Expression of carnitine palmitoyl-CoA transferase-1B is influenced by a cis-acting eQTL in two chicken lines selected for high and low body weight

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Ka S, Markljung E, Ring H, Albert FW, Harun-Or-Rashid M, Wahlberg P, Garcia-Roves PM, Zierath JR, Denbow DM, Pääbo S, Siegel PB, Andersson L, Hallböök F. Expression of carnitine palmitoyl-CoA transferase-1B is influenced by a cis-acting eQTL in two chicken lines selected for high and low body weight. Physiol Genomics 45: 367–376, 2013. First published March 19, 2013; doi:10.1152/physiolgenomics.00078.2012.—Carnitine palmitoyl-CoA transferase-1B is a mitochondrial enzyme in the fatty acid oxidation pathway. In a previous study, CPT1B was identified as differentially expressed in the hypothalamus of two lines of chickens established by long-term selection for high (HWS) or low (LWS) body weight. Mammals have three paralogs (CPT1a, b and c) while nonmammalian vertebrates only have two (CPT1A, B). CPT1A is expressed in liver and CPT1B in muscle. CPT1C is expressed in hypothalamus, where it regulates feeding and energy expenditure. We identified an intronic length polymorphism, fixed for different alleles in the two populations, and mapped the hitherto missing CPT1B locus in the chicken genome assembly, to the distal tip of chromosome 1p. Based on molecular phylogeny and gene synteny we suggest that chicken CPT1B is pro-orthologous of the mammalian CPT1c. Chicken CPT1B was differentially expressed in both muscle and hypothalamus but in opposite directions: higher levels in hypothalamus but lower levels in muscle in the HWS than in the LWS line. Using an advanced intercross population of the lines, we found CPT1B expression to be influenced by a cis-acting expression quantitative trait locus in muscle. The increased expression in hypothalamus and reduced expression in muscle is consistent with an increased food intake in the HWS line and at the same time reduced fatty acid oxidation in muscle yielding a net accumulation of energy intake and storage. The altered expression of CPT1B in hypothalamus and peripheral tissue is likely to be a mechanism contributing to the remarkable difference between lines.

body weight; chromosomal mapping; fatty acid; genotyping; hypothalamus; malonyl-CoA; skeletal muscle; lipid metabolism; mitochondrial; mRNA expression; pectoral muscle

CARNITINE PALMITOYL-COENZYME A TRANSFERASE-1 (CPT1; palmitoyl-CoA: L-carnitine O-palmitoyltransferase, EC 2.3.1.21) is a key enzyme in the control of fatty acid oxidation, which catalyzes the rate-limiting step of β-oxidation by translocating fatty acids across the mitochondrial membranes. Malonyl-coenzyme A (CoA), an intermediate in fatty acid synthesis, inhibits CPT1 action, thus blocking the oxidation of fatty acids during times of fatty acid synthesis and energy surplus (26). There are three mammalian CPT1 paralogs. CPT1a is predominantly expressed in liver, CPT1b in muscle, while CPT1c is mainly expressed in the brain (30). Only two paralogs have been described in chicken, denoted CPT1A and B, but only CPT1A is present in the chicken genome assembly (WASHUC2, May 2006), whereas CPT1B is only known from cDNA sequences (36). Malonyl-CoA as an intermediate metabolite in the fatty acid metabolism has recently been shown to be involved in hypothalamic regulation of energy expenditure and food intake (23, 27, 32, 40) and serves as an indicator of the energy status in hypothalamic neurons. Experimental manipulation of the malonyl-CoA system alters feeding behaviors (10, 17, 34). Although CPT1c is structurally similar to its mammalian paralogs CPT1a and b, it does not seem to catalyze the prototypical fatty acid transport (40). CPT1c is expressed in the mammalian hypothalamus, and knockout mice exhibit a marked reduction in food intake, lower body weight, and less body-fat content than their wild-type littermates. This knockout phenotype is consistent with a role for CPT1c as an energy-sensing malonyl-CoA target (40), which regulates energy homeostasis via the hypothalamic (20).

We have studied the chicken CPT1A and B in two chicken lines established by divergent selection for body weight at 56 days of age for >50 generations from a founder population of White Plymouth Rock chickens (8, 25, 35). The two populations, the high-weight (HWS) and the low-weight (LWS) selection lines, now have more than a ninefold difference in body weight at selection age. Several behavioral, metabolic, immunological, and endocrine differences between lines have evolved during the course of the selection experiment (5, 7, 18, 19). Among the correlated responses to the selection for body weight are differences in feeding behavior and food consumption (8). The involvement of the hypothalamus in these phenotypic differences was implied after lesioning of the ventromedial hypothalamic nucleus, which affected the feeding behavior (4). Interestingly, only minor differences were seen between lines when we analyzed the hypothalamic neuropeptide mediators of appetite such as the melanocortin receptors (13, 15), indicating
that the behavioral alteration cannot be explained solely by changes in the hypothalamic neuropeptide regulatory system. Analysis of global gene expression in hypothalamus of the two lines have identified multiple differentially expressed genes in networks and processes regulating neuronal plasticity and development, DNA metabolism and repair, and induction of apoptosis (13). Although CPT1B, which is mainly expressed in muscle, was identified as one of the most differentially expressed genes in hypothalamus by the expression analysis, its contribution to the phenotypes of these lines could not be pursued until now because its chromosomal location was not known.

In this work we follow up on the observation that CPT1B was differentially expressed in our earlier array analysis of hypothalamus of the two selected lines (13). We confirmed that CPT1B, but not CPT1A, has higher expression levels in hypothalamic tissue from the HWS than from the LWS line. Interestingly, expression change in the opposite direction was found for CPT1B in muscle. These results suggested the hypothesis that the regulation of the expression of CPT1B has been a target for the divergent selection with differential CPT1B expression in the two lines as the result. We tested this by identifying a genetic polymorphism in the CPT1B gene that was first used to determine the hitherto unknown position of CPT1B in the chicken linkage map. The CPT1B polymorphism was then genotyped in an advanced F9 intercross between the two chicken lines. Using body weight and CPT1B muscle expression data in the F9 animals, we found that CPT1B expression is affected by an expression quantitative trait locus (eQTL). The data expose one possible regulatory mechanism that underlies the genetics of variable behaviors to satisfy the quest for energy and food in vertebrates and shed light on the molecular evolution and establishment of novel functions after gene duplications in this important gene family.

MATERIALS AND METHODS

Animals and tissues. The LWS and HWS lines were established from a common founder population generated by crosses among seven inbred lines of White Plymouth Rock chicken. The lines have been maintained as closed populations by continuous selection for high or low body weight at 56 days of age. Descriptions of the selection program and various correlated responses to the selection within the lines are provided elsewhere (8, 11). For example, each selected generation of the parental lines is hatched annually the first Tuesday in March, and dietary formulation has remained constant throughout. Feed and water were supplied ad libitum. Animal handling and care were performed according to the National Research Council publication Guide for Care and Use of Laboratory Animals and were approved by the Virginia Tech Institutional Animal Care and Use Committee. The experiment adheres to American Physiological Society’s Guiding Principles in the Care and Use of Vertebrate Animals in Research and Training.

HWS and LWS chickens from generation 45 (G45) were used for the quantitative reverse transcription polymerase chain reaction (qRT-PCR) analysis in peripheral and brain tissues. Five males and five females at 56 days (selection age) and three males and seven females at 4 days of age from each selected line and four White Leghorn chickens were used for tissue dissections. Liver, pectoral muscle, adipose tissue, total brain, brain regions according to Fig. 1 including hypothalamus, and a region containing diencephalon, mesencephalon, pons, and medulla (DMPM) were dissected at 56 days after hatch, immediately frozen in liquid nitrogen, and stored at −70°C until used.

A reciprocal advanced intercross population between HWS and LWS chickens was produced with the main purpose of identifying genes that explain the large difference in body weight and growth between the parental lines. The intercross was initiated from G41 of the
In two chicken lines, the parental lines. Eight HWS males were mated to 22 LWS females, and 8 LWS males were mated to 19 HWS females to generate 150 F1 progeny in 40 families. Thereafter 40 pair-matings with one male and one female from each family were done for each generation during nine generations (F9 intercross) as in Ref. 29 to minimize genetic drift. The husbandry of the intercross was identical to that of Refs. 11, 28. Body weights at 56 days were recorded for all individuals, and 42 male and 38 female F6 chickens from the advanced intercross were CPT1B genotyped. Pectoral muscle tissue from 28 females and 25 males was dissected for total RNA preparation and used for analysis of relative CPT1B mRNA levels.

**RNA preparation and quantitative RT-PCR.** Total RNA was isolated with TRIzol (Invitrogen, Carlsbad, CA) purified with RNeasy mini kit (Qiagen, Valencia, CA), the quality was checked with an Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA), and the RNA samples were frozen at −70°C until used. Complementary DNA synthesis from total RNA and two-step quantitative (q)PCR were performed as described (14). Random primers were used for first-strand cDNA synthesis (Superscript III RT, Invitrogen). Briefly, qRT-PCR was performed using the qSYBR Green supermix (Bio-Rad Laboratories) with MyiQ Single-Color Real-Time PCR Detection System (Bio-Rad). Primers were designed with Primer Express v2.0 (Applied Biosystems, Carlsbad, CA) with the default settings Tm 60°C, 50% G/C, amplicon size minimum 100 base pairs. Each primer sequence was BLASTed separately against GenBank and EMBL, and only primers with one perfect match within the target sequence and with the second best hit <75% identity were used. The primer pairs were checked for PCR efficiency, linear dynamic range, and specificity. To confirm identity of amplified PCR products, dissociation curve analysis and agarose gel electrophoresis were performed after analysis. The initial mRNA levels were first normalized to β-actin and TATA-box binding protein (TBP) mRNA levels to correct for variations in the cDNA syntheses and experimental procedure. We validated the use of β-actin and TBP for normalization purposes by testing for the most stable mRNA expression of TBP, β-actin, β-2-microglobulin, and glyceraldehyde 3-phosphate dehydrogenase over the time points and tissues. The software geNorm (also included in Bio-Rad MyIq software package) was used. Control reactions containing primers but without reverse transcriptase were analyzed in parallel. The data were analyzed by the 2^−ΔΔCT method (21). Analysis of variance (ANOVA) was used for the statistical analysis.

**Phylogenetic and synteny analysis.** Maximum likelihood phylogenetic trees were based on deduced amino acid sequences of all predicted and annotated CPT1 family homologs available in Ensembl and constructed using the Ensemble on-line analysis software package Gene Tree. The reference tree is available on http://www.ensembl.org (GeneTree ENSGTO055000743443) (37). Syntenic regions in the chicken and human genome hosting CPT1 paralogs were identified by whole genome alignment using BlastZ-net/Lastz-net pairwise alignment analysis available in the Ensemble on-line analysis software package (16, 33).

**Discovery of an intronic polymorphism and genotyping.** A region from the end of exon 23 to the beginning of exon 24 (numbering based on human CPT1B) from two HWS and four LWS chickens was amplified and sequenced with primers CPT1ex23F and CPTex24R (Table 1), and an intronic polymorphism was identified. A genotyping assay for the two intronic sequence alleles was designed. We used a fluorescently labeled common forward primer located in exon sequence and two different reverse primers located in intronic sequence (Table 1), giving a four-base-pair size difference between the two alleles (155 and 159 base pairs). The PCR reaction contained 0.2 μM of each primer and PCR Buffer II, 1.5 mM MgCl2, 0.2 mM dNTP, 1 U AmpliTaq GOLD polymerase (Applied Biosystems), and 40 ng of DNA. The PCR cycling conditions were 95°C for 5 min, 8 touchdown cycles 95°C 30 s, 65°C–58°C 30 s, 72°C 20 s, 40 cycles 95°C 15 s, 58°C 15 s, 72°C 20 s, and 72°C for 5 min. The difference in the fragment length was detected using a MegaBACE 1000 DNA Analysis System (Amersham Biosciences/GE Healthcare, Uppsala, Sweden) and analyzed with Genetic Profiler (GE Healthcare). We genotyped 47 parental animals (25 HWS and 22 LWS) and 10 F1 animals to assess fixation of the alleles in the two chicken lines. We used this assay to genotype 80 individuals from the F9 intercross, and a subset of F2 individuals (n = 108) from a large intercross pedigree between the HWS and LWS lines (38) was used for linkage analysis to map CPT1B on the chicken linkage map. The analysis was carried out with the CRI-MAP software package as previously described (38). A genome-wide set of 432 markers previously scored in the pedigree was included in a two-point linkage analysis.

**Western blotting.** Pectoral muscle tissue was dissected, frozen on dry ice, and later homogenized in a lysis buffer containing 20 mM HEPES pH 7.4, 100 mM NaCl, 100 mM NaF, 1% NP-40, 1 mM Na3VO4, 5 mM EDTA, and 1 μg/mL protease inhibitor cocktail (Halt; Thermo Scientific, Rockford, IL). The protein lysate was subjected to two cycles of freezing and thawing on dry ice to release the mitochondrial proteins. Protein concentrations were determined with the DC Protein Assay

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**Table 1. Antibodies and PCR primer sequences**

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<th>Antibody/Primer Name</th>
<th>Antigen, Species/Sequence</th>
<th>Catalog/Accession ID</th>
<th>Note</th>
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<td>mouse</td>
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<td>H_R</td>
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F, forward; R, reverse primer.
Differential expression of CPT1B in two chicken lines

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We separated 20 μg protein per sample on 10% denaturing SDS-polyacrylamide-electrophoresis Mini-Protean TGX Precast gels (Bio-Rad) and electrophoretically transferred that to Immun-Blot PVDF membrane (Bio-Rad) with the recommended buffers. Nonspecific binding was blocked in 4% bovine serum albumin in TBST buffer (20 mM Tris, 140 mM NaCl, 0.05% Tween-20) for 1 h at room temperature. The membrane was incubated with primary antibody diluted in 1% bovine serum albumin in TBST at 4°C overnight. Primary antibodies are listed in Table 1. After washing the membrane, we incubated it with horseradish peroxidase-conjugated secondary antibodies (Jackson ImmunoResearch Laboratories, West Grove, PA) that were detected by chemiluminescence with the ChemiDoc MP Imaging System (Bio-Rad) and quantified with the software Image Lab (Bio-Rad) (9). Each sample was normalized to the actin level and related to the mean levels of the female LWS protein. The same filter was used for all four primary antibodies. ANOVA with Tukey’s multiple-comparison post hoc test was used for the statistical analysis.

RESULTS

Organ-specific expression of CPT1B and CPT1A. Our earlier microarray analysis indicated that CPT1B is expressed in nervous tissue (13). Using qRT-PCR we re-examined the expression of CPT1A and B mRNA in peripheral and brain tissues from White Leghorn chickens. Expression of CPT1B mRNA in brain tissue was confirmed at levels similar to those in adipose tissue, but 100 times lower than in pectoral muscle. Background levels were seen in liver tissue (Fig. 1A). When brain regions from 1 wk old chicks were analyzed, the highest expression was found in hypothalamus, mesencephalon, and optic tectum (Fig. 1B). Levels of CPT1A mRNA were high in liver compared with the other analyzed tissues (Fig. 1C) and were not elevated in hypothalamus compared with the other brain regions (Fig. 1D).

Differential CPT1B mRNA expression between HWS and LWS chicken in muscle and hypothalamus. The overall relative CPT1B mRNA levels in muscle, liver, adipose, and brain tissue from the two selection lines were similar to those in White Leghorn chicken tissue. However, in a comparison of the two lines, the expression in muscle was significantly higher ($P < 0.01$) (adipose tissue borderline significantly higher, $P = 0.06$) in the LWS than HWS line (Fig. 2A). A differential hypothalamic CPT1B expression between the lines was initially suggested by one probe set in an Affymetrix array analysis (13).
having 99.9% sequence identity to the chicken CPT1B (accession number DQ314726) (Fig. 2B). This differential expression, with higher levels in the HWS than LWS line, was confirmed by qRT-PCR analysis in both hypothalamus from 4 and 56 days of age and from both sexes (Fig. 2B) but not in whole brain tissue, cerebellum, optic tectum, or in telencephalon (Fig. 2C). It is noteworthy that the differential CPT1B mRNA expression with high levels in the LWS line in muscle and adipose tissue was reversed in hypothalamus with significantly lower levels ($P < 0.05$) in the LWS than HWS line. Differential CPT1A expression was not seen (Fig. 2D).

**Phylogeny and evolution of the vertebrate CPTI gene family members.** CPT1c has only been found in mammalian genomes. Using maximum likelihood molecular phylogeny analysis of all available CPT1 amino-acid sequences, we generated a tree in which CPT1c sequences formed a separate clade containing solely mammalian species. This clade was positioned inside the branch holding both mammalian and nonmammalian vertebrate CPT1B sequences. Both CPT1B- and CPT1A-like sequences were found in genomes throughout the vertebrate species (Fig. 3A).

**Chicken HWS and LWS line-specific CPT1B DNA sequence polymorphism.** The significant differential CPT1B expression between the lines implied that the expression level may have been targeted by the divergent selection for body weight and may be due to genetic changes at cis-acting and/or trans-acting regulatory elements. To distinguish between these possibilities, it is necessary to examine patterns of DNA polymorphism around the gene. However, the CPT1B gene has not been mapped, nor has the genomic sequence been retrieved in the chicken genome assembly. To find a polymorphism that could be used for genotyping and for linkage mapping of the chicken CPT1B locus we amplified intronic sequences. Primers based on the partial chicken CPT1B cDNA sequence located in adjacent exons deduced by the gene structure of orthologous genes were used, and only a few of several intron-spanning primer pairs gave a specific amplification product. We amplified a region from the end of deduced exon 23 to the beginning of exon 24 (numbering based on human CPT1B) from two HWS and four LWS chickens. Sequencing of the PCR product confirmed the identity of the sequence but revealed that the intronic sequence largely contained tandem repeats. Due to the highly repeated nature of the DNA sequence, only partial DNA sequence from the fragment could be obtained (data not shown). One sequence length polymorphism was found, and sequence of several individuals indicated that the HWS and LWS birds were homozygous for two different alleles. Using the MegaBACE 1000 DNA Analysis System we designed a genotyping assay that distinguished between the two alleles by PCR fragment length (155 and 159 base pairs) (Fig. 4A). Out of 47 tested, all HWS (25) and all LWS (22) birds were confirmed to be homozygous for different alleles, and 10 F1...
animal were heterozygous, implying that the alleles were fixed or close to fixation in the two parental lines.

Assignment of CPT1B to the distal tip of chicken chromosome 1p. The genotyping assay was used for typing 108 individuals from a F2 intercross pedigree between the HWS and LWS lines (38), and two-point linkage analysis revealed highly significant evidence for linkage between CPT1B and one marker RBL438 (LOD score 28.0, recombination fraction 2.6%) located at the distal tip of chicken chromosome 1p at position 308,721 base pairs (Table 2). The order between CPT1B and RBL438 in relation to the other markers could not be established due to the few recombination events between them and the long distance to the next markers.

The chromosomal position on the tip of chromosome 1p was supported by comparison of gene synteny in the human and chicken genomes. Chicken and human orthologs of CPT1B are syntenic with several of the same genes on both chicken chromosome 1p and human chromosome 11 and CPT1A with genes on chicken chromosome 5 and human chromosome 22q. The human CPT1c gene is on chromosome 19 in a region without any clear homology to any region in the chicken genome (Fig. 3B).

Polymorphism and genotyping of the F9 intercross. We genotyped 80 individuals of an F9 advanced intercross of the HWS and LWS lines (Fig. 4B), previously developed for analyzing the contribution of gene regions to the phenotypes of...
the two lines. Body weight measurements and skeletal muscle tissue had been collected from each individual in the F9 intercross. The body weight at 8 wk was 200–900 g in females and 600–1,200 g in males (Fig. 4C). Comparisons of HWS and LWS genotypes and body weights did not reveal any significant association even when stratified for sex (Fig. 4, D–F). A trend for association between lower body weight and the LWS genotype in females could be seen \((P = 0.06, \text{Fig. 4F})\). The relative \textit{CPT1B} mRNA levels in pectoral muscle from the F9 intercross individuals were analyzed by qRT-PCR and were compared with the genotypes of the individuals. \textit{CPT1B} mRNA levels were significantly associated with genotype in females (Table 3). Although the association was significant when all individuals were taken into consideration, it was not when analyzed only for males (Fig. 4, G–I).

The association, after nine generations of intercrosses, between genotype (LWS \textit{CPT1B} allele) and high mRNA levels in female pectoral muscle (Fig. 4G) showed that the \textit{CPT1B} locus is linked to an eQTL for \textit{CPT1B} expression in muscle in these lines. We could not analyze the expression in hypothalamus because hypothalamus was not sampled at the time when the F9 intercross was collected. \textit{CPT1A} mRNA expression was also analyzed, but no differential expression between genotypes in the F9 intercross was seen (data not shown), in line with the observation of no difference between the lines (Fig. 2D). When we re-examined the QTL data from previous intercross analysis with respect to the markers on the tip of chromosome 1p with the \textit{CPT1B} gene, there was no evidence for a significant QTL for growth that overlapped with the RBL438 marker (11, 28, 38). This indicated that the \textit{CPT1B} locus is not a major QTL for growth under the investigated experimental conditions.

**Mitochondrial proteins in muscle of HWS and LWS lines.**

The differential expression of \textit{CPT1B} mRNA in muscle suggested that mitochondria or mitochondrial biosynthesis may be different in the two lines and that differential mitochondrial function may be a contributing factor to the divergent line phenotypes. We analyzed the protein levels by Western blot of \textit{CPT1B}, NADH-ubiquinol oxidoreductase, and succinate-ubiquinol oxidoreductase. NADH-ubiquinol oxidoreductase and succinate-ubiquinol oxidoreductase represent the mitochondrial oxidative chain complexes and are used to monitor the overall synthesis of mitochondrial proteins in a sample. No significant differences of the analyzed mitochondrial protein levels between genotypes were seen (Fig. 5, A–D), indicating that there are no gross differences in mitochondrial protein levels in pectoral muscle from the lines. However, borderline significantly differential \textit{CPT1B} levels \((P = 0.054)\) in female pectoral muscle supported the observed differential mRNA expression (Fig. 5, A and D).

**DISCUSSION**

The HWS and LWS lines are characterized by marked differences in growth, feeding behavior, food consumption, and a ninefold difference in body weight by 56 days. \textit{CPT1B} was differentially expressed in the lines in both hypothalamus and muscle but with the opposite relation in the two tissues: lower levels in hypothalamus in the LWS line than HWS line, but higher in muscle in LWS than HWS line. The difference attracted our interest, and initially we hypothesized, based on the function of \textit{CPT1B}, that expression differences could have direct contributions to the establishment of the phenotypes of the two chicken lines. \textit{CPT1B} and \textit{CPT1A} catalyze the rate-limiting step of \(\beta\)-oxidation by transporting fatty acids into mitochondria, a function that is essentially conserved throughout the vertebrate tree. The combination of low \textit{CPT1B} expression in muscle that may reflect a low fatty acid \(\beta\)-oxidation, with high feed consumption both seen in the HWS line, could result in increased fat accumulation and a higher body weight. The reverse relationship, with high mitochondrial fatty acid metabolism and low appetite, would result in lean chickens with a low body weight as seen in the LWS chickens. The finding is fully consistent with a previous study showing that the LWS chickens have a higher rate of lipolysis than HWS chickens (5). The observation in this work that \textit{CPT1B} is expressed in chicken hypothalamus and that the expression has been a subject of change in the LWS and HWS lines during selection for growth is intriguing. The \textit{CPT1B} expression in chicken central nervous system (CNS) was not observed in previous studies (36). However, \textit{CPT1B} expression has been recently reported in the brain of the sea bream, another non-mammalian vertebrate species (2).

Our results are consistent with reduced feeding in the \textit{CPT1c} knockout mice and the proposed regulatory role for the mammalian brain-specific \textit{CPT1c} gene in sensing energy status and regulating food intake (27, 30, 40). The function of \textit{CPT1c} has been proposed to be a mammalian innovation and even to represent a gene neofunctionalization (30, 39). The observation that chicken \textit{CPT1c} is expressed in both hypothalamus and muscle and that its expression is different between these lines implies that chicken \textit{CPT1c} may have dual roles, the role both of mammalian \textit{CPT1b} in muscle and that of \textit{CPT1c} in hypothalamus. This would also imply that the proto-ortholog of \textit{CPT1b} and \textit{CPT1c} had roles in both CNS and muscle.

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<th>Genotype</th>
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<th>Females</th>
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<tbody>
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<td>LWS/LWS</td>
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<td>1.43 ± 0.10*</td>
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<td>LWS/HWS</td>
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<td>1.23 ± 0.11</td>
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<tr>
<td>HWS/HWS</td>
<td>1.02 ± 0.11</td>
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Means ± SE. *Female low weight selection (LWS)/LWS vs. female high weight selection (HWS)/HWS, \(P = 0.012\). All other comparisons, not significant. One-way ANOVA, Tukey’s post hoc test.

**Table 3. Least square mean analysis of \textit{CPT1B} muscle expression in the F9 intercross using a model with \textit{CPT1B} genotype and sex**
Mammals have three CPT1 paralogs, while nonmammalian vertebrates have two. Orthologs of CPT1A and CPT1B are found in genomes throughout the vertebrate tree, and phylogeny displays two monophyletic clades joined by a common root shared with agnathan and nonvertebrate CPT1 homologs. CPT1A and B are both located in two well-characterized paralogs that were formed by the two total genome doublings at the base of the vertebrate tree (24). This strongly indicates that vertebrate CPT1A and CPT1B were generated by these genome doublings. All hitherto identified CPT1c orthologs form one clade within the branch with CPT1B sequences, separate from those of CPT1A (Fig. 3A), and since CPT1c only has been found in mammalian genomes, we conclude that CPT1c was formed by a duplication after the divergence of sauropsids including chicken but before the mammalian species radiation. Our data showing a resemblance between mammalian CPT1c and chicken CPT1B but not CPT1A in the mode of regulation also suggest that chicken CPT1B rather than CPT1A represents the proto-orthologous homolog to mammalian CPT1c (and CPT1b). Furthermore, when the expression of CPT1A and B was analyzed in hypothalamus, CPT1B but not CPT1A levels were elevated in hypothalamus compared with the other brain regions. We suggest that the gene function in the proto-orthologous CPT1b/c was divided on the mammalian CPT1b and CPT1c paralogs and is therefore an initial subfunctionalization event with a rapidly diverging CPT1c gene taking on the regulatory CNS functions but leaving the metabolic functions in muscle to the other paralog: CPT1b. We also suggest that the fixation of two such gene functions would have been accelerated by the presence of different regulatory genetic polymorphisms, similar to what have been suggested in this study.

The phenotypes of the HWS and LWS chicken are a result of selection at multiple loci across the genome. A recent genome-wide analysis of 60,000 single nucleotide polymorphisms in the lines identified >100 chromosomal regions that have been divergently selected for during the 50 generations after the start of the selection (12). The analysis was restricted to sequences present in the chicken genome assembly, and therefore the CPT1B region not analyzed. The distal portion of chicken chromosome 1p, which is present in the assembly and presumably is adjacent to the CPT1B-region, shows a small but significant elevation of the signal for divergent selection in the lines (12). This suggests that the marked allele frequency difference at the CPT1B locus between the lines is not a result of genetic drift during the development of the HWS and LWS lines. It was unexpected that the allele frequency of the CPT1B HWS allele had dropped from 0.5 in the F1 generation to ~0.35 in the F6 generation (Fig. 4B) as the design with 40 pairmatings in each intercross generation should reduce random genetic drift. However, at present we cannot exclude the possibility that this change in allele frequency is due to drift, but an alternative explanation would be that the HWS homozygotes have a lower viability or reduced fertility.

At least 13 QTL modifying growth have been detected (11, 28, 38). CPT1B was assigned by linkage analysis to the distal tip of chromosome 1p. The absence of a QTL for growth on the tip of chicken chromosome 1 shows that the CPT1B locus is not a major QTL for growth in these lines. However, there are several reasons why our QTL analysis may have failed to detect a QTL although it exists. First, it may be due to lack of power, although an F2 generation of ~800 birds was used. Our previous studies have shown that a large number of QTL each with a rather small individual effect are underlying the dramatic phenotypic differences between the HWS and LWS lines. Second, epistatic interaction between QTL has contributed significantly to the selection response in these lines (6), making QTL detection even more challenging. Third, most F2
individuals have an intermediate body weight, and it is possible that the CPT1B locus has a more pronounced effect at the more extreme body weights present in purebred HWS and/or LWS chickens. The preserved association between high CPT1B mRNA expression in pectoral muscle and the LWS genotype even after nine generations of intercrosses strongly suggests that the differential expression of CPT1B has a genetic component (Fig. 4G). We therefore conclude that the differential expression in muscle between lines most likely is caused by a cis-acting eQTL.

It is very unlikely that the line-specific intronic sequence polymorphism that was used for mapping and genotyping in this study is by itself the regulatory mutation. Repeated attempts were made to isolate and sequence other nonexonic regions of the gene but were not successful. The difficulties in amplifying and sequencing the intron sequence and the fact that the region containing CPT1B on the distal chromosome 1p is missing from the chicken genome assembly suggest that the region contains DNA with a repetitious nature that is difficult to sequence or even amplify. The poor coverage of this region may in fact have affected the result in the previously performed QTL analyses.

The gene structure of chicken CPT1B is not known, but other CPT1 homologs all have a complex gene structures with >18 exons and alternative splicing in the 5'-end of the gene (42). Transcripts with different 5'-exons encoding different 5'-untranslated region (UTR) sequences indicate different transcriptional start sites and the existence of multiple regulatory elements that each separately may confer tissue-specific expression (http://www.ensembl.org; human CPT1A ENSG00000110090, CPT1B ENSG00000205560, CPT1C ENSG00000169169). The hypothalamic and muscle-specific chicken CPT1B expressions can therefore be regulated separately by unique regulatory elements that would allow for accumulation of cis- as well as trans-acting mutations with opposite effects in the two lines during the course of divergent selection. Such a mode of regulation is consistent with results showing that the human CPT1c 5'-UTR contains repressing sequences under the regulation of specific conditions of cellular energy availability (22).

Malonyl-CoA regulates lipid and glucose metabolism in skeletal muscle (3, 31). The levels of malonyl-CoA are physiologically regulated by fasting and feeding, and increasing amounts of evidence support a role for malonyl-CoA as a signaling mediator of energy balance in the CNS (10). Pharmacological inhibition of CPT1 in the CNS inhibits food intake, suggesting that malonyl-CoA may suppress food intake through a CNS-expressed CPT1 (27). A similar regulatory role in the chicken brain is suggested by the differential expression of CPT1B without a general change in mitochondrial biogenesis and regulation at 56 days as indicated by similar levels of NADH-ubiquinol oxidoreductase and succinate-ubiquinol oxidoreductase in muscle in the lines (Fig. 5). The AMP-activated protein kinase modulates the malonyl-CoA concentrations by regulating Acetyl-CoA carboxylases and is thereby linked via the malonyl-CoA signaling mechanism to the role of CPT1 (1). In a recent experiment, food intake was studied after stimulation or inhibition of the AMP-activated protein kinase in the chicken lines used in this study (41). The result showed differences between the lines in the responses after the activity of the AMP-activated protein kinase was manipulated. The differential CPT1B expression identified in this study may be one of the factors that contribute to these different responses.

We propose that altered regulation of CPT1B expression in both hypothalamus and peripheral tissue is one important mechanism underlying the remarkable differences in appetite, fat deposition, and growth between the HWS and LWS lines. This is supported by the findings that 1) the two lines are fixed or nearly fixed for different CPT1B alleles and 2) a cis-acting eQTL affects CPT1B expression at least in muscle. Our genetic data and expression data suggest that both cis-acting and trans-acting factors contribute to the differential CPT1B expression in these lines. The increased expression of CPT1B in hypothalamus and its reduced expression in muscle are consistent with increased appetite and food intake in the HWS line and at the same time reduced fatty acid oxidation in muscle, yielding a maximum net accumulation of energy intake and storage. This inverse regulation of CPT1B expression, uncovered by the divergent selection for growth, may constitute a mechanism that promotes fast accumulation of energy stores by combining large appetite and low fatty acid oxidation and metabolism in the peripheral tissues. In nature this kind of regulation may have been favorable for animals when efficient and fast accumulation of sufficient energy stores is required, for example during preparations for winter hibernation or long-distance migration that are performed by many birds every year. The normal satiety mechanisms should in such cases be set out of play, in order for the individual to collect sufficient reserves of energy. The results presented in this study thus uncover one link in the complex network that regulates energy homeostasis and appetite, which underlies the genetic foundation for our variable responses that drive behaviors to satisfy our quest for energy and food.

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DISCLOSURES

No conflicts of interest, financial or otherwise, are declared by the author(s).

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REFERENCES


