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CLINICAL STUDY

# Impact of phosphodiesterase 8B gene rs4704397 variation on thyroid homeostasis in childhood obesity

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## Abstract

*Context*: Several studies demonstrated that obese children have higher TSH than normal-weight children. The polymorphism rs4704397 in the phosphodiesterase 8B (*PDE8B*) gene showed an association with TSH.

*Objectives*: i) To assess the effect of *PDE8B* on TSH in obese children; ii) to dissect the role of obesity degree in modulating this association; and iii) to stratify the individual risk to show hyperthyrotropinaemia according to *PDE8B* genotype.

*Methods*: Eight hundred and sixty-seven Italian obese children were investigated. Clinical data and thyroid hormones were evaluated and the *PDE8B* rs4704397 was genotyped.

*Results*: *PDE8B* A/A homozygous subjects showed higher TSH ($P=0.0005$) compared with A/G or G/G. No differences were found for peripheral thyroid hormones. Among A/A children, 22% had hyperthyrotropinaemia, compared with 11.6% of heterozygotes and 10.8% of G/G ($P=0.0008$). Consistently, A/A had an odds ratio (OR) to show abnormal TSH level of 2.25 ($P=0.0004$). Body mass index (BMI) appeared correlated with TSH ($P=0.0001$), but the strength of the effect of *PDE8B* on TSH was independent of BMI ($P=0.1$).

Children were subdivided into six groups according to obesity degree and genotypes. *PDE8B* A/A with BMI SDS above 3 had the highest OR (OR 2.6, $P=0.0015$) to have hyperthyrotropinaemia, whereas G/G with BMI SDS below 3 showed the lowest possibilities (OR 0.3, $P=0.005$).

*Conclusions*: We have shown: i) in obese children, *PDE8B* is associated with TSH; ii) the interaction between adiposity and *PDE8B* on TSH is not synergistic, but follows an additive model; and iii) impact of this association in the stratification of individual risk to have hyperthyrotropinaemia.

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## Introduction

Attention to thyroid function in obese children has increased in recent years (1). Hypothyroidism has often been thought to be the cause of obesity, and thyroid function test is still one of the most commonly performed laboratory analysis in this group of patients. Several studies have demonstrated that obese children show higher thyroid-stimulating hormone (TSH) levels than normal-weight subjects, as well as a positive correlation between TSH levels and body mass index (BMI) (2, 3, 4, 5, 6, 7).

Isolated hyperthyrotropinaemia is a condition characterised by serum TSH level above the statistically defined upper limit of the reference range, with normal or slightly high serum-free thyroxine ($fT_4$) and serum-free triiodothyronine ($fT_3$) concentrations (8). Whether or not increased TSH level affects the metabolic and cardiovascular profile in obese children and adolescents remains unclear, as well as the TSH level decrease after weight loss (5, 6). Thereby, there is still considerable disagreement regarding treatment (8).

TSH serum concentration also has genetic determinants, as proven in several populations (9). Recently, in a genome-wide association scan among more than 350 000 single nucleotide polymorphisms (SNP), the rs4704397 SNP in the phosphodiesterase 8B (*PDE8B*) gene has been shown to be associated with circulating TSH levels. This SNP, in the general population, accounted for 2.3% of the variance in TSH (10). Each copy of the minor A allele was found to be associated with an increase in TSH concentration of 0.13 mIU/l. Remarkably, this polymorphism is located in intron 1 of *PDE8B*, a gene that encodes a high-affinity cAMP-specific PDE expressed in the thyroid gland and, likely, regulating TSH signalling (10, 11).

In another study, this polymorphism has been associated with TSH variations during pregnancy, a condition in which screening for hypothyroidism has been recommended for the possible negative



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consequences on the foetus of maternal abnormal thyroid function (12).

This result, suggesting a genetic contribution to TSH variation during pregnancy, may have implications in the treatment of pregnant women considered, under current guidelines, to be affected by subclinical hypothyroidism (12).

Finally, a recent meta-analysis confirmed that the *PDE8B* rs4704397 polymorphism is associated with high TSH in normal subjects, and is also weakly associated with low $fT_4$ levels although this association is lost in individuals on levothyroxine treatment (13).

The objectives of this study were to: i) verify the presence of the association between this polymorphism and TSH in obese children, a group of patients at increased risk to show elevated TSH levels; ii) dissect the potential role of obesity degree in modulating this association; and iii) use this polymorphism in the stratification of the individual risk of obese children to develop abnormally elevated TSH levels.

## Patients and methods

### *Cohort description and clinical evaluation*

We examined 927 children and adolescents referred to our ward (Childhood Obesity Service, Department of Paediatrics, Second University of Naples) for obesity between 1999 and 2008. Subjects with a history of diabetes or using medications that altered blood pressure, glucose or lipid metabolism, with goitre or known thyroid disease, were excluded. Sixty patients (60/927: 6%) were identified as having autoimmune thyroiditis following positive autoantibodies and ultrasonography and were, therefore, excluded from the study. The Ethics Committee of the Second University of Study of Naples approved the study. Informed consent was obtained from parents and, when appropriate, from children.

Of the 867 subjects enrolled, 425 were girls. Obesity was defined as a BMI at or above the 95th percentile for age and sex, using the definition of the International Task Force for Obesity in Childhood and the charts for the Italian population (14). Obesity degree was evaluated using the Z-score BMI (BMI SDS), calculated with the least mean square (LMS) method (15).

Waist circumference was measured by the same operator to the nearest centimetre with a flexible steel tape while the subjects were standing, after gently exhaling, and is the minimal circumference measurable on the horizontal plane between the lowest portion of the rib cage and iliac crest. The intra-operator coefficient of variation (CV) was 1.3%.

The average value of two waist measurements was obtained and, as an indirect measure of the amount of abdominal fat, the ratio between waist and height was calculated.

Systolic blood pressure (SBP) and diastolic blood pressure (DBP) were measured three times while the subjects were seated; the two last measurements were averaged for the analysis, and we calculated S.D. according to normative values (16).

Pubertal stage was assessed using Tanner criteria (17).

After an overnight fasting, a blood sample was obtained for triglycerides, high-density lipoprotein cholesterol (HDL-C), insulin, serum glucose and thyroid hormones (TSH, $fT_3$ and $fT_4$).

Serum fasting glucose level was measured with the glucose oxidase method. Triglycerides and HDL-C were measured using an Olympus AU 560 apparatus by an enzymatic colorimetric method.

Immunoreactive insulin was assayed by IMX chemical analyser (Abbott Diagnostics, Santa Clara, CA, USA). The mean intra- and inter-assay CV were 4.7 and 7.2% respectively. The degree of insulin resistance was determined using a homeostasis model assessment (HOMA): (insulin (mU/l)$\times$glucose level (mmol/l)/22.5) (18).

Thyroid hormones (TSH, $fT_3$ and $fT_4$) were determined by highly specific solid-phase technique–chemiluminescence immunoassays (PerkinElmer, Turku, Finland).

Isolated hyperthyrotropinaemia was diagnosed when TSH level was higher than 4.2 μUI/ml (97.5th for our assay), with normal $fT_3$ and $fT_4$ levels and no signs or symptoms of hypothyroidism.

### *Genotyping*

Patients were genotyped for *PDE8B* rs4704397 G to A variant in intron 1. The following primers were used: F: 5′-GGCGCTACTCTAGGTTTGGA-3′ and R: 5′-GTCT-GCTCCTTGGCTTTTCC-3′. The BslI restriction enzyme was used to identify the variant, since the A allele eliminates a BslI restriction site. Random samples were confirmed by direct genotyping that provided concordant results in all cases.

### *Statistical analysis*

A $\chi^2$ test was used to verify whether the genotypes were in Hardy–Weinberg equilibrium and to compare categorical variables. Differences among genotypes for continuous variables were evaluated by a general linear model. When it was appropriate, age, gender and BMI SDS were used as covariates.

Levene's test of equality of variance was used to test the differences of the variance of the quantitative trait TSH according to the *PDE8B* genotypes. This test is based on the fact that, under plausible scenarios of gene–gene or gene–environment interaction, the variance of a quantitative trait (e.g. TSH levels) is expected to differ among the three possible genotypes of a biallelic SNP (e.g. *PDE8B*) (19). Regression lines were compared

**Table 1** Clinical and laboratory characteristics of the children involved in the study. Values are expressed as mean±S.D.s (ranges).

| Characteristics | Values |
|---|---|
| *n* | 867 |
| Male/female | 412/455 |
| Prepubertal (%) | 50.3 |
| Age (years) | 10.5±2.8 (4–16) |
| BMI SDS | 2.9±0.7 (1.5–8.5) |
| Waist to height ratio | 0.61±0.06 (0.42–0.89) |
| SBP-SDS | 0.6±1.1 |
| DBP-SDS | 0.1±0.8 |
| HOMA | 5.3±3.7 (0.3–25) |
| Triglycerides (mg/dl) | 95±52 (18–344) |
| HDL-C (mg/dl) | 43±26 (26–147) |
| TSH (mUI/l) | 2.7±1.3 (0.5–10) |
| $FT_4$ (pg/ml) | 9.9±2.2 (0.93–15.9) |
| $FT_3$ (pg/ml) | 3.9±0.7 (1.9–6.8) |

BMI SDS, body mass index SDS; DPB-SDS, diastolic blood pressure SDS; SBP-SDS, systolic blood pressure SDS; HOMA-IR, homeostatic model of assessment of insulin resistance index; HDL-C, high-density lipoprotein cholesterol.

to examine the influence of the genotypes on the relationship between TSH and BMI SDS.

Non-normally distributed variables were log transformed before the analysis, but raw means are shown. A logistic regression was performed to calculate the odds of showing abnormal levels of TSH according to the genotypes. Age, gender and, when appropriate, BMI SDS were used as covariates.

Stat-Graph 3.0 Software for Windows was used for all the statistical analyses. All data are expressed as mean±S.D. $P$ values $<0.05$ were considered statistically significant and, where appropriate, were adjusted for multiple comparisons.

## Results

Distribution of the different *PDE8B* rs4704397 genotypes was in Hardy–Weinberg equilibrium ($P>0.05$).

Two hundred and fifty-nine patients were homozygous for the wild-type allele (G/G), 438 were A/G and 170 were A/A. The clinical characteristics of the patients involved in the study are shown in Table 1. Abnormally high TSH level (above 4.2 UI/l) was observed in 117 out of 867 patients (13%). The difference in circulating TSH levels according to the different *PDE8B* genotypes was shown, with the higher levels observed in the children carrying the A/A genotype ($P=0.0012$). The difference remained statistically significant after adjusting for age, gender, pubertal stage and BMI SDS ($P=0.0005$; Table 2).

No variations among genotypes were found for BMI SDS, total cholesterol, HDL-C, triglycerides, HOMA, $fT_3$ or $fT_4$ (Table 2).

Thirty-eight out of 170 A/A homozygous patients (22%) had abnormally high TSH levels compared with 11.6% (51/438) of heterozygotes and 10.8% (28/259) of homozygotes for the G major allele ($P=0.0008$). Consistently, children homozygotes for the A allele had an odds ratio (OR) to show abnormal TSH level of 2.25 mUI/l (95% CI: 1.5–3.5, $P=0.0004$) compared with the patients with the other genotypes.

Based on the theoretical observation that the within genotype variance of a quantitative trait will vary when a genetic or an environmental interaction is present, we explored the presence of an interacting covariate on the genetic effect of *PDE8B* on serum TSH levels. Levene's test of equality of variance ($P=0.2$) did not suggest the presence of an interacting covariate.

Nevertheless, considering that BMI SDS, as expected, correlated with TSH level ($P=0.00001$), we focused on the possible modulating role of obesity degree on the effect of *PDE8B* polymorphism on TSH levels.

Relationship between BMI SDS and TSH levels was, therefore, analysed in function of the different *PDE8B* genotypes. Comparison of the slopes of relative regression lines was not significant ($P=0.1$; Fig. 1). This further strengthens the concept that the effect of *PDE8B* rs4704397 on TSH levels is independent of BMI. Together, rs4704397 and BMI SDS explained 8.4% of the variability of TSH. The effect of the genetic component was 2.5% and the specific quantitative contribution of each minor (A) allele to TSH circulating concentration was 0.14 mIU/l, which is in line with what was shown in large cohorts of adults previously described (10).

In order to obtain a complete risk stratification of the possibilities to have abnormal TSH levels, we subdivided the population of obese children into six groups according to BMI SDS (below or above 3, the generally accepted cut-off to define severe obesity) and *PDE8B* genotypes (G/G, A/G or A/A).

**Table 2** Clinical and laboratory characteristics of obese patients stratified by *PDE8B* genotype. Values are expressed as mean±S.D.s. General linear model analysis including gender, age and pubertal stage as covariates have been used to compare continuous variables.

| | GG | GA | AA | *P* values |
|---|---|---|---|---|
| *n* (%) | 259 (29.9%) | 438 (50.5%) | 170 (19.6%) | |
| Age (years) | 10.6±2.9 | 10.5±2.8 | 10.7±2.7 | 0.7 |
| BMI SDS | 3±0.7 | 2.9±7 | 2.9±0.7 | 0.2 |
| Waist to height ratio | 0.60±0.05 | 0.61±0.05 | 0.60±0.06 | 0.7 |
| SBP-SDS | 0.76±1 | 0.67±1 | 0.63±1.1 | 0.4 |
| DBP-SDS | 0.29±0.8 | 0.15±0.7 | 0.2±0.7 | 0.06 |
| HOMA-IR | 5.7±4.8 | 5.5±3.6 | 5.1±3.8 | 0.7 |
| HDL-C (mg/dl) | 41±16 | 43±34 | 45±14 | 0.35 |
| Triglycerides (mg/dl) | 96±46 | 97±44 | 107±73 | 0.1 |
| TSH (mUI/l) | 2.6±1.16 | 2.7±1.25 | 3±1.5 | 0.0012 |
| $FT_4$ (pg/ml) | 10±2.3 | 9.9±2.3 | 9.9±3.5 | 0.9 |
| $FT_3$ (pg/ml) | 3.9±0.7 | 3.9±0.8 | 3.8±0.9 | 0.5 |

BMI SDS, body mass index SDS; DPB-SDS, diastolic blood pressure SDS; SBP-SDS, systolic blood pressure SDS, HOMA-IR, homeostatic model of assessment of insulin resistance index; HDL-C, high-density lipoprotein cholesterol.

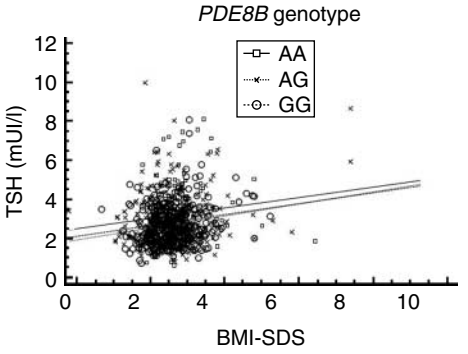


**Figure 1** Association between TSH levels and BMI SDS according to the *PDE8B* genotypes. Regression analysis describing in 867 obese children the relationship between TSH levels and BMI-SDS in patients homozygous for *PDE8B* G variant, heterozygous and homozygous for *PDE8B* A variant. The three regression lines are not significantly different as to slopes ($P=0.7$). Patients homozygous for A variant are shown as unfilled squares; patients heterozygous are indicated as crosses and patients G/G are shown as unfilled dots.

As shown in Table 3, the prevalence of children with high TSH level is particularly elevated in the group of patients with severe obesity homozygous for the A allele (27%), while children homozygous for the G allele and less severely obese had the lowest prevalence of abnormal TSH levels (5.3%; $P=0.0001$).

Logistic regression analysis showed that subjects homozygous for the *PDE8B* minor allele (A/A) and with BMI SDS above 3 (category I) had the highest OR (OR 2.6 (CI: 1.5–4.7) $P=0.0015$) to develop abnormally elevated (>4.2 UI/l) TSH, and that OR progressively reduced in the other groups of patients according to the simply additive model of interaction between BMI SDS and *PDE8B* genotype (Table 3).

In fact, children homozygous for the *PDE8B* common allele (G/G) and with BMI SDS equal or below 3 (category VI) showed the lowest possibilities to have abnormal TSH level (OR 0.3 (CI: 0.1–0.6) $P=0.005$; Table 3).

## Discussion

Higher serum TSH concentrations are found in obese children and adults compared with normal-weight individuals (4, 5, 20, 21). Furthermore, TSH appears to be positively related to the degree of obesity. A positive correlation has been identified between serum leptin and serum TSH (22, 23), which could reflect the association between TSH and BMI reported in some studies (4, 8, 9, 24). Recent papers, investigating normal subjects or pregnant women, have shown that the rs4704394 polymorphism in the *PDE8B* gene is associated with variations in TSH levels (12, 13). In line with the data previously reported, we have shown in a group of 867 Italian obese children and adolescents that this polymorphism is associated with TSH levels. Furthermore, we have expanded the knowledge about the clinical impact of this *PDE8B* variant demonstrating the lack of association with BMI degree, abdominal fat and some component of the metabolic syndrome, such as SBP and DBP, dyslipidemia and insulin resistance. No association has been found with $fT_3$ and $fT_4$. The polymorphism, therefore, appears to be associated with changes in thyroid homeostasis, but not with changes in obesity-linked cardiovascular and metabolic risk factors.

The second question we have faced in this work was the dissection of the interaction between BMI degree and the *PDE8B* variant in modulating TSH levels in childhood obesity. Particularly, we have analysed whether the phenotypic (BMI increase) and the genetic (*PDE8B* polymorphism) elements work following a synergistic or an additive model in increasing TSH levels. Both the analysis of equality of variance and the comparison of slopes of the regression lines between BMI SDS and TSH in function of the different *PDE8B* genotypes suggested an additive model of interaction. In other words, the strength of the effect of *PDE8B* rs4704394 on TSH levels is not modulated by obesity degree. The lack of synergy of the interaction between BMI and *PDE8B* in increasing TSH levels may be attributable to their different pathophysiological actions. Adiposity and *PDE8B* likely modulate thyroid homeostasis at different steps.

*PDE8B* encodes a cyclic AMP PDE enzyme (11, 25), strongly expressed in the thyroid gland (26, 27, 28) but undetectable in the pituitary gland, and its influence on thyroid hormone parameters should be via hydrolysis and inactivation of cAMP in the thyroid, in response to

**Table 3** Risk showing abnormal TSH levels in 867 obese children stratified in six categories according to body mass index SDS (BMI SDS) and *PDE8B* genotype. TSH values are expressed as mean ± S.D.s. Logistic regression analysis has been used to calculate the odds ratios (OR) to have TSH >4.2 mUI/l for each category of patients (from I to VI) compared with the entire cohort of children.

| Categories | BMI SDS | *PDE8B* genotype | Patient number | TSH (mUI/l) | Patients (%) with TSH >4.2 mUI/l | OR (CI) *P* value |
|---|---|---|---|---|---|---|
| I | >3 | AA | 70 | 3.3±1.6 | 27.1 | 2.6 (1.5–4.7) 0.0015 |
| II | >3 | AG | 278 | 2.7±1.2 | 11.5 | 0.8 (0.5–1.5) 0.5 |
| III | >3 | GG | 110 | 2.8±1.3 | 18.8 | 1.5 (0.9–2.5) 0.1 |
| IV | ≤3 | AA | 160 | 2.8±1.4 | 19 | 1.6 (0.9–2.7) 0.1 |
| V | ≤3 | AG | 278 | 2.7±1.2 | 11.8 | 1.1 (0.7–2) 0.5 |
| VI | ≤3 | GG | 149 | 2.4±1.1 | 5.3 | 0.3 (0.1–0.6) 0.005 |

TSH signalling. Variations in *PDE8B* may, therefore, influence the thyroid hormone set point by making the thyroid less responsive to TSH (11).

Among the several mechanisms suggested to explain increased TSH levels in obesity, the most favoured one is increased leptin-mediated production of pro-TRH (3, 28, 29, 30). Leptin innervates hypothalamic TRH-synthesising neurons (31) and stimulates TSH production through the hypothalamic pituitary axis. Therefore, in agreement with our hypothesis, adiposity could exert its action on thyroid homeostasis at a different step (i.e. central action) compared with the step (i.e. peripheral action) of *PDE8B* variant.

Nevertheless, considering that both pregnant women and obese children represent two particular groups of subjects with frequently increased TSH, the possibility that the *PDE8B* gene is more an amplification gene for mildly failing or challenged thyroid function than a strong determinant of the TSH set-point cannot be excluded a priori. This also considering that in the first paper showing the association between the *PDE8B* rs4704394 SNP and TSH, the first population investigated (Sardinian) is a low iodine-intake population, the replication group is an ageing population, and the second replication group is the Amish population (32), a group known to exhibit close to 20% of thyroid autoimmunity features.

In the third part of this work, we have stratified the entire population of obese children on the basis of their *PDE8B* genotypes and severity of their obesity (below or above 3 BMI SDS) in six groups with different possibilities to show abnormally elevated TSH levels. The prevalence of patients with altered TSH levels ranged from 5 to 27% according to *PDE8B* genotype and BMI measure.

Endocrinologists and paediatricians frequently face the decision of what to do about an obese child who has normal $fT_3$ and $fT_4$ levels and TSH levels slightly above the upper range (1). For these clinicians, it may be of interest to know more about the intriguing relationship between thyroid and obesity and, therefore, about the individual risk of obese children to have abnormal TSH levels.

In fact, in patients whose TSH level is shifted towards the upper limits, such as in obese patients, the clinical impact of *PDE8B* polymorphism is more relevant as it increases the number of patients recognised as having hyperthyrotropinaemia.

In conclusion, we have studied for the first time the rs4704394 *PDE8B* polymorphism in a group of obese patients and, particularly, in a cohort of obese children and we have: i) confirmed, also in these kind of patients, the association with TSH levels; ii) demonstrated that the interaction between adiposity and *PDE8B* in elevating TSH levels is not synergistic, but follows an additive model; and iii) highlighted the clinical impact of this association, stratifying the individual risk to develop abnormally elevated TSH levels on the basis of the interaction between the *PDE8B* genotype and the degree of obesity.

## 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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