## **CHARTER IV**

# RESULTS



## 1. Sequence analysis in the $TR\beta$ gene

From the six unrelated individuals, only one patient had a mutation in exon 9 of the  $TR\beta$  gene. Analysis of the  $TR\beta I$  gene by PCR-sequencing revealed that the proband harbored a heterozygous missense mutation (c.1223T>C) resulting in a methionine (ATG) to threonine (ACG) substitution at codon 313 (p.M313T). This was a *de novo* mutation as her unaffected parents did not carry this mutation (figure 18).



Figure 18 Mutation analysis. An electropherogram of the proband showing a heterozygous missense mutation (an arrow) resulting in a methionine (ATG) to threonine (ACG) substitution at codon 313 (p.M313T) (the middle panel). The identified mutation was not detected in her parents (the left and right panels).

This mutation has been previously reported in other populations but never been investigated for its functional significance. A previous report identified one Japanese patient with goiter<sup>[48]</sup>. Thyroid function tests were shown in table 14.

**Table 14** Thyroid function tests of a Thai patient and a Japanese patient with asimilar mutation in the  $TR\beta I$  gene.

	Thai patient	Japanese patient	Normal range
FT <sub>3</sub> (pg/ml)	12.03	6.10	1.6- 4.0
$FT_4$ (ng/dl)	4.52	4.97	0.8-1.8
TSH (mU/ml)	1.41	1.20	0.3-4.1

From the structure of TR $\beta$ , the p.M313T mutation is located at the T<sub>3</sub>-binding domain (figure 19)<sup>[11]</sup>. The uncharacterized p.M313T mutation could be pathogenic by impairing T<sub>3</sub>-mediated transcriptional activity and interfering with the function of the wild type TR $\beta$ .



**Figure 19** Structure of the  $TR\beta$  isoform<sup>[11]</sup>. Star (\*) indicates the position of the p.M313T.

#### 2. Functional analysis of mutant $TR\beta$ 1s.

#### 2.1 T<sub>3</sub>-dependent transactivation activity

The objective of this experiment is to determine the effect of the mutant TR $\beta$ 1s on T<sub>3</sub>-transcriptional activity using the luciferase reporter system. The Palx3-Luc is a positively regulated reporter containing a binding site for TRs. In the presence of T<sub>3</sub>, the TR $\beta$ 1 can effectively activate the Luc gene expression. In transient co-transfection, the wild-type or mutant TR $\beta$ 1s were cotransfected with the Palx3-Luc into COS-7 cells. For efficient activation, 10<sup>-7</sup> M of T<sub>3</sub> were added to the culture media. This concentration of T<sub>3</sub> was previously used and shown to have a significant effect. The transactivation activity was represented as relative luciferase activity (firefly luciferase activity was normalized with renilla luciferase activity). All experiments were performed in triplicate and repeated two times. Cotransfection with the renilla luciferase reporter was used as the internal control to minimize the variability of the obtained results caused by differences in the transfection efficiency between different samples of the transfected cells (figure 20).



Figure 20 Firefly and Renilla luciferase activities in testing of T<sub>3</sub>-dependent transactivation.

Panel A shows activities of Firefly and Renilla luciferases in each culture without  $T_3$ . Panel C shows activities of Firefly and Renilla luciferases in each culture with  $10^{-7}M$  T<sub>3</sub>. Panel B shows normalization of luciferase in each culture without  $T_3$ . Panel D shows normalization of luciferase in each culture with  $10^{-7}M T_3$ .

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#### Statistical analysis

All data of the luciferase activity were calculated as relative luciferase activity and shown as fold induction (relative to the luciferase activity of the control vector  $pcDNA^{TM}$  3.1/myc-His B). All experiments were performed in triplicate and repeated two times. The results were reported as fold induction  $\pm$  SD. Statistical analyses were performed using ANOVA (figure 4).

At  $10^{-7}$  M of T<sub>3</sub>, the T<sub>3</sub>-dependent transactivation of the Palx3-Luc reporter observed in the COS-7 cells transfected with the wild-type TR $\beta$ , was significantly abolished when cells were transfected with each of the mutant TR $\beta$ s except for the I276L and G344A mutants. The mutant I276L had transcriptionally activity close to the wild-type response (I276L = 20-fold; wild-type = 28-fold), and the mutant G344A showed normal transactivation activity at  $10^{-7}$  M of T<sub>3</sub> (G344A = 32-fold; wild-type = 28-fold). This suggested that the I276L and G344A mutants retained their transactivation properties at  $10^{-7}$  M of T<sub>3</sub> (figure 21).



**Figure 21** T<sub>3</sub>-dependent transactivation of the Palx3-Luc reporter in COS-7 cells transfected with different constructs. All except the I276L and G344A mutants showed a significant reduction of the T<sub>3</sub>-dependent transactivation activity compared with that of the WT TRβ1. Data were represented in fold induction relative to the luciferase activity of the vector control. Relative stimulation in the presence of T<sub>3</sub> treatment is indicated above the bars.

### 2.2 Dominant negative effect (DNE)

Dominant negative effect was tested by transfection of the all mutant TR $\beta$ 1s exhibited a dominant negative effect in the presence of 10<sup>-7</sup> M of T<sub>3</sub> together with equal and quadruple amounts of each mutant TR $\beta$ 1 to COS-7 cells in the presence of 10<sup>-7</sup> M T<sub>3</sub>. The firefly luciferase activity was normalized with renilla luciferase activity. Experiments were performed twice with triplicate per experiment.



Figure 22 Firefly and Renilla luciferase activities in testing of dominant negative effect in each culture with 10<sup>-7</sup>M T<sub>3</sub>.

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Panel A shows activities of Firefly and Renilla luciferase at ratio of WT:MT=1:1. Panel C shows activities of Firefly and Renilla luciferase at ratio of WT:MT=1:4. Panel B shows normalization of luciferase at ratio of WT:MT=1:1. Panel D shows normalization of luciferase at ratio of WT:MT=1:4.

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#### Statistical analysis

In cotransfection experiments to test for dominant negative effect, all mutant TR $\beta$ 1s exhibited a dominant negative effect in the presence of 10<sup>-7</sup>M of T<sub>3</sub> providing strong evidence supporting the pathogenic mechanism of these mutant TR $\beta$ 1s identified in patients with RTH (figure 23).



