

## Triiodothyronine ( $T_3$ ) induces *HIF1A* and *TGFA* expression in MCF7 cells by activating PI3K



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### ABSTRACT

High expression levels of hypoxia inducing factor 1 alpha are related to mammary carcinogenesis. In previous studies, we demonstrated that expression of transforming growth factor alpha increases upon treatment with triiodothyronine, but this expression does not occur in cellular models that do not express the estrogen receptor, or when cells are co-treated with the anti-estrogen, tamoxifen. The aim of this study was to determine the effect of the hormone triiodothyronine on the expression of the genes *HIF1A* and *TGFA* in the breast cancer cell line MCF7. The cell line was subjected to treatment with triiodothyronine at the supraphysiological dose of  $10^{-8}$  M for 10 min, 30 min, 1 h, and 4 h in the presence or absence of actinomycin D, the gene expression inhibitor, cycloheximide, the protein synthesis inhibitor, and LY294002, the phosphoinositide 3 kinase inhibitor. *HIF1A* and *TGFA* mRNA expression was analyzed by reverse transcription polymerase chain reaction. For data analysis, we used analysis of variance complemented by Tukey test and an adopted minimum of 5% significance. We found that *HIF1A* and *TGFA* expression increased in the presence of triiodothyronine at all times studied. *HIF1A* expression decreased in triiodothyronine-treated cells when gene transcription was also inhibited; however, *TGFA* expression decreased after 10 and 30 min of treatment even when transcription was not inhibited. We found that activation of PI3K was necessary for triiodothyronine to modulate *HIF1A* and *TGFA* expression.

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### 1. Introduction

Despite the significant advances in diagnosis and treatment, breast cancer (BC) remains an important and ongoing challenge for those responsible for public health [1]. The hormone triiodothyronine ( $T_3$ ) stimulates the proliferation of multiple types of non-malignant cells [2–4], including breast [5] and thyroid [6] cells. Several studies on the influence of thyroid hormone (TH) in breast carcinomas, including work by our group, have reported a higher frequency of hyperthyroidism in postmenopausal patients with breast cancer [7–9].

Many tumors induce transcription of angiogenesis-related genes, including the hypoxia inducing factor (*HIF1*) and transforming growth factor alpha (*TGFA*). *HIF1* induces the translation of angiogenesis-related genes favoring this route of carcinogenesis [10]. Previous studies demonstrated that overexpression of *HIF1* and *TGFA* is positively correlated with tumor aggressiveness and malignant progression of human neoplasms [11–13]. Zhong et al. [14] showed that the alpha subunit of

*HIF1*, *HIF1A*, is overexpressed in various human tumors (colon, breast, stomach, lung, skin, ovary, prostate, kidney, and pancreatic carcinomas), and that *HIF1A* is more pronounced in pre-malignant lesions than in benign lesions [14].

*TGFA*, which encodes a mammalian growth factor that can be affected by diet and hormones, is located on chromosome 2p13, comprises 80 kb of genomic DNA, and has six exons [15–16]. *TGFA* is produced by tumor cells and secreted by many tumors [17]. Overexpression of *TGFA* may occur during malignant progression [11].

In previous work, we demonstrated that *TGFA* expression increases after treatment with triiodothyronine ( $T_3$ ) in MCF7 cells the same effect was observed in primary cultures [18,19].

Although  $T_3$  often acts through the classic genomic regulation of gene transcription, a number of effects of  $T_3$  occur rapidly and are not affected by inhibitors of transcription or by protein synthesis [20–22]. In these instances,  $T_3$  may act via a mechanism that requires sites on the plasma membrane. For example, it may act through the activation of integrin  $\alpha\beta_3$ , which activates ERK1/2 and culminates in local membrane events, such as  $Na^+/H^+$  ion transport systems, or through complex cellular events, such as cell proliferation. Alternatively,  $T_3$  may act through the cytoplasm. The TH can activate the mitogen-activated

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protein kinase (MAPK) and phosphoinositide 3 kinase (PI3K). PI3K activation subsequently can result in  $T_3$ -dependent transcription of specific genes, insertion of the  $Na^+ K^+$ -ATPase into the plasma membrane, and modulation of the ATPase activity. Studies using cell lines have shown changes in the expression of several genes after treatment with  $T_3$ -dependent PI3K [23–25]. The objective of this study was to determine the effect of  $T_3$  hormone at supraphysiological doses on the activation of the PI3K pathway by measuring the expression of *HIF1A* and *TGFA* in MCF7 breast cancer cells.

## 2. Materials and methods

### 2.1. Reagents

RPMI 1640 medium, fetal bovine serum (FBS), and antibiotic solution with 1:100 dilution were purchased from Gibco BRL (Grand Island, NY, USA). Actinomycin D (ACTD), cycloheximide (CHX), triiodothyronine ( $T_3$ ), LY294002 (LY), dimethylsulfoxide (DMSO), sodium hydroxide (NaOH), and charcoal-stripped FBS were purchased from Sigma Aldrich (St Louis, MO, USA).

### 2.2. Cell culture

Project approved by the Research Ethics Committee of Botucatu Medical School, protocol 3367-2009.

The MCF7 cell line (BC immortalized cells) was initially obtained from a primary culture of breast cancer cells originating from the pleural effusion of a female patient with metastasis [26]. These cells express ER  $\alpha$  and  $\beta$ , as well as TR  $\alpha$  and  $\beta$  [18,27–28]. The human breast cancer cell line MCF7 [kindly provided by Prof. Dr. Maria Mitzi Brentani, Laboratory of Oncology, FMUSP, and initially purchased from the American Type Culture Collection (ATCC), Manassas, Virginia, USA] were expanded, grown, and maintained in the cell bank of the Clinical Medicine Experimental Laboratory, UNESP, Botucatu. All experiments were repeated in triplicate for all treatments and times, between the second and third passages. The MCF7 cells were cultivated in RPMI 1640 medium supplemented with 1.2 g/L  $NaHCO_3$ , 10 mM HEPES, pH 7.4, and 10% FBS. The cell lines were maintained at 37 °C in 5%  $CO_2$ . The medium was changed every 2 d. Before starting the inhibitor and hormone treatments, the medium was replaced with a phenol red-free medium to remove all hormones in the medium. The cells then were incubated with 10% charcoal-stripped FBS. After incubation, the cells were treated with 10 nM  $T_3$  for 10 min, 30 min, 1 h and 4 h; all treatments were initiated together and, subsequently, the cells were collected at the end of the respective treatment durations. The inhibitors and the  $T_3$  hormone were added in the following amounts: actinomycin D (ACTD, 5.0  $\mu$ g/mL,  $T_3$  associate ACTD group); cycloheximide (CHX, 50  $\mu$ M,  $T_3$  associate CHX group); and LY294002 (50  $\mu$ M,  $T_3$  associate LY group). ACTD was used as a transcription inhibitor; CHX was used as a translation inhibitor; and LY294002 to verify the involvement of the PI3K pathway. The untreated, control group received only 0.1% NaOH (diluent:  $T_3$ ). The inhibitors LY294002 and CHX were added to the medium 1 h prior to  $T_3$  treatment.

### 2.3. Gene expression

Total RNA was extracted from the MCF7 cells using Trizol (Invitrogen, San Paulo, Brazil), according to the manufacturer's instructions. The High Capacity cDNA reverse transcription kit for RT-PCR® (Invitrogen, São Paulo, Brazil) was used for the synthesis of 20  $\mu$ L of complementary DNA (cDNA) from 1000 ng of the total RNA. *HIF1A* expression levels (Hs00153153\_m1, Applied Biosystems) and *TGFA* expression levels (Hs00608187\_m1, Applied Biosystems) were determined using qRT-PCR. Quantitative analysis was performed using the Applied Biosystems StepOne Plus system with the TaqMan qPCR commercial kit (Applied Biosystems), according to the manufacturer's

instructions. The amplification conditions were as follows: activation of the enzyme at 50 °C for 2 min, denaturation at 95 °C for 10 min, and cDNA amplification during the 40 cycles comprising denaturation at 95 °C for 15 s and extension at 60 °C for 1 min. All experiments were performed in duplicate. Gene expression was quantified, relative to the data obtained from the control group, after normalization with an internal control (GAPDH, Hs02758991\_g1), using the  $2^{-\Delta\Delta Ct}$  method, as described previously [29].

### 2.4. Statistical analysis

For the statistical analysis, we used ANOVA in conjunction with the Tukey test and the Student's *t*-test, with a minimum significance of 5%. The data are expressed as mean  $\pm$  standard deviation.

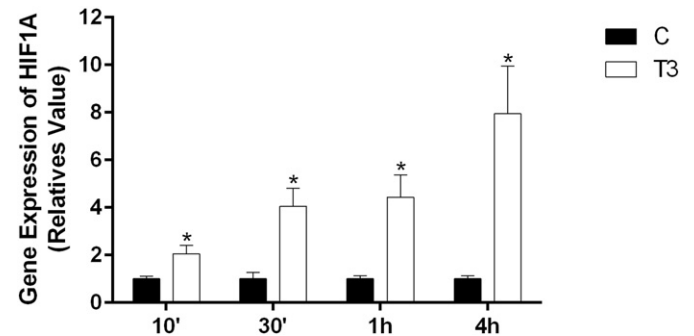
## 3. Results

**Treatment with  $T_3$  increases *HIF1A* and *TGFA* expression.** Figs. 1 and 2 represent *HIF1A* and *TGFA* expression, respectively, in MCF7 cells treated with  $T_3$  for 10 min, 30 min, 1 h, and 4 h. The results demonstrate that treatment with  $T_3$  promotes a significant, time-dependent increase in *HIF1A* and *TGFA* expression in breast cancer cells.

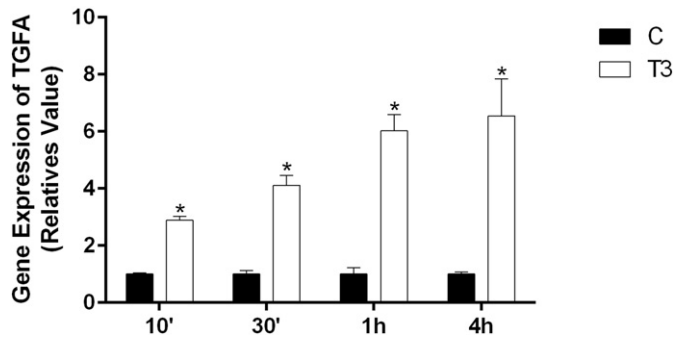
**Treatment with inhibitors actinomycin D, cycloheximide and LY294002 had no effect on *HIF1A* and *TGFA* expression in breast cancer cells.** Figs. 3 and 4 represent *HIF1A* and *TGFA* expression, respectively, in MCF7 cells treated with inhibitors actinomycin D (ACTD), cycloheximide (CHX) and LY294002 (LY) for 10 min, 30 min, 1 h and 4 h. The results showed that there was no statistical difference in the control group compared to inhibitors. C, Control; actinomycin D (ACTD), cycloheximide (CHX) and LY294002 (LY). Comparison com C  $\times$  ACTD; C  $\times$  CHX, C  $\times$  LY.

**Inhibition of RNA synthesis with actinomycin D affects  $T_3$ -mediated increases in *HIF1A* expression and *TGFA* expression.** To determine if the effect of  $T_3$  on the expression of *HIF1A* and *TGFA* requires mRNA synthesis, we inhibited mRNA synthesis in breast tumor cells with actinomycin D (ACTD). When comparing *HIF1A* expression in cells treated with  $T_3$  alone to expression in cells treated with  $T_3$  and ACTD, we found that *HIF1A* mRNA levels higher at all time points (Fig. 5). This result suggests that gene transcription is required for the action of  $T_3$ . *TGFA* expression was significantly higher in  $T_3$  treated cells than in cells treated with  $T_3$  and ACTD for 10 min; however, after 30 min, there was no statistical difference between the two treatments (Fig. 6).

**Inhibition of protein synthesis with cycloheximide affects  $T_3$ -mediated increases in *HIF1A* expression and *TGFA* expression.** To determine if  $T_3$ -dependent regulation of *HIF1A* and *TGFA* mRNA levels requires protein synthesis, breast cancer cells were incubated in the presence of  $T_3$ , and with or without cycloheximide (CHX). Figs. 7 and 8 show the combined effect of  $T_3$  and CHX on *HIF1A* and *TGFA* expression, respectively, when compared to the effect of  $T_3$  alone. In relation



**Fig. 1.** Time-dependent effect of  $T_3$  on *HIF1A* mRNA at 10 min, 30 min, 1 h, and 4 h in MCF7 cells.  $T_3$  = 10 nM  $T_3$ , C = no  $T_3$ . Data are expressed as mean  $\pm$  standard deviation values and were analyzed using the Student's *t*-test. \**p* < 0.05 in the C associate  $T_3$  comparison. *n* = 3 for each treatment.



**Fig. 2.** Time-dependent effect of  $T_3$  on *TGFA* mRNA at 10 min, 30 min, 1 h, and 4 h in MCF7 cells.  $T_3 = 10$  nM  $T_3$ , C = no  $T_3$ . Data are expressed as mean  $\pm$  standard deviation values and were analyzed using the Student's *t*-test. \* $p < 0.05$  in the CxT3 comparison.  $n = 3$  for each treatment.

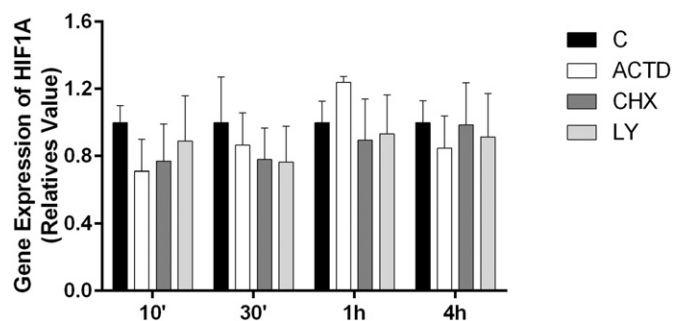
the group  $T_3$  associate CHX compared to  $T_3$ , was significantly higher in  $T_3$  treated cells than in cells treated with  $T_3$  and CHX in *HIF1A* and *TGFA* expression at all time points studied.

**Inhibition of P13K signaling affects  $T_3$ -mediated increases in *HIF1A* expression and *TGFA* expression.** To determine if the activation of the PI3K pathway is required for the regulation of *HIF1A* and *TGFA* expression by  $T_3$ , breast cancer cells were incubated in the presence of  $T_3$  and with or without the P13K inhibitor, LY294002 (LY). As shown in Figs. 9 and 10, there was significantly higher in  $T_3$  treated cells than in cells treated with  $T_3$  and LY in *HIF1A* and *TGFA* expression at all time points studied.

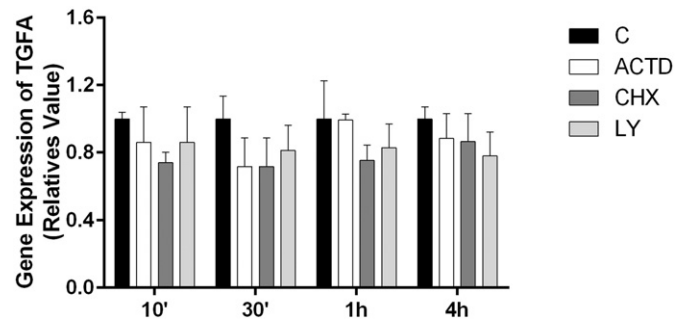
#### 4. Discussion and conclusions

Cellular hypoxia and metabolic stress occurs in many cancers. *HIF1A* is a central regulator of oxygen homeostasis. Previous studies indicated that *HIF1A* is overexpressed in many types of cancer, primarily BC, whereas mediate *HIF* proteins the adaptation to cellular hypoxia [14, 30–31]. High *HIF1A* expression in human breast cancer cells are related to breast cancer and the molecular changes that result from tumor vascularization. Like *HIF1A*, *TGFA* is also secreted by many tumors and possesses angiogenic properties [17]. The involvement of *TGFA* in the interaction between neoplastic epithelial cells and stromal cells has been intensively studied in recent years [17,32–33]. *TGFA* recognizes binds to the epithelial growth factor (EGF) receptor and, like EGF, is a potent inducer of mitosis during breast development [34].

Studies have described the antiproliferative effect of TH [5] on BC in ER positive cells and have demonstrated the ability of  $T_3$  to increase cell proliferation in the presence of the TH receptor by inducing the expression of genes normally stimulated by  $E_2$ , including the progesterone receptor (*PgR*), *TGFB1*, and *TGFA* [35–36].



**Fig. 3.** Treated with inhibitors ACTD, CHX and LY were compared to control cells on the modulation *HIF1A* mRNA at 10 min, 30 min, 1 h and 4 h in MCF7 cells. ANOVA, supplemented by the Tukey test, in the CxACTD; CxCHX and CxLY comparison.  $n = 3$  for each treatment.



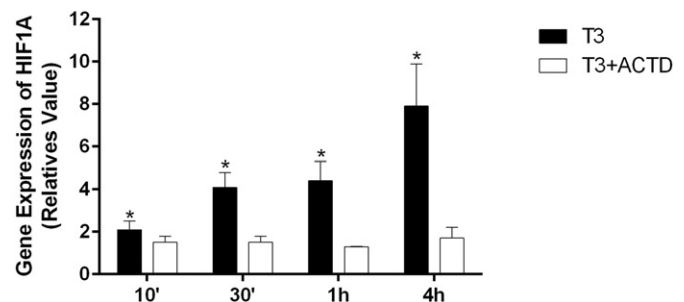
**Fig. 4.** Treated with inhibitors ACTD, CHX and LY were compared to control cells on the modulation *TGFA* mRNA at 10 min, 30 min, 1 h and 4 h in MCF7 cells. ANOVA, supplemented by the Tukey test, in the CxACTD; CxCHX and CxLY comparison.  $n = 3$  for each treatment.

Previous studies have indicated that  $T_3$  promotes gene expression by binding to the nuclear TH receptor [37]. Recent studies also have suggested that cytosolic cascades are the underlying mechanism of  $T_3$  action [38–39]. The present study confirms the action of  $T_3$  on breast cancer cells (MCF7), showing an increase in *HIF1A* and *TGFA* expression as a result of treatment with  $T_3$  for different times (Figs. 1 and 2). These results correlate with studies that demonstrated increased expression of a number of genes, such as amphiregulin (*AREG*) in MCF7 cells [40], leptin in adipocytes 3T3-L1 cells [41], and *HIF1A* in human fibroblast cells [39], upon treatment with  $T_3$ . Taken together, these results show that  $T_3$  affects the transcription of *HIF1A* and *TGFA* at both short periods of time.

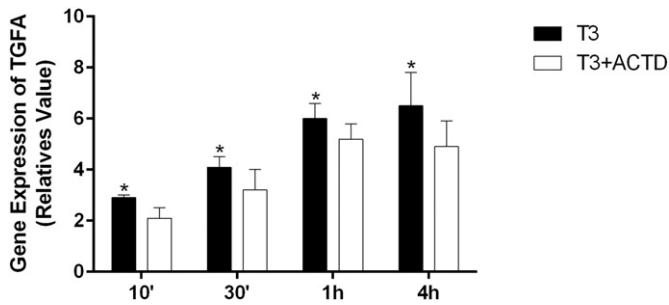
Our results show that, as compared to the results for control-treated cells, treatment with inhibitors alone had no effect on *HIF1A* and *TGFA* expression in breast cancer cell lines.

Our next step was to determine if  $T_3$  acts to stabilize *HIF1A* and *TGFA* mRNA using ACTD. ACTD is a general transcriptional inhibitor with anticancer activity, and is approved for the treatment of sarcomas, Wilms' tumor trophoblasts, and germ cells [42–43]. As shown in Fig. 4, after 10 min of treatment with ACTD, *TGFA* expression decreases. After 30 min of treatment, there was no difference in *TGFA* expression, demonstrating stability of the mRNA. Our results are in agreement with the study of Volpato et al. [44] who tested whether the increase in *GLUT4* expression after treatment of 3T3-L1 cells with  $T_3$  for 30 min is maintained in the presence of ACTD. The authors found that ACTD did not prevent the action of  $T_3$  [44].

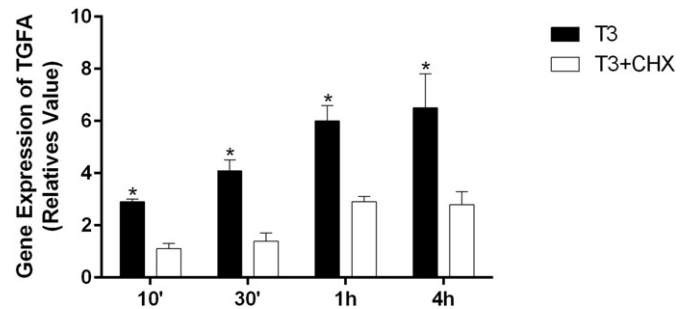
Extra-nuclear mechanisms can potentially influence gene expression. Although the onset of action is via an extra-nuclear mechanism that relies on alternative routes, the consequences of that action can include increased transcription [25]. This suggests that there might be an interrelationship between nuclear and extra-nuclear events of TH. With regard to extra-nuclear events, we can distinguish two classes of target genes by the actions of  $T_3$  that occur using the PI3K pathway: 1) a class of genes induced directly by the action of this pathway in which protein



**Fig. 5.** Effect of  $T_3$  and  $T_3 +$  ACTD on the modulation of *HIF1A* mRNA at 10 min, 30 min, 1 h and 4 h. ANOVA, supplemented by the Tukey test, \* $p < 0.05$ ;  $n = 3$  for each treatment.



**Fig. 6.** Effect of  $T_3$  and  $T_3$  associate ACTD on the modulation of *TGFA* mRNA levels at 10 min, 30 min, 1 h and 4 h. ANOVA, supplemented by the Tukey test, \* $p < 0.05$ ;  $n = 3$  for each treatment.



**Fig. 8.** Effect of  $T_3$  and  $T_3$  associate CHX on the modulation of *TGFA* mRNA levels at 10 min, 30 min, 1 h and 4 h. ANOVA, supplemented by the Tukey test, \* $p < 0.05$ ;  $n = 3$  for each treatment.

synthesis is not required “a priori” for the treatment to influence the action of the hormone, and 2) a class of genes whose expression is altered in the presence of the hormone, but is dependent on the synthesis of a specific protein previously known to be indirectly affected by extra-nuclear  $T_3$  [39].

In order to determine whether  $T_3$  directly or indirectly regulates *HIF1A* and *TGFA*, we used CHX to inhibit protein synthesis. We found that CHX reduces the action of  $T_3$ , leading to decreased levels of *HIF1A* and *TGFA*, at all treatment times, (Figs. 5 and 6, respectively), indicating that the effects of  $T_3$  on these genes requires prior protein synthesis and that  $T_3$  acts on these genes indirectly. Studies by Moeller et al. [39] with human fibroblasts show that the action of  $T_3$  on *HIF1A* is direct because expression was not affected by the presence of CHX, suggesting there was no need for a precursor protein to stimulate the expression of *HIF1A*. However, the expression of *Glut1*, *PFKP*, and *MCT4* decreased in the presence of CHX, suggesting a precursor protein was needed in order for  $T_3$  to indirectly regulate these genes [39].

The PI3K pathway functions in a wide variety of cellular processes, including intracellular pathways, cytoskeletal organization, cell growth and transformation, and the prevention of apoptosis [45–46]. The PI3K pathway also affects differentiation of multiple cell lineages [47–48]. The concept of the effect of TH was diverse, including extra-nuclear actions of  $T_3$  and  $T_4$ .  $T_3$  activates the PI3K pathway, which leads to an increase in the expression of several genes, including *HIF1A* and the calcineurin inhibitor, *ZAKI-4 $\alpha$*  [25,39].

Several studies using cell lines highlight changes in gene expression after treatment with  $T_3$  that are dependent on the PI3K pathway [23–25, 39,41]. Among the genes stimulated by treatment with  $T_3$  via the PI3K pathway, we focused on genes related to energy metabolism, including *HIF1A*, *GLUT1*, *PFKP*, and *MCT4*. Studies from our group recently suggested that leptin is modulated by  $T_3$  in a PI3K-dependent manner in 3T3-L1 adipocytes [41]. In all of these studies, alteration in gene expression occurred through a non-nuclear mechanism of action of the thyroid hormone that was dependent on PI3K signaling, because all expression

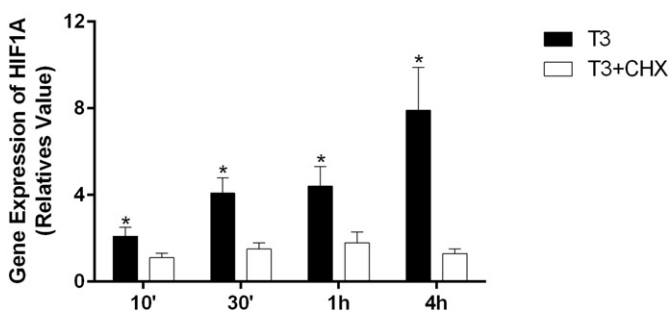
was inhibited by concomitant treatment with the PI3K – specific inhibitor, LY294002.

In this study, we used LY294002 to determine if activation of the PI3K pathway is required for  $T_3$ -mediated regulation of *HIF1A* and *TGFA* expression. As shown in our results, *HIF1A* and *TGFA* expression increased upon treatment with  $T_3$ , but not upon treatment with  $T_3$  and LY294002 (Fig.7 and Fig.8). The use of PI3K inhibitors like LY demonstrates that this effect is dependent on a TH signaling cascade that is initiated by PI3K. This result suggests that the increase in transcriptional regulation of *HIF1A* and *TGFA* is possibly mediated by the PI3K pathway, which is activated by  $T_3$ . Moeller et al. [39] showed that  $T_3$ -dependent activation of *HIF1A* in a human fibroblast cell line is likely independent of PI3K activation. Cao et al. [38] reported that  $T_3$  interacts with the p85A subunit of PI3K by binding to TR $\beta$  in the cytosol. This binding leads to activation of PI3K and the subsequent activation of a signaling cascade comprising sequential phosphorylation of protein kinase b (Akt), protein target of rapamycin in mammals (mTOR), and its substrate, ribosomal protein S6 kinase 70 (p70S6K). This signaling occurs very rapidly, with the mTOR phosphorylation occurring within 10 min after treatment with  $T_3$  [49]. Other studies indicate that the extra-nuclear activity of TH occurs through the activation of PI3K, with the phosphorylation of proteins that are already present in the cytoplasm [50–52].

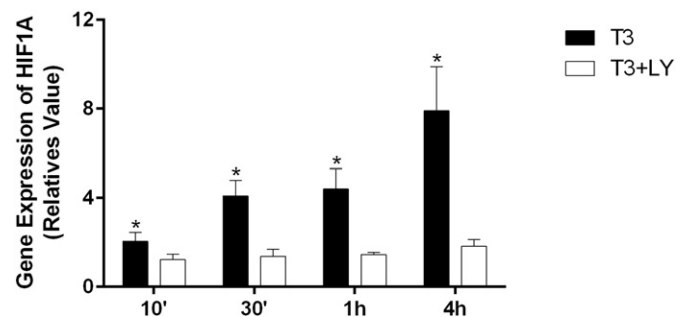
Studies demonstrating the mechanism by which TH can alter the expression of genes linked to breast cancer proliferation or to other cancer therapies offer alternative approaches for the treatment of this disease. Our study confirms that  $T_3$  hormone acts through the activation of the extra-nuclear pathway for the expression of *HIF1A* and *TGFA* in the MCF7 cell lines, involving the PI3K signaling pathway.

#### Declaration of interest

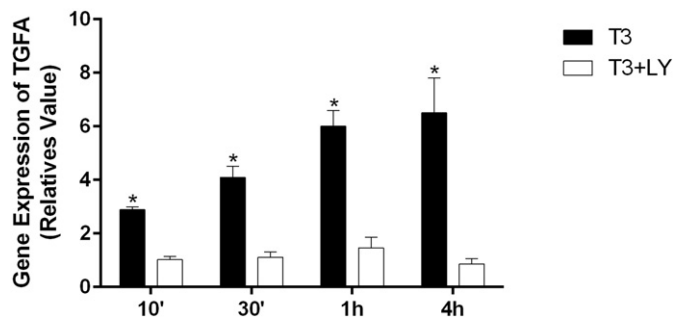
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of this review.



**Fig. 7.** Effect of  $T_3$  and  $T_3$  associate CHX on the modulation of *HIF1A* mRNA levels at 10 min, 30 min, 1 h and 4 h. ANOVA, supplemented by the Tukey test, \* $p < 0.05$ ;  $n = 3$  for each treatment.



**Fig. 9.** Effect of  $T_3$  and  $T_3$  associate LY on the modulation of *HIF1A* mRNA levels at 10 min, 30 min, 1 h and 4 h. ANOVA, supplemented by the Tukey test, \* $p < 0.05$ ;  $n = 3$  for each treatment.



**Fig. 10.** Effect of  $T_3$  and  $T_3$  associate LY on the modulation of *TGFA* mRNA levels at 10 min, 30 min, 1 h and 4 h. ANOVA, supplemented by the Tukey test, \* $p < 0.05$ ;  $n = 3$  for each treatment.

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