

ORIGINAL RESEARCH

A Study of *RET/PTC1* and *RET/PTC3* Gene Rearrangement in Papillary Thyroid Carcinoma with Clinico-Pathological Association in a Tertiary Care Centre of Karnataka

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ABSTRACT

Introduction: Papillary carcinoma of thyroid (PTC) is the commonest malignancy of thyroid. Various genetic alterations like gene mutation, gene amplification, gene translocation and gene methylation results in PTC. The prevalence of *RET/PTC* in papillary carcinomas shows significant geographic variation between 2.5% to 67%. There are more than 13 different types of *RET/PTC* translocations with *RET/PTC1* and *RET/PTC3* being commonest, accounting for >90% of all rearrangements. Many studies have correlated *RET/PTC1* and *RET/PTC3* with clinicopathological features and found varying results. Thus, we intend to study the frequency of *RET/PTC* gene rearrangement among PTC at our institute and see the association of *RET/PTC1* and *RET/PTC3* gene rearrangement with various histomorphological features. **Methods:** The study was conducted on histopathologically proved PTC cases. The Hematoxylin and eosin (H&E) stained slides prepared from formalin fixed paraffin embedded (FFPE), tissue blocks were evaluated and the area of interest with presence of >50% tumour area and absence of haemorrhage, necrosis and stromal desmoplasia was selected for PCR. The RNA was extracted followed by singleton Taqman gene expression assay for *RET/PTC1* and *RET/PTC3* rearrangement using Ag-PATH one step RT-PCR. *ACTB* gene was used as internal control. The results were correlated with various clinicopathological features for statistical significance. **Results:** A total of 18 PTC cases were included in the study. There were 6 (33.3%) males and 12 (66.6%) females with age range from 21 years to 68 years. On microscopic examination, conventional PTC, were seen in 10 cases (55.6%) and follicular variant seen in 8 cases (44.4%). The *RET/PTC* gene arrangement was seen in 3 out of 18 cases (16.6%) with *RET/PTC1* gene arrangement seen in 1 cases (5.6%) and *RET/PTC3* gene arrangement seen in 2 cases (11.1%). No statistically significant association of *RET/PTC* gene arrangement with age, gender, size of the lesion and microscopic type were noted.

Key words: PTC, *RET/PTC1*, *RET/PTC3*, Clinico-pathological Correlation, No statistically significant association

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INTRODUCTION

Thyroid cancer is a common endocrine malignancy that has shown a rapid increase in the global incidence in recent decades. The incidence rates have increased by about 58.1% between 1970 to 2003 ⁽¹⁾. In India, over the past decade there is a significant raise in the incidence of PTC by about 62% in females and 48% in males⁽²⁾. Papillary carcinoma of thyroid (PTC) is the most common thyroid malignancy seen between third to fourth decades of life accounting for 70% of

the thyroid carcinomas ⁽³⁾. Various types of genetic alterations like gene mutation (BRAF gene), gene translocation (*RET/PTC* rearrangement) and gene methylation has been identified as driver genetic alteration resulting in PTC. ^(4,5)

The prevalence of *RET/PTC* rearrangement in PTC has shown significant geographic variations of 20-70 %⁽⁶⁾. In India, there are no larger studies to know the prevalence of *RET/PTC* rearrangement in PTC across

the country. Some of the studies have shown the prevalence rate to range between 25-86.6% (7,8)

There are more than 13 different types of *RET/PTC* translocations, all resulting from the fusion of the tyrosine kinase domain of *RET* to the 5' portion of different genes (6). *RET/PTC1* and *RET/PTC3* are the most common types, accounting for >90% of all rearrangements (9,10).

There is some evidence that different types of *RET/PTC* may be associated with distinct biologic properties of papillary carcinomas. Some of the studies have shown that *RET/PTC1* tends to be more common in tumours with typical papillary growth and micro-carcinoma with a more benign clinical course, whereas *RET/PTC3* shows a strong correlation with the solid variant of papillary carcinoma with more aggressive tumour behaviour (9). Thus, we intend to study the frequency of *RET/PTC* gene rearrangement among PTC at our institution and see the association between *RET/PTC1* and *RET/PTC3* gene rearrangement with various histomorphological features of PTC.

METHODOLOGY

The study was conducted retrospectively on histopathologically proved PTC cases over a period of two years after obtaining institutional ethical

committee clearance. The patient's demographic details and gross specimen details were documented from hospital records. The Hematoxylin and eosin (H&E) stained slides prepared from formalin fixed paraffin embedded (FFPE) tissue blocks were evaluated for various histopathological features like pattern of tumour cell arrangement, extra thyroidal extension and Lymph node involvement. The area of interest from the tumour block, with presence of >50% tumour cellularity and absence of haemorrhage, necrosis and stromal desmoplasia were selected for Polymerase chain reaction (PCR). The RNA was extracted with RNeasy FFPE Kit (Qiagen), and the quality of the RNA extracted was checked using multisiskan Skyhigh spectrophotometer. The RNA was subjected to single step cDNA conversion and Taqman gene expression assay using Ag-Path one step RT-PCR Reagent (Applied biosystems). A singleplex RT-PCR was performed using 2x RT-PCR Buffer of 12.5 µL, 25x RT-PCR Enzyme Mix 1 µL, RNA sample of 2 µL, Forward and reverse Taqman primer –probe mixture of 2 µL, nuclease free water of 7.5 µL with the total reaction volume of 25 µL. *ACTB* gene (Thermoscientific) was used as internal control for the PCR. The primer – probes [7] used in the reaction are as shown in table 1.

TABLE 1: shows the primer - probe used in the Taqman gene expression assay:

GENE	PRIMER/PROBE TYPE	SEQUENCE
<i>RET/PTC1</i>	FORWARD PRIMER	CGCGACCTGCGCAA
	REVERSE PRIMER	CAAGTTCTTCCGAGGGAATTCC
	PROBE	6FAMCAAGCGTAACCATCGAGGATCCAAAGT TAMRA
<i>RET/PTC3</i>	FORWARD PRIMER	CCCCAGGACTGGCTTACCC
	REVERSE PRIMER	CAAGTTCTTCCGAGGGAATTCC
	PROBE	6FAM AAAGCAGACCTTGGAGAACAGTCAGGAGGTAMRA
<i>ACTB</i>	FORWARD PRIMER	TGACGGGGTCACCCACACTGTGCCCATCTA
	REVERSE PRIMER	CTAGAAGCATTGCGGTGGACGATGGAGGG
	Probe	6FAMCCG GCT TCG CGG GCG AC - TAMRA

The reaction was performed on Quantstudio 5 with the PCR condition as mentioned in Table 2. The results of *RET/PTC1* and *RET/PTC3* gene expression

assay was correlated with various clinicopathological features using descriptive statistics.

Table 2: Shows PCR conditions used for *RET/PTC 1* and *3* and *ACTB* gene Taqman gene expression assay.

Settings	Step 1	Step 2	Step 3	
stage	Reverse transcription	Denaturation	PCR (Denature)	PCR (anneal /extend)
temperature	45 ⁰	95 ⁰	95 ⁰	60 ⁰
time	10 mins	10 mins	15 sec	45

The results were looked for association with various clinico-pathological features for statistical significance. The data was analyzed using descriptive

statistics and association between *RET/PTC* rearrangement and various histomorphological features were assessed using Fisher's Exact Test,

Likelihood ratio and Liner – by linear association tests.

RESULTS

A total of 18 PTC specimens were included in the study. There were 6 (33.3%) males and 12 (66.7%) females with age range from 21 years to 68 years and mean age of 38.5 yrs. Majority of the cases were between 30-39 years of age (55.6%).

On gross examination 5 cases (27.8%) had tumour size < 2 cms, 8 cases (44.4%) had tumour size of 2 to

4 cms and 5 cases (27.8%) had tumour size of > 4 cms. On microscopic examination conventional PTC with papillary pattern was seen in 10 cases (55.6%) and follicular variant of PTC seen in 8 cases (44.4%). *RET*/PTC rearrangement was seen in 3/18 cases (16.7%) with *RET*/PTC1 rearrangement being positive in 1/18 case (5.6%) and *RET*/PTC3 rearrangement being positive in 2/18 cases (11.1%) as seen in **figure 1**.

Figure 1: showing RT-PCR amplification plot for *RET*/PTC gene rearrangement with *ACTB* (β actin) as internal control.

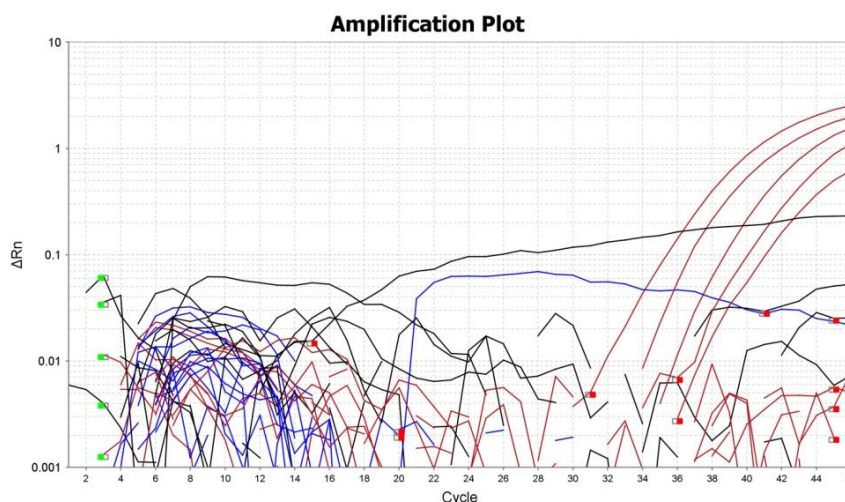


Image ■ betaactin ■ RET/PTC1 ■ RET/PTC3 **shows**

amplification plot of *RET*/PTC in (black) and *ACTB* gene (red) as internal control.

The association of *RET*/PTC rearrangement with various histomorphological features are as shown in table 3.

Table 3: shows association of *RET*/PTC rearrangement with various histomorphological features

SI No	VARIABLE	No of cases with percentage	RET/PTC (type)	
1.	Male	6 (33.3%)	1(5.6%)	RET/PTC1
	Female	12 (66.7%)	2 (11.1%)	RET/PTC1 RET/PTC3
2	Age	21 - 68 years	21, 40 yrs	RET/PTC3
			60 yrs	RET/PTC1
3. Gross	<2 cms	5 (27.8%)	1 (5.6%)	RET/PTC3
	2-4 cms	8 (44.4%)	1 (5.6%)	RET/PTC3
	>4 cms	5 (27.8%)	1 (5.6%)	RET/PTC1
4. microscopy	Papillary	10(55.6%)	1 (5.6%)	RET/PTC3
	follicular	8(44.4%)	2 (11.1%)	RET/PTC1, RET/PTC3
5.	Multi-focality	4/18 (22.2%)	No statistically significant association noted	
6.	Lymph node involvement	2/18 (13.3%)	No statistically significant association noted	
7.	Extra-thyroidal extension	3/18 (20.0%)	No statistically significant association noted	

DISCUSSION

Thyroid is an endocrine organ with malignancy rate accounting for approximately 1% of all newly diagnosed cancer cases. The most frequent type of thyroid malignancy is PTC, which constitutes for more than 80% of all cases⁽¹²⁾.

The incidence of PTC increases with age, and women are more frequently affected than men, in the ratios of 2:1 to 4:1⁽¹²⁾. The female to male ratio in our study was 2:1, which is similar to another study done in Italy by Basolo et al which showed male : female ratio of 2.2:1⁽¹³⁾

Various genetic alterations that can be seen in PTC are *BRAF* mutation, *RET/PTC* translocation, *RAS* gene mutation, mutation in *TERT* promoter gene and *ALK* translocation⁽⁴⁾

In a study conducted by George N et al in North India to study the prevalence of genetic alterations in Endemic goitre population found no cases with *RET/PTC* translocation out of 109 cases that they studied⁽¹⁴⁾

Among the 13 different types of *RET/PTC* rearrangements, the *RET/PTC1* and *RET/PTC3*, are the commonest type of rearrangements seen in PTC. The most common *RET* fusions in PTC are *CCDC6-RET* (also named *RET/PTC1*) and *NCOA4-RET* (also named *RET/PTC3*), accounting for about 90% of all the *RET* gene fusion-positive cases⁽¹⁵⁾. Both *RET/PTC1* and *RET/PTC3* are intrachromosomal paracentric inversions as both the genes participating in the fusion are located on chromosome 10q^(16, 17, 18)

There is paucity of literature in studies of *RET/PTC* translocation in PTC in India. A study conducted by Mishra A et al.⁽¹⁹⁾ studied the prevalence of *RET/PTC* translocation in PTC by immunohistochemistry in endemic goitre areas of India and found the prevalence to be 44%.

The study by Liu RT et al showed *RET* rearrangements in 8 of 105 (8%) sporadic PTCs in Taiwan, which was a much lower prevalence than previously reported for this population but comparable to those reported in other nations using similar methodology⁽²⁰⁾. Whereas according to a study conducted by Zhu Et al the prevalence of *RET/PTC* translocation varied from 17-40% based on the technique used for detection of *RET/PTC* activation⁽²¹⁾

The molecular genetic study by Puxeddu et al demonstrated, positivity of *RET/PTC1* and *RET/PTC3* in 13 of 48 tumors (27.1%), and an exclusive or preferential *RET-TK* expression was seen in 17 cases (35.4%)⁽²²⁾.

In our study 3/18 cases (16.7%) showed *RET/PTC* rearrangement, with *RET/PTC1* seen in 5.6% and *RET/PTC 3* seen in 11.1% cases.

Fenton et al showed that among adults, *RET/PTC1* was common and may be associated with an aggressive clinical course. They described that the incidence and significance of *RET/PTC* rearrangements were less well understood among

children. In their study out of 74 children with PTC, no correlation between the *RET/PTC* rearrangement with age, tumor size, focality, and the extent of disease at the time of diagnosis, or recurrence were noted⁽²³⁾

In the study by Erdogan M et al, on 101 patients with PTC, showed *RET/PTC* positivity in 67 (66.3%) cases with p value of <0.001. *RET/PTC1* was positive in 32(31.7%), and *RET/PTC3* in 21(20.8%) cases, with both rearrangements being positive in 10 (9.9%) cases. Their study showed no significant association between *RET/PTC* expression and the clinical and pathological features⁽²⁴⁾.

In 2018, Khan et al studied *RET/PTC* rearrangement among 40 cases of PTC in Kashmiri's and observed that *RET/PTC* rearrangements were confined to 10/40 (20.83%) cases. Presence of *RET/PTC* rearrangement significantly correlated with gender, elevated TSH levels and lymph node metastasis. They concluded that *RET/PTC3* rearrangement was a frequent event in the oncogenesis of thyroid⁽⁷⁾

In 2014, Rao et al did quantitative estimation of *RET/PTC1* and *RET/PTC3* gene rearrangements by real-time PCR on 30 cases of PTC. They showed no statistically significant differences between positive and negative *RET/PTC3* mRNA expression with clinico- pathological features. They concluded that *RET/PTC3* gene rearrangements were the most prevalent form of rearrangements in PTCs among Chennai population⁽⁸⁾.

In the study by Lee et al, on 11 PTC patients, two PTC had *RET/PTC1*, 3 had *RET/PTC2*, and 1 case had *RET/PTC3* rearrangement. Although the cause of high frequency of *RET/PTC* rearrangement in Chinese papillary thyroid carcinomas was unknown, their study showed that *RET* rearrangement is an important genetic lesion underlying the development of thyroid papillary carcinoma in Taiwan⁽²⁵⁾.

Our study showed no statistically significant association between sex, gross size of PTC, microscopic pattern, extra thyroidal extension, lymph node metastasis and multifocality of the lesion with *RET/PTC* translocation which might translate that *RET/PTC* may not be implicated in prognosis or the outcome of the disease process. The findings of our studies are similar to another study done in Italy by Basolo et al⁽¹³⁾.

CONCLUSION

In our study, the frequency of *RET/PTC* gene translocation in PTC was 16.7%, with *RET/PTC1* and *RET/PTC3* gene rearrangement being 5.6% and 11.1% respectively. No statistically significant association of *RET/PTC* gene translocation with various clinico-pathological features were noted. To the best of our knowledge, this is a first study from Karnataka on prevalence and clinico-pathological association of PTC with *RET/PTC* gene rearrangements. Larger studies in this regard are essential to confirm whether *RET/PTC* is a driver

genetic alteration in PTC and if there are other genetic events in addition to *RET*/PTC activation responsible for malignant phenotype and cancer progression.

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