Thyroid hormone induced angiogenesis through the integrin αvβ3/protein kinase D/histone deacetylase 5 signaling pathway

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Key Words
- thyroid hormone
- angiogenesis
- integrin αvβ3
- protein kinase D
- histone deacetylase 5
- basic fibroblast growth factor
- human umbilical vein endothelial cells

Abstract

Thyroid hormone is reported to induce angiogenesis, which is mediated by the membrane receptor integrin αvβ3, but the precise signaling pathway is still not very clear. Recently, studies have shown that protein kinase D (PKD) regulates the recycling of integrin αvβ3, which is required for cell migration. Moreover, phosphorylated PKD stimulates histone deacetylase 5 (HDAC5) phosphorylation and nuclear export in endothelial cells. As a potent pro-angiogenic growth factor, basic fibroblast growth factor (bFGF (FGF2)) is a downstream target gene of HDAC5. Therefore, we examined the hypothesis that a novel signaling pathway through integrin αvβ3/PKD/HDAC5 might contribute to thyroxine (T4)-induced angiogenesis. We selected human umbilical vein endothelial cells (HUVECs) for treatment. Angiogenesis was assessed using wound-healing and tubulogenesis assays. Signaling molecules, including phosphorylated PKD and HDAC5, were measured by western blotting. bFGF mRNA was analyzed by real-time PCR. Our results showed that T4 (100 nmol/l) stimulated the migration and formation of tube-like structures of HUVECs, whereas tetraiodothyroacetic acid (Tetrac, 100 nmol/l) inhibited T4-induced cell migration. Importantly, T4 promoted the phosphorylation of PKD and HDAC5. These effects were inhibited respectively by Tetrac, PKC inhibitor (2.5 µmol/l) and PKD siRNA. Meanwhile, T4 could promote the cytoplasmic accumulation of phosphorylated HDAC5 in HUVECs. In addition, bFGF mRNA expression in HUVECs significantly increased within 2 h of T4 treatment, but was decreased by Tetrac. Our findings indicate that T4 increases the expression of bFGF mRNA via the integrin αvβ3/PKD/HDAC5 signaling pathway, which plays an important role in angiogenesis.

Introduction

Angiogenesis, the formation of new blood capillaries, is an important component of embryonic vascular development, wound healing and organ regeneration. It also contributes to pathological processes, including diabetic retinopathy, atherosclerosis and tumor growth (Folkman 1995, Carmeliet et al. 2003, Ferrara et al. 2003). The process of angiogenesis includes coordinated endothelial cell proliferation, invasion, migration, and tube formation. It is orchestrated by different growth factors, such as vascular endothelial growth factor (VEGF),...
angiopoietins, basic fibroblast growth factor (bFGF) and so on (di Blasio et al. 2010).

Recently, effects of thyroid hormones, including l-thyroxine (T4), and 3,5,3′-triiodo-l-thyronine (T3), on angiogenesis have been observed in studies of the chick chorioallantoic membrane model (Davis et al. 2004, Mousa et al. 2006a,b) and the human dermal microvascular endothelial cell microtubular model (Mousa et al. 2006a,b). Bergh et al. (2005) identified integrin αvβ3 as a cell surface receptor for thyroid hormone (T4) and as the initiation site for T4-induced angiogenesis. The extracellular domain of integrin αvβ3 includes an Arg-Gly-Asp (RGD) recognition site that is an important verification domain for the ligands of the protein (Plow et al. 2000). The thyroid hormone receptor on integrin αvβ3 is located at or near the RGD recognition site. It is reported that T4 is bound with greater affinity to integrin than T3. By binding to integrin αvβ3, the thyroid hormone signal is transduced by the MAPK (extracellular regulated kinase 1/2, ERK1/2) cascade (Davis et al. 2004, Bergh et al. 2005). Several complex downstream events occur as a result of the activation of ERK1/2, including regulation of the activity of the plasma membrane Na+/H+ antiporter (D’Arezzo et al. 2004), an increase in activity of cell membrane Na+, K+-ATPase (sodium pump) (Lei et al. 2008), secretion of some vascular growth factors including bFGF, consequent angiogenesis (Davis et al. 2004), etc. However, the precise signaling system of T4-induced angiogenesis has not been discovered yet.

There is recycling of integrin αvβ3 in cells, which is required for cell migration (Ramsay et al. 2007, Mai et al. 2011). di Blasio et al. (2010) found that protein kinase D1 (PKD1), a novel serine/threonine protein kinase, promotes integrin αvβ3 recycling and inhibits its endocytosis. PKD1 is also reported to be phosphorylated in endothelial cells in response to VEGF and serves as a histone deacetylase (HDAC) kinase (Vega et al. 2004a,b). This signaling was confirmed by Ha et al. (2008a,b) to mediate VEGF-induced angiogenesis. They suggested that through a VEGF receptor 2-phospholipase Cγ (PLCγ)–protein kinase C (PKC)–PKD1-dependent pathway, VEGF stimulates HDAC5 phosphorylation and nuclear export in endothelial cells, which induces gene expression and angiogenesis. Besides HDAC5, another class II a HDAC family member, HDAC7, which was also reported by Ha et al. (2008a,b), is activated through the VEGF–PKD1-dependent pathway and accumulates in the cytoplasm of endothelial cells.

HDAC5-dependent regulation of gene expression is well known to control angiogenesis. By binding to the promoter of the bFGF (FGF2) and SLIT2 genes, HDAC5 represses the expression of these pro-angiogenic genes, whereas HDAC5 silencing promotes capillary sprouting of endothelial cells (Urbich et al. 2009). Accordingly, we propose that a new signaling pathway of integrin αvβ3/PKD/HDAC5 is involved in regulating bFGF expression, which further affects the angiogenesis induced by thyroid hormone.

Materials and methods

Materials

L-T4 and tetraiodothyroacetic acid (Tetrac) were purchased from Sigma–Aldrich. MAB to GAPDH, β-actin and PKC inhibitor (bisindolylmaleimide I, HCl, Bis) were purchased from Santa Cruz Biotechnology, Inc. The Nuclear and Cytoplasmic Protein Extraction Kit was obtained from KeyGEN BioTECH (Nanjing, Jiangsu, China). Anti-phosphorylated PKD, PKD, phosphorylated HDAC5 and HDAC5 were obtained from Cell Signaling Technology (Beverly, MA, USA). Matrigel was obtained from BD Biosciences (Franklin Lakes, NJ, USA). GenMute siRNA Transfection Reagent was purchased from SignaGen Laboratories (Ijamsville, MD, USA).

Cell culture and treatment

Human umbilical vein endothelial cells (HUVECs, ATCC, Manassas, VA, USA) were cultured in DMEM/F12 (Invitrogen) supplemented with 1000 U/l penicillin, 1 mg/ml streptomycin and 10% (v/v) fetal bovine serum (FBS) in an atmosphere of 5% CO2 at 37 °C. For experimental purposes, 80% confluent HUVECs were preincubated for 24 h in a serum-free medium, the cells were treated for 15, 30, and 45 min with vehicle or T4 (100 nmol/l). Tetrac (100 nmol/l) and Bis (2.5 μmol/l) were used to pretreat the cells for 30 min before adding T4

Western blotting

Whole-cell lysates were prepared in RIPA buffer (Sigma–Aldrich) containing complete protease inhibitors (Roche Diagnostics Ltd), and protein concentration was determined using the Pierce BCA Protein Assay Kit (Thermo Fisher Scientific UK Ltd, Leicestershire, UK). Thirty micrograms of proteins were separated on an 8% SDS–polyacrylamide gel and transferred onto a nitrocellulose membrane for immunodetection. The membrane was then blocked in Tris-buffered saline with 0.25% Tween 20 (TBST) containing 5% (w/v) dried skimmed milk powder.
followed by overnight incubation at 4 °C with gentle shaking with primary antibody. The membrane was washed four times in TBST and incubated with the appropriate HRP-conjugated secondary antibody (Dako, Ely, UK) for 60 min at room temperature. The membrane was washed four times again in TBST. ECL plus reagents (GE Healthcare, Princeton, NJ, USA) were added to the membrane following the manufacturer’s protocol. Any differences in protein phosphorylation due to variations in loading were routinely corrected by normalization to the levels of the appropriate total protein.

Nuclear and cytoplasmic protein extraction

HUVECs (5 × 10⁶–1 × 10⁷/ml) were collected and washed with cold PBS. The pellet was added with 200 µl cytoplasmic lysis buffer (with 0.5 µl 10 mM di-dithiothreitol, 1 µl 100 mM phenylmethylsulphonyl fluoride (PMSF), and 0.5 µl 1 mM protease inhibitors) and placed on ice for 15 min. Then the cells were centrifuged at 16 000 g for 5 min at 4 °C. The supernatant was carefully collected and cytoplasmic protein extract was obtained. One hundred microliters of nuclei lysis buffer (with 0.1 µl di-dithiothreitol, 0.5 µl 100 mM PMSF, and 0.1 µl protease inhibitors) were added to resuspend centrifugal precipitate (nuclear), which was placed on ice for 40 min, then centrifuged at 16 000 g for 15 min at 4 °C. The supernatant was carefully removed and nuclear protein extract was obtained.

RNA interference

Cells were transfected with control siRNA (negative control, Shanghai GenePharma Co., Ltd, Shanghai, China) or siRNA specific to PKD (Shanghai GenePharma Co., Ltd) using GenMute transfection reagent (SigmaGen Laboratories) according to the manufacturer’s protocols (Table 1). HUVECs were seeded at a concentration of 5 × 10⁵ cells in six-well plates containing DMEM/F12 without FBS for 24 h. On the day of transfection, the siRNA–transfection reagent complex was prepared by diluting 25 nmol/l siRNA. This was followed by the addition of GenMute transfection reagent, gentle mixing and incubation for 20 min at room temperature. The siRNA–GenMute transfection reagent complexes were added dropwise to the cells. Cells were gently mixed and incubated for 6 h, following which T₄ and DMEM/F12 without FBS were added. Cells were incubated for 48 h before RNA or protein extraction.

Real-time PCR

Cells were harvested in TRIzol (Invitrogen) and total RNA was extracted according to the manufacturer’s protocol. Primer pairs for bFGF were designed using the Primer3 software (http://bioinfo.ut.ee/primer3-0.4.0/). Basic Local Alignment Search Tool (BLAST) was used to ensure the specificity of the primer pair. RNA (2 µg) was subjected to RT-PCR using the Access RT-PCR system (Promega). Total RNA was reverse transcribed into cDNA at 70 °C for 5 min, then at 42 °C for 60 min. Second-strand synthesis and PCR amplification were performed for 40 cycles with denaturation at 95 °C for 30 s, annealing at 58 °C for 60 s, and extension at 70 °C for 120 s, with final extension at 68 °C for 7 min after completion of all cycles. All of the quantitative real-time RT-PCR measurements were performed using a CFX96 Touch Real-Time PCR Detection System (Bio-Rad Laboratories, Inc.) with SYBR Premix Ex Taq (Takara Bio, Inc., Shiga, Japan), according to the manufacturer’s instructions. The primer pairs were as follows: bFGF, forward: 5’-TGG CTA TGA AGG AAG ATG GA-3’ and reverse: 5’-ACT GCC CAG TTC GTT TCA GT-3’; and UBC, forward: 5’-GAT CAT CGC TGT GAT CGT CAC-3’ and reverse: 5’-GTG TAC TGG GCT CAA CCT CG-3’. UBC was used as the control amiplocon. The results were measured by the formula: 2⁻ΔΔCt = −ΔΔCt = −((target gene in sample Ct−UBC gene in sample Ct)−(target gene in control Ct−UBC gene in control Ct)).

Wound-healing assay

HUVECs were seeded in six-well plates with growth medium containing 10% FBS. The cells were allowed to grow to form a confluent monolayer. The wound-induced migration was triggered by scraping the cells with a plastic pipette tip, and the wound was imaged immediately.

Table 1 Oligonucleotide sequences of siRNA

<table>
<thead>
<tr>
<th>siRNA sequence</th>
<th>PKD(1)</th>
<th>PKD(2)</th>
<th>PKD(3)</th>
<th>Negative FAM control</th>
<th>Negative control</th>
<th>GAPDH positive control</th>
</tr>
</thead>
<tbody>
<tr>
<td>Forward</td>
<td>5’-CUGGUACGUCAAGUCUUATT-3’</td>
<td>5’-UAAGACCUUGACGACCCAGTT-3’</td>
<td>5’-CAACACUGAGUGCUUUAATT-3’</td>
<td>5’-UUCUCGGAACGUGUCACCUUTT-3’</td>
<td>5’-AAUGACACGUGUGACGUAAUATT-3’</td>
<td>5’-CUUGGCUUGUGCUAAUACTT-3’</td>
</tr>
<tr>
<td>Reverse</td>
<td>3’-UAUAUGUGUAUGUGUGCUAAGUTT-3’</td>
<td>3’-AAUACGUACACGUGUCAAAUATT-3’</td>
<td>3’-AACUACUGUAAACUGUGCUU-3’</td>
<td>3’-AAUGUGAACGUGUGACGUAAUATT-3’</td>
<td>3’-UCGUCAGUGUGUCAAAUATT-3’</td>
<td>3’-CUUGGACGUUGUGCUAAUATT-3’</td>
</tr>
</tbody>
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The cells were then treated with T₄ or Tetrac. The wound was imaged at different intervals as indicated using an inverted phase-contrast microscope. The wound gap was measured on the images and the distance of migration was calculated as wound gap at 0 h − wound gap at x h, where x is the time point of measurement, and the average wound-healing time was calculated based on at least nine determinations of the wound (Sharlow et al. 2008).

**Tubulogenesis assay**

The effect of thyroid hormone on tubulogenesis was tested by determining the formation of capillary-like tubes in 96-well plates loaded with Matrigel. Matrigel was thawed at 4 °C overnight before use. A total of 440 μl of Matrigel were mixed with 2×10⁴ HUVECs in a total volume of 220 μl. A 50 μl aliquot of the Matrigel cell mixture was then added to each well and incubated at 37 °C for 30 min to allow gel formation. This was followed by the addition of 250 μl culture medium and incubation at 37 °C for 48 h. After washing, the cell medium was replaced with culture medium mixed with thyroid hormone (T₄: 100 nmol/l), which was replaced every 24 h for 2 days. The tube-like structures inside the wells were fixed with 4% formaldehyde and photographed (Zhang et al. 2010). The total length of the capillary-like network that was formed within the Matrigel was measured using Image J software (National Institutes of Health, Bethesda, MD, USA).

**Statistical analysis**

The data were summarized as mean ± S.E.M. Unpaired Students’ t-test was used for comparisons between two groups. For multiple comparisons, statistical analysis was performed by ANOVA. P values < 0.05 were considered to be significant.

**Results**

**T₄ promoted the migration and tubulogenesis of HUVECs**

The effect of T₄ on cell migration was examined by wound-healing assay in HUVECs. Confluent HUVECs were wounded and then treated with T₄ or Tetrac. We found that the migration ability of HUVECs changed with time and was different in each group (Fig. 1). The T₄ (100 nmol/l) group showed a longer distance of migration than the control group, whereas the Tetrac (100 nmol/l) + T₄ group showed a shorter distance of migration than T₄ group at 8, 12, and 24 h (*P < 0.05), which indicated that T₄ was able to induce HUVEC migration, and that Tetrac significantly

**Figure 1**

Effects of T₄ and Tetrac on migration of HUVECs in wound-healing assay. HUVECs were grown to 70% confluence in six-well plates. The monolayer was wounded and imaged immediately (0 h). Growth media containing a vehicle (PBS) or T₄, Tetrac, or and Tetrac + T₄ was added to every well. In the Tetrac + T₄ group, HUVECs were pretreated with Tetrac for 30 min, then treated with T₄. The concentration of T₄ and Tetrac were both 100 nmol/l. Wound closure was recorded at 8, 12, and 24 h. The width of the wound was the average of nine determinations per time point. Distance of migration was calculated at each time point as described in Materials and methods. Phase-contrast images of the wounds were taken at × 100 magnification. The experiment was repeated three times and results of a representative experiment are shown. *P < 0.05 when compared with the control group, #P < 0.05 when compared with the T₄ group at the same time.
The signaling pathway of angiogenesis induced by T4

T4 induced the phosphorylation of PKD To examine the potential role of PKD in the T4-stimulated signaling pathway, we first observed PKD phosphorylation in HUVECs in response to T4. HUVECs were stimulated with T4 (100 nmol/l) at different times as indicated. As shown in Fig. 3A, T4 rapidly induced PKD phosphorylation within 15 min (P<0.05). This higher activation was inhibited by Tetrac. The effect of Tetrac alone on cell migration did not result in a significant difference from the control group (P>0.05). In addition, we investigated the effects of T4 on the capability of HUVECs to form capillary-like structures in Matrigel and quantified it by measuring the number and length of capillary-like structures. Our results showed that the number of tube-like structures obviously increased in the T4 group (P<0.05) compared with the control group (Fig. 2). These results indicated that T4 had a strong ability to induce capillary-like tube formation and migration of HUVECs.

The signaling pathway of angiogenesis induced by T4 T4 stimulated HDAC5 phosphorylation and cytoplasmic accumulation Figure 3D shows that the expression of phosphorylated HDAC5 in the T4 group was nearly 1.5-fold higher than that in the control group (P<0.05). Compared with the T4 group, different concentrations of Tetrac effectively inhibited T4-induced HDAC5 phosphorylation (P<0.05). However, we barely observed any significant difference in HDAC5 phosphorylation with different concentrations of Tetrac + T4 (P>0.05, Fig. 3D). In addition, nuclear export of HDAC5 depended on its phosphorylation, which further affected the downstream gene expression. To confirm the subcellular location of phosphorylated HDAC5 in T4-activated signaling events, we examined the cytoplasmic localization of T4-induced HDAC5 phosphorylation in HUVECs. Our results showed that there was cytoplasmic accumulation of phosphorylated HDAC5 after administration of T4 for 15 min (1.39-fold when compared with the control group, P<0.05). While Bis and Tetrac inhibited T4-induced cytoplasmic accumulation of phosphorylated HDAC5 (Fig. 4). Collectively, these results suggested that T4 induced the cytoplasmic accumulation of phosphorylated HDAC5 in HUVECs by activating the integrin αvβ3/PKC pathway.

T4-induced phosphorylation of HDAC5 mediated by PKD To further define the role of PKD in T4-induced HDAC5 phosphorylation, we knocked down the endogenous PKD in HUVECs using siRNA specifically targeting human PKD. All three PKD siRNAs significantly inhibited the expression of PKD (PRKD1) mRNA and protein (Fig. 5A, B). Particularly, PKD siRNA significantly repressed T4-induced HDAC5 phosphorylation (Fig. 5C). Here, we confirmed an essential role of PKD in T4-induced HDAC5 phosphorylation in HUVECs.
T4 increased the expression of bFGF mRNA via the integrin αvβ3/PKD/HDAC5 signaling pathway

As a potent pro-angiogenic factor, bFGF is one of the numerous target genes regulated by HDAC5. To investigate whether the pro-angiogenic action of T4 was related to induction of bFGF expression via the integrin αvβ3/PKD/HDAC5 pathway, we examined the expression of bFGF with real-time PCR. HUVECs were treated with T4 or Tetrac for 2–6 h. The results showed that an increase in bFGF expression was obvious after 2 h of T4 treatment (2.637-fold when...
molecule. Both T_4 and 3,3',5-triiodothyronine (rT_3) exert direct, positive control of the quantity of polymerized actin in cultured astrocytes without affecting gene expression.

In our study, T_4 was also discovered to be associated with angiogenesis in HUVECs. We found that T_4 promoted HUVEC migration and formation of tube-like structures. Meanwhile, Tetrac, a pure inhibitor of the binding of T_4 and T_3 to integrin αβ_3 (Bergh et al. 2005, Davis et al. 2009), prevented T_4-induced cell expansion. Our results indicated that T_4 showed a strong ability to regulate HUVEC angiogenesis, which was initiated at the membrane receptor integrin αβ_3, and the use of Tetrac was appropriate for investigating the participation of the receptors in actions of thyroid hormone analogs. This result is consistent with previous research showing that integrin αβ_3 is required in thyroid-hormone-induced angiogenesis. Studies report that the extracellular domain of integrin αβ_3 includes an RGD recognition site, which is an important verification domain for the ligands of the protein. The thyroid hormone receptor domain is at or near the RGD recognition site on integrin αβ_3 (Bergh et al. 2005, Cody et al. 2007). By binding to integrin αβ_3, thyroid hormone activates several downstream signaling molecules to regulate signal transduction.

Integrin αβ_3 contains two thyroid hormone-binding sites, denoted as S_1 and S_2, which translate the thyroid hormone signal differently (Davis et al. 2011). Several studies have shown that the signaling pathway of angiogenesis induced by T_4 is mediated by S_2, and ultimately activates the ERK1/2 pathway (Lin et al. 2009). Interestingly, there is recycling of integrin αβ_3 in cells, i.e. from endosomal compartment to plasma membrane, which is required for cell migration (Pellinen & Ivaska 2006, Shattil et al. 2010). There are some signaling molecules involved in regulating this complicated cellular recycling. Among them, PKD1 can interact with integrin αβ_3 in endothelial cells and regulate its trafficking in two different ways: on the one hand, it promotes integrin αβ_3 recycling, and on the other hand, it inhibits integrin αβ_3 endocytosis (di Blasio et al. 2010). Wong & Jin (2005) also confirmed that PKD, as a downstream target, is involved in VEGF-induced MAPK signaling and proliferation of endothelial cells. This evidence indicates a potential signaling role of PKD, which is activated by T_4 binding to integrin αβ_3, involved in T_4-induced angiogenesis. Thus, we evaluated the phosphorylation of PKD in our model and found that T_4 increased PKD phosphorylation in HUVECs, whereas Tetrac inhibited T_4-induced PKD phosphorylation. However, the dose-dependent inhibitory effect of Tetrac
Many studies report that the phosphorylation of PKD depends on the activation of PKC (Vega et al. 2004a,b). To further clarify the role of PKC in T₄-induced PKD phosphorylation, we pretreated HUVECs with PKC inhibitor. Our results showed that T₄-stimulated PKD phosphorylation was reduced by PKC inhibitor. The data implied that the integrin αβ3/PKC signaling pathway was involved in PKD activation induced by T₄.

In contrast to the previous studies, we first reported that through activation of the integrin αβ3/PKC/PKD pathway, T₄ induced the phosphorylation of HDAC5. We used both Tetrac and PKC inhibitor to block the signaling pathway and discovered that HDAC5 phosphorylation stimulated by T₄ was reduced. We also designed PKD siRNA to inhibit PKD expression and found that cellular HDAC5 phosphorylation significantly decreased. Class II a HDAC family members, especially HDAC5 and HDAC7,
have been identified as important downstream regulators of PKD. They are reported to be involved in VEGF-induced gene expression and angiogenesis (Ha et al. 2008a,b). Ha et al. (2008a,b) also demonstrated that once HDAC5 is phosphorylated, it would be exported from the nucleus, resulting in the relaxation of nucleosomes, thereby beneficial for transcription of downstream target genes. To investigate the nuclear export of HDAC5 in response to T4, we extracted cytoplasmic protein and found that phosphorylated HDAC5 was increased in the cytoplasm of HUVECs, while the effects of Tetrac and PKC inhibitor were in contrast to this, which indicated that there was nuclear–cytoplasmic shuffling of HDAC5 in response to T4. Therefore, it is speculated that the pro-angiogenic action of T4 is initiated at the cell surface integrin αvβ3 and ultimately activates the PKD/HDAC5 signaling pathway. HDAC5 phosphorylation and nuclear export promoted by T4 regulate histone acetylation and chromatin remodeling and further affect pro-angiogenic factor transcription.

Acetylation of chromatin proteins and transcription factors is part of a complex signaling system that is mainly involved in the control of gene expression (McKinsey & Olson 2005, Backs & Olson 2006). Histone acetyltransferases and HDACs act in an opposing manner to control the acetylation state of nucleosomal histones. HDAC5 has been shown to act as a signal-responsive repressor of cardiac hypertrophy, skeletal muscle differentiation and bone development (McKinsey et al. 2000, Zhang et al. 2002, Vega et al. 2004a,b). There are numerous target genes regulated by HDAC5, among which bFGF was discovered and also the transcriptome of cells transfected with HDAC5 siRNA was profiled by Urbich et al. (2009). Among the significantly regulated genes with altered RNA levels are the genes involved in angiogenesis, including angiogenic growth factors and receptors (e.g. bFGF, neuropilin 2, and VEGF receptor 2), guidance molecules (e.g. Slit2) and transcription factors. bFGF, SLIT2, and EPHB4 are time-dependently and significantly upregulated in HDAC5 siRNA-transfected HUVECs. Here, we selected the pro-angiogenic bFGF as a target gene of HDAC5 and assessed its mRNA expression. The results showed that T4 increased the expression of bFGF mRNA within 2 h, and Tetrac decreased the expression of bFGF mRNA. Due to the shorter time of exposure, this effect is considered to be different from thyroid-hormone-induced genomic effects resulting from binding to thyroid hormone nuclear receptor. Our findings indicate that T4-induced angiogenesis is regulated by the integrin αvβ3/PKD/HDAC5-dependent upregulation of bFGF.

Many studies report that T4-induced angiogenesis is regulated by a complicated signaling system. Here, we demonstrated a new signaling pathway through integrin αvβ3/PKD/HDAC5, in which T4 stimulates HDAC5 nuclear export and increases bFGF mRNA expression that contributes to angiogenesis in HUVECs. The reduction of thyroid hormone in circulation or the inhibition of thyroid hormone actions at the integrin αvβ3 receptor would consequently produce a reduction in the proliferative and angiogenic effects of thyroid hormone. Al Husseini et al. (2013) also found that thyroidectomy mitigates hypoxia-induced pulmonary hypertension, and that the mechanism is associated with a reduced proliferation of endothelial cells and reduced angiogenesis. Therefore, targeting thyroid hormone actions could be an alternative adjuvant therapy against cancer proliferation and angiogenesis. Our study would facilitate exploration of the potential therapeutic targets and help us to control pathological angiogenesis.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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