Thyroid hormones act indirectly to increase sex hormone-binding globulin production by liver via hepatocyte nuclear factor-4α

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Abstract

Thyroid hormones increase hepatic sex hormone-binding globulin (SHBG) production, which is also regulated by hepatocyte nuclear factor-4α (HNF-4α) in response to changes in the metabolic state of the liver. Since the human SHBG promoter lacks a typical thyroid hormone response element, and because thyroid hormones influence metabolic state, we set out to determine whether thyroid hormones mediate SHBG expression indirectly via changes in HNF-4α levels in HepG2 human hepatoblastoma cells, and in the livers of transgenic mice that express a 4.3 kb human SHBG transgene under the control of its own 0.8 kb promoter sequence. Thyroid hormones (triiodothyronine (T₃) and thyroxine (T₄)) increase SHBG accumulation in HepG2 cell culture medium over 5 days, and increase cellular SHBG mRNA levels. In addition, T₄ treatment of HepG2 cells for 5 days increased HNF-4α mRNA and HNF-4α levels in concert with decreased cellular palmitate levels. Plasma SHBG levels were also increased in mice expressing a human SHBG transgene after 5 days treatment with T₄ along with increased hepatic HNF-4α levels. In HepG2 cells, the human SHBG promoter failed to respond acutely (within 24 h) to T₄ treatment, but a 4-day pre-treatment with T₄ resulted in a robust response that was prevented by co-treatment with HNF-4α siRNA, or by blocking the β-oxidation of palmitate through co-treatment with the carnitine palmitoyltransferase I inhibitor, etomoxir. These data lead us to conclude that thyroid hormones increase SHBG production indirectly by increasing HNF-4α gene expression, and by reducing cellular palmitate levels that further contribute to increased HNF-4α levels in hepatocytes.

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Introduction

Thyroid hormones influence plasma sex hormone-binding globulin (SHBG) levels under both normal and pathological conditions (Anderson 1974) by altering the production of SHBG by hepatocytes (Rosner et al. 1984). In addition, blood levels of SHBG in infants increase within the first 2–3 weeks after birth, and this has been attributed to a postnatal maturation of hepatic sensitivity to thyroid hormones (Leger et al. 1990). Plasma SHBG levels are also commonly elevated beyond normal reference ranges in patients with hyperthyroidism (Anderson 1974), but are not increased in individuals suffering from familial thyroid hormone resistance, despite their very high blood levels of thyroid hormones (Sarne et al. 1988). Since the latter is likely due to defects in thyroid hormone action in the liver, it has been proposed that plasma SHBG measurements can be used clinically to assess end-organ sensitivity to thyroid hormones (Sarne et al. 1988).

Human HepG2 hepatoblastoma cells have been widely used as a model for the studies of thyroid hormone action in the liver (Rosner et al. 1984, Raggatt et al. 1992, Kester et al. 2006). These cells express the type I iodothyronine deiodinase that converts the pro-hormone thyroxine (T₄) into the receptor-active triiodothyronine (T₃) in the normal liver, but they lack the type III iodothyronine deiodinase: a key enzyme responsible for deactivating thyroid hormones in the liver and other tissues (Kester et al. 2006). On the other hand, HepG2 cells express the glucuronidases responsible for the metabolic clearance of thyroid hormones in the liver (van Stralen et al. 1996). The human SHBG gene is also expressed in HepG2 cells and their production of SHBG is enhanced by thyroid hormone treatments in concert with an increase in SHBG mRNA levels (Rosner et al. 1984, Mercier-Bodard et al. 1991, Raggatt et al. 1992).

In earlier studies, increases in plasma SHBG have been noted in hypothyroid patients several days after the initiation of treatment with T₃ (Sarne et al. 1988), and this is consistent with studies in which treatment of HepG2 cells with thyroid hormones increase SHBG production after 2–3 days (Rosner et al. 1984, Raggatt et al. 1992). It has been assumed that these responses are mediated directly by the thyroid hormone receptor.
(TR) acting at the level of the human SHBG gene. Thyroid hormones exert their effects at the gene level via the TR, which generally binds as a heterodimer with the retinoid X receptor to cis-acting elements that are referred to as thyroid hormone response elements (TREs) within target gene promoters. A typical TRE is a tandem repeat of the consensus AGGTCA separated by four nucleotides (Zhang & Lazar 2000), and is classified as a direct repeat-4 (DR-4) element. It was therefore of interest that a bioinformatic scan failed to identify a DR-4-like element that might act as a TRE within the human SHBG promoter responsible for controlling its expression in the liver (Jänne & Hammond 1998).

Since thyroid hormones influence the metabolic state of the liver (Malik & Hodgson 2002) and because we have recently demonstrated that SHBG gene expression in hepatocytes is dynamically regulated by changes in their metabolic state (Selva et al. 2007), we set out to determine whether thyroid hormone-induced changes in the metabolic state of HepG2 cells and the liver could account for changes in SHBG expression.

Materials and methods
Cell culture experiments
Cell culture reagents were from Life Technologies Inc. (Invitrogen). HepG2 hepatoblastoma cells (catalog no. HB-8065; ATCC, Manassas, VA, USA) were routinely maintained in DMEM supplemented with 10% FBS and antibiotics (100 U penicillin/ml and 100 μg streptomycin/ml). For experiments, HepG2 cells were cultured to 30–50% confluence prior to the addition of supplements: glucose (Sigma–Aldrich Canada Ltd), T3 (Sigma–Aldrich), T4 (Sigma–Aldrich) or etomoxir (Sigma–Aldrich), as indicated. Palmitate levels in HepG2 cells were determined as described previously (Selva et al. 2007).

Transient transfections of human SHBG promoter-driven luciferase reporter plasmids together with a pCMVlacZ control plasmid (Jänne & Hammond 1998, Selva et al. 2007) were performed using the HiPerfect Transfection Reagent (Qiagen). The siRNA experiments were carried out using HiPerfect Transfection Reagent together with either a control siRNA (catalog 1022076) or an hepatocyte nuclear factor-4α (HNF-4α) siRNA (catalog 00161546) obtained from Qiagen. Two days after transfection, the cells were washed twice with PBS and harvested by scraping. After centrifugation, cell pellets were resuspended in 100 μl 250 mM Tris–Cl, pH 7.8, and cells were lysed by three freeze–thaw cycles. Appropriate aliquots of cell extracts were used for measurements of luciferase and β-galactosidase activity.

To correct for transfection efficiency, light units from the luciferase assay were divided by the OD reading from the β-galactosidase assay.

SHBG measurements
Human SHBG levels in culture medium taken from HepG2 cells were measured using a time-resolved immunofluorometric assay (Niemi et al. 1988).

RNA analysis
Total RNA was extracted from HepG2 cells using TRIzol reagent (Invitrogen). Reverse transcription (RT) was performed at 42°C for 50 min using 3 μg of total RNA and 200 U of Superscript II together with an oligo(dT) primer and reagents provided by Invitrogen. An aliquot of the RT product was amplified in a 35-μl reaction using PCR SuperMix (Invitrogen) with appropriate oligonucleotide primer pairs corresponding to human HNF-4α (forward primer 5’-GCTCTCTCCCTTGCTGTCGC and reverse primer 5’-GGAAGAGCTTGAGACAGGCC), SHBG (forward primer 5’-GTTGCTACTACTGGTGCACAC and reverse primer 5’-GCCATCTCCATCATGGGCG), TR1-α (forward primer 5’-CCGCCACACATCCAGGACA and reverse primer 5’-GGGAATGTGGATCAGATCCC), and cyclophilin A (forward primer 5’-ATGGTCACCCCCCCCGTG and reverse primer 5’-CGCAATTTTGGATCAGATCCC). The PCR was performed for 40 cycles at 94°C for 15 s, 57–65°C for 30 s, and 72°C for 1 min, and PCR products were resolved by electrophoresis in a 1% agarose gel.

Treatment of human SHBG transgenic mice with thyroid hormone
Mice that express a 4.3 kb human SHBG transgene in the liver (Jänne et al. 1998) were routinely maintained on standard laboratory chow and water provided ad libitum. The human SHBG transgene in these mice is expressed in the liver under the control of its own ~800 bp promoter sequence that corresponds to the same sequence we have studied in the context of a luciferase reporter gene (Jänne & Hammond 1998, Selva et al. 2007). For the experiment, female mice (n = 3) were treated with water (controls) or water containing T3 (0.5 mg/l) for 5 days. Blood samples were taken by saphenous vein sampling for measurements of plasma SHBG levels (Selva et al. 2007) immediately before the treatment, and on day 5 of treatment when livers were also taken for RNA and protein extraction (see below). Animals were weighed before and after treatment and no change in weights were observed in either group over
the 5 days of treatment. This animal protocol was approved by the Animal Use Subcommittee of the University Council on Animal Care at The University of British Columbia.

**Total cellular and nuclear protein extracts**

After treatments, mouse livers or HepG2 cells were harvested and homogenized in 50 mM Tris–HCl, pH 7-9, 300 mM KCl, 1·5 mM MgCl₂, 0·1% Nonidet P-40, and 20% glycerol supplemented with Complete protease inhibitor cocktail (Roche Diagnostics) at 4 °C, followed by centrifugation (11 000 g for 10 min) to obtain total protein extracts. For nuclear protein extracts, the HepG2 cells were first incubated on ice for 10 min with hypotonic buffer (10 mM HEPES, pH 7·9, 1·2 M KCl, 1 mM EDTA, 1 mM EGTA, 0·5 mM dithiothreitol (DTT), 0·2 mM phenylmethylsulfonyl fluoride (PMSF), and the Complete protease inhibitor cocktail) and centrifuged through a 3 ml 1 M sucrose cushion at 4 °C for 30 min to obtain a nuclear extract, which was dialyzed overnight against 20 mM Tris, pH 7·9, 100 mM KCl, 1 mM EDTA, 1 mM EGTA, and 0·5 mM DTT containing 10% glycerol.

**Western blot analysis**

Total cell protein and nuclear protein extracts were used for western blotting with antibodies against human HNF-4α (C-19; catalog sc-6556; Santa Cruz Biotechnology Inc., Santa Cruz, CA, USA) and human cyclophilin A (SA-296; BIOMOL Int., Plymouth Meeting, PA, USA). Specific antibody–antigen complexes were identified using an HRP-labeled goat anti-rabbit IgG or rabbit anti-goat IgG and chemiluminescent substrates (Pierce Biotechnology Inc., Rockfort, IL, USA) by exposure to X-ray film.

**Statistical analyses**

Data were analyzed using one-way ANOVA, and P values of <0·05 were considered significant.

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**Results**

**Thyroid hormones only increase SHBG production by HepG2 cells after 2 days of treatment**

We first examined the effects of daily supplementation with T₃ (100 nM) or T₄ (100 nM) on SHBG production by HepG2 cells over the course of 5 days, by comparing medium concentrations of SHBG on days 1 and 5 of thyroid hormone treatments. This showed that T₃ and T₄ stimulated SHBG production (P<0·001), and that T₄ was more effective than T₃ (Fig. 1A). In addition, the amount of SHBG mRNA was clearly increased in relation to the cyclophilin A mRNA control in HepG2 cells after 5 days treatment with T₄, but this was not as obvious after treatment with T₃ (Fig. 1B).

The effect of T₄ on SHBG gene expression in HepG2 cells was then studied over a 3-day treatment period during which 100 nM T₄ was added daily to the cultures, coincident with the collection of culture media for measurements of SHBG production rates (Fig. 1C). This demonstrated that the T₄-induced increases in SHBG production are only apparent (P<0·05) after 2 days of treatment, and increase substantially between treatment days 2 and 3 (P<0·001). We also explored the possibility that the delayed response to thyroid hormone in HepG2 cells might be due to an increase in TR expression, but within the time frame of our experiments in which HepG2 cells were treated with T₄ there was no change in their TR1-α mRNA levels, as assessed by RT-PCR (Fig. 1D).

We next examined whether T₄ (100 nM) treatments influence SHBG production by HepG2 cells over a 5-day period when the cells were cultured in high concentrations of glucose. This demonstrated that T₄ increased SHBG production by HepG2 cells regardless of whether they were maintained in the presence of 100 μM glucose (control) or 10 mM glucose, added as daily supplements (Fig. 1E).

**Human SHBG promoter lacks a TRE and only responds in HepG2 cells after several days pre-treatment with T₄**

We have previously demonstrated that the 803 bp human SHBG promoter, which controls its activity in the liver, is influenced by a polymorphic TAAAA repeat sequence in the distal promoter sequence (Hogeveen et al. 2001) as well as a Sp1 site (Fig. 2A). However, when these upstream sequences are removed, the proximal 299 bp promoter sequence is not only generally more active in HepG2 cells (Jänne & Hammond 1998), but also retains its responsiveness to changes in metabolic state (Selva et al. 2007), or to treatments with drugs that act via the peroxisome proliferator receptor γ that binds to the DR-1 element in the 299 bp human
SHBG promoter and represses its transcriptional activity (Selva & Hammond 2009). This DR-1 sequence can also bind HNF-4α as well as COUP-TF, but does not appear to have much influence on the basal transcriptional activity of the human SHBG promoter in HepG2 cells. This DR-1 sequence can also bind HNF-4α as well as COUP-TF, but does not appear to have much influence on the basal transcriptional activity of the human SHBG promoter in HepG2 cells. By contrast, the ‘TATA-less’ human SHBG promoter (Jänne & Hammond 1998) contains another binding site for HNF-4α and COUP-TF, which is located in the position where a TATA box would normally be positioned (Fig. 2A), and this appears to serve as the major on–off switch for SHBG transcription: such that occupancy of this site by HNF-4α promotes transcription while COUP-TF binding represses transcription (Jänne & Hammond 1998, Selva et al. 2007). The 299 bp human SHBG promoter sequence also contains a binding site for USF transcription factors (Fig. 2A) that play a key role in controlling the expression of the SHBG gene in testicular cell types, but has no obvious role in hepatocytes (Selva et al. 2005).

Although an analysis of the 803 bp human SHBG promoter failed to identify a sequence that resembles a typical TRE (Zhang & Lazar 2000), a DR-8 sequence that has been reported to function as an atypical TRE (Bouterfa et al. 1995) overlaps the DR-1 element within the 299 bp SHBG proximal promoter (Fig. 2A). However, the half-site of this DR-8 sequence extends outside the DNase 1 footprinted region in which this DR-1 element is located (Jänne & Hammond 1998).

Since we found that T₄ was clearly more effective than T₃ in increasing SHBG production by HepG2 cells (Fig. 1), we used T₄ to treat HepG2 cells in subsequent experiments to explore its mechanism of action. When the activities of the 803 and 299 bp human SHBG promoter sequences were tested in the context of a luciferase reporter gene assay after treatment with T₃ and T₄ increase SHBG production via HNF-4α. By contrast, the ‘TATA-less’ human SHBG promoter (Jänne & Hammond 1998) contains another binding site for HNF-4α and COUP-TF, which is located in the position where a TATA box would normally be positioned (Fig. 2A), and this appears to serve as the major on–off switch for SHBG transcription: such that occupancy of this site by HNF-4α promotes transcription while COUP-TF binding represses transcription (Jänne & Hammond 1998, Selva et al. 2007). The 299 bp human SHBG promoter sequence also contains a binding site for USF transcription factors (Fig. 2A) that play a key role in controlling the expression of the SHBG gene in testicular cell types, but has no obvious role in hepatocytes (Selva et al. 2005).

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Figure 1 Increases in human SHBG production by HepG2 cells occur after 2 days treatment with thyroid hormone. (A) HepG2 cells were cultured in medium containing FBS for 5 days and treated daily with or without 100 nM T₃ or T₄. Accumulation of human SHBG in the medium was measured using an immunofluorometric assay. Data points are shown as mean ± S.D. of triplicates. ***P<0.001 compared with the control. (B) Semi-quantitative RT-PCR analysis of SHBG mRNA levels in HepG2 cells cultured for 5 days with daily addition of 100 μM glucose and PBS vehicle (control), 100 nM T₃ or T₄ (100 nM). Cyclophilin A (CypA) mRNA was amplified as an internal control. (C) HepG2 cells were cultured in medium containing FBS for 3 days and treated with thyroid hormone (100 nM T₄ in PBS) or PBS control. Accumulation of human SHBG in the medium was measured every 24 h using an immunofluorometric assay. Data points are mean ± S.D. of triplicates. *P<0.05 and ***P<0.001 compared with the control. (D) Semi-quantitative RT-PCR analysis of TR1-α mRNA levels in HepG2 cells cultured for 5 days with PBS vehicle (control) or 100 nM T₄. Cyclophilin A (CypA) mRNA was amplified as an internal control. Data points are mean ± S.D. of triplicates. *P<0.05 and ***P<0.001 compared with the control. (E) HepG2 cells were cultured in medium containing FBS for 5 days and treated daily with 100 μM glucose (control) or 10 mM glucose in the presence or absence of 100 nM T₄. Accumulation of human SHBG in the medium was measured using an immunofluorometric assay. Data points are shown as mean ± S.D. of triplicates. ***P<0.001 compared with the control.
levels in HepG2 cells after a 5-day treatment with T₄. This indicated that the amounts of HNF-4α mRNA were substantially increased after treatment with 100 nM T₄ (Fig. 3A), and that this resulted in an increase in SHBG in total cell protein extracts as well as a substantial increase in HNF-4α within nuclear extracts, as demonstrated by western blotting (Fig. 3B). To confirm that this effect of thyroid hormone on increasing the production of SHBG is associated with an increase in hepatic HNF-4α levels in vivo, we treated mice expressing a human SHBG transgene in the liver with T₃ by adding it to their drinking water. This almost doubled the plasma levels of human SHBG (P<0.05) after 5 days of T₃ treatment (Fig. 4A), and resulted in a similar increase in hepatic HNF-4α levels (P<0.01) as assessed by western blotting (Fig. 4B).

In order to demonstrate that the thyroid hormone effect on SHBG expression in HepG2 cells is mediated through increasing HNF-4α levels, we pre-treated the cells daily for 4 days with or without 100 nM T₄, and examined the activity of the 299 bp human SHBG promoter in the context of a luciferase reporter gene assay after co-transfection with either a control siRNA or a siRNA for HNF-4α. The results clearly indicate that the increased SHBG promoter activity seen after 4 days pre-treatment with 100 nM T₄ can be abrogated (P<0.001) by treatment with the siRNA for HNF-4α (Fig. 5A). As expected, the siRNA for HNF-4α also reduced SHBG promoter activity in untreated HepG2 cells (P<0.01), but the magnitude of the decrease was less than that seen in the T₄-treated cells (Fig. 5A). As a control for the effectiveness of the siRNA treatment,
Western blots from nuclear extracts of cells treated under the same conditions reveal a substantial increase in nuclear HNF-4α protein levels when the HepG2 cells were treated with 100 nM of T4, while treatment with siRNA for HNF-4α reduces the protein levels of HNF-4α in cells pre-treated with either the vehicle control or 100 nM T4 (Fig. 5B). Inhibition of β-oxidation blocks the thyroid hormone effect on SHBG production and HNF-4α levels in HepG2 cells

Recently, we have demonstrated that HNF-4α levels in HepG2 cells decrease in response to increased lipogenesis and cellular palmitate levels, and that this leads to a reduction in SHBG gene expression (Selva et al. 2007). We therefore measured the palmitate content of HepG2 cells treated for 5 days with 100 nM T4 versus untreated cells, and found lower levels of palmitate in the T4-treated cells (6.4 μg/10^6 cells). Since thyroid hormones increase metabolic rate and influence cellular levels of carnitine palmitoyltransferase I (CPTI), the rate-controlling enzyme in the fatty acid oxidation pathway (McGarry & Brown 1997), we performed an experiment in which HepG2 cells were treated with 100 nM of T4 or vehicle control alone or in the presence of etomoxir, a CPTI inhibitor (Murthy & Pande 1990). This showed that treatment with 5 or 10 μM etomoxir did not influence SHBG production by control cells, but reduced (P<0.05 and P<0.01 respectively) the increase in SHBG production by T4-treated HepG2 cells (Fig. 6A), as well as the increase in HNF-4α protein levels that occurs in response to T4 treatment (Fig. 6B).

**Discussion**

T4 increases the production and secretion of SHBG by HepG2 cells, and this response is only apparent after 2–5 days of treatment, as reported previously (Rosner et al. 1984). In our experiments, equimolar amounts of T4 were consistently more effective than T3 in these in vitro experiments, and this may be due to differences in their transport into cells in culture when compared with the liver in vivo, as well as differences in their metabolism in HepG2 cells versus normal hepatocytes. By contrast, our experiments using a transgenic mouse western blots from nuclear extracts of cells treated under the same conditions reveal a substantial increase in nuclear HNF-4α protein levels when the HepG2 cells were treated with 100 nM of T4, while treatment with siRNA for HNF-4α reduces the protein levels of HNF-4α in cells pre-treated with either the vehicle control or 100 nM T4 (Fig. 5B).
Most importantly, these results demonstrate that the effect of thyroid hormone on SHBG gene expression only requires sequences within the proximal promoter, and we found this to be remarkable because it lacks a typical TRE. Moreover, the fact that the SHBG promoter failed to respond to either $T_3$ or $T_4$ within 48 h suggests that the thyroid hormone-induced increase in SHBG gene expression is mediated indirectly through some other mechanism, and we excluded the possibility that this might involve thyroid hormone-mediated changes in the expression of the TR itself.

We have recently found that the human SHBG gene in HepG2 cells, as well as in a transgenic mouse model, responds to changes in metabolic state brought about by increased lipogenesis after treatment with glucose or fructose (Selva et al. 2007). Importantly, these studies demonstrated that this effect is mediated by alterations in cellular HNF-4α levels, which acts as a key regulator of SHBG transcription (Jänne & Hammond 1998). Since HNF-4α responds to and modulates the metabolic state of the liver (Sladek 1993, Jump 2004), and because thyroid hormones increase the basal metabolic rate of the liver (Malik & Hodgson 2002), we explored the possibility that the changes in SHBG expression in HepG2 cells after 5 days treatment with thyroid hormones involves changes in HNF-4α expression and/or its accumulation. Our results support this because we observed an increase in cellular HNF-4α mRNA content, as well as an increase in nuclear HNF-4α levels, in concert with an increase in SHBG mRNA levels after the cells were treated with $T_4$, and the $T_4$-mediated increase in SHBG production by HepG2 cells occurs regardless of whether the cells were cultured in the presence of low or high levels of glucose. We also found that the addition of $T_3$ to the drinking water of mice that express a human SHBG transgene in their liver results in an increase in the blood levels of human SHBG in these mice, and that this occurs in parallel with an increase in hepatic HNF-4α levels in the same animals. While there is no evidence that thyroid hormones directly regulate the HNF-4α gene in the liver, a change in the metabolic state of the liver after $T_4$ treatment could in turn influence HNF-4α expression.

The essential role of HNF-4α in enhancing SHBG transcription in HepG2 cells in response to thyroid hormones was demonstrated by blocking the increase in cellular HNF-4α levels by using a siRNA approach. It was considered important to do this because thyroid hormones could increase the expression of other transcription factors that might influence SHBG expression, or coactivators, such as Trp-3, PGC-1α, Src-1, and Src-3 (Zhang & Lazar 2000) that influence the activities of transcription factors, including HNF-4α (Wang et al. 1998, Yoon et al. 2001, Iwahashi et al. 2002). We therefore also studied the effects of the thyroid hormone treatments on the levels of Trp-3, PGC-1α, HNF-4α, and CypA.
and Src-3 mRNA levels in the HepG2 cells, and failed to observe any changes in semi-quantitative RT-PCR assays (data not shown). Moreover, our results imply that the effect of thyroid hormone on human SHBG expression is entirely due to the increase in HNF-4α levels, because siRNA suppression of the T₄-induced HNF-4α levels in HepG2 cells completely blocked the T₄-induced increase in SHBG promoter activity.

It is possible that HNF-4α levels in HepG2 cells are also influenced by their overall metabolic state because we have previously observed that HNF-4α levels are reduced in concert with increases in the cellular content of palmitate after treatment of HepG2 cells with either monosaccharides or palmitoyl CoA (Selva et al. 2007). Our present experiments further support this by showing that a reduction in cellular palmitate levels after T₄ treatment occurs in concert with an increase in HNF-4α levels. It is also known that thyroid hormones increase the expression of CPTI (Mynatt et al. 1994), and this likely explains the reduced palmitate levels in HepG2 cells treated with T₄. Taken together therefore, these observations have led us to conclude that the lipid content of the cells must in some way influence the production and/or the accumulation of HNF-4α, which in turn plays a pivotal role in controlling SHBG gene expression. This is further supported by our experiment in which HepG2 cells were treated with T₄ in the presence or absence of a CPTI inhibitor to block palmitate oxidation, which resulted in a loss of the thyroid hormone stimulated increase in HNF-4α levels and a concomitant reduction in production of SHBG by HepG2 cells.

In conclusion, our studies demonstrate that the well-known effect of thyroid hormones on increasing plasma SHBG levels reflects an alteration in the metabolic state of hepatocytes resulting in increased nuclear HNF-4α levels, which in turn act on the SHBG promoter to increase its transcriptional activity. It remains to be determined whether thyroid hormones act directly or indirectly to alter HNF-4α gene expression in hepatocytes, but our data do imply that changes in metabolic state contribute in part to an increase in HNF-4α levels within hepatocytes treated with thyroid hormones.

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Declaration of interest

The authors declare that there is no conflict of interest that would prejudice the impartiality of this scientific work.

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