

# ISSN: 2690- 912X

## Journal of Genetic Engineering and Biotechnology Research

## **Research Article**

## Two Sequences Variations of the E768D Mutation Found in Familial Medullary **Thyroid Carcinomas**

### A Chikouche<sup>1\*</sup>, N Habak<sup>1</sup>, N Ould Bessi<sup>1</sup>, M Boudissa<sup>2</sup>

<sup>1</sup>Laboratory of Biochemistry, Center Pierre et Marie Curie, Algiers, Algeria

<sup>2</sup>Department of Endocrinology, Center Pierre et Marie Curie, Algiers, Algeria

#### \*Corresponding author

A Chikouche, Laboratory of Biochemistry, Center Pierre et Marie Curie, Algiers, Algeria.

Submitted: 10 Nov 2021; Accepted: 17 Nov 2021; Published: 22 Dec 2021

Citation: A Chikouche, N Habak, N Ould Bessi, M Boudissa. (2021). Two Sequences Variations of the E768D Mutation Found in Familial Medullary Thyroid Carcinomas. J Gene Engg Bio Res, 3(2), 40-44.

#### Abstract

Medullary thyroid cancer or MTC is present in sporadic form (75% of cases) and in familial form (25% of cases), in this latter situation, the MTC is a part of Multiple Endocrine Neoplasia type 2 (MEN 2). The MEN2 is divided into MEN2A, MEN2B and FMTC or isolated familial MTC. The MEN2 are rare hereditary disease, transmitted as an autosomal dominant mode, linked to mutations of the RET gene.

The discovery of a mutation in the RET proto-oncogene by molecular biology techniques in a index case of MTC confirms the diagnosis of familial and allows the genetic testing of healthy clinically related index case: those who carry the genetic mutation, will be offered prophylactic thyroidectomy before any biological or clinical manifestation.

The genetic analysis of the RET gene was performed by PCR / sequencing. The E768D mutation was found in the exon 13 of the RET gene in 2 differences sequences forms (GAG/GAC et GAG/GAT). This mutation, already described, found in the FMTC.

Keywords: Multiple Endocrine Neoplasia Type 2, Medullary Thyroid Carcinoma, FMTC, Proto-oncogene RET, Mutation, Genetic Screening

#### Introduction

Medullary thyroid carcinoma or MTC is a C-cell tumor with secretion of calcitonin (CT).

MTC, which may be preceded by C-cell hyperplasia of the thyroid gland, has a very early metastatic spread that can be at the micro carcinoma stage [1].

There are two ways to reach the diagnosis of MTC before surgery: fine-needle aspiration and above all, CT [2-5]. It occurs sporadically in 75% and in a familial form in 25% of cases. These familial forms constitute Multiple Endocrine Neoplasia type 2 or MEN2. These are rare hereditary diseases, with autosomal dominant inheritance, almost complete penetrance and are characterized by the constant presence of medullary thyroid carcinoma (MTC) associated or not with the involvement of the adrenal and parathyroid medulla [6]. Behave FMTC, or familial isolated medullary thyroid carcinoma where MTC is the only clinical manifestation without

other associated endocrine tumors, represents 35% of the MEN2 [7]. MEN2A or Sipple syndrome is the most common form (60% of MEN2) with medullary thyroid cancer often associated with pheochromocytoma and / or hyperparathyroidism [8]. MEN2B or Gorlin syndrome, the rarest form (5%) associated with MTC, pheochromocytoma, developmental abnormalities and mucosal neurons [9].

The predisposition gene for different forms of MEN2 is the proto-oncogene RET (rearranged during transfection), identified by Takahashi in 1985 and located on chromosome 10 (10q11.2) by Ishizaka in 1989 [10-14]. It consists of 21 exons which codes for a transmembrane receptor with tyrosine kinase activity [15-17].

This membrane receptor is composed of an N-terminal extracellular region with a cysteine-rich domain (CRD), a transmembrane region and a C-terminal intracellular region that contain two domains with tyrosine kinase activity [18].

The activation of the RET receptor proceeds in the following manner: a homodimeric ligand of the GFL family (GDNF Family Ligand) whether it be GDNF (Glial cell line-Derived Neurotrophic Factor), Neurturin, Artemin or Persephin linked to a specific GFR $\alpha$  receptor (GDNF family receptors- $\alpha$ 1 to 4). The ligand-coreceptor binding in dimeric form causes the dimerization of the receptor RET and its activation. Germline mutations of this gene have been identified in 95% of FMTCs [10, 19]. The mutations found in the FMTC result in permanent activation of the receptor. These are point mutations or duplications, which sit in order of frequency at exons 10, 11, 13, 14, 15, 8 and 16 (the 7 most frequently mutated exons) and lead to a change of codon type false sense which affect specific coding regions of RET. These mutations result in the substitution of one amino acid for another.

Some mutations are FMTC specific and others are common to MEN2A and FMTC [10, 20].

The identification of these mutations by molecular biology techniques confirms the diagnosis of MEN2.

Molecular screening has taken an important place in family forms in search of relatives carrying the family mutation.

#### **Materials and Methods**

Blood samples from a male adult patient and a patient with medullary thyroid cancer without further clinical manifestations. Whole blood samples are taken on tube with EDTA.A request for a genotypic analysis was sent to us accompanied by a letter of consent and a sheet which gives the diagnosis, a clinical summary and a report of the biological exploration and imaging Subsequently samples of 11 relatives were sent to us (Table I).

DNA extraction Genomic DNA was extracted from peripheral blood leukocytes by the salt technique.

A decision algorithm was decided according to the order of the most frequently mutated exon. We start with the analysis of exons 10, 11 and 13 and if the mutation is not found, the analysis of exons 14, 15, 8 and 16 will be performed. PCR conditions. The amplification of exon 13 of the RET proto-oncogene was performed using the following primers provided by Applied Bio Systems.

Exon 13F; 5' TGACCTGGTATGGTCATGGA 3' Exon 13R; 5' GGAGAACAGGGCTGTATGGA 3'

The PCR conditions used are 4  $\mu$ l of DNA (25 ng /  $\mu$ l), 2.5  $\mu$ l  $\mu$ l of 10X PCR buffer; 1.25  $\mu$ l of dNTPs (2 mM, 1.5  $\mu$ l 25 mM MgCl 2, 1.25  $\mu$ l of 2 mM dNTPs, 1.25  $\mu$ l of 5 pmol /  $\mu$ l sense and antisense primers), 0.1  $\mu$ l Taq polymerase Roche (5U /  $\mu$ I) and 13.15  $\mu$ I of H2O.

The amplification is programmed as follows; an initial denaturation step of 5 minutes at 94° C., then 35 amplification cycles (comprising denaturation of one minute at 94° C., hybridization

of one minute at  $60^{\circ}$  C. and elongation of one minute at  $72^{\circ}$  C.) followed by a final elongation step of 10 minutes at  $72^{\circ}$  C.

The amplicons are tested by electrophoresis in 2% agarose gel with Roche Size VII marker. The size of amplicon 13 is 250pb. Sequence PCR. The PCR products are purified on Millipore (Manu 30) plates and the sequence PCR reaction is carried out with 1.5  $\mu$ l of purified PCR product; 0.8  $\mu$ l of Big Dye terminator V1.1 (Applied Bio system); 3.6  $\mu$ l of 5X buffer (V1.1) and 2  $\mu$ l of sense or antisense primer (5 pmol /  $\mu$ l).

The amplification is programmed with 25 cycles comprising a step of 30 seconds at 95° C. followed by a step of 4 minutes at 60° C. The sequence PCR products are purified to remove dNTPs, unincorporated free dideoxynucleotides and excess primers by a method based on the use of Sephadex G 50 gel on MultiScreen MAHV N45 plates (Millipore). Purified PCR sequence products are passed to the Applied Bio System 3130 Sequencer which performs capillary electrophoresis using POP 7 gel (Applied Bio systems).

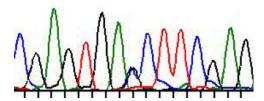
#### **Results and Discussion**

The genotypic analysis of the two index cases with isolated medullary cancer found a mutation in the heterozygous state, due to a base substitution, at codon 768 of exon 13 of proto-oncogene RET. In the first index case, male, aged 50, the mutation found is due to a G> C transversion of c.2304 nucleotide and the GAG codon will give the GAC codon (Figure 1).

Whereas in the 40-year-old female index case, the mutation found is due to a G> T transversion of c.2304 nucleotide and therefore the GAG codon will give the GAT codon (Figure 2).

The GAG codon corresponds to glutamic acid represented by the letter E whereas the GAC and GAT codons correspond to the aspartic acid represented by the letter D. So in both cases, there is a change of glutamic acid at position 768 to aspartic acid. This germline mutation noted E768D was found in the FMTC [21]. It is considered specific FMTC where it is found in 8% [11].





**Figure 1:** Chromatogram of the E768D mutation (GAG / GAC) found in exon 13.

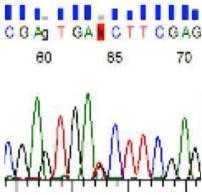


Figure 2: Chromatogram of the E768D mutation (GAG / GAT) found in exon 13.

**Table I: List of related relatives** 

Family Number	Status	Sex	Age	Mutation
1	Index case: Father	M	50 years	Mut htz G768D (gag/gac)
	Child	F	20 years	Mut htz G768D (gag/gac)
	Child	M	18 years	RAS
	Child	M	17 years	RAS
	Child	M	15 years	Mut htz G768D (gag/gac)
	Child	M	13 years	RAS
	Child	F	12 years	RAS
	Child	F	07 years	RAS
2	Index case: Female	F	40 years	Mut htz G768D (gag/gat)
	Mother	F	69 years	Mut htz G768D (gag/gat)
	Sister	F	46 years	RAS
	Sister	F	39 years	RAS
	Sister	F	33 years	Mut htz G768D (gag/gat)

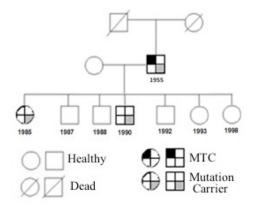


Figure 3: family tree of the family No. 1 studied.

After the mutation in the first index case was found, a study of the family was performed, 07 apparently healthy children benefited from genotypic analysis. 02 out of 07 children carry the E768D mutation (Figure 3).

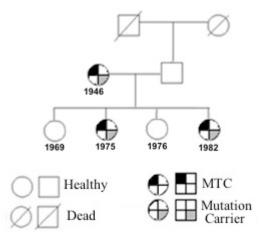


Figure 4: family tree of the N ° 2 family studied.

After the mutation in the 2nd index case was found, a family study was performed, the affected mother and sister and 2 apparently healthy sisters benefited from the genotypic analysis. 02 of the 04 are carriers of the E768D mutation (Figure 4).

#### **Conclusion**

Two index cases, which have isolated medullary thyroid carcinoma, carry a mutation in exon 13 of the RET gene, the E768D but in the form of two sequence variations. This mutation was detected using molecular biology techniques (PCR / sequencing). This discovery led to the diagnosis of familial MTC.

This mutation, already described, found only in the FMTC, exempts the carriers of a surveillance of the parathyroid glands and medulla-adrenal glands.11 relatives of both families benefited from genotypic analysis (Table I).02 children among the siblings of 07 children of the 1st family (Figure 3) are carriers of the family mutation and have benefited from a prophylactic thyroidectomy. Among the 04 relatives of the second family (Figure 4), the mother and a sister are affected and carry the mutationOther relatives who do not carry the mutation are considered to be free and thus are not supervised.

#### Acknowledgement

We thank all the staff of the Laboratory of Biochemistry, Pierre and Marie Curie Center, Algiers. We thank Dr. Daoud Chafia for help in the development of the article.

#### **Conflict of Interest**

No conflict of interest related to the article exists.

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