



# BRAF<sup>V600E</sup> Mutation Analysis in Fine-Needle Aspiration Cytology of Fixed Slide Specimens in Patients with Papillary Thyroid Carcinoma

Sara Cheraghi<sup>1</sup>, Maryam Honardoost<sup>1</sup>, Fereshteh Abdolmaleki<sup>1</sup>, Mohammad E. Khamseh<sup>1\*</sup>

Received: 13 Dec 2023

Published: 22 Jul 2024

## Abstract

**Background:** Papillary thyroid carcinoma is the most frequent type of thyroid cancer. The BRAF<sup>V600E</sup> mutation is associated with tumor progression. We explored the utility of the BRAF molecular testing on fine needle aspiration fixed specimens of patients with confirmed diagnoses of papillary thyroid carcinoma.

**Methods:** Fixed thyroid cytology slide specimens of 19 patients with Bethesda II to VI reports were used to detect BRAF<sup>V600E</sup> mutation by pyrosequencing of extracted DNA.

**Results:** BRAF<sup>V600E</sup> mutation was detected in 25% of the specimens with Bethesda category III and IV nodules and in 73% of the nodules with Bethesda category V and VI.

**Conclusion:** BRAF mutation analysis can be performed on fixed fine needle aspiration cytology specimens. Although the frequency of the mutation is higher in specimens with higher Bethesda category scores, it could support clinical decision-making in thyroid nodules with intermediate Bethesda category scores.

**Keywords:** Papillary Thyroid Cancer, Fine Needle Aspiration, BRAFV600E

**Conflicts of Interest:** None declared

**Funding:** This study was supported by Iran University of Medical Sciences.

\*This work has been published under CC BY-NC-SA 1.0 license.

Copyright© Iran University of Medical Sciences

**Cite this article as:** Cheraghi S, Honardoost M, Abdolmaleki F, Khamseh ME. BRAF<sup>V600E</sup> Mutation Analysis in Fine-Needle Aspiration Cytology of Fixed Slide Specimens in Patients with Papillary Thyroid Carcinoma. *Med J Islam Repub Iran.* 2024 (22 Jul);38:83. <https://doi.org/10.47176/mjiri.38.83>

## Introduction

Thyroid cancers are the most prevalent neoplasms found in the endocrine system. Generally, differentiated thyroid lesions can be divided into two categories: papillary thyroid cancer (PTC) and follicular thyroid cancer (FTC). PTC accounts for approximately 73.9%, while the Follicular Variant of PTC carcinoma accounts for approximately 26.1% (1). Surgery is the primary treatment, and radioiodine therapy has also been used to treat certain types of thyroid cancer. Multi-kinase and tyrosine kinase inhibitors are used for iodine-resistant patients (2, 3). The inhibitory drugs target genes such as BRAF<sup>V600E</sup>, RET, and TRK (3).

The BRAF gene, located on chromosome 7 (7q34), encodes a cytoplasmic serine/threonine kinase enzyme. This enzyme is critical in regulating the induction of the mitogen-activated protein kinase (MAPK) signaling pathway,

which mediates cell proliferation, differentiation, survival and growth (4).

Pathogenic mutations in the BRAF gene occur in more than 19% of cancers. More than 90% of BRAF mutations are V600E mutations (5, 6).

The BRAF gene mutation has been identified in 70% of melanoma, 45% of thyroid cancer, 40% of pancreatic cancer, and 20% of colon cancer patients (7). In thyroid cells, the BRAF gene mutation has been associated with hypermethylation. The prevalence rate of the BRAF gene mutation has been reported 45% in thyroid cancer (8).

Detection of somatic variants in tumor tissue is a major challenge due to the high heterogeneity of cancer cells. Tumor tissue cells often have a limited number of mutated cells, which are surrounded by a large number of normal

**Corresponding author:** Dr Mohammad E. Khamseh, [khamseh.m@iums.ac.ir](mailto:khamseh.m@iums.ac.ir)

<sup>1</sup> Endocrine Research Center, Institute of Endocrinology and Metabolism, Iran University of Medical Sciences, Tehran, Iran

### ↑What is “already known” in this topic:

A molecular marker combined with cytology analysis can improve the diagnosis accuracy in thyroid nodules.

### →What this article adds:

Based on the results, the detection of BRAFV600E gene mutation in the cytology specimens could improve clinical decisions in thyroid nodules with undetermined statue, but further investigation should be done.

cells. Somatic mutations occur at low frequencies and require high-sensitivity methods for detection. Molecular detection methods such as PCR-based methods, including allele-specific PCR (AS-PCR) (9), real-time PCR, HRM (10), COLD-PCR, ddPCR (11), immunohistochemistry (IHC), sequencing methods such as Sanger (12), pyrosequencing (13), and next-generation sequencing (NGS) are used to detect variants. The sensitivity and specificity of detection methods are varying, except ddPCR, most of them have 1-5% sensitivity. The sensitivity of qPCR and NGS methods is approximately 5%. Although Sanger sequencing has high specificity, its sensitivity is relatively low at 15-20% (12). Pyrosequencing has higher sensitivity than Sanger and is able to detect about 5% of mutant alleles (14). A pyrosequencing assay was used in this study to increase the detection sensitivity of the low-frequency mutant alleles.

### Methods

**Study population:** This case series study included 19 patients with Bethesda II-VI thyroid nodules admitted to the thyroid clinic of the Endocrinology and Metabolism Institute, Iran University of Medical Sciences. Cytology specimens were collected from all patients suspected of PTC. The samples were obtained via a Fine Needle Aspiration (FNA) procedure under guided ultrasound. A written consent was obtained from the included patients, and they were informed about the objective of this study. The cytological evaluation was performed by a single expert pathologist. The presence of malignant cells was confirmed and the Bethesda groups were also identified.

**Sample preparation:** Alcohol-fixed smears that contained lesion cells were utilized for BRAF<sup>V600E</sup> molecular analysis. For DNA extraction from alcohol-fixed FNA specimens, the FNA slides were first de-coverslipped by soaking in xylene at room temperature for up to 72 hours. The decoverslip slides were resoaked in xylene for five minutes to remove the remaining mounting media. During this process, cellular contents adhere well to the slide. Cells on glass slides were collected by scraping the slides with a sterile scalpel blade. The processes were carried out by wetting the slide with approximately 30 µl of lysis buffer to help collect the cells as clump form into 2ml tubes. DNA extraction was conducted using a commercially available kit of Qiagen (Valencia, California, USA). DNA was evaluated for quantity and quality through a Nano-drop spectrophotometer (MAESTRO-Gene, Taiwan).

**Molecular detection:** Pyrosequencing technology was employed to identify BRAF<sup>V600E</sup>. In order to evaluate the target gene, the 205 bp region of exon 15 containing codon 600 of the BRAF gene was amplified using the PCR method. The sequence of primers includes BRAF\_F:5'-

ATGCTTGCTCTGATAGGAA-3' and BRAF\_R: 5'-TCAGTGGAAAAATAGCCTCAATTC-3'. The reverse primer was biotinylated at its 5' end to facilitate the pyrosequencing process. Each PCR reaction contained 20 to 50 ng of genomic DNA, 10 picomoles of each primer and 25 microliters of Taq DNA Polymerase Master Mix RED enzyme buffer (Amplicon, Denmark) in a total volume of 50 microliters. The PCR process (Applied Biosystems, USA) was carried out using temperature cycling, which includes initial denaturation at 95°C for 10 minutes, followed by 35 cycles at 95°C for 30 seconds, 59°C for 30 seconds, and 72°C for 45 seconds. The final amplification was performed at 72°C for 2 minutes. To verify the accuracy and specificity of the amplification, we observed 5 microliters of PCR product on a 2% agarose gel. Then, 20 microliters of the biotin PCR product were added to 6 microliters of streptavidin sepharose beads. The temperature was increased to make single-stranded DNA (ssDNA), biotinylated ssDNA attached to streptavidin sepharose beads. PyroMark Q48 (QIAGEN) used dispense sequence to identify sequence variation. The primer was designed to analyze codons 599 to 602.

### Statistical analysis

In this study, the descriptive analysis of quantitative variables was carried out by reporting the mean and standard deviation. The descriptive analysis of qualitative parameters was performed using frequencies and regarded percentages. The chi-squared test and the Fisher exact test were used to compare the BRAFV600E mutation between different subgroups. Mann-Whitney test was also implemented to compare the means of age and tumor size based on the status of BRAF V600E mutation. All statistical analyses were performed using SPSS version 20. A *P* value of <0.05 was considered statistically significant.

### Results

The average age of the patients at the time of diagnosis was 45.2 (±9.3) years. Seventy-four percent (N=14) of the participants were female. Table 1 provides detailed information about the clinical characteristics of the participants. Cytology examination of the specimens classified 15 patients as Bethesda category V & VI. In addition, 4 patients were classified as Bethesda category III & IV. The average size of the nodules was 2.4 cm (±1.5). Of all cases with available relevant data (N=11), 54.5% of the patients had suspicious cervical lymph nodes detected by ultrasound imaging.

The pyrosequencing began with the analysis of codon 599 and ended with codon 602 analysis. Therefore, a T>A sequence analysis of codon 600 was performed to identify

Table 1. Characteristics of the study participants

	Bethesda III-IV	Bethesda V-VI
Age_Median(Min_Max yrs.)	52.5 (34-59)	42 (33-59)
Nodule size (cm, Min_Max)	2.5 (0.3-4)	2.2 (0.3-6)
Lymphatic node involvement (%)**	1(50%)	5(55.5%)
BRAF V600E (%)	1 (25)	11 (73.33)

\*Min: Minimum. Max: Maximum, \*\* based on available data

the mutation. The results showed that 73.33% of the patients with Bethesda V & VI categories and 25% with Bethesda III & IV categories had the mutation. There was no significant statistical relationship between age, gender, and tumor size with the occurrence of the BRAF<sup>V600E</sup> mutation ( $P > 0.05$ ).

### Discussion

BRAF mutation has been reported in 60-74% of people with PTC, 4-45% in ATC, and 1.7% in FTC (15). The prevalence of BRAF<sup>V600E</sup> mutation in PTC (51%) is higher compared to FVPTC (24.1%) and FTC (14%). In PTC patients, the presence of the BRAF<sup>V600E</sup> mutation is associated with some clinical features, including age at diagnosis, distant and lymph node metastases, progression of TNM stage, and risk of recurrence (16, 17).

BRAF<sup>V600E</sup> mutation has been identified in 43.6% of papillary microadenomas and 42.4% of small PTC (18). 80-83% of this mutation occurs in tall cells and 12-18% in follicular cells of PTC patients (6). BRAF p.V600E mutation results in thymine to adenine change at position 1799 and as a result of substituting valine (V) to glutamate (E) at amino acid codon 600. Less frequent mutations at position 1799 include V600K (valine to lysine), V600R (valine to arginine), and V600M (valine to methionine) (5, 6). Studies have shown that the BRAF<sup>V600E</sup> mutation usually occurs in younger individuals, whereas the V600K mutation is more common in older patients and tends to affect the head and neck region (19). In the study of Al-Masri et al. (2021), the frequency of BRAF<sup>V600E</sup> in patients with PTC was reported to be 71%. In this study, genetic testing was performed on FFPE tissue and an inverse relationship was observed between tumor size and the presence of mutation ( $P = 0.009$ ) (20). In a study on the Iranian population, the frequency of BRAF<sup>V600E</sup> mutation was reported at 77.8% in FFPE tissue samples with PTC (21). In the study of Dadgarnia et al. the prevalence of the BRAF<sup>V600E</sup> mutation in Iranian patients with suspected PTC (76 FNA samples) has been reported at 21.1%. The results showed a significant relationship between the mutation and pathological findings ( $P = 0.001$ ) (22). BRAF<sup>V600E</sup> mutation is associated with an increased risk of recurrence as well as reduce the effectiveness of treatment and radioiodine therapy (23). To improve PTC detection in uncertain cytology, analyzing BRAF<sup>V600E</sup> in aspiration samples may increase the accuracy rates of diagnostic (24). In addition, detecting the mutation in low-risk patients before surgery may provide a valuable prognosis for disease management (25). It has been observed that mutations in the BRAF gene occur with a frequency of 90.2% in Asiana PTC patients. The prevalence of BRAF<sup>V600E</sup> in East Asia is reported to be 76.4%. However, there is weak evidence about the frequency of the variant in the population of Iran, Thailand, Singapore, and other countries (26).

In this study, we investigated the frequency of the mutation in cytology samples in the two groups of patients with suspected PTC (Bethesda III-VI). The results indicated the presence of eleven samples with BRAF<sup>V600E</sup> mutation in the Bethesda V-VI (positive PTC) and one BRAF<sup>V600E</sup> mutation in the Bethesda III-IV group. In our study, the rate of

BRAF<sup>V600E</sup> detection was 63.1% among the patients included. Analysis of molecular markers and cytology of FNA samples can improve the accuracy of thyroid nodule diagnosis before surgery (27). Only 5-15% of thyroid nodules are reported as malignant and require surgery based on the FNA cytology test. However, a histological study will be necessary in 30% of patients for cytological features alone can't provide an accurate diagnosis (28). BRAF variant assay on FNA samples showed higher sensitivity in diagnosing thyroid nodules compared to cytology analysis alone (29-31).

### Conclusion

Our research found that the BRAF<sup>V600E</sup> mutation was present in over 73.3% of patients with Bethesda V & VI, while it was found in only 25% of patients classified as Bethesda III & IV. Therefore, identifying the BRAF gene mutation in cytology samples can be a valuable diagnostic tool for diagnosing PTC from suspected PTC.

### Authors' Contributions

Conception and design: MH and MEK; Development of methodology: MH and FA; Acquisition, analysis, and interpretation of data: SC; Writing, review, and/or revision of the manuscript: SC and MEK; Administrative, technical, or material support: MEK and MH; Study supervision: MEK; All authors read and approved the final manuscript.

### Ethical Considerations

All phases of the study were approved by the Ethics Committee of the Iran University of Medical Sciences No. IR.IUMS.REC.1396.30870.

### Acknowledgment

We extend our heartfelt appreciation and thanks to everyone who contributed to this study.

### Conflict of Interests

The authors declare that they have no competing interests.

### References

- Henke LE, Pfeifer JD, Baranski TJ, DeWees T, Grigsby PW. Long-term outcomes of follicular variant vs classic papillary thyroid carcinoma. *Endocr Connect*. 2018;7(12):1226.
- Haddad RI, Nasr C, Bischoff L, Busaidy NL, Byrd D, Callender G, et al. NCCN guidelines insights: thyroid carcinoma, version 2.2018. *J Natl Compr Cancer Netw*. 2018;16(12):1429-40.
- Marotta V, Chiofalo MG, Di Gennaro F, Daponte A, Sandomenico F, Vallone P, et al. Kinase-inhibitors for iodine-refractory differentiated thyroid cancer: Still far from a structured therapeutic algorithm. *Crit Rev Oncol Hematol*. 2021;162:103353.
- Loo E, Khalili P, Beuhler K, Siddiqi I, Vasef MA. BRAF V600E mutation across multiple tumor types: correlation between DNA-based sequencing and mutation-specific immunohistochemistry. *Appl Immunohistochem Mol Morphol*. 2018;26(10):709-13.
- Long GV, Menzies AM, Nagrial AM, Haydu LE, Hamilton AL, Mann GJ, et al. Prognostic and clinicopathologic associations of oncogenic BRAF in metastatic melanoma. *J Clin Oncol*. 2011;29(10):1239-46.
- Santonastaso C, Di Paolo M, Tommaselli A, Morelli L, Pugliese S, Troisi A, et al. A simple and high sensitive method for detection of BRAF 1799T>A (V600E) mutation in the thyroid fine needle aspirate. *World Cancer Res J*. 2019;6:e1291.
- Yi JW, Ha SY, Jee HG, Kim K, Kim SJ, Chai YJ, et al. Induction of the

- BRAFV600E Mutation in Thyroid Cells Leads to Frequent Hypermethylation. *Clin Exp Otorhinolaryngol.* 2022;15(3):273-82.
8. De Monaco A, Faioli D, Di Paolo M, Catapano O, D'Orta A, Del Buono M, et al. Pharmacogenomics markers for prediction response and toxicity in cancer therapy. *World Cancer Res J.* 2014;1(3):e276.
  9. Sapio MR, Posca D, Troncone G, Pettinato G, Palombini L, Rossi G, et al. Detection of BRAF mutation in thyroid papillary carcinomas by mutant allele-specific PCR amplification (MASA). *Eur J Endocrinol.* 2006;154(2):341-8.
  10. Pichler M, Balic M, Stadelmeyer E, Ausch C, Wild M, Guelly C, et al. Evaluation of high-resolution melting analysis as a diagnostic tool to detect the BRAF V600E mutation in colorectal tumors. *Mol Diagn.* 2009;11(2):140-7.
  11. Pinzani P, Santucci C, Mancini I, Simi L, Salvianti F, Pratesi N, et al. BRAFV600E detection in melanoma is highly improved by COLD-PCR. *Clin Chim Acta.* 2011;412(11-12):901-5.
  12. Oh H-S, Kwon H, Park S, Kim M, Jeon MJ, Kim TY, et al. Comparison of immunohistochemistry and direct sanger sequencing for detection of the BRAFV600E mutation in thyroid neoplasm. *J Endocrinol Metab.* 2018;33(1):62-9.
  13. Laurini JA, Aoun P, Iqbal J, Chan W, Greiner TC. Investigation of the BRAF V600E mutation by pyrosequencing in lymphoproliferative disorders. *Am J Clin Pathol.* 2012;138(6):877-83.
  14. Mauger F, How-Kit A, Tost J. COLD-PCR technologies in the area of personalized medicine: methodology and applications. *Mol Diagn Ther.* 2017;21(3):269-83.
  15. Prete A, Borges de Souza P, Censi S, Muzza M, Nucci N, Sponziello M. Update on fundamental mechanisms of thyroid cancer. *Front Endocrinol.* 2020;11:102.
  16. Kebebew E, Weng J, Bauer J, Ranvier G, Clark OH, Duh Q-Y, et al. The prevalence and prognostic value of BRAF mutation in thyroid cancer. *Ann Surg.* 2007;246(3):466.
  17. De Leo A, Serban D, Maloberti T, Sanza V, Coluccelli S, Altimari A, et al. Expanding the Spectrum of BRAF Non-V600E Mutations in Thyroid Nodules: Evidence-Based Data from a Tertiary Referral Centre. *Int J Mol Sci.* 2023;24(4):4057.
  18. Silver JA, Bogatchenko M, Pusztaszeri M, Forest V-I, Hier MP, Yang JW, et al. BRAF V600E mutation is associated with aggressive features in papillary thyroid carcinomas ≤ 1.5 cm. *Otolaryngol Head Neck Surg.* 2021;50:1-8.
  19. Zablocka T, Kreismane M, Pjanova D, Isajevs S. Effects of BRAF V600E and NRAS mutational status on the progression-free survival and clinicopathological characteristics of patients with melanoma. *Oncol Lett.* 2023;25(1):1-9.
  20. Al-Masri M, Al-Shobaki T, Al-Najjar H, Iskanderian R, Younis E, Abdallah N, et al. BRAF V600E mutation in papillary thyroid carcinoma: its relation to clinical features and oncologic outcomes in a single cancer centre experience. *Endocr Connect.* 2021;10(12):1531-7.
  21. Ranjbari N, Almasi S, Mohammadi-Asl J, Rahim F. BRAF mutations in Iranian patients with papillary thyroid carcinoma. *Asian Pac J Cancer Prev.* 2013;14(4):2521-3.
  22. Dadgarnia M, Abouii M, Baradaranfar M, Vaziribozorg S, Zand V. BRAF Gene Mutation (V600E) in Aspiration Cytology of Patients With Suspected Papillary Thyroid Carcinoma. *Acta Med Iran.* 2021:524-9.
  23. Ayala MD, Rodríguez AE, González AB, Gabiña PM, Rodríguez TG, de Zarate ERO, et al. BRAF V600E mutation in papillary thyroid cancer and its effect on postoperative radioiodine (131I) therapy: should we modify our therapeutic strategy? *Cir Esp. (English Edition).* 2018;96(5):276-82.
  24. Chakraborty A, Narkar A, Mukhopadhyaya R, Kane S, D'Cruz A, Rajan M. BRAF V600E mutation in papillary thyroid carcinoma: significant association with node metastases and extra thyroidal invasion. *Endocr Pathol.* 2012;23:83-93.
  25. Czarniecka A, Oczko-Wojciechowska M, Barczyński M. BRAF V600E mutation in prognostication of papillary thyroid cancer (PTC) recurrence. *Gland Surg.* 2016;5(5):495.
  26. Rashid FA, Munkhdelger J, Fukuoka J, Bychkov A. Prevalence of BRAFV600E mutation in Asian series of papillary thyroid carcinoma—a contemporary systematic review. *Gland Surg.* 2020;9(5):1878.
  27. Titov SE, Ivanov MK, Demenkov PS, Katanyan GA, Kozorezova ES, Malek AV, et al. Combined quantitation of HMGA2 mRNA, microRNAs, and mitochondrial-DNA content enables the identification and typing of thyroid tumors in fine-needle aspiration smears. *BMC cancer.* 2019;19:1-14.
  28. Kim DL, Song KH, Kim SK. High prevalence of carcinoma in ultrasonography-guided fine needle aspiration cytology of thyroid nodules. *Endocr J.* 2008;55(1):135-42.
  29. Ohori NP, Singhal R, Nikiforova MN, Yip L, Schoedel KE, Coyne C, et al. BRAF mutation detection in indeterminate thyroid cytology specimens: underlying cytologic, molecular, and pathologic characteristics of papillary thyroid carcinoma. *Cancer Cytopathol.* 2013;121(4):197-205.
  30. Marchetti I, Lessi F, Mazzanti CM, Bertacca G, Elisei R, Coscio GD, et al. A morpho-molecular diagnosis of papillary thyroid carcinoma: BRAF V600E detection as an important tool in preoperative evaluation of fine-needle aspirates. *Thyroid.* 2009;19(8):837-42.
  31. Kim SW, Lee JI, Kim J-W, Ki C-S, Oh YL, Choi Y-L, et al. BRAF V600E mutation analysis in fine-needle aspiration cytology specimens for evaluation of thyroid nodule: a large series in a BRAF V600E-prevalent population. *J Clin Endocrinol Metab.* 2010;95(8):3693-700.