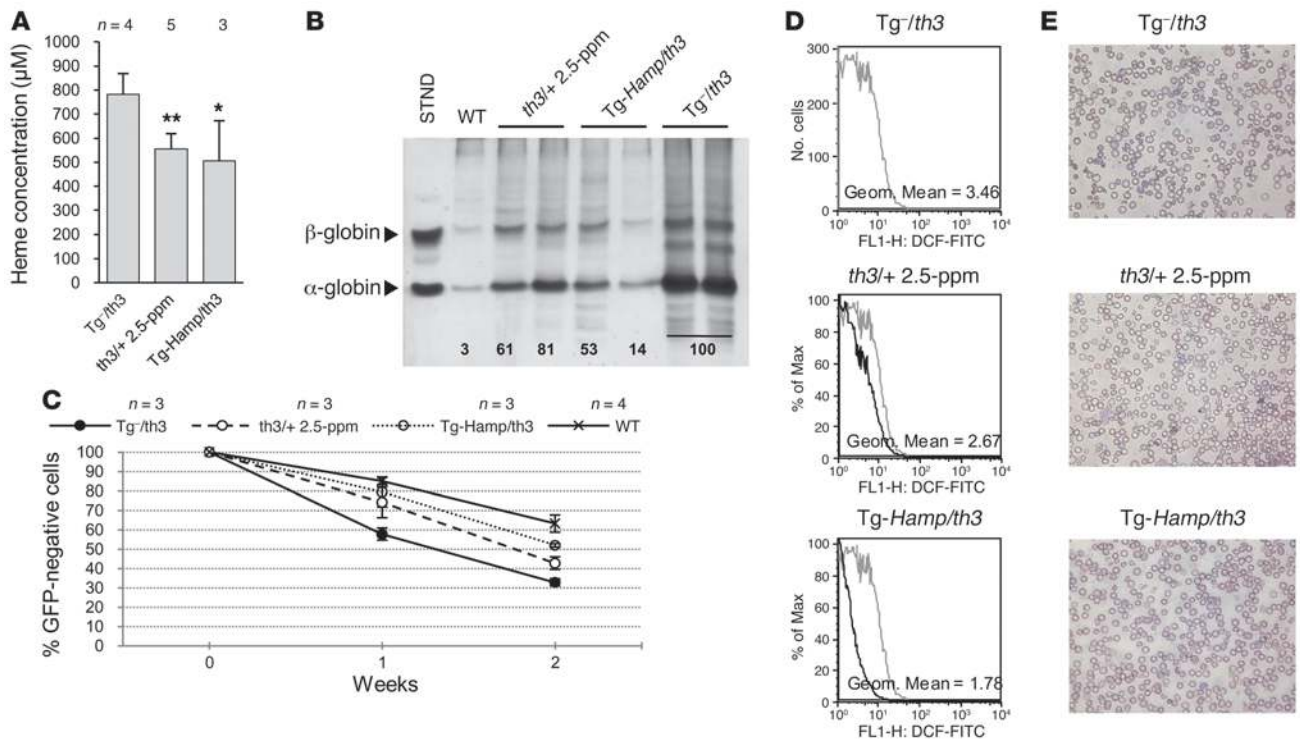


Figure 6 Overexpression of transgenic *Hamp1* improves erythropoiesis in *th3/+* mice. **(A)** Quantification of the heme content in *th3/+* mice fed the 2.5-ppm iron diet, Tg-/th3, and Tg-Hamp/th3 mice, using the same number of rbc from each mouse. **(B)** rbc membrane fractions analyzed by TAU gel electrophoresis to determine the amount of bound globins. The membrane fractions prepared from the same number of rbc have been loaded in each lane. The number under each lane represents the α-globin band intensity expressed as percentage of the mean band intensity of the 2 *th3/+* mice. **(C)** rbc life spans measured as a percentage of that of GFP-negative cells collected from GFP-positive mice injected with blood from WT mice, *th3/+* mice fed the 2.5-ppm iron diet, Tg(-)/th3, and Tg-Hamp/th3 mice. Data are presented as mean ± SD. **(D)** ROS measured in the peripheral blood of 3 representative mice, a *th3/+* fed the 2.5-ppm diet, a Tg-/th3, and a Tg-Hamp/th3 using CM-H₂DCFDA. Both the Tg-Hamp/th3 mouse and the *th3/+* mouse on the 2.5-ppm diet showed reduced fluorescence compared with the Tg-/th3 mouse (in gray). **(E)** Blood smears stained with May-Grunwald-Giemsa stain, showing the rbc morphology of representative mice, a *th3/+* fed the 2.5-ppm iron diet, a Tg-/th3, and a Tg-Hamp/th3. Original magnification, ×400. Data are presented as mean ± SD.

in the spleen decreased (Figure 4, A–C). In a subset of thalassemic mice, we analyzed erythroid cells from both spleen and BM by FACS analysis using a recently described technique that enables a more discrete resolution of the distinct stages in erythroid differentiation using the Ter119 and CD44 antibodies. This assay allows the separation of erythroid cells into distinct populations corresponding to proerythroblasts (fraction I), basophilic (II), polychromatic (III), orthochromatic cells, and reticulocytes (IV), and mature rbc (V) (Supplemental Figure 6, only spleen is shown; similar results were observed in the BM) (18). This analysis confirmed that both the percentage and the absolute number of immature erythroid progenitor cells in the spleen decreased as seen using the CD71 and Ter119 markers.

Low serum iron and Tf saturation levels were very low to undetectable at 1 month. Furthermore, iron content in the livers, spleens, and kidneys was reduced (Figure 3C and Supplemental Figure 3C). We also observed a reduction of splenomegaly (Figure 4D), a more normal architecture of the spleen (Supplemental Figure 7A), and a reduction of EMH in the liver (Supplemental Figure 7B). A single Tg-Hamp/th3 animal (Figure 3D) exhibited high hepcidin expression, approximately 9 times that of the average observed in the Tg-/th3 mice. This HHE mouse also displayed a

low level of Hb (4 g/dl; Figure 3A) and reduced iron in the liver but no change in its splenic iron content compared with control mice (Figure 3C). Iron present in the spleen was mostly sequestered in macrophages, indicating that high levels of hepcidin prevent normal iron recycling, resulting in a markedly negative effect on rbc production. The *Hamp1* transgenic transcript of the HHE-3 mouse was sequenced in order to exclude the presence of mutations acquired during transgenesis (not shown).

We then quantified the mRNA levels in the Northern blots shown in Figure 3D and correlated the results with a series of parameters, such as Hb, liver and spleen iron, and splenomegaly (Figure 5). This analysis indicated that moderate overexpression of *Hamp1* (up to 4-fold that of endogenous levels, excluding the HHE mouse) had a positive effect or no effect on Hb synthesis (Figure 5A) and correlated inversely with a decreased liver and spleen iron load and amelioration of splenomegaly (Figure 5, B–D). These observations, together with those of the blood profile (Figure 3) and the decrease in the number of immature erythroid cells (Figure 4C), indicate that reduction of erythroid activity ameliorates the morphology of the spleen (Figure 5H and Supplemental Figure 7A) in these mice and reverses splenomegaly (Figure 5B). In contrast, analysis of the HHE mouse indicated that excessive hepcidin production

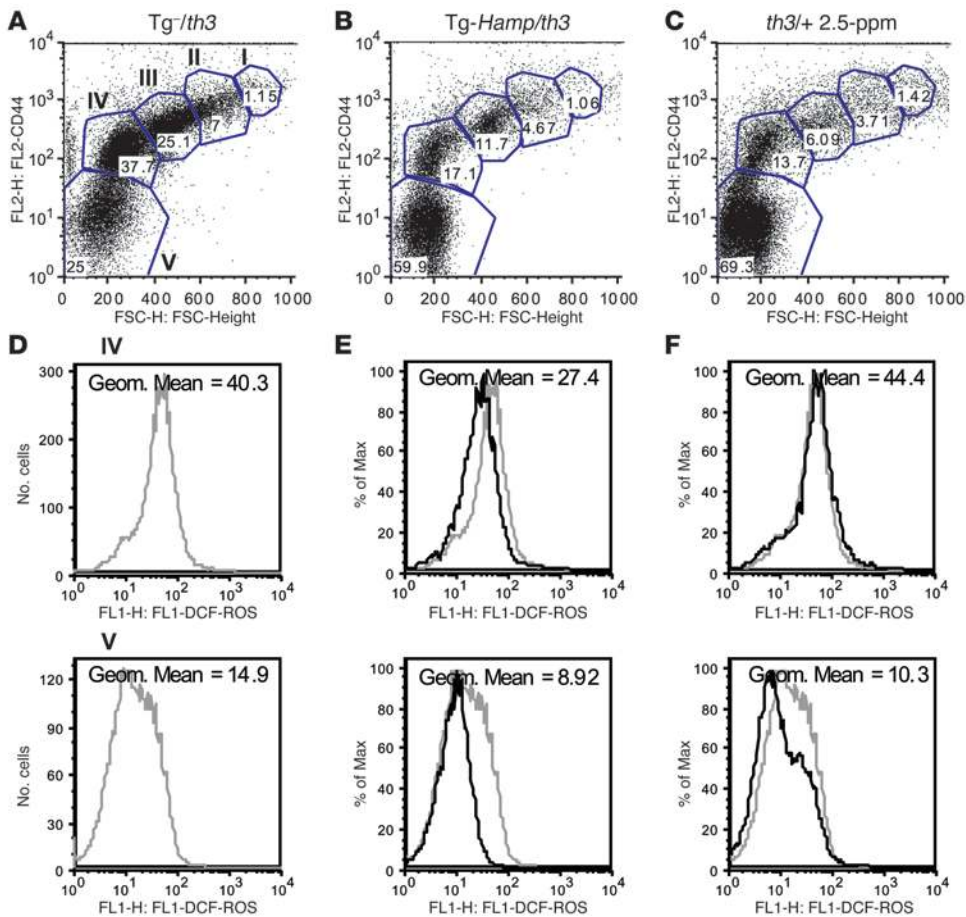


Figure 7 Different stages of erythroid differentiation in the spleens of *th3/+* mice fed the 2.5-ppm iron diet or overexpressing *Hamp1*. FACS analysis of representative mice (A) *Tg-/th3*, (B) *Tg-Hamp/th3*, and (C) *th3/+* on the 2.5-ppm diet mice. D, E, and F show representative analyses of ROS for stages IV (upper panel) and V (lower panel) using CM-H₂DCFDA. Data are presented as mean ± SD.

in β -thalassemia is detrimental, as indicated by the low Hb level (Figure 5A), iron overload in the spleen (Figure 5, D and G), and splenomegaly (Figure 5B), emphasizing the fact that a therapeutic benefit would depend upon the level of *Hamp1* achieved.

At 5 months, the *Tg-Hamp/th3* mice still exhibited reduced organ iron contents (although the heart was not affected; Figure 3C and Supplemental Figure 3C) and improved erythropoiesis compared with *Tg-/th3* mice (Figure 3A). The *Tg-Hamp/th3* mice exhibited increased levels of serum iron and Tf saturation, as did the WT mice overexpressing transgenic *Hamp1* (not shown).

Overexpression of transgenic Hamp1 also improves erythropoiesis in th3/+ mice. To identify the causes leading to amelioration of erythropoiesis in these mice, we analyzed additional *th3/+* mice maintained on the 2.5-ppm iron diet and *Tg-Hamp/th3* mice on the 35-ppm iron diet and compared them to *Tg-/th3* control mice, also on the 35-ppm diet (respectively, $n = 5, 3,$ and 4 mice per group). As observed previously, *th3/+* mice on the 2.5-ppm iron diet and *Tg-Hamp/th3* mice exhibited improved erythropoiesis compared with *Tg-/th3* control mice (not shown). In particular, a reduced MCH was corroborated by direct quantification of the heme content using the same number of rbc from each mouse (Figure 6A). This led us to hypothesize that a reduced heme level would limit the formation of insoluble globins (α chain/heme aggregates) and thereby reduce their potential toxicity when they adhere to rbc membranes and produce ROS (19). Thus, a reduction in insoluble α -globins could improve the quality and survival of erythroid cells, leading to a larger number of rbc in the circulation and amelioration

of the IE and anemia. To test this hypothesis, we prepared membrane fractions and determined the amount of bound globins by triton acetic acid urea (TAU) gel electrophoresis. *th3/+* mice on the 2.5-ppm iron diet and *Tg-Hamp/th3* mice showed a reduction of membrane-associated α chains compared with *Tg-/th3* control mice (Figure 6B); this was confirmed by HPLC using the same membrane fractions (Supplemental Figure 8).

Splenomegaly exacerbates anemia both by sequestering rbc and augmenting their removal by erythrophagocytosis. Since we observed that the spleen was reduced in *th3/+* mice on the 2.5-ppm iron diet and *Tg-Hamp/th3* mice, we devised a new method to evaluate the lifespan of rbc to avoid the potentially confusing factor of splenomegaly. We transfused blood from WT, *th3/+* on the 2.5-ppm iron diet and *Tg-Hamp/th3* mice into GFP-transgenic mice, which exhibit normal spleen sizes. rbc from the latter group of mice are fluorescent and easy to distinguish from donor rbc by FACS analysis. The rbc from *th3/+* mice on the 2.5-ppm iron diet and *Tg-Hamp/th3* mice also exhibited longer life spans, similar to WT rbc (Figure 6C). The rbc from *Tg-Hamp/th3* mice exhibited a more normal morphology (Figure 6E). Additionally, a ROS indicator, 5-(and-6)-chloromethyl-2',7'-dichlorodihydrofluorescein diacetate, acetyl ester (CM-H₂DCFDA), was added to peripheral blood, spleen, and BM cells. This compound permeates into the cells and is oxidized in the presence of ROS or free heme. Oxidation was detected by monitoring the increase in fluorescence by flow cytometry. This analysis indicated that rbc (Figure 6D) from *th3/+* mice on the 2.5-ppm diet and *Tg-Hamp/th3* mice have

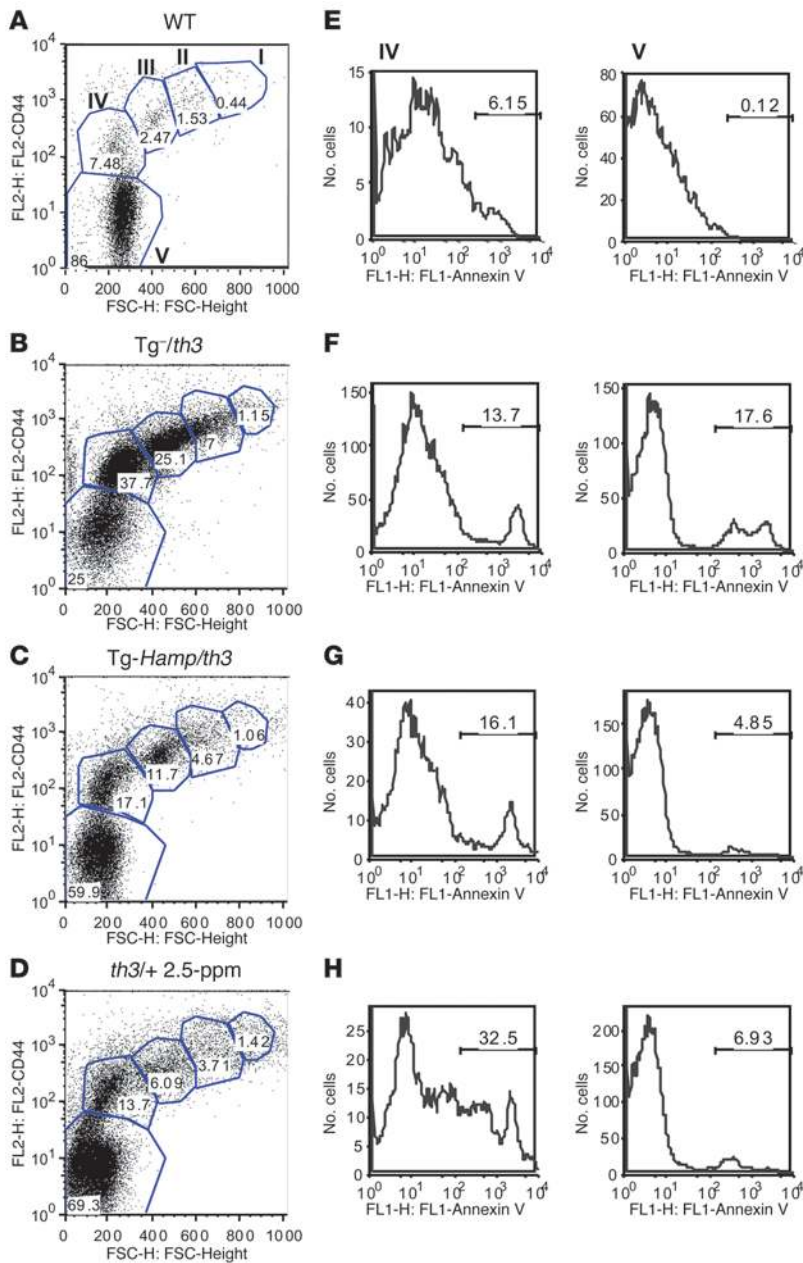


Figure 8 Different stages of erythroid differentiation in the spleens of *th3/+* mice fed the 2.5-ppm iron diet or overexpressing *Hamp1*. FACS analysis of representative mice (A) WT, (B) *Tg/th3*, (C) *Tg-Hamp/th3*, and (D) *th3/+* on the 2.5-ppm diet mice. Numbers indicate the percentage of cells measured in each distinct erythroid population. E, F, G, and H show representative analyses of membrane phosphatidylserine exposure for stages IV (left panel) and V (right panel) using annexin V. Data are presented as mean \pm SD.

reduced fluorescence, and by implication, reduced ROS and/or free heme, when compared with cells from *Tg/th3* control mice. Furthermore, we analyzed distinct erythroid populations from both spleen and BM by FACS analysis using the Ter119 and CD44 antibodies (Figure 7, A–C, only spleen is shown) and investigated in these fractions the level of ROS (18). The analysis of the distinct erythroid populations in the spleen indicates that ROS were reduced in both *Tg-Hamp/th3* mice (both fractions

IV and V) and *th3/+* mice fed the low-iron diet (fraction V) compared with *Tg/th3* controls (Figure 7, D–F).

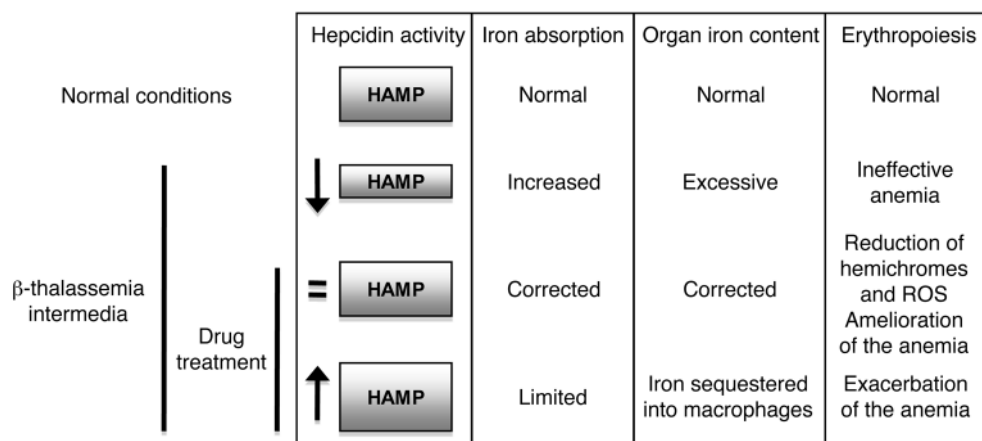
Furthermore, WT mice and untreated *Tg/th3* mice have different patterns of erythroid differentiation and apoptosis in the BM and spleen. The relative percentage of erythroid cells increases, approximately 2-fold at each stage of differentiation (from fraction I to IV), likely reflecting 1-cell divisions, in WT mice (Figure 8A). In contrast, untreated *Tg/th3* mice increase 3 to 6 times (Figure 8B) between fractions I and II as well as between II and III. This observation corroborates previous studies that indicate that β -thalassemic erythroid cells exhibit increased cell proliferation and reduced cell differentiation compared with those from normal mice (20). However, comparing the FACS profiles of WT and *Tg/th3* mice (Figure 8, A and B, respectively) with those of *Tg-Hamp/th3* mice (Figure 8C), we observed that the latter group of mice exhibited an improved profile both in the spleen and BM (not shown), as indicated by a reduction in the number of cells in fractions II to IV, a more balanced ratio of the number of cells between these fractions and a relative increase in terminally differentiated cells in fraction V.

Although we observed similar results in *th3/+* mice on the 2.5-ppm iron diet (Figure 8D), further analysis using annexin V identified a large proportion of erythroid precursors undergoing apoptosis (orthochromatic cells and reticulocytes in fraction IV) or exhibiting an abnormal rbc membrane (mature rbc in fraction V, comparing Figure 8, E–G with H). This was not the case in *Tg-Hamp/th3* mice.

In conclusion, our data suggest that modest overexpression of hepcidin limits the formation of toxic α chain/heme aggregates, reduces free heme and/or ROS formation, and improves both rbc lifespan and anemia. Moreover, it reduces IE by restoring to normal the relative proportion of cells at different stages of erythroid differentiation rather than by triggering cell death of erythroid precursors.

Discussion

Iron balance must be carefully regulated to provide iron as needed while avoiding the toxicity associated with its excess. Tissue iron overload is a primary focus of β -thalassemia management, and if not prevented or adequately treated, is fatal in both transfused and nontransfused patients. NTBI in the circulation damages the heart, endocrine organs, and liver (21). NTBI serves as a catalyst for the formation of ROS, which can cause myocyte damage, arrhythmias, and congestive heart failure, the main causes of death in patients with β -thalassemia (22). Therefore, development of new strategies to reduce excessive iron absorption and tissue iron overload is one of the primary goals of improved management for β -thalassemic patients.

**Figure 9**

Potential effects of hepcidin agonists or activators on iron absorption under normal and β -thalassemic conditions. =, normal; ↓, abnormally low; ↑, abnormally high hepcidin expression levels.

For this reason, we considered the possibility that iron overload could be avoided by limiting the amount of iron absorbed. Such an approach might serve as a substitute for or adjunct to iron chelation therapy in patients affected by β -thalassemia intermedia who exhibit increased iron absorption. In fact, it might be superior to iron chelation since it would be expected to prevent exposure to excessive and possibly toxic iron, obviating the need to eliminate an excess sequestered in vital organs. Although it is unclear how much iron is acquired through increased intestinal absorption in patients who require chronic blood transfusions, even minimal iron absorption would be potentially damaging. Therefore, in chronically transfused patients, we propose that limiting or blocking dietary iron absorption will increase the efficacy of their iron chelation therapy.

We hypothesize that the amount of iron absorbed from a standard iron diet is in excess of that required for erythropoiesis in $th3/+$ mice. The unchanged Hb levels (~8 g/dl; Figure 1A) in both WT and $th3/+$ mice fed the 2.5-ppm diet supports this notion. In other words, β -thalassemic mice require less iron to produce 8 g/dl of Hb than what is required by normal mice to produce 15 g/dl of Hb. Theoretically, then, iron intake in β -thalassemic patients who do not require chronic blood transfusions might be restricted so as to reduce organ iron levels without any detrimental effect on Hb levels.

Because the main cause of increased iron absorption in β -thalassemia intermedia is the low expression of *Hamp1* (13, 14), we utilized transgenic mice overexpressing hepcidin to limit iron overload as a complementary approach to dietary iron restriction. Taken together, our data indicate that a moderate increase in the expression of *Hamp1* in $th3/+$ mice led to hepatic iron levels identical to those in normal mice while splenic iron levels were 4 times less than those in untreated β -thalassemic mice (Figure 3C). These reduced organ iron levels were associated with amelioration of anemia, splenomegaly, and EMH compared with untreated $th3/+$ mice (Figure 3A, Figure 4D, and Supplemental Figure 7B). Taken together, these observations demonstrate that iron overload may play an important role in exacerbating IE, increasing splenomegaly, and decreasing Hb levels over time, perhaps by interfering with erythroid maturation or rbc formation.

After 5 months, both normal and $th3/+$ mice that overexpressed *Hamp1* exhibited increased serum iron levels compared with mice evaluated after 1 month. This occurred despite similar levels of transgenic *Hamp1* expression in all mice indicating that other factors, in addition to the level of *Hamp1* expression, control ongoing iron absorption, at least in mice. One possibility is that the level

of *Fpn1* increases over time, allowing more iron to enter through the duodenum. However, *Fpn1* expression did not increase in mice overexpressing *Hamp1* (Supplemental Figure 9). We cannot exclude the possibility that additional factors modify the translation, maturation, secretion, and ultimately, the serum levels of *Hamp*.

Both $th3/+$ mice fed the 2.5-ppm iron diet and *Tg-Hamp/th3* mice increased their Hb levels, decreased reticulocyte counts, and reversed IE and splenomegaly. Additionally, reduced MCH and heme levels were observed in these mice (Figures 1–4 and Figure 6A). Thus, even though the total heme and Hb content in individual rbc decreased, anemia was reduced because of increased production of rbc. Moreover, while the number of rbc increased, the number of reticulocytes was reduced. This indicates that the IE in these mice was less severe than in untreated mice. We conclude that the toxicity of free heme and α chains is reduced, thereby making erythropoiesis more efficient.

Therefore, by limiting the availability of iron to erythroid precursors, hepcidin agonists might improve the efficiency of erythropoiesis and the survival of the resulting reticulocytes and erythrocytes, by decreasing the synthesis of heme and, perhaps, α -globin chains. Recently, *th1/th1* mice, a model of β -thalassemia intermedia (23) similar to $th3/+$, treated with apo-Tf demonstrated a significant reduction of splenomegaly and IE, an increase in Hb and rbc concentrations, and higher hepcidin expression, suggesting that maldistribution of iron in β -thalassemia might also contribute to IE (24). In this study, MCH was also decreased. These complimentary observations suggest that decreasing iron availability for erythropoiesis may be beneficial in limiting abnormal rbc production. Decreased iron availability likely results in more effective erythropoiesis, as less iron is available during erythroid development to generate free heme or α -globin precipitates, factors associated with shortened rbc survival. Previously presented data demonstrate that the absence of heme-regulated inhibitor (HRI) kinase, which controls Hb synthesis (25), exacerbates the β -thalassemia phenotype (26), while lack of heme exporter feline leukemia virus subgroup C cellular receptor (FLVCR), which controls heme export (27), impairs rbc formation (28). These observations, along with our new data, suggest that an excess of iron and/or heme (in addition to α -globin) in erythroid cells might be deleterious to erythropoiesis. Moreover, modulation of erythroid iron intake or heme synthesis might also affect the stability of excess α -globin chains or selectively influence the synthesis of α - versus β -globin chains. In the first scenario, in the absence of heme molecules, α -globin chains might be extreme-



ly unstable and rapidly eliminated, thereby obviating any toxicity. Alternatively, under conditions of reduced erythroid iron intake, α chains might be produced at a lower rate than β chains, with HRI potentially playing a role in this process. However, Q-PCR analysis of the α -globin mRNA transcript in control and experimental mice did not show any difference (not shown). Additional experiments are required to evaluate the stability and/or degradation of free α chains and their rate of synthesis under condition of low iron.

Furthermore, while the number of rbc were increased in Tg-*Hamp*/*th3* mice, the number of reticulocytes, the proportion of immature erythroid precursors, and the total number of erythroid precursors in the spleen were reduced (Figures 3 and 4). Moreover, the Epo levels in these mice were unchanged from those in *th3*/*+* mice (Supplemental Figure 2B). Accordingly, we can also hypothesize that an excess of iron might alter the ratio between proliferation and differentiation of erythroid cells when the synthesis of globin chains is impaired. Additional studies will be required to determine whether reduced iron intake can variably modulate the synthesis of α - and β chains, the role of heme and ROS in erythroid differentiation/proliferation, and the mechanisms by which hepcidin agonists affect erythropoiesis.

In our study we also identified a small subset of mice, indicated as HHE (both normal and *th3*/*+*), that exhibited reduced Hb levels and elevated iron deposition in splenic macrophages. These findings were associated with elevated *Hamp1* expression levels. Thus, although our data demonstrates as proof of concept that increased hepcidin levels can reduce tissue iron overload and improve erythropoiesis in β -thalassemia intermedia mice, this approach will require titration of HAMP or a HAMP agonist to avoid sequestration of iron in macrophages and thus exacerbation of anemia (Figure 9). Further studies are necessary to explore the potential use of hepcidin agonists/activators to prevent iron overload or reverse its toxic effects in β -thalassemia. Nevertheless, our data represent a proof of concept that increased hepcidin levels can reduce tissue iron overload and improve erythropoiesis in β -thalassemia intermedia and support our hypothesis that hepcidin therapy may be beneficial in this disorder.

Methods

Generation of thalassaemic mice and transgenic mice overexpressing *Hamp1*. WT and *th3*/*+* embryos were genotyped at 13.5–15.5 days of gestation and the hematopoietic fetal liver cells (HFLCs) harvested as described (29). These HFLCs were then transplanted into WT syngeneic recipients (C57BL/6) (29). Transgenic mice overexpressing *Hamp1* in their hepatocytes (Tg-*Hamp* mice, C57BL/6 background) have already been described (16). The studies described were carried out using defined diets containing 35 and 2.5 ppm of iron (Harlan-Teklad). Pathological analysis of tissues was as previously described (8). All studies were conducted under protocols approved by the Institutional Animal Care and Use Committee (IACUC) of Weill Cornell Medical College.

Hematological studies. Blood samples were obtained by retro-orbital puncture under anesthesia. Complete blood counts (CBC) were measured on an Advia 120 analyzer (H-System; Bayer Corp.).

Measurement of tissue iron content, serum iron, heme, and Tf saturation. The iron content of the liver and spleen as well as serum iron and Tf saturation levels were determined as described in our previous publications (8, 26). The amount of heme in the rbc was quantified using the QuantiChrom Heme colorimetric assay (BioAssay Systems) according to the manufacturer's instructions.

Q-PCR. RNA samples extracted from the liver and duodenum of adult mice were retrotranscribed by using the SuperScript II First Strand Kit (Invitrogen). cDNAs were analyzed by Q-PCR with primers specific for *Hamp1* (Fw: 5'-TGAGCAGCACCTATCTC-3' and Rev: 5'-ACT-

GGGAATTGTTACAGCATTT-3'; GenBank sequence NM_032541), *Hfe* (Fw: 5'-GCAATCTCAGGCCATGATTA-3' and Rev: 5'-ATTCCAACCAAGAAGATGGC-3'; GenBank NM_010424), and *Fpn1* (Fw: 5'-CAAGAATGAGCTCCTGACCA-3' and Rev: 5'-GCCACAACAACAATC CAGTC-3'; GenBank NM_016917). Mouse Gapdh (Applied Biosystems) or mouse β -actin (Fw: 5'-GTGGGCGCTCTAGGCACCA-3' and Rev: 5'-CGGTTGGCCTTAGGGTTCA-3'; GenBank NM_007393) were used as Q-PCR endogenous controls. Q-PCR reactions were performed by using the ABI Prism 7900HT Sequence Detection System (Applied Biosystems), with TaqMan (TaqMan PCR 2X Master Mix; Applied Biosystems) and SYBR Green (iQ SYBR Green Supermix; Bio-Rad Laboratories) chemistry.

Sequencing. In order to sequence the transgenic *Hamp1* mRNA, we utilized 2 primers that resulted only in the retrotranscription of the transgenic *Hamp1*. One oligonucleotide (Fw: 5'-TCCTTAGACTGCACAGCAGAA-3') recognizes a sequence at the beginning of *Hamp1*, in exon 1, before the ATG start codon. The second oligonucleotide (Rev: 5'-AATCAAGGTCCCAAACTC-3') hybridizes with a sequence in the β -globin poly(A) sequence, which is present only in the transgenic mRNA.

Northern blot analysis. RNA samples are analyzed as described by Roy et al. (16). Band intensity is quantified using the ImageQuant TL software (GE Healthcare/Amersham).

CD71, Ter119, CD44, ROS, and annexin V analyses by flow cytometry. BM and spleen cells were incubated with FITC-labeled anti-mouse CD71 and APC-conjugated anti-mouse Ter119 antibodies (BD Biosciences – Pharmingen). In a subset of mice, the cells were also stained with a PE-conjugated anti-mouse CD44 marker (BD Biosciences – Pharmingen) together with the aforementioned antibodies. ROS were detected in peripheral blood and in immature erythroid cells from the spleen and BM with the indicator CM-H₂DCFDA (Invitrogen). The FITC Annexin V kit (BD Pharmingen) was utilized according to the instructions provided by the manufacturer. For all the analyses, cells were sorted using a FACSCalibur instrument (BD) and the results analyzed with FlowJo software (Tree Star, Inc.).

Measurement of rbc lifespan. To evaluate whether the lifespan of rbc from *th3*/*+* mice fed the 2.5-ppm iron diet, and Tg-*Hamp*/*th3* mice fed the 35-ppm diet was extended compared with that of Tg/*th3* mice, we injected 400 μ l of blood from each *th3*/*+* mouse ($n = 3$ per group) into mice whose erythrocytes express GFP and that were previously phlebotomized, withdrawing the same volume of blood. The percentage of GFP-negative rbc from the donor mice was measured by FACS analysis 24 hours after injection (time 0) and again after 1 and 2 weeks. Blood from WT mice injected into GFP mice was used to measure the lifespan of normal erythrocytes. WT mice were also used to measure the rbc lifespan with a sulfo-NHS-biotin reagent (Pierce) that binds to the surface of erythrocytes in order to establish that both methods were comparable. A single dose of 1 mg of sulfo-NHS-biotin was injected into mice intravenously. After 24 hours, a drop of blood was collected from the tail and incubated with a fluorochrome-conjugated streptavidin, then analyzed by flow cytometry. FACS analyses were performed for 2 weeks after injection to measure the progressive clearance of the biotin-labeled erythrocytes from circulation. We did not observe any difference in the lifespan of WT rbc determined by the 2 methods (not shown).

Analyses of α - and β -globin chains in plasma and on rbc membranes. To visualize soluble as well as membrane-bound globins, we utilized TAU gel electrophoresis, which resolves α - and β -globin subunits under denaturing conditions (19, 30). The fraction of sample loaded on the TAU gel was adjusted relative to the number of rbc from CBC, so that the same number of erythrocytes (150×10^6) is represented in each lane.

Statistics. Data are presented as mean \pm SD. Unpaired 2-tailed Student's *t* test was performed using Microsoft Excel, Mac 2008 software. $P < 0.05$ was considered statistically significant.



Acknowledgments

The authors thank Kimberly Young and the members of the Pasta and Red Cells Society of New York for technical support and helpful discussions. This work is supported by the Cooley's Anemia Foundation (CAF), the Associazione Veneta Lotta alla Talassemia (AVLT) (Veneta Association for the Fight Against Thalassemia – Italy) (to S. Gardenghi and L. Breda). This work is supported by grants from the Carlo and Micol Schejola Foundation and the Children's Cancer and Blood Foundation; NIH grant NIDDK-1R01DK090554-01 (to S. Rivella) and R01DK55463 (to R.W. Grady); a grant from the American Portuguese Biomedical Fund (APBRF, USA)/Inova (to P. Ramos), and

NIH grants KO1DK065635 (to C.N. Roy) and 5R01DK082717 (to E. Nemeth). S. Gardenghi is a fellow of the Cooley's Anemia Foundation. P. Ramos is a fellow of the Fundação para a Ciência e Tecnologia, Portugal (SFRH/BD/24813/2005).

Received for publication November 10, 2009, and accepted in revised form September 29, 2010.

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