SREBP-2-deficient and hypomorphic mice reveal roles for SREBP-2 in embryonic development and SREBP-1c expression

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Abstract  Cholesterol and fatty acid biosynthesis are regulated by the sterol regulatory element-binding proteins (SREBPs), encoded by Srebf1 and Srebf2. We generated mice that were either deficient or hypomorphic for SREBP-2. SREBP-2 deficiency generally caused death during embryonic development. Analyses of Srebf2−/− embryos revealed a requirement for SREBP-2 in limb development and expression of morphogenic genes. We encountered only one viable Srebf2−/− mouse, which displayed alopecia, attenuated growth, and reduced adipose tissue stores. Hypomorphic SREBP-2 mice (expressing low levels of SREBP-2) survived development, but the female mice exhibited reduced body weight and died between 8 and 12 weeks of age. Male hypomorphic mice were viable but had reduced cholesterol stores in the liver and lower expression of SREBP target genes. Reduced SREBP-2 expression affected SREBP-1 isoforms in a tissue-specific manner. In the liver, reduced SREBP-2 expression nearly abolished Srebf1c transcripts and reduced Srebf1a mRNA levels. In contrast, adipose tissue displayed normal expression of SREBP target genes, likely due to a compensatory increase in Srebf1a expression. Our results establish that SREBP-2 is critical for survival and limb patterning during development. Reduced expression of SREBP-2 from the hypomorphic allele leads to early death in females and reduced cholesterol content in the liver, but not in adipose tissue.—Vergnes, L., R. G. Chin, T. de Aguiar Vallim, L. G. Fong, T. F. Osborne, S. G. Young, and K. Reue. SREBP-2-deficient and hypomorphic mice reveal roles for SREBP-2 in embryonic development and SREBP-1c expression. J. Lipid Res. 2016. 57: 410−421.

Supplementary key words  sterol regulatory element-binding protein 2 • sterol regulatory element-binding protein 1c • gene regulation • cholesterol synthesis

Cholesterol is a precursor for the biosynthesis of steroid hormones, bile acids, and vitamin D, and is a critical determinant of cell membrane permeability and fluidity (1, 2). Cholesterol biosynthesis and homeostasis are regulated by the sterol regulatory element-binding protein (SREBP) transcription factor family. SREBPs are basic-helix-loop-helix-leucine zipper transcription factors, which are activated in response to low cellular sterol levels by a series of protein cleavage/transport events (3–5). There are three SREBP isoforms, which originate from two genes. Srebf1 encodes SREBP-1a and SREBP-1c, which have distinct promoters and 5′ exons. Srebf2 encodes SREBP-2. SREBP-1c is the predominant isoform in metabolic tissues such as liver and adipose tissue, but has a relatively weak transcription-activation domain compared with the other SREBPs. There is overlap in the activities of the SREBP isoforms, but it is generally held that SREBP-1c primarily targets genes implicated in fatty acid synthesis, whereas SREBP-2 preferentially regulates genes involved in cholesterol synthesis (5–8). SREBP-1a is a potent activator of both triacylglyceride and cholesterol biosynthetic pathways, but is expressed at low levels in metabolic tissues, making the physiological role of the protein unclear (9). SREBP-1c, itself, is regulated by SREBPs, indicating a high degree of cross-talk among SREBP proteins, making it difficult to assign distinct physiological functions to individual SREBP proteins.

Abbreviations: Acc, acetyl-CoA carboxylase; AER, apical ectodermal ridge; BMP, bone morphogenetic protein; FGF, fibroblast growth factor; Grem1, gremlin 1; Hmgcr, HMG-CoA reductase; Hmgcs, HMG-CoA synthase; Insig, insulin-induced protein; Ldlr, LDL receptor; MEF, mouse embryonic fibroblast; Peh1, patched 1; SCAP, SREBP cleavage-activating protein; Sels, sterol-CoA desaturase 1; SHH, sonic hedgehog; SREBP, sterol regulatory element-binding protein; WAT, white adipose tissue; ZPA, zone of polarizing activity.

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SREBP activity is regulated by the nutritional status of the cell (10, 11). When cellular sterol concentrations are high, SREBP precursors are bound to SREBP cleavage-activating protein (SCAP) in the endoplasmic reticulum membrane. SCAP, in turn, interacts with insulin-induced proteins (Insigs), which serve to retain the SCAP-SREBP complex within the endoplasmic reticulum membrane. When sterol concentrations are low, SCAP-bound SREBPs are translocated to the Golgi where they undergo a two-step cleavage process (by S1P and S2P proteases), thereby releasing the N-terminal active domain (nuclear SREBP).

Studies with genetically modified mice have provided insight into the physiological roles of the three SREBP isoforms [reviewed in (3, 5)]. The characterization of transgenic mice with expression of constitutively active nuclear forms of SREBP-1a, -1c, or -2 led to the identification of preferential target genes for SREBP-1 (lipogenesis genes) and SREBP-2 (cholesterol synthetic genes) (9, 12, 13). However, the physiological roles of the SREBP proteins cannot be fully delineated with constitutively active transgenes that lack the capacity to be regulated by sterols. Studies with gene knock-out models have largely confirmed the gene targets for SREBP-1 and have provided additional insights into the physiological roles of this protein. Because of the critical functions of the SREBP pathway, SREBP-1 deficiency is lethal in utero in 50–85% of mice (14). Although no analysis of SREBP-2-deficient mice has been published, Shimano et al. (14) did comment that SREBP-2 deficiency is lethal during embryogenesis. Also, deficiency in S1P, which is required for activation of all SREBP isoforms, is lethal in utero (15). SCAP and S1P function has been examined with conditional gene activation of all SREBP isoforms, is lethal in utero (15). SCAP (14) did comment that SREBP-2 deficiency is lethal during embryogenesis, the role of each protein during development has not been studied in detail. It is intuitive that lipid homeostasis should be critical for normal development, because upregulation of cholesterol and phospholipid synthesis is required to satisfy the demand for membrane biogenesis during periods of rapid cell proliferation. Also, it is well-documented that impaired sterol synthesis results in developmental defects in humans and animals (17–20). However, the activities of SREBP-1 and SREBP-2 that make them indispensable for development have not been identified. In the current study, we set out to elucidate the physiological role of SREBP-2 during embryonic development and in the liver and adipose tissue of adult mice. Both of these objectives were approachable after identifying a gene-trap allele for Srebh2. That mutant allele made it possible to generate both SREBP-2-deficient mice and hypomorphic SREBP-2 mice.

**MATERIALS AND METHODS**

**Generation of mutant mice**

Mouse embryonic stem cells containing a gene-trap insertion in Srebh2 (cell line XD155) were obtained from BayGenomics (now http://www.genetrap.org) (21, 22). Insertion of the gene-trap vector pGTLx into Srebh2 was verified by direct sequencing of cDNA obtained by 5′ rapid amplification of cDNA ends (5′-RACE). Male chimeric mice from blastocyst microinjections were then bred with C57BL/6J females to generate mice carrying the mutant Srebh2 allele. The site of the gene-trap insertion within intron 1 of the Srebh2 gene was determined by inverse PCR. Offspring were genotyped by PCR of genomic DNA with primers specific for the WT Srebh2 allele (5′-tgaaatggtggcatgcaacctc-3′, 5′-gctgtgaactctgactgattac-3′; 483 bp) and for the mutant allele carrying the insertion mutation (5′-gattcgacgaactgtaaag-3′, 5′-gctgaaagtctgactgatg-3′; 482 bp). To generate Srebh2 hypomorphic mice, Srebh2+/- mice were crossed with an Hprt-Cre transgenic mice (23). The Cre-mediated recombination event eliminated the floxed splice acceptor site in the gene-trapped allele; recombination was detected by a shift in the size of the PCR product generated from the mutant allele (from 482 to 136 bp). The Cre transgene was detected by PCR (primers 5′-accacgagcataactc-3′, 5′-ttaactggtgaaccaggag-3′; 199 bp). Mice were housed in a 12 h light/dark cycle and fed a Purina 5001 chow diet. Samples were collected around 1:00 PM, after 5 h fasting. Mouse studies were performed under approval from the University of California at Los Angeles Institutional Animal Care and Use Committee.

**Tissue staining and histology**

Fresh tissues were fixed in 4% paraformaldehyde and then processed as described (24). Tissues and embryos were stained for β-galactosidase expression, as described (25) with minor modifications. Tissue samples were directly embedded in OCT (Sakura Finetek) and frozen. Fresh 10 μm sections were fixed with 2% formaldehyde and 0.2% glutaraldehyde in PBS for 5 min and incubated in X-gal solution at 37°C overnight. For whole embryos, samples were fixed in 4% paraformaldehyde for 5 min, washed three times in PBS, and stained. Skeletal staining was performed with Alizarin red and Alcian blue as described (www.hhmi.ucla.edu/derobertis/).

**Whole mount in situ hybridization**

Mouse in situ hybridization on whole mounts was performed as described (www.hhmi.ucla.edu/derobertis/). The probes were described previously (26–28).

**Cell culture and cholesterol depletion**

Mouse embryonic fibroblasts (MEFs) were prepared from embryos harvested 11.5 days post coitus. Cells were maintained at 37°C in 5% CO2 with DMEM containing 10% FBS, penicillin/streptomycin, 1 mM pyruvate, 2 mM glucose, and nonessential amino acids. Cells were immortalized by continuous passaging. For cholesterol-depletion studies, MEFs were plated on 12-well plates (100,000 cells/well) on day 1. On day 2, the cells were treated overnight with DMEM containing 10% charcoal-stripped FBS (Gibco, 12676-011), 0.5% (2-hydroxypropyl)-β-cyclodextrin (Sigma, C0926), and 20 μM mevastatin (Tocris, 1526). The same results were obtained with two independent WT and Srebh2-/- cell lines.

**Gene expression analyses**

Total RNA was isolated from mouse tissues and MEFs by extraction with TRIzol (Invitrogen). cDNA synthesis, RT-PCR, and quantitative (q)PCR were performed as described (24). Gene expression was normalized to B2 microglobulin and 36b4. All primer sequences used in this study are presented in supplementary Table 1. Relative miR-35a expression was determined by TaqMan RT-PCR using a predesigned probe set (Applied Biosystems).

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from cDNA synthesized from 100 ng total RNA (Applied Biosystems) and normalized to SnoRNA 202.

Western blot analyses

Livers were rinsed in cold PBS and homogenized in buffer A [10 mM HEPES (pH 7.4), 0.42 M NaCl, 2.5% glycerol, 1.5 mM MgCl₂, 0.5 mM Na-EDTA, 0.5 mM EGTA]. Nonhomogenized tissue was removed with a 10 μm cell strainer, and the homogenate was centrifuged at 4,000 rpm for 15 min at 4°C. The supernatant fluid was centrifuged again at 13,000 rpm for 10 min at 4°C. The resulting pellet was resuspended in buffer B (buffer A containing 100 mM NaCl) to generate the cytosolic fraction. The original pellet was resuspended in buffer C [10 mM HEPES (pH 7.4), 0.42 M NaCl, 2.5% glycerol, 1.5 mM MgCl₂, 0.5 mM Na-EDTA, 0.5 mM EGTA]. Twenty micrograms of these fractions were used for Western blot studies. Protein visualization was performed with rabbit anti-mouse SREBP-2 antibodies (1:5,000 (29)) followed by an HRP-conjugated goat anti-rabbit IgG (1:20,000), and detected with an ECL+ kit (GE Healthcare).

Lipid analysis

For tissue lipid analysis, samples were processed as described (24). Total proteins were quantified for normalization between samples (BCA kit, Pierce).

Steroid hormone quantification

Plasma hormones were determined by the Endocrine Support Core Lab at Oregon National Primate Research Center.

RESULTS

SREBP-2 is required for viability and for limb bud development during mouse embryogenesis

To generate mouse models with absent or reduced SREBP-2, we used a gene-trap allele containing an inser-
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serum (to reduce exogenous cholesterol in the medium). Sterol deprivation in MEFs had similar effects as Srebf2 deficiency: Bmp2 gene expression was induced, whereas Bmp4 and Fgf8 were downregulated (Fig. 3). These results indicate that SREBP-2 and cellular cholesterol homoeostasis have a role in regulating limb development-related genes.

SREBP-2 is critical for embryonic hepatic lipid homeostasis

To assess the role of SREBP-2 on cholesterol homeostasis in the liver during embryonic development, we collected embryos at E11.5 and assessed expression of Sreb
Reduced fat reserves in an adult SREBP-2-deficient mouse

We recovered one viable Srebf2−/− mouse from a total of ~200 progeny from Srebf2+/−×Srebf2+/− intercrosses. At 2 months of age, the SREBP-2-deficient mouse was hairless and weighed 40% less than its littermates (Fig. 5A). Srebf2 deficiency was confirmed by an absence of SREBP-2 protein in the liver (Fig. 5B). The size of the liver was similar to that of heterozygous littermates when normalized to body weight (Fig. 5C). The Srebf2−/− mouse had dramatically reduced fat reserves, with nearly undetectable gonadal white adipose tissue (WAT) and markedly reduced inguinal subcutaneous WAT mass (Fig. 5C). Histological examination of tissue harvested from the perigonadal fat pad revealed smaller adipocytes with reduced lipid accumulation (Fig. 5D, top). Sections through the skin showed strata of dermal, adipose, and its target genes in the liver; we also extracted lipids from the remainder of the embryo. Whole body cholesterol and triglyceride levels were similar in WT and Srebf2−/− embryos (Fig. 4A). As expected, Srebf2 mRNA levels in liver were nearly undetectable, and target genes involved in cholesterol synthesis [HMG-CoA synthase (Hmgcs), HMG-CoA reductase (Hmgcr)], SREBP protein processing (Insig1), and cellular cholesterol uptake [LDL receptor (Ldlr)] were significantly reduced (Fig. 4B). Also reduced by 70–80% were Srebf1a and Srebf1c transcript levels (Fig. 4C), consistent with a feed-forward regulatory loop between SREBP-2 and SREBP-1c (37, 38). We also found reduced transcripts for SREBP1-regulated fatty acid synthesis genes [acetyl-CoA carboxylase (Aco), Fasn, stearoyl-CoA desaturase 1 (Scd1)] (Fig. 4B). Thus, Srebf2-deficient embryos displayed reduced expression of both SREBP-1c and SREBP-2 target genes.
The single adult \textit{Srebf2}^{+/−} mouse provided an opportunity to assess effects of SREBP-2 deficiency on liver and adipose tissue lipids and on gene expression levels. The effects of \textit{Srebf2}^{−/−} deficiency in adult liver mirrored those observed in \textit{Srebf2}^{+/−} embryos, although statistical analysis was not possible due to availability of only a single muscle tissue in WT mice, but subdermal adipose tissue was virtually undetectable in the \textit{Srebf2}^{−/−} mouse (Fig. 5D, bottom). Even though limb bud abnormalities were encountered in \textit{Srebf2}^{+/−} embryos, the skeleton of the sole surviving \textit{Srebf2}^{−/−} mouse appeared normal (Fig. 5E).

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\begin{figure}[h]
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\caption{Lipid levels and gene expression in \textit{Srebf2}^{+/−} embryos. A: Cholesterol (Chol) and triacylglycerol (TAG) levels in E11.5 whole embryos. Expression levels of steroidogenic-related (B) and fatty acid synthesis-related (C) genes in liver of E11.5 embryos. All WT values are set at 1. Data represent the mean ± SD (n = 4). *P < 0.05, **P < 0.01 versus WT. Mvk, mevalonate kinase.}
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\caption{Characterization of an adult \textit{Srebf2}^{+/−} mouse. A: Photo of the 2-month-old \textit{Srebf2}^{+/−} mouse with a \textit{Srebf2}^{+/+} littermate. B: Immunoblot analysis of SREBP-2 from livers of \textit{Srebf2}^{+/−} and \textit{Srebf2}^{−/−} mice. C: Percent body weight of liver, gonadal WAT (gWAT), inguinal WAT (iWAT), kidney, and spleen. D: Hematoxylin/eosin staining of gWAT and iWAT. E: Alizarin red (bone) and Alcian blue (cartilage) staining of the skeleton.}
\end{figure}
Srebf2⁻/⁻ mouse, hepatic cholesterol levels in the Srebf2⁻/⁻ mouse were reduced by 40% and triacylglycerol levels were reduced by 60% (Fig. 6A). Transcript levels for Srebf1a and Srebf1c in the liver were reduced, as were the transcripts for most SREBP target genes analyzed (Fig. 6B). In inguinal WAT, cholesterol levels were reduced by approximately one-half compared with heterozygous littermates, but triacylglycerol levels (normalized to protein) were similar (Fig. 6C). In contrast to the liver of the Srebf2⁻/⁻ mouse, most SREBP target genes in WAT were expressed at levels similar to those in WT mice (Fig. 6D). Interestingly, Srebf1a mRNA levels in WAT were elevated 5-fold, whereas Srebf1c mRNA levels were normal. In addition, the expression levels for Acc, Fasn, and Scd1 were equal to (or exceeded) those in Srebf2⁻/⁻ mice. Thus, in the adipose tissue of the Srebf2⁻/⁻ mouse, higher levels of Srebf1a expression may have partially compensated for the loss of SREBP-2.

Srebf2 hypomorphic mice exhibit reduced adiposity and sex-specific lethality as young adults

While we were able to study a single viable Srebf2⁻/⁻ mouse, embryonic lethality prevented us from thoroughly investigating SREBP-2 function in adult mice. To circumvent this issue, we used Cre recombinase to remove the splice acceptor in the gene-trap allele, with the goal of restoring limited amounts of normal mRNA splicing and creating mice with a hypomorphic Srebf2 allele (Srebf2hyp). Intercrosses of Srebf2⁻/⁻ and Srebf2hyp mice generated 127 live offspring, 19% of which (compared with 25% expected) were compound heterozygotes for the hypomorphic and null alleles (Srebf2⁻/hyp). Hepatic SREBP-2 protein levels in the Srebf2⁻/hyp mice were 80–90% lower than in WT mice (Fig. 7B). Srebf2⁻/hyp mice appeared grossly normal during the neonatal period, but the females had reduced body weight beginning at 4 weeks of age (Fig. 7C), and 50% of these animals died between 8 and 12 weeks of age (Fig. 7D). Male Srebf2⁻/hyp mice exhibited normal body weight and survived until the study was terminated at 12 weeks of age. Compared with WT mice, male Srebf2⁻/hyp mice had 20–40% lower fat pad tissue mass and 15% lower liver mass (relative to total body weight) (Fig. 7E).

We hypothesized that impaired steroid hormone synthesis might contribute to lethality in female Srebf2⁻/hyp mice. However, our analyses of hormone levels did not reveal a likely cause of the premature death in females. Plasma estradiol and progesterone levels were normal in females. Male Srebf2⁻/hyp mice actually had elevated levels of aldosterone and corticosterone in the plasma (Table 1).

Effects of reduced Srebf2 gene expression in liver and adipose tissue

We studied adult Srebf2⁻/hyp mice to assess effects of reduced SREBP-2 expression on cholesterol homeostasis. At 12 weeks of age, Srebf2⁻/hyp males had reduced cholesterol levels in the liver, but not in adipose tissue; tissue triacylglycerol levels were normal (Fig. 8A, C). Reduced SREBP-2 expression also led to lower expression of cholesterol biosynthetic and lipogenic genes in the liver (Fig. 8B), but not in adipose tissue (Fig. 8D). Srebf2⁻/hyp mice had reduced cholesterol levels in the liver, but not in adipose tissue; tissue triacylglycerol levels were normal (Fig. 6A). Transcript levels for Srebf1a and Srebf1c in the liver were reduced, as were the transcripts for most SREBP target genes analyzed (Fig. 6B). In inguinal WAT, cholesterol levels were reduced by approximately one-half compared with heterozygous littermates, but triacylglycerol levels (normalized to protein) were similar (Fig. 6C). In contrast to the liver of the Srebf2⁻/⁻ mouse, most SREBP target genes in WAT were expressed at levels similar to those in WT mice (Fig. 6D). Interestingly, Srebf1a mRNA levels in WAT were elevated 5-fold, whereas Srebf1c mRNA levels were normal. In addition, the expression levels for Acc, Fasn, and Scd1 were equal to (or exceeded) those in Srebf2⁻/⁻ mice. Thus, in the adipose tissue of the Srebf2⁻/⁻ mouse, higher levels of Srebf1a expression may have partially compensated for the loss of SREBP-2.

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SREBP-2 influences limb development and SREBP-1 regulation

The gene expression patterns in tissues of Srebf2+/H11002/H11002 and Srebf2−/− hyp mice could have been influenced by secondary compensatory responses. To verify the effects of SREBP-2 deficiency on gene expression, we assessed basal gene expression and sterol regulation of gene expression in Srebf2+/H11002/H11002 MEFs. Under basal conditions (DMEM with 10% FBS; shown in the left two bars of each graph), several cholesterol biosynthetic genes [Hmgcs, Hmgcr, mevalonate kinase (Mvk)] and Ldlr were expressed at significantly lower levels in the Srebf2+/H11002/H11002 MEFs (Fig. 9A), mirroring the gene expression findings in the liver of Srebf2−/− hyp mice (Fig. 8B). SREBP-2 deficiency in MEFs led to nearly undetectable Srebf1c mRNA levels, but to increased levels of Srebf1a transcripts (Fig. 9B). SREBP-2 deficiency also reduced Srebf1 gene expression, with 90% lower Srebf1c mRNA levels in liver and 70% lower Srebf1c levels in adipose tissue. Srebf1a levels were modestly altered in both tissues (Fig. 8B, D). The adipose tissue of Srebf2−/− hyp mice displayed a 6-fold increase in transcripts for the LDL receptor (Fig. 8D). Given that the gene for miR-33a resides within an intron of Srebf2, we assessed whether the Srebf2 gene-trap allele leads to altered miR33a mRNA expression. miR-33a RNA levels and mRNA levels for several miR-33a target genes were similar in livers of Srebf2−/− hyp and WT mice (Fig. 8E, F). Glucose-6-phosphatase (G6pc) mRNA levels were decreased in the hypomorphic mice, but because miR-33a and other target genes tested were expressed at WT levels, this is unlikely a result of altered miR-33a regulation.

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acid synthesis and cholesterol biosynthesis, respectively (7). However, the activities of the two transcription factors overlap, making it challenging to decipher their unique physiological functions. Previously published studies characterized effects of SREBP-1 deficiency in the mouse (14), but the impact of SREBP-2 deficiency was not characterized. Here, we used a combination of two mutant Srebf2 alleles to investigate the roles of SREBP-2 in mouse development and in adult mice. We identified a crucial role for SREBP-2 in survival and in limb patterning through effects on the SHH pathway. We also demonstrated a key role for SREBP-2 in maintaining hepatic cholesterol content and in regulating Srebf1 gene expression, in addition to regulating well-established SREBP-2 target genes.

DISCUSSION

It has long been appreciated that SREBP-2 is a crucial transcriptional regulator of lipid homeostasis. SREBP-1 and SREBP-2 preferentially target genes involved in fatty acid synthesis and cholesterol biosynthesis, respectively (7). However, the activities of the two transcription factors overlap, making it challenging to decipher their unique physiological functions. Previously published studies characterized effects of SREBP-1 deficiency in the mouse (14), but the impact of SREBP-2 deficiency was not characterized. Here, we used a combination of two mutant Srebf2 alleles to investigate the roles of SREBP-2 in mouse development and in adult mice. We identified a crucial role for SREBP-2 in survival and in limb patterning through effects on the SHH pathway. We also demonstrated a key role for SREBP-2 in maintaining hepatic cholesterol content and in regulating Srebf1 gene expression, in addition to regulating well-established SREBP-2 target genes.
SREBP-2 influences limb development and SREBP-1 regulation

SREBP-2 deficiency is incompatible with normal embryonic development; most Srebf2−/− embryos died by 14.5 days post coitus. This finding likely explains why no one has encountered or studied a human subject with complete SREBP-2 deficiency. In the mouse, a spontaneous Srebf2 missense mutation was associated with cataracts and persistent skin wounds (41), but the effect of the amino acid substitution on SREBP-2 activity is unknown, but unlikely to abolish activity. The cause of death in Srebf2−/− embryos is unclear, given that Srebf2 expression is expressed widely and multiple organ systems could have been compromised by the absence of SREBP-2.

A striking phenotype of Srebf2−/− embryos was abnormal digit formation. At 13.5 days post coitus, Srebf2 expression is detectable in the limb buds of WT embryos in the regions destined to undergo apoptosis during digit specification. The absence of digit formation in Srebf2−/− embryos confirmed a requirement for SREBP-2 in this process. This finding is in accord with previous work showing that in the developing limb bud, there is spatial concordance between cholesterol biosynthetic gene activity and the apoptotic process that defines the digits (40). Gene expression analyses in Srebf2−/− embryos revealed alterations in pathways that regulate limb morphogenesis, including components of the SHH signaling axis. Limb buds of Srebf2−/− embryos exhibited increased Shh transcript level, but reduced expression of downstream components of the signaling pathway (Ptch1, Bmp4). Given that both SHH and Ptch1 both contain sterol-sensing domains (41), it is interesting to speculate that SREBP-2 regulation of cholesterol levels in the developing embryo may play a role in the proper functioning of this pathway, but additional work is required.

Our results in the Srebf2−/− mice demonstrate that low levels of SREBP-2 expression are sufficient for survival during embryogenesis. Srebf2−/− mice are born at a near-normal frequency; the viability of males appeared normal, but the females exhibited failure-to-thrive and most succumbed during the first few months of life. An analysis of steroid hormones was not helpful in explaining the differences in the survival of males and females. Studies of adult male Srebf2−/− mice revealed a complex relationship between Srebf2 expression and the regulation of Srebf1. Previous work established that loss of SREBP-1 leads to increased hepatic SREBP-2 transcript and protein levels, increased expression of cholesterol biosynthetic genes, and a 3-fold increase in hepatic cholesterol content (14). We found that reduced SREBP-2 expression in Srebf2−/− mice resulted in tissue-specific alterations in Srebf1 expression. In the liver, the Srebf2−/− mice had nearly undetectable levels of Srebf1c transcripts and an 80% reduction in Srebf1a transcripts. The low levels of SREBPs in these mice were accompanied by...
40% lower stores of cholesterol in the liver. In contrast, the cholesterol content of adipose tissue and embryonic fibroblasts was maintained despite a 70% reduction in Srebf1a expression levels, perhaps because of slightly increased Srebf1c fibroblasts was maintained despite a 70% reduction in the cholesterol content of adipose tissue and embryonic cholesterol efflux, such as following transcription of the Srebf2 gene (42–45). miR-33a targets transcripts from multiple genes involved in cellular cholesterol efflux, such as Abca1 and Abec1, and miR-33a inhibition has been proposed as an anti-atherosclerosis treatment (46, 47). It is thought that the coordinate expression of Srebf2 and miR-33a represents a mechanism to maintain cellular cholesterol homeostasis by enhancing cholesterol synthesis while limiting sterol efflux. Because miR-33a is present within the cholesterol synthesis while limiting sterol efflux. Because miR-33a levels would be reduced in our Srebf2-deficient mice. However, the expression of miR-33a and several target genes were not perturbed in the liver, suggesting that the Srebf2 mutant allele did not disrupt miR-33a expression. Furthermore, the phenotypes of our mice did not recapitulate those of miR-33a-deficient mice, which manifest hepatic steatosis and are prone to increased body weight on chow and high-fat diets (48). It is possible that miR-33a production is unaffected by our gene-trapped alleles or that there are compensatory changes in our mice that serve to maintain transcript levels for miR-33a target genes.

Finally, these studies provide a proof-of-principle for generation of hypomorphic alleles from gene-trap insertions. Gene trapping has been a valuable adjunct to standard homologous recombination approaches for deciphering gene function in mice (21, 22). Regardless of which technique is used, it is often the case that knocking out a gene in mice results in lethality during embryonic development. In those cases, most investigators rely on the production of tissue-specific knockout mice to assess gene function. In the current study, we showed that the creation of a hypomorphic allele from the gene-trap insertion represents a useful approach for deciphering gene function. We used Cre recombinase to remove the slice acceptor site in the gene-trap allele, which restored a low level of SREBP-2 transcripts and led to markedly reduced SREBP-2 levels throughout the body. Of note, this approach is not limited to creating a “global hypomorphic mouse;” it would have been possible to use a cell type-specific Cre transgene to create mice that express low amounts of SREBP-2 in a tissue.

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REFERENCES


