

Thyroid

THYROID HORMONE METABOLISM AND ACTION

T₃-Dependent Transcriptional Programming by TR β in Thyroid Cells Requires SWI/SNF Chromatin Remodelers

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Transcriptional regulation in response to thyroid hormone (T₃) is a dynamic and cell-type specific process that maintains cellular homeostasis and identity. A bimodal switch model, where T₃ binding alters the co-regulator profile of a constitutively DNA-bound thyroid hormone receptor (TR) to affect downstream gene expression, is widely used to describe the interaction between TR β and chromatin. To test this model on a genome-wide scale, we used an integrated genomics approach to profile and characterize the cistrome of TR β by CUT&RUN, map changes in chromatin accessibility by ATAC-seq, and capture the transcriptomic changes in response to T₃ by RNA-seq in the normal thyroid cell line, Nthy-ORI. Our CUT&RUN data demonstrated that T₃ binding causes significant shifts in TR β genomic occupancy; these shifts are associated with differential chromatin accessibility. Most of the T₃-induced differentially expressed genes have a TR β binding site associated with the proximal promoter region within one kilobase of the transcriptional start site, suggesting that these are direct TR β regulatory target genes. Remarkably, the majority of TR β binding sites were found in transgenic regions and distal regulatory elements. In order to identify the co-regulatory proteins that are required for execution of a T₃-dependent transcriptional program in our thyroid cells, we used a TR β -miniTurboID fusion construct to perform a proximity ligation assay followed by mass spectrometry. We identified 1,138 nuclear proteins that interact with TR β . Of these proteins, 75 interact preferentially in the presence of T₃ and 68 in the absence of T₃. All of the core SWI/SNF complex subunits from both of the major subtypes (BAF and PBAF) were identified as TR β . Interestingly, we found that the PBAF-specific subunit, PBRM1, was significantly enriched in the presence of T₃. BAF complex-specific subunits, such as ARID1A, were also present in our dataset. To test whether TR β could differentially recruit BAF and PBAF complexes to its binding sites, we performed CUT&RUN targeting BRG1, PBRM1, and ARID1A to determine the degree of co-occupancy with TR β . Based on our comprehensive genomic and proteomic analyses, we propose a new model for selective recruitment of BAF and PBAF SWI/SNF complexes to TR β binding sites for differential functions in regulating chromatin accessibility.

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T₃ Enters Axon Terminals of Mouse Cortical Neurons, Is Retrogradely Transported to the Cell Nucleus and Activates Gene Expression

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Thyroid hormone (TH) is critical for brain development and function. T₃ enters neurons through membrane transporters and reaches the cell nucleus where it binds to receptors (TR) to regulate gene transcription. However, neurons also express the type 3 deiodinase (D3), which is located in the cellular and nuclear membranes and inactivates T₃. Here, we investigated the fate and biological impact of T₃ that enters neurons through axons. Primary cortical neurons were isolated from E16.5 embryos of the TH action indicator (THAI) mice, which were engineered with a TH-responsive transgene where three copies of a T₃-responsive element drive a luciferase (Luc) reporter. Neurons were seeded on a microfluidic device consisting of two independent compartments: (i) cellular, where about 70-90,000 cell bodies were located, and (ii) axonal, where a few hundred distal axons were located. Fluidic isolation of the compartments was monitored with Alexa Fluor 594 hydrazide. In the first set of experiments (repeated 3 times), 8-10-day old cultures were incubated for 48h with medium containing 1% charcoal-stripped serum (Tx-medium). Subsequently, 10nM T₃ was added to the axonal compartment, and 24h later cell bodies were harvested and Luc mRNA measured by RT-qPCR. There was a 2.4 ± 0.7-fold increase in Luc mRNA levels, but the addition of 2uM Silychristin (MCT8 inhibitor) to the axonal compartment reduced T₃ induction of Luc mRNA by 32 ± 4.2%. In the second set of experiments (repeated 3 times), 4.9 ± 2.2pM ¹²⁵I-T₃ (final concentration) was added to the cellular or axonal compartments. Medium was sampled and ¹²⁵I-T₃ and its metabolites were separated/quantified via UPLC linked to a flow scintillation detector. After 72h of adding ¹²⁵I-T₃ to the axonal compartment, about 0.73 % ¹²⁵I-T₃ (0.052 ± 0.025pM) was found in the cellular compartment. In addition, 3,3'-¹²⁵I-T₂ and ¹²⁵I (0.011 ± 0.003 and 0.052 ± 0.023pM, respectively) were also detected. When ¹²⁵I-T₃ was added to the cellular compartment, about 1.6% ¹²⁵I-T₃ (0.048 ± 0.027pM), no metabolites, was detected in the axonal compartment. Only background radioactivity was detected in the opposing compartment when ¹²⁵I-T₃ was added in the absence of cells. We conclude that T₃ can be taken up by neuronal axons, partly via MCT8, and transported retrogradely to the cell nucleus to initiate TH signaling. D3-generated T₃ metabolites exit the cell body alongside with small amounts of intact T₃. This pathway could explain how D2-generated T₃ in tanycytes is taken up by TRH-secreting neurons to mediate negative T₃ feedback. Anterograde T₃ transport was also detected, the significance of which remains unknown.

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The Effects of Energy Restriction on Thyroid Hormone Dynamics

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