COMMENTARY

The C282Y Mutation Causing Hereditary Hemochromatosis Does Not Produce a Null Allele

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Targeted mutagenesis was used to produce two mutations in the murine hemochromatosis gene (Hfe) locus. The first mutation deletes a large portion of the coding sequence, generating a null allele. The second mutation introduces a missense mutation (C282Y) into the Hfe locus, but otherwise leaves the gene intact. This mutation is identical to the disease-causing mutation in patients with hereditary hemochromatosis. Mice carrying each of the two mutations were bred and analyzed. Homozygosity for either mutation results in postnatal iron loading. The effects of the null mutation are more severe than the effects of the C282Y mutation. Mice heterozygous for either mutation accumulate more iron than normal controls. Interestingly, although liver iron stores are greatly increased, splenic iron is decreased. We conclude that the C282Y mutation does not result in a null allele.

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HEREDITARY HEMOCHROMATOSIS is a common, autosomal recessive disorder affecting approximately one million people in the United States. The gene responsible for most cases was identified by positional cloning in 1996.1 Termed HFE, it encodes an atypical member of the class I major histocompatibility protein family that heterodimerizes with β2-microglobulin. Most affected patients are homozygous for a unique missense mutation that results in a tyrosine for cysteine substitution at amino acid 282 (C282Y).1 It is not clear whether heterozygosity for the C282Y mutation, by itself, can predispose to iron overload. The C282Y mutation disrupts an intramolecular disulfide bond, and may interfere with β2-microglobulin binding.2 Mice deficient in β2-microglobulin and mice deficient in Hfe both develop systemic iron overload.3,4 The function of HFE and its role in iron metabolism remain unknown. We created two mutant mouse strains to investigate whether the C282Y mutation results in total loss of protein function, and to develop a model system to study the pathogenesis of hemochromatosis.

MATERIALS AND METHODS

The murine Hfe gene resembles its human ortholog. Codon 282 is 49 nucleotides upstream of an exon-intron junction. We used site-directed mutagenesis (QuickChange kit; Stratagene, La Jolla, CA) to introduce the C282Y mutation into murine codon 282. Genomic Hfe DNA was inserted into the pTKLNCL targeting vector (from R. Mortenson, Brigham and Women’s Hospital), such that the C282Y mutation was close to the neomycin resistance cassette (Fig 1). The construct was electroporated into TC-1 embryonic stem (ES) cells,5 and recombinant clones were selected as previously described.6 We anticipated that most targeting events would involve recombination between homologous sequences located further from the selectable marker than the site of the mutation and would, therefore, result in introduction of the C282Y mutation into the mouse genome. This proved to be true. Targeting vector sequences were located within an intron, between loxp sites. A second targeting vector was similarly used to construct an Hfe null allele (Fig 1).

Correctly targeted ES cell clones were injected into mouse blastocysts to generate chimeric mice carrying each mutant allele. Inbred mouse strains vary markedly in parameters of iron metabolism7 (and our unpublished data). For this reason, the original chimeric mice were bred to two different inbred strains. First, they were bred to 129/SvEvTac mice from which the TC-1 ES cell line was derived,7 to place the C282Y mutation close to the neomycin resistance cassette.8 This maneuver deleted vector sequences located further from the selectable marker than the site of the mutation and would, therefore, result in introduction of the C282Y mutation into the mouse genome. This proved to be true. Targeting vector sequences were located within an intron, between loxp sites. A second targeting vector was similarly used to construct an Hfe null allele (Fig 1).

Animals were maintained on standard mouse diet and iron status was evaluated at various ages as previously described.6 RESULTS AND DISCUSSION

As shown in Fig 2, genotype correlated strongly with iron loading. Mice heterozygous for either mutant allele showed more iron loading than wild-type mice of the same genetic background (Fig 2a). Similar to previously reported results,4 mice homozygous for the null allele developed massive iron loading early in life. This occurred postnatally; wild-type and mutant iron levels were identical at 3 days of age, and iron loading occurred more rapidly on the 129/SvEvTac background (data not shown). C282Y homozygotes had a phenotype intermediate between null homozygotes and wild-type mice. Results were confirmed by Prussian blue staining of liver tissue (Fig 2b). These results indicate that the C282Y mutation does not completely disrupt the function of Hfe, and is not a null mutation. Interestingly, mice began to accumulate hepatic iron before circulating transferrin was fully saturated. At 4 weeks of age, on the 129/SvEvTac background, nonfasting transferrin saturations were 84.0 ± 1.1, 89.5 ± 1.3, and 88.3 ± 1.4 for wild type, C282Y homozygotes, and null homozygotes, respectively. These blood samples were obtained by retroorbital bleeding or

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Fig 1. Targeting constructs used to create mutant Hfe alleles. The structures of the two targeting constructs are shown, with reference to the murine Hfe locus. In each case, the intron/exon structure of the genomic clone is shown on the top line, the structure of the targeting construct is shown on the second line, and the structure of the correctly targeted mutant locus is shown on the third line. Black boxes are Hfe exons. Translational start (ATG) and stop (STOP) sites are indicated. 5' 8 homology (5' hom) and 3' homology (3' hom) regions are indicated for each targeting vector. The locations of the neomycin resistance (NEO) and cytosine deaminase (CD) cassettes are shown. Hatched boxes represent loxP sites. The asterisk (*) shows the site of codon 282. (a) Summarizes the strategy used to make the null allele; (b) summarizes the strategy used to introduce the C282Y missense mutation. The final line in (b) shows the structure of the C282Y allele after vector sequences have been removed by Cre-mediated recombination between loxP sites.

Fig 2. Iron metabolism in Hfe mutant mice. (a) Liver iron content was determined for 4-week-old 129/SvEvTac mice as previously described and expressed as micrograms per gram wet weight ± standard error. Genotypes are abbreviated as follows: wild-type (+/+), Hfe C282Y homozygous (Y/Y), and Hfe null homozygous (−/−). All differences between genotypes were statistically significant when P values were determined by Welch correction of the unpaired t-test. (b) Hepatic iron was visualized by Prussian blue staining of tissue sections from wild-type and mutant F2 mice with a C57BL/6J × 129/SvEvTac background. Nonheme iron deposits appear blue. (c) Spleen iron was determined for 4-week-old 129/SvEvTac mice using the same method as was used for liver iron, and expressed as microgram per gram wet weight ± standard error. Differences between wild-type mice and each mutant strain were statistically significant according to P values determined by Welch correction of the unpaired t-test. The mutant strains were not significantly different from each other.
cardiac puncture; it remains possible that portal transferrin saturations are higher. Mice homozygous for each \( Hfe \) mutation had less splenic nonheme iron than wild-type mice, despite systemic iron overload (Fig 2c). This may be because mouse spleen is an active site of erythropoiesis, and most splenic storage iron is found in macrophages. This may be analogous to human hemochromatosis, where patients have been shown to have decreased iron in bone marrow macrophages.\(^9\)

In conclusion, the C282Y mutation clearly predisposes to iron loading, but is not as severe as a null allele. Heterozygosity for either mutant \( Hfe \) allele results in increased iron stores, consistent with the notion that the prevalence of the human mutation may result from heterozygote advantage. Analogous to human patients, mice carrying \( Hfe \) mutations also have depleted splenic iron stores, further confirming that these mouse mutants offer a valid system for studying the human disease. Finally, liver iron loading begins before circulating transferrin is fully saturated, suggesting that it may occur in the absence of significant levels of nontransferrin-bound iron. This has implications for the mechanism of hepatic iron loading, and suggests that it may begin earlier than generally appreciated in hemochromatosis patients.

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