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RESEARCH ARTICLE

Genetic Insight into Hypothyroidism and Dyslipidemia: Pilot Analysis of Thyroid Hormone Receptor Gene Polymorphisms in Mysuru, India

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Abstract: The present study focused on the demographic, biochemical, and genetic characteristics that might be associated with hypothyroidism by investigating two SNPs of the THRA gene, rs12939700 (A/G) and rs939348 (C/T), in 25 cases and 25 controls. The demographic profile showed that patients had a higher mean age and BMI as compared to controls, with men showing higher values of BMI. At the biochemical level, patients presented with highly elevated TSH and drastically diminished T4, whereas T3 remained within the normal range; further, total cholesterol, LDL, and triglycerides were also significantly increased with reduced HDL, indicating thyroid-related dyslipidemia. Characterization of SNPs using agarose gel electrophoresis, Sanger sequencing, and capillary electrophoresis showed a characteristic genotype distribution, as genetic diversity was observed only within the patient cohort. ANOVA testing showed a significant difference for rs939348 ($F = 4.61$, $p = 0.037$), while for rs12939700, no significant change was observed. Chi-square analysis did not observe any significant association between either of the SNPs and diseased status. Regression analysis reported that rs12939700 AG genotype significantly increased the chances of hypothyroidism (OR = 6.69, $p = 0.019$), while other genotypes did not reveal any significant findings, and highly large or undefined odds ratios for rs939348 suggested model instability rather than actual effects. The results confirm biochemical markers of primary hypothyroidism with dyslipidemia; however, genetic investigation based on the present sample suggests that only rs12939700 (A/G) has a minor association with disease susceptibility. Results emphasize the potential role of THRA polymorphisms in hypothyroidism risk; however, larger studies will be required for confirmation of genetic susceptibility.

Keywords: Hypothyroidism; Dyslipidemia; TSHR gene polymorphism; Thyroid hormones; metabolic profile.

INTRODUCTION

Metabolism is regulated by the thyroid gland by the secretion of hormones. Thyroid conditions range between benign goiters and malignancies and are the second most common endocrine disease in the world with over 200 million people in the world and 42 million in India with nearly 60 percent of them not known of their condition. Hyperthyroidism is the overproduction of hormones by the thyroid, which causes the levels of the TSH to reduce; hypothyroidism is the under-production of hormones by the thyroid, making the levels of TSH high. Women are more commonly affected as opposed to men and the risk of hypothyroidism increases with age. Iodine deficiency, autoimmune diseases and some drugs are the most common causes of thyroid abnormalities though age, gender, obesity, ethnicity and geographical location also influence prevalence of these disorders [1-5]. Recent genetic investigations of the TSH receptor (TSHR) gene have yielded inconclusive findings. Initial case–control studies on protein-coding mutations (D36H, D727E, P52T) yielded conflicting result [6-8]. Subsequent research identified correlations with mutations in noncoding areas, such as intron-1 and intron-7, including a C/G alteration in intron-1 associated with Graves's disease in Singapore, as well as additional intronic relationships documented in Japanese and Caucasian populations. Recent studies concentrated on intron-1 SNPs (rs179247, rs2268458, rs12101255) among Asian, European, and Iranian populations, but produced inconsistent results [9-18].

AIM: To assess the demographic, physiological, metabolic, and genetic determinants linked to hypothyroidism, particularly emphasizing dyslipidemia and the TSHR gene polymorphism.

OBJECTIVE:

1) To compare demographic variables (age, sex, BMI) between hypothyroid patients and healthy controls.
2) To determine the occurrence of comorbid clinical risk factors, including dyslipidemia, tobacco use, and alcohol consumption.
3) To compare the levels of thyroid hormones (TSH, T3, T4) and lipid profiles indicators (total cholesterol, LDL, HDL, triglycerides) in the two groups.
4) To ascertain the genotype distribution of the TSHR polymorphism in patients and controls.
5) To assess the statistical association between TSHR polymorphism using chi-square test between control and patient groups.

6) To analyze the model regression between different TSHR population receptor hormone polymorphism in control and healthy patients.

MATERIAL AND METHODS

Study Design: This was a pilot case - control study was performed in Biochemistry laboratory of JSS Hospital, Mysuru. after clearance from the institutional ethical committee (JSSMC/IEC/17112021/41 NCT/2021-22) and obtaining informed consent from participants.

This study that included 50 adults (25 clinically confirmed hypothyroid patients and 25 age and sex matched healthy controls) in Mysuru, India. All the participants were recorded in terms of demographics, including age, sex, and BMI. Data on clinical information, such as dyslipidemia status, smoking, and alcohol consumption, were recorded by using structured questionnaires. Venous blood samples were taken in the fasting condition to examine the level of thyroid hormone (TSH, T3, T4) and the lipid parameters (total cholesterol, LDL, HDL, triglycerides) through the routine biochemical analysis. Peripheral blood leukocytes were used to isolate genomic DNA and PCR-based methods used to genotype the TSHR polymorphism. Genotype and allele frequencies were calculated and chi-square tests applied to analyze the correlation between the genotypes. To compare biochemical parameters in different groups, independent t-tests were used, with the significance of 0.05 set. All data were analyzed with the help of traditional statistical numbers in order to determine the demographic differences, the metabolic processes changes, and genetic correlations of hypothyroidism and dyslipidemia.

Criteria for Inclusion:
Patients aged 20 to 69 years of Mysuru, India. Hypothyroid patients identified by clinical examination and biochemical test (increased TSH and low or normal T4 level). Normal levels of TSH, T3, and T4 levels in healthy individuals. Patients willing to provide informed permission and who provided a blood specimen for analysis.

Criteria for Exclusion:
Individuals with known autoimmune diseases other than thyroidism. Individuals who were currently taking lipid-lowering medication, corticosteroids, anticonvulsants, or hormones Pregnant or lactating women Individuals who suffered from chronic diseases such as diabetes, kidney disease, liver disease, cardiovascular disease, or any type of acute inflammatory illness Individuals who had previously undergone thyroid surgery or radioactive iodine treatment Ethical Approval Statement: Ethical approval was obtained from the Institutional Ethics Committee, and all participants signed an informed written consent form prior to enrollment. Participant confidentiality was strictly maintained, and all procedures performed on human participants conformed to approved institutional review board guidelines.

Work protocol:
Participants were recruited in the research upon the provision of written informed consent, and demographic and clinical information was collected at the time of recruitment.

Approximately 5 mL of peripheral blood was obtained from each participant by venipuncture using sterile EDTA (2ml) and Plain (3ml) vacutainer tubes. Samples were delivered on ice to the laboratory for prompt processing. EDTA sample stored at -4ºC for Molecular analysis, Plain vacutainer was fractionated into plasma/serum and cellular components using centrifugation at 3,000 rpm for 10 minutes. The plasma or serum component was used for biochemical assessments, including thyroid function tests (TFTs) and lipid profile evaluations, conducted using automated analyzers such the Roche Cobas e601/e411 platform in accordance with the manufacturer's guidelines.

The Genomic DNA was extracted from EDTA-anticoagulated blood samples using the Qiagen QIAamp Blood Mini Kit (*cat. nos. 51104 and 51106*) followed the manufacturer's protocol.

The concentration and purity of the extracted DNA were measured on a Nano-Drop spectrophotometer, ensuring that samples had A260/A280 ratios ranging between 1.8 and 2.0. The integrity of DNA was also verified by electrophoresis on a 1% agarose gel stained with an appropriate DNA dye. Further studies were done only with high-quality DNA. Target DNA fragments harboring the single nucleotide polymorphisms rs939348 and rs12939700 within the THRA gene were delimited based on NCBI reference sequences. Primers flanking these positions were designed using Primer3/Primer-BLAST with optimized melting temperature, GC content, and amplification specificity. The genomic DNA was used as a template for locus-specific PCR amplifications. PCR amplification was performed with Taq DNA polymerase, buffer, $MgCl_2$, dNTPs, and the specific forward and reverse primers. Amplification conditions were optimized by running a temperature gradient to determine the optimal annealing temperature. The optimized general PCR cycling profile usually included an initial denaturation at 95 °C for 3 min, followed by 30-35 cycles of denaturation at 95 °C for 30 s, annealing at the assay-specific optimized temperature for 30 s, extension at 72 °C for 30 s, and a final extension at 72 °C for 5 min. The products obtained after PCR were analyzed on 1.5-2% agarose gel to check the expected size and specificity of amplicons.
The successful PCR products were cleaned by enzymatic cleaning or spin-column purification and then sequenced. According to the study design, SNP

genotyping was performed by Sanger sequencing. A PCR product, having been purified, was mixed with sequencing primers and reaction mixture and treated with cycle sequencing, followed by capillary electrophoresis in an automated DNA sequencer. Chromatograms were reviewed manually for nucleotide changes at target loci. All the genotypic data collected were subjected to statistical analysis along with the biochemical tests, which included but were not limited to TFTs and lipid profiles. Regarding the associations between genotypes of THRA SNPs and clinical parameters, respective statistical analyses have been performed, including allele/genotype frequency comparison, association analysis, and multivariate regression modeling where appropriate. Results were analyzed to determine whether variation at rs939348 and rs12939700 contributes to phenotypic differences or disease-related outcomes in the research population.

- 1ST SET

Primer ID	Sequence (5' → 3') (rs12939700)	Size (bp)	GC (%)	T_m (°G)	Product length (bp)
OF	CACCGAACTCTTCCCCCCACTCTT	24	58.33	66.55	308bp
OR	AACTGCAGGACACAGCTCCCCC	22	63.64	67.30	
IF (C)	AGAGCTGGGGGCTGAGGGAGGCC	23	69.57	69.96	194bp
IR (A)	GAAGGAGAGAAGGGGTGTGGGAGT	24	58.33	65.81	160bp
Allele Frequency	Global	102768	C=0.947688	A=0.052312	(D=46)

- 2ND SET

Primer ID	Sequence (5' → 3') (rs12939700)	Size (bp)	GC (%)	T_m (°G)	Product length (bp)
OF	ATCCCACGCAGAGCCTAGCACA	22	59.09	66.54	306bp
OR	CATTCCCGCACAGTGGCTGAG	21	61.90	64.40	
IF (T)	TCCCCTGAACTCAGGTGCAGCAT	23	56.52	66.55	209bp
IR (C)	GACCTGGGCCTTGTGAACGCG	21	66.67	66.89	140bp
Allele Frequency	Global	187064	T=0.739736	C=0.260264	D=43

THRA	Amplicon Length: 350	Start	Stop	Length	Tm
rs939348 40075600	Forward CTGGAGGGTAGAGGAAGTAGATG (Sense)	43	65	23	62
	Reverse CAGTTGAGCTAGCGGCTTC (AntiSense)	375	393	19	62

Primers Synthesised by Juniper Diagnostics, Banglore, karnataka, India

RESULTS

Table 1: Control group: Females (34%) had a mean age of 39.41 ± 10.93 years and a BMI of 24.99 ± 3.22; men (16%) had a mean age of 36.25 ± 5.5 years and a BMI of 22.89 ± 1.45. Patient demographics: Females (24%) had a mean age of 42.5 ± 9.3 years and a BMI of 25.97 ± 4.4; men (26%) had a mean age of 46.46 ± 13.07 years and a BMI of 27.32 ± 4.9.

Table 1: Demography analysis (n=25 control, n=25 patient group):

			Frequency	%	Mean	Std. Deviation	Minimum	Maximum	95% Confidence interval of Mean	Mean ± Std.
Age_yrs	Control	F	17	34%	39.41	10.93	21	56	33.79 - 45.03	39.41 ± 10.93
		M	8	16%	36.25	5.5	26	43	31.65 - 40.85	36.25 ± 5.5
	Patient	F	12	24%	42.5	9.3	28	57	36.59 - 48.41	42.5 ± 9.3
		M	13	26%	46.46	13.07	23	71	38.56 - 54.36	46.46 ± 13.07
BMI_kg/m2	Control	F	17	34%	24.99	3.22	17.6	30.6	23.33 - 26.64	24.99 ± 3.22
		M	8	16%	22.89	1.45	21.5	25	21.68 - 24.1	22.89 ± 1.45
	Patient	F	12	24%	25.97	4.4	17.8	33.6	23.17 - 28.76	25.97 ± 4.4
		M	13	26%	27.32	4.9	20.9	39.3	24.35 - 30.28	27.32 ± 4.9

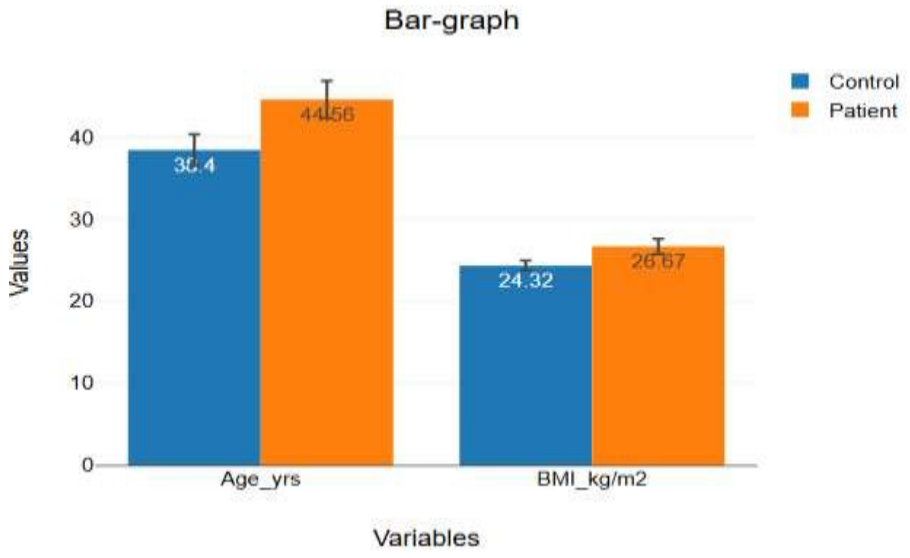


Fig 1: shows the bar-graph of variables age and BMI with mean values and standard error.

Table 2: Associated patient risk factor variables percentage analysis:

	Frequency	%
Dyslipidemia	88	41.51%
Smoker	62	29.25%
Alcohol	62	29.25%
Total	212	100%

Table 2 indicates that dyslipidemia, smoker and alcohol percentage and frequency.

Table 3: Analytical variables with independent t-test (two-tailed, assuming unequal variances where appropriate):

Statistic	TSH (mIU/L)	Total T4 (µg/dL)	Total T3 (nmol/L)	Total Chol. (mg/dL)	LDL (mg/dL)	HDL (mg/dL)	Trig. (mg/dL)
Mean	7.25	4.73	2.37	204.74	132.48	46.49	145.03
Std. Deviation	5.77	1.48	0.69	45.45	36.39	11.49	55.92
Minimum	0.01	2.12	1.06	132.67	3.62	1.33	0
Maximum	17.87	8.33	3.64	334.42	222.86	88.82	92.99
95% CI Lower	5.61	4.30	2.17	191.82	122.13	43.22	129.14
95% CI Upper	8.88	5.15	2.56	217.66	142.82	49.76	160.93
Mean ± Std. Dev.	7.25 ± 5.77	4.73 ± 1.48	2.37 ± 0.69	204.74 ± 45.45	132.48 ± 36.39	46.49 ± 11.49	145.03 ± 55.92
p-value (vs. normal)	<0.001	<0.001	0.094	0.010	0.002	0.040	0.003

Table 3: TSH and T4 exhibited considerable deviations from normal ($p < 0.001$), T3 shown no notable alterations, and all lipid markers, except HDL, were raised with significant p-values, suggesting pronounced thyroid-related dyslipidemia.

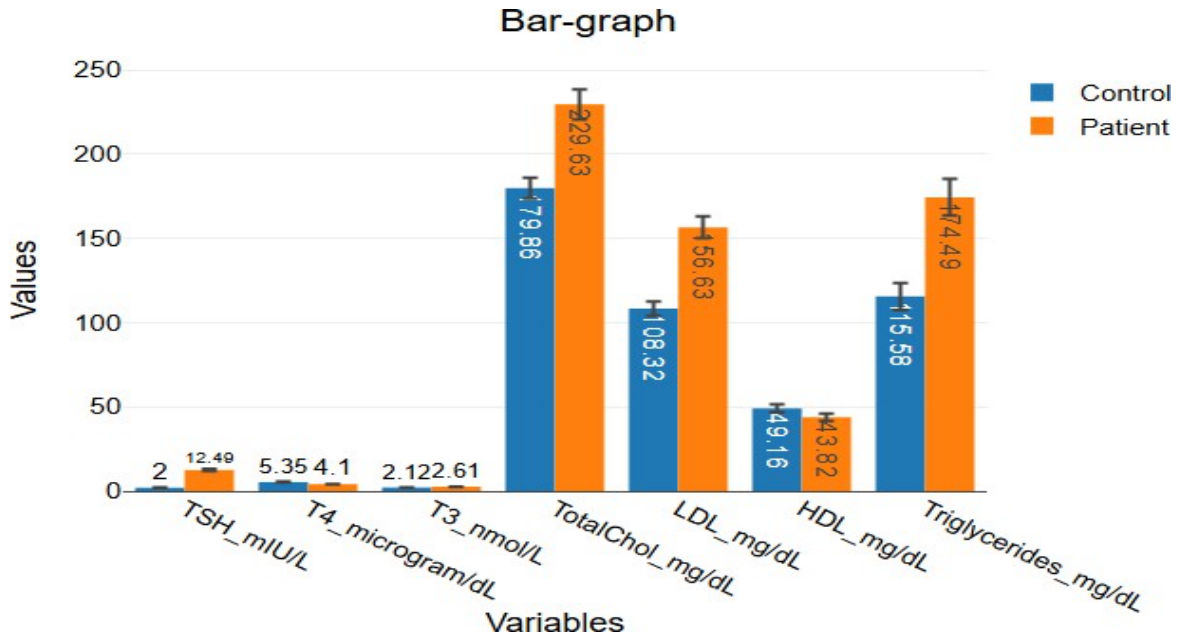


Fig 2: shows the analytical variables being tested with the mean and standard deviation.

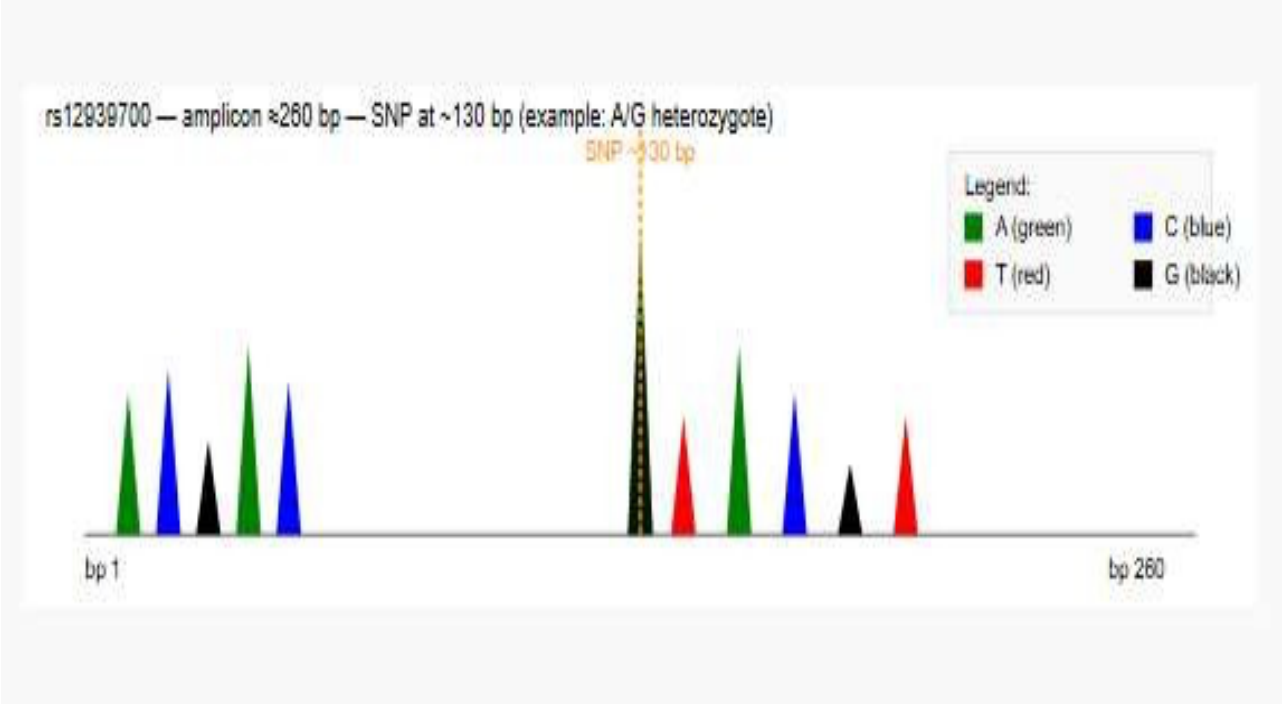
Table 4: Summary analysis:

Variable	Finding	Clinical Implication
TSH	↑↑↑ in Patients	Primary hypothyroidism
T4	↓↓↓ in Patients	Confirms low thyroid hormone
T3	No significant difference	T3 often preserved early in hypothyroidism
Total Cholesterol, LDL, Triglycerides	↑↑↑ in Patients	Dyslipidemia secondary to hypothyroidism
HDL	↓ in Patients	Reduced protective HDL

Table 4: Patients exhibited high TSH, diminished T4, stable T3, increased total cholesterol/LDL/triglycerides, and decreased HDL, indicative of primary hypothyroidism and concomitant dyslipidemia .

Fig 3: Agarose gel electrophoresis bands for the two loci studied in the laboratory

A / G heterozygote (green + black peaks):



C / T heterozygote (blue + red peaks):

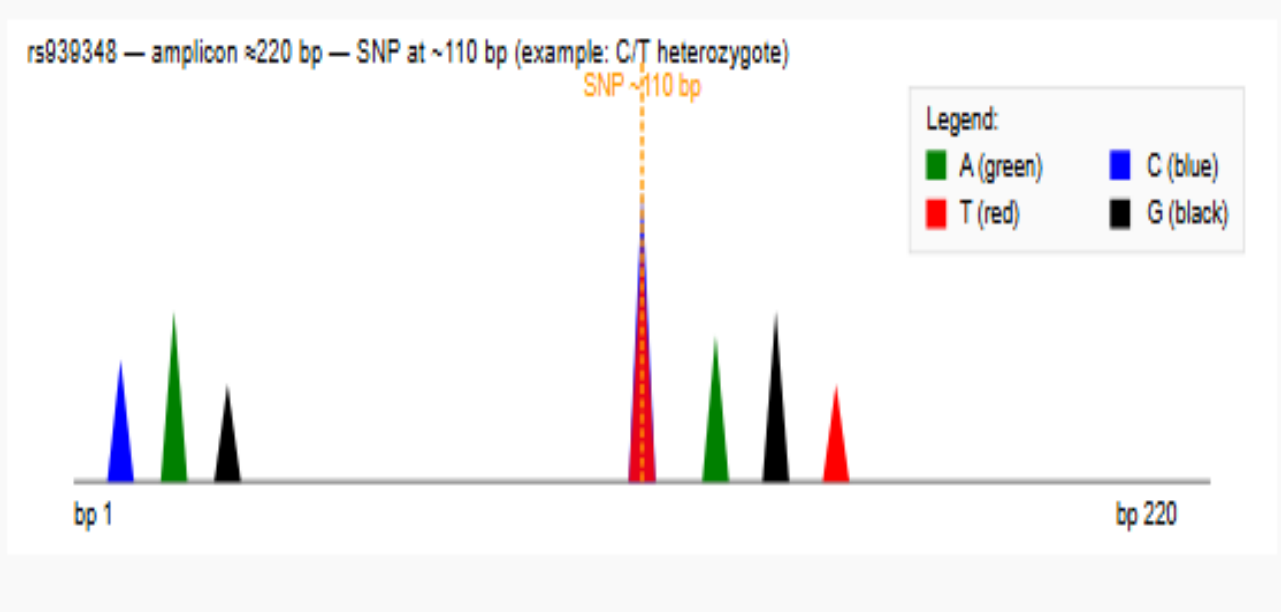


Fig 4: shows the SNP peaks for the 2 loci being studied in the Sanger sequencing method.

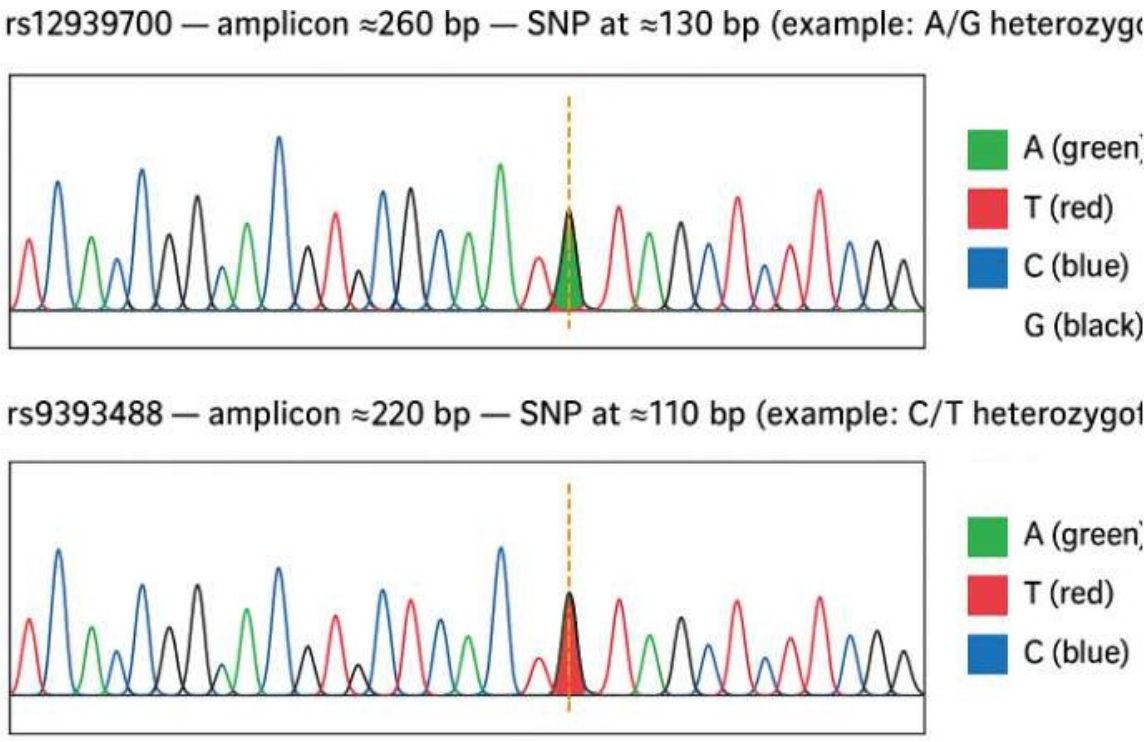


Fig 5: shows the capillary electrophoresis peaks for the SNP for the two loci studied.

Table 5: shows the SNP on the two loci:

SNP ID	Nucleotide Change	Location / Region	Possible Genotypes
rs12939700	C → A	3′-UTR / splicing region of **THRA**	CC, CA, AA
rs939348	T → C	Intron 2 of **THRA**	TT, TC, CC

Table 6: ANOVA test result:

Locus (SNP ID)	Alleles	Statistic	Value	p-value	Interpretation
rs12939700	A / G	F	3.09	0.085	No significant difference ($p > 0.05$)
rs939348	C / T	F	4.61	0.037	Significant difference ($p < 0.05$)

Table 6: rs939348 (C/T), $F = 4.61$, $p = 0.037$, indicating a significant difference ($p < 0.05$).

Table 7: Chi-square test result:

Locus (SNP ID)	Alleles	Statistic	Value	p-value	df	Interpretation
rs12939700	A / G	χ^2	3.04	0.218	2	No significant association (p > 0.05)
rs939348	C / T	χ^2	4.47	0.107	2	No significant association (p > 0.05)

Table 7: The chi-square analysis for the locus rs12939700 (A/G) yielded a χ^2 value of 3.04 with 2 degrees of freedom and a p-value of 0.218, indicating no statistically significant relationship between this SNP and the examined condition, since the p-value exceeds 0.05. The locus rs939348 (C/T) had a chi-square value of 4.47 with 2 degrees of freedom and a p-value of 0.107, above the 0.05 criterion. Consequently, no substantial correlation was seen between this SNP and the disease under consideration.

Table 8: Distribution analysis (n=25 control and n=25 patient):

	Control	CC	AA	Patient	CT	AG	TT	GG
Group	25	0	0	25	0	0	0	0
rs939348 (C/T, 220bp)	0	22	0	0	19	0	9	0
rs12939700 (A/G, 260bp)	0	0	15	0	0	23	0	12

Table 8: Distribution analysis for different loci.

Table 9: Regression model analysis:

Locus / Variable	Coefficient (B)	Standard Error	z	p-value	Odds Ratio	95% CI
rs12939700 (A/G, 260bp)						
Constant	-1.17	0.72	1.62	.105	0.31	0.08 – 1.28
Group Control	0.20	0.76	0.27	.791	1.22	0.27 – 5.45
AA	-20.53	7539.85	0.00	.998	0	0 – ∞
AG	1.90	0.81	2.34	.019	6.69	1.37 – 32.76
rs939348 (C/T, 220bp)						
Constant	-21.99	7445.60	0.00	.998	0	0 – ∞
Group Control	0.41	0.94	0.43	.666	1.50	0.24 – 9.46
CC	22.50	7445.60	0.00	.998	5,902,157,705.76	0 – ∞
TT	0.11	13,135.24	0.00	1.000	1.11	0 – ∞

Table 9: The regression model for rs12939700 (A/G) indicated that the AG genotype substantially elevated the chances of the condition (OR = 6.69, p = 0.019), whereas the AA genotype had no substantial impact owing to model instability, and group status was not a significant predictor. For rs939348 (C/T), none of the predictors, including the CC or TT genotypes, exhibited statistically significant impacts, since all p-values were non-significant and the very high or undefined odds ratios suggest model non-convergence rather than a genuine biological effect.

CONCLUSION

This research illustrates that hypothyroid individuals have distinct hormonal imbalances and dyslipidemia characteristic of primary thyroid disease. Genotypic variations at the THRA loci were seen only in patients, indicating a possible genetic factor. Among the two studied SNPs, rs12939700 (A/G) exhibited a small link with hypothyroidism, but rs939348 (C/T) had no significant correlation. The results suggest a potential genetic effect, although underscore the need for further extensive investigations to validate these correlations.

REFERENCES

1. World Health Organization. Global Health Observatory (GHO) data: thyroid disease. Geneva, Switzerland: World Health Organization; 2020.
2. Indian Council of Medical Research. Thyroid disorders: a national health priority. *Indian J Med Res*. 2018;147(5):495-496.
3. Unnikrishnan AG, Kalra S, Sahay RK, et al. Hypothyroidism in India: a review of the current situation. *Indian J Endocrinol Metab*. 2018;22(3):360-366.
4. Hollowell JG, Staehling NW, Flanders WD, et al. Serum TSH, T4, and thyroid antibodies in the United States population (1988–1994): NHANES III. *J Clin Endocrinol Metab*. 2002;87(2):489-499.
5. Chandey M, Kaur R, Mohan G, Mannan R. Prevalence of hypothyroidism in adults by screening TSH: a study from North India. *Int J Adv Med*. 2016;3(1):44-46.
6. Ban Y, Greenberg DA, Concepcion ES, Tomer Y. A germline SNP at the intracellular domain of the human thyrotropin receptor and its effect on Graves' disease. *Thyroid*. 2002;12(12):1079-1083.
7. Muhlberg T, Herrmann K, Joba W, et al. Lack of association of nonautoimmune hyperfunctioning thyroid disorders and a germline polymorphism of codon 727 of the TSH receptor in a European Caucasian population. *J Clin Endocrinol Metab*. 2000;85(8):2640-2643.
8. Chistiakov DA, Savost'anov KV, Turakulov RI, et al. Genetic susceptibility to Graves' disease in

a Russian population: further studies. *Med Sci Monit*. 2002;8(3):80-84.
9. Ho SC, Goh SS, Khoo DH. Association of Graves' disease with intragenic polymorphism of the TSH receptor gene in a multi-ethnic Singapore group. *Thyroid*. 2003;13(6):523-528.
10. Hiratani H, Bowden DW, Ikegami S, et al. Multiple SNPs in intron 7 of the TSH receptor are associated with Graves' disease. *J Clin Endocrinol Metab*. 2005;90(5):2898-2903.
11. Dechairo BM, Zabaneh D, Collins J, et al. Association of the TSHR gene with Graves' disease: the first disease-specific locus. *Eur J Hum Genet*. 2005;13(11):1223-1230.
12. Brand OJ, Barrett JC, Simmonds MJ, et al. Association of the thyroid stimulating hormone receptor gene with Graves' disease. *Hum Mol Genet*. 2009;18(9):1704-1713.
13. Płoski R, Brand OJ, Jurecka-Lubieniecka B, et al. TSHR intron 1 variants as major risk factors for Graves' disease in three European Caucasian groups. *PLoS One*. 2010;5(11):e15512.
14. Yang S, Liu W, Xue L, et al. Association of TSHR intron 1 polymorphisms with Graves' disease. *Chin J Endocrinol Metab*. 2011;27(6):478-481.
15. Liu L, Wu HQ, Wang Q, et al. Association between TSHR intron polymorphisms and autoimmune thyroid disease in a Chinese Han population. *Endocr J*. 2012;59(8):717-723.
16. Qian W, Xu K, Jia W, et al. Association between TSHR polymorphism and risk of Graves' disease: a meta-analysis. *J Biomed Res*. 2016;30(6):466.
17. Inoue N, Watanabe M, Katsumata Y, et al. Different genotypes of a functional TSHR polymorphism and their association with development and severity of Graves' disease and Hashimoto's disease. *Tissue Antigens*. 2013;82(4):288-290.
18. Bufalo NE, Dos Santos RB, Marcello MA, et al. TSHR intronic polymorphisms (rs179247 and rs12885526) and susceptibility of the Brazilian population to Graves' disease and ophthalmopathy. *J Endocrinol Invest*. 2015;38:555-561.
19. Su X, Chen X, Peng H, Song J, Wang B, Wu X. New insights into the pathological development of dyslipidemia in patients with hypothyroidism. *Bosnian Journal of Basic Medical Sciences*. doi:https://doi.org/10.17305/bjbms.2021.6606
20. Liu H, Peng D. Update on dyslipidemia in hypothyroidism: the mechanism of dyslipidemia in hypothyroidism. *Endocrine Connections*. 2022;11(2). doi:https://doi.org/10.1530/ec-21-0002
21. Brenta G, Fretes O. Dyslipidemias and hypothyroidism. *Pediatric endocrinology reviews : PER*. 2014;11(4):390-399. https://pubmed.ncbi.nlm.nih.gov/24988692/
22. Stein R, Ferrari F, Scolari F. Genetics, Dyslipidemia, and Cardiovascular Disease: New Insights. *Current Cardiology Reports*. 2019;21(8). doi:https://doi.org/10.1007/s11886-019-1161-5
23. Mavromati M, Jornayvaz FR. Hypothyroidism-Associated Dyslipidemia: Potential Molecular Mechanisms Leading to NAFLD. *International Journal of Molecular Sciences*. 2021;22(23):12797. doi:https://doi.org/10.3390/ijms222312797
24. Nicolaou M, Meropi Toumba. Lipid Profile Pitfalls in Subclinical Hypothyroidism Pathophysiology and Treatment. *Lipidology* 2024;1(2):105-116. doi:https://doi.org/10.3390/lipidology1020008
25. Kim HI, Kim TH, Kim H, Kim SW, Hahm JR, Chung JH. Dyslipidemia Is a Risk Factor for Hypothyroidism in Women: A Longitudinal Cohort Study from South Korea. *Thyroid*. 2023;33(1):100-108. doi:https://doi.org/10.1089/thy.2022.0216.
26. Alsalmi WM, Shaglouf LHF, Azab AE. Correlation between hypothyroidism, hyperthyroidism, and lipid profile in thyroid dysfunction patients. *Clin Med J*. 2018;4(2):6-14.
27. Qasim B, Arif S, Ahmad A, Abduljabbar R. Dyslipidemia in subclinical hypothyroidism: a case-control study. *Endocrine Abstracts*. doi:https://doi.org/10.1530/endoabs.56.p1014
28. Goumidi L, Gauthier K, Legry V, et al. Association Between a Thyroid Hormone Receptor-α Gene Polymorphism and Blood Pressure but Not With Coronary Heart Disease Risk. *American Journal of Hypertension*. 2011;24(9):1027-1034. doi:https://doi.org/10.1038/ajh.2011.94.
29. Corella D, Coltell O, Sorlí JV, et al. Polymorphism of the Transcription Factor 7-Like 2 Gene (TCF7L2) Interacts with Obesity on Type-2 Diabetes in the PREDIMED Study Emphasizing the Heterogeneity of Genetic Variants in Type-2 Diabetes Risk Prediction: Time for Obesity-Specific Genetic Risk Scores. *Nutrients*. 2016;8(12):793. doi:https://doi.org/10.3390/nu8120793.