

Distribution of *RET* Mutations in Multiple Endocrine Neoplasia 2 in Denmark 1994–2014: A Nationwide Study

Jes Sloth Mathiesen,^{1,2} Jens Peter Kroustrup,³ Peter Vestergaard,³ Kirstine Stochholm,⁴ Per Løgstrup Poulsen,⁴ Åse Krogh Rasmussen,⁵ Ulla Feldt-Rasmussen,⁵ Mette Gaustadnes,⁶ Torben Falck Ørntoft,⁶ Thomas van Overeem Hansen,⁷ Finn Cilius Nielsen,⁷ Kim Brixen,⁸ Christian Godballe,¹ and Anja Lisbeth Frederiksen⁹

Background: Germline mutations of the *RE*arranged during *Transfection* (*RET*) proto-oncogene cause multiple endocrine neoplasia 2 (MEN2). It is unclear whether the distribution of *RET* mutations varies among populations. The first nationwide study of the distribution of *RET* mutations was conducted, and the results were compared to those of other populations.

Methods: This retrospective cohort study included 1583 patients who underwent *RET* gene testing in one of three centers covering all of Denmark between September 1994 and December 2014. Primary testing method was Sanger sequencing, which included exons 8–11 and 13–16. Mutations were defined according to the ARUP database July 1, 2016.

Results: *RET* mutations were identified in 163 patients from 36 apparently unrelated families. Among the 36 families 13 (36.1%) carried mutations in codon 611, four (11.1%) in codon 618, three (8.3%) in codon 620, one (2.8%) in codon 631, six (16.7%) in codon 634, one (2.8%) in codon 790, one (2.8%) in codon 804, one (2.8%) in codon 852, one (2.8%) in codon 883, and five (13.9%) in codon 918. Among the 13 families with codon 611 mutations, 12 had the p.C611Y mutation.

Conclusions: The distribution of *RET* mutations in Denmark appears to differ from that of other populations. Mutations in codon 611 were the most prevalent, followed by more frequently reported mutations. This might be due to a possible founder effect for the p.C611Y mutation. However, further studies are needed to find possible explanations for the skewed mutational spectrum in Denmark.

Keywords: epidemiology, genetics, molecular biology, medullary thyroid carcinoma, medullary thyroid carcinoma—genetics

Introduction

MULTIPLE ENDOCRINE NEOPLASIA 2 (MEN2) is an autosomal dominant inherited cancer syndrome subdivided into MEN2A and MEN2B. MEN2A associates medullary thyroid carcinoma (MTC), pheochromocytoma (PHEO), hyperparathyroidism (HPTH), cutaneous lichen amyloidosis (CLA), and Hirschsprung's disease (HD).

MEN2B associates MTC, PHEO, ganglioneuromatosis of the aerodigestive tract, and facial, ophthalmologic, and skeletal abnormalities (1).

MEN2A and 2B are caused by activating missense germline mutations of the *RE*arranged during *Transfection* (*RET*) proto-oncogene. These pivotal discoveries were made in 1993 and 1994 (2–5), and since then, >100 mutations have been identified (1).

Departments of ¹Otolaryngology—Head and Neck Surgery, ⁸Endocrinology, and ⁹Clinical Genetics, Odense University Hospital, Odense, Denmark.

²Department of Clinical Research, University of Southern Denmark, Odense, Denmark.

³Department of Clinical Medicine and Endocrinology, Aalborg University Hospital, Aalborg, Denmark.

Departments of ⁴Internal Medicine and Endocrinology and ⁶Molecular Medicine, Aarhus University Hospital, Aarhus, Denmark.

⁵Department of Endocrinology; ⁷Center for Genomic Medicine; Copenhagen University Hospital, Copenhagen, Denmark.

Codon 634 mutations are reported as the most prevalent in both European (6–16) and non-European families (17–25). However, a recent Greek study of 58 *RET* positive families found mutations of codon 533 to be predominant (26). Smaller studies from Portugal (27), Cyprus (28), and Sardinia (29) revealed mutations prevailing in codons 611, 618, and 804, respectively. Also, a large multicenter study of 250 families from Italy showed an unusually high prevalence of codon 804 and 891 mutations (7). A high prevalence of codon 790 mutations has been noted in Germany (6). Consequently, it is unclear whether the distribution of *RET* mutations is comparable among populations or whether geographical differences exist.

The first nationwide study of the distribution of *RET* mutations was conducted, and the results were compared to those of other populations.

Patients and Methods

Patients

This retrospective cohort study included 1583 unique patients who underwent *RET* gene testing in one of three centers covering all of Denmark between September 1994 and December 2014. At the end of the study period on January 1, 2015, the population of Denmark was 5,659,715 (www.dst.dk).

RET testing was performed in 1056, 459, and 104 patients at (i) the Center for Genomic Medicine, Copenhagen University Hospital, (ii) the Department of Molecular Medicine, Aarhus University Hospital, and (iii) the Department of Endocrinology and Medicine, Aalborg University Hospital, respectively. If tested in more than one center, patients were considered only once. One patient was tested in all three centers, while 34 patients were tested in two centers. This yielded a total of 1583 unique patients of which 164 were positive and 1419 negative for a *RET* mutation (Fig. 1).

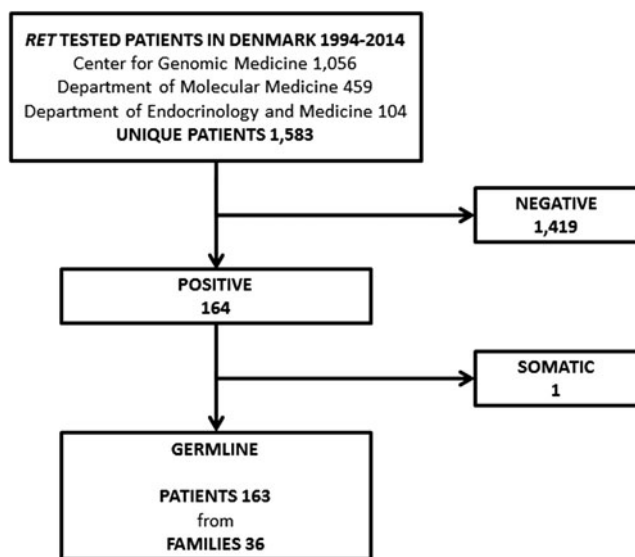


FIG. 1. Flow chart showing patients and families tested for REarranged during Transfection (*RET*) mutations in Denmark 1994–2014. The Center for Genomic Medicine, Department of Molecular Medicine, and Department of Endocrinology and Medicine are part of Copenhagen University Hospital, Aarhus University Hospital, and Aalborg University Hospital, respectively.

RET testing was performed on genomic DNA extracted from whole blood in 1581 patients. One patient harbored the p.C634Y + p.Y791F tandem germline mutation. The ARUP database classifies the p.Y791F sequence change as uncertain (www.arup.utah.edu/database/) (30). However, because recent evidence has classified the sequence change as neutral, the patient was counted as a p.C634Y mutation alone (31,32).

Two patients with MTC were tested using formalin-fixed paraffin-embedded tissue. Both patients were deceased at the time of testing. One was tested using normal tissue, and one using submandibular tissue suspected of MTC metastasis. The latter proved positive for the L790F mutation, but due to suspicion of a somatic mutation in the local metastasis, the patient was excluded from our *RET* germline mutation cohort (Fig. 1). The patient has been described elsewhere (33).

A MEN2 family was defined by (i) clinical workup in one of the four MEN2 management centers in Denmark, (ii) a unique mutation, or (iii) a molecular proven *de novo* mutation (both parents of the index case tested mutation negative).

Indications for testing included MTC, PHEO, HPTH, HD, and relatives at risk of MEN2, among others.

Methods

To assess criterion (i), data were provided by collaborators from the four MEN2 management centers. For criteria (ii) and (iii), data were provided by the three *RET* testing centers. Sequence changes were defined as mutations if classified as pathogenic in the continually updated ARUP database on July 1, 2016 (30).

RET testing centers

Center for Genomic Medicine, Copenhagen University Hospital. From September 1994 to December 1995, Sanger sequencing of *RET* exons 10 and 11 was performed. Since January 1996, June 1997, February 2000, and September 2007, analysis was expanded to exons 16, 13+14, 15, and 8+9, respectively. Since October 2014, next-generation sequencing (NGS) of all *RET* exons has been performed. Predictive testing of relatives at risk of MEN2 was performed in the relevant exon only.

Polymerase chain reaction (PCR) was performed using the primers described in Table 1. Sanger sequencing was carried out in both directions using an ABI377 DNA sequencer as previously described (33,34) or an ABI3730 genetic analyzer, and the sequences were analyzed manually or by the use of SeqScape (Applied Biosystems).

NGS was carried out using biotinylated oligos (Roche NimbleGen) designed to capture all exons from the NM_020975 transcripts. Library construction was carried out using 500 ng of genomic DNA. The DNA was fragmented into an average size of 200 bp using a Covaris S2 AFA ultrasonicator, and adaptors from Illumina or Roche NimbleGen were ligated to the fragments. Illumina adaptors included in the TruSeq DNA LT Sample Preparation Kit were attached using an SPRI-works System I for the Illumina Genome Analyzer (Beckman Coulter). Adaptor sequences provided by Roche NimbleGen (SeqCap Adaptor Kit A/B) were ligated using the KAPA HTP Library Preparation Kit Illumina on a Sciclone G3 NGS Workstation (PerkinElmer). Sequence capture was performed using a double capture protocol (Roche NimbleGen), where 6–12

TABLE 1. PRIMERS AND POLYMERASE CHAIN REACTION CONDITIONS FOR AMPLIFICATION OF *RET* EXONS FROM THE TWO MAJOR *RET* TESTING CENTERS IN DENMARK

<i>RET center</i>	<i>Exon</i>	<i>Primer sequences</i>	
Center for Genomic Medicine, Copenhagen University Hospital	8	5'-CTG TCT TTG CTG CCC TGG GTC TGT CAC-3' 5'-CGT TTC CAC CGG TGC CAT-3'	
	9	5'-GCT GGC AAG GCT CTG TAT ATG GT-3' 5'-GGA GGC TCA GCT TGA TGC ATA GAA C-3'	
	10	5'-TCA GAA AGG CAC TGT GAC CAA GC-3' 5'-TCC TGG GTG GAG TAA CAG AGG C-3'	
	11	5'-GAG CAT ACG CAG CCT GTA CCC AG-3' 5'-GAA ATG GGG GCA GAA CAC A-3'	
	13	5'-CAG GAA CAT AAT GCC ACA TAC AC-3' 5'-CCG TGG ACT CAG CTA GAC ACA-3'	
	14	5'-GCT CCT GGA AGA CCC AAG-3' 5'-TGG TGG AGT CAG GGT GTG ACA-3'	
	15	5'-CAG GTC TCA CCA GGC CGC TAC-3' 5'-AAG GGC CTC GGG TCA GTA TGC T-3'	
	16	5'-CTG TGC CCA GGA GTG TCT ACA GC-3' 5'-CCA GCC ATT TGC CTC ACG AAC ACA T-3'	
	Department of Molecular Medicine, Aarhus University Hospital	8	5'-CCT TGG GCT CCA TCC GT-3' 5'-CCC CAG GAC CCC GTT T-3'
		9	5'-TAT GGT GTT TCC CTA CTC A-3' 5'-CAG GTT TCC CCT ACT ATC-3'
		10	5'-GCG CCC CAG GAG GCT GAG TG-3' 5'-TGC TGT TGA GAC CTC TGT GG-3'
		11	5'-CTC GAT GGG GTG TTC TCA GG-3' 5'-GGA GGG CAG GGG ATC TTC-3'
		13	5'-GCA GGC CTC TCT GTC TGA ACT T-3' 5'-GGA GAA CAG GGC TGT ATG GA-3'
		14	5'-TCC TGG AAG ACC CAA GCT GC-3' 5'-CAT GGT GGG CTA GAG TGT GG-3'
		15	5'-CCC CCG GCC CAG GTC TCA C-3' 5'-GCT CCA CTA ATC TTC GGT ATC TTT-3'
		16	5'-TCT CCT TTA CCC CTC CTT CC-3' 5'-CCT GGC CAA GCT GCA CAG AC-3'

RET, REarranged during Transfection.

samples are multiplexed prior to hybridization. Finally, 2×76 bp paired-end sequencing was performed on the Illumina MiSeq platform to an average depth of at least 100×.

Department of Molecular Medicine, Aarhus University Hospital. From October 1995 to January 1996, Sanger sequencing of exons 10 and 11 was performed. Since February 1996, October 1996, December 1998, September 2004, and September 2007, testing was expanded to exons 16, 13+14, 8+9, and 15, respectively. Until 2000, only the cysteine domains were tested. As testing has improved, some old blood samples initially negative of *RET* mutations were re-tested. Predictive testing of relatives at risk of MEN2 was performed in the relevant exon only.

PCR was carried out using genomic DNA extracted from EDTA-stabilized blood. The primers are shown in Table 1. Sequencing was carried out in both directions on an ABI3130XL or ABI350XL Genetic Analyzer, and sequences were analyzed using Gensearch[®] software (Phenosystems).

Department of Endocrinology and Medicine, Aalborg University Hospital. From November 1996 to July 2002, primer-specific PCR amplification to detect the p.C611Y

mutation was performed. The method has been described in detail previously (35).

Approvals

The investigation was approved by the Danish Health Authority (3-3013-395/2) and the Danish Data Protection Agency (13/19275).

Results

RET testing of 1583 patients detected 14 different germline mutations in 163 patients from 36 apparently unrelated families. Twelve families were defined by either a unique or *de novo* mutation, while the remaining were defined by clinical workup (Table 2). Of the 36 families, 30 (83%) had MEN2A and six (17%) had MEN2B.

Accounting for 36% of all families, *RET* germline mutations of codon 611 were the most frequent. Subsequently, mutations of codons 634 (17%), 918 (14%), 618 (11%), 620 (8%), 631 (3%), 790 (3%), 804 (3%), 852 (3%), and 883 (3%) followed (Table 3). No mutations of codons 292, 515, 533, 609, 630, 666, 750, 768, 891, 904, or 912 were identified.

Among the 13 families with codon 611 mutations, 12 had the p.C611Y mutation, while one had the p.C611W mutation.

TABLE 2. FAMILIES WITH DETECTED *RET* GERMLINE MUTATIONS^a IN DENMARK FROM 1994 TO 2014 ACCORDING TO FAMILY NUMBER, EXON, NUCLEOTIDE AND SEQUENCE CHANGE, *RET* STATUS IN TESTED CASES, AND REFERENCE OF EARLIER REPORT

Family no.	Exon	Nucleotide change	Sequence change	<i>RET</i> + ^b / <i>RET</i> -	Ref.
1 ^c	10	c.1833C>G	p.C611W	6/11	
2	10	c.1832G>A	p.C611Y	2/0	(43)
3	10	c.1832G>A	p.C611Y	1/0	
4	10	c.1832G>A	p.C611Y	8/3	
5	10	c.1832G>A	p.C611Y	15/13	
6	10	c.1832G>A	p.C611Y	2/0	(34)
7	10	c.1832G>A	p.C611Y	9/7	(34)
8	10	c.1832G>A	p.C611Y	2/6	
9	10	c.1832G>A	p.C611Y	26/27	
10	10	c.1832G>A	p.C611Y	30/30	(44)
11	10	c.1832G>A	p.C611Y	1/3	
12	10	c.1832G>A	p.C611Y	5/18	(45)
13	10	c.1832G>A	p.C611Y	7/8	
14	10	c.1853G>T	p.C618F	1/1	
15	10	c.1853G>T	p.C618F	2/1	(34)
16	10	c.1853G>A	p.C618Y	5/9	
17	10	c.1853G>A	p.C618Y	3/3	(34)
18	10	c.1858T>C	p.C620R	6/5	
19	10	c.1858T>C	p.C620R	3/3	(34)
20 ^d	10	c.1858T>C	p.C620R	1/3	(34)
21 ^c	11	c.1891G>T	p.D631Y	1/0	
22	11	c.1900T>C	p.C634R	1/1	
23	11	c.1900T>C	p.C634R	1/2	(34)
24	11	c.1900T>C	p.C634R	3/11	(44)
25	11	c.1900T>C	p.C634R	1/5	(34)
26 ^{c,e}	11	c.1901G>A	p.C634Y	2/0	
27 ^{c,e}	11 + 13	c.1901G>A+c.2372A>T	p.C634Y+Y791F	1/2	
28 ^c	13	c.2370G>T	p.L790F	5/2	
29 ^c	14	c.2410G>A	p.V804M	2/1	
30 ^c	14	c.2556C>G	p.I852M	3/4	
31 ^{c,d}	15	c.2647_2648GC>TT	p.A883F	1/3	(46)
32 ^d	16	c.2753T>C	p.M918T	1/4	(47)
33 ^d	16	c.2753T>C	p.M918T	1/3	
34	16	c.2753T>C	p.M918T	1/2	
35 ^d	16	c.2753T>C	p.M918T	3/2	(48)
36	16	c.2753T>C	p.M918T	1/1	
Total	36			163/194	

^aSequence changes classified as pathogenic in the ARUP database July 1, 2016 (30).

^b*RET*+ includes index cases.

^cFamilies with unique mutations in Denmark.

^dFamilies in which both parents of the index case were tested mutation negative.

^eFamilies immigrated to Denmark. Family 26 and family 27 originate from Greece and Latvia, respectively.

The distribution of *RET* germline mutations reported in European and non-European studies is shown in Tables 3 and 4.

Discussion

In this nationwide study of 1583 patients who were *RET* tested from 1994 to 2014, 14 different *RET* germline mutations were identified in 163 patients from 36 apparently unrelated MEN2 families. Mutations of codon 611 were the most prevalent (36%), followed by mutations of codon 634 (17%).

Limitations

To estimate the true number of *RET* mutations in a country, the entire population needs to be tested. However, this would result in both immense socioeconomic and ethical chal-

lenges. For the best possible estimate under the given circumstances, this study included all *RET* tested patients in Denmark since testing became available and for more than two decades onwards.

To capture yet unrecognized MEN2 patients, the Danish MEN taskforce has recommended routine *RET* screening in all patients with MTC, PHEO, C-cell or parathyroid hyperplasia, familial/recurrent HPTH, and HPTH <40–50 years of age (36,37). Unfortunately, the completeness of *RET* screening in these patient groups is unknown and will require further studies. In most other studies, only patients with MTC, clinically diagnosed MEN2, or relatives at risk of MEN2 were submitted to mutational analysis of *RET* (7–29,38,39).

To establish a nationwide *RET* positive MEN2 cohort, data were collected in collaboration with the *RET* testing and MEN2 management centers in Denmark. This might cause

TABLE 3. DISTRIBUTION OF *RET* GERMLINE MUTATIONS^a IN EUROPE^b

RET mutation	Denmark		Greece		Germany		Italy		Poland		Spain		Slovenia		Czechia		France		Spain	
	N	n (%)	S	n (%)	S	n (%)	M	n (%)	S	n (%)	S	n (%)	S	n (%)	M	n (%)	M	n (%)	n	(%)
p.V292M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p.C515S	0	0	0	0	0	0	1 (0)	0	0	0	0	0	0	0	0	0	0	0	0	0
p.G533C	0	0	21 (36)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p.C609R/G/F/S/Y	0	0	0	0	1 (1)	0	6 (3)	0	3 (13)	0	1 (4)	0	0	0	1 (5)	0	1 (1)	0	0	0
p.C611R/G/F/S/W/Y	13 (36)	0	0	0	6 (3)	0	1 (0)	0	0	0	0	0	0	1 (5)	0	1 (1)	0	1 (2)	0	0
p.C618R/G/F/S/Y	4 (11)	0	4 (7)	0	11 (6)	0	15 (6)	0	2 (9)	0	1 (4)	0	4 (31)	0	0	6 (6)	0	3 (7)	0	0
p.C620R/G/F/S/W/Y	3 (8)	0	5 (9)	0	14 (7)	0	9 (4)	0	4 (17)	0	1 (4)	0	0	0	12 (12)	0	0	1 (2)	0	0
p.C630R/F/Y	0	0	0	0	1 (1)	0	4 (2)	0	0	0	0	0	0	0	0	0	0	0	0	0
p.D631Y	1 (3)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p.C634R/G/F/S/W/Y	6 (17)	0	19 (33)	0	73 (38)	0	85 (37)	0	9 (39)	0	17 (68)	0	6 (46)	0	11 (52)	0	46 (47)	0	36 (88)	0
p.K666E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p.A750P	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p.E768D	0	0	1 (2)	0	2 (1)	0	9 (4)	0	0	0	1 (4)	0	0	0	1 (5)	0	2 (2)	0	0	0
p.L790F	1 (3)	0	0	0	26 (14)	0	8 (3)	0	0	0	0	0	3 (23)	0	0	4 (4)	0	0	0	0
p.V804L/M	1 (3)	0	3 (5)	0	19 (10)	0	52 (22)	0	1 (4)	0	0	0	0	0	3 (14)	0	15 (15)	0	0	0
p.I852M	1 (3)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p.A883F/T	1 (3)	0	0	0	0	0	1 (0)	0	0	0	0	0	0	0	0	0	0	0	0	0
p.S891A	0	0	0	0	6 (3)	0	23 (10)	0	1 (4)	0	1 (4)	0	0	0	0	0	7 (7)	0	0	0
p.S904F	0	0	0	0	0	0	1 (0)	0	0	0	0	0	0	0	0	0	0	0	0	0
p.R912P	0	0	0	0	0	0	0	0	1 (4)	0	0	0	0	0	0	0	0	0	0	0
p.M918T	5 (14)	0	5 (9)	0	32 (17)	0	17 (7)	0	2 (9)	0	3 (12)	0	0	0	4 (19)	0	3 (3)	0	0	0
Total	36 (100)	58 (100)	191 (100)	232 (100)	232 (100)	232 (100)	232 (100)	232 (100)	23 (100)	25 (100)	25 (100)	13 (100)	21 (100)	97 (100)	41 (100)	41 (100)	41 (100)	41 (100)	41 (100)	41 (100)

Due to rounding up, not all sums of the numbers fit.

^aSequence changes classified as pathogenic in the ARUP database July 1, 2016 (30).

^bIncluding series with a minimum of 10 European *RET* families (27–29) excluded, a minimum of exons 10–11 and 13–16 tested ((16) excluded), and specifying familial prevalence. N, nationwide; S, single center; M, multicenter; n, number of families.

TABLE 4. DISTRIBUTION OF *RET* GERMLINE MUTATIONS^a OUTSIDE EUROPE^b

Exon	RET mutation	China	China	India	Iran	China	Korea
		S (17) n (%)	S (18) n (%)	S (19) n (%)	M (20) n (%)	(21) n (%)	M (22) n (%)
5	p.V292M	0	1 (9)	0	0	0	0
8	p.C515S	0	0	0	0	0	0
8	p.G533C	0	0	0	0	0	0
10	p.C609R/G/F/S/Y	0	0	2 (13)	0	0	0
10	p.C611R/G/F/S/W/Y	0	0	0	1 (9)	0	0
10	p.C618R/G/F/S/Y	2 (20)	1 (9)	1 (7)	1 (9)	0	3 (23)
10	p.C620R/G/F/S/W/Y	0	0	0	0	0	0
11	p.C630R/F/Y	0	0	0	1 (9)	0	0
11	p.D631Y	0	0	0	0	0	0
11	p.C634R/G/F/S/W/Y	6 (60)	8 (73)	9 (60)	6 (55)	15 (75)	10 (77)
11	p.K666E	0	0	0	0	0	0
12	p.A750P	0	0	0	0	0	0
13	p.E768D	0	0	0	0	0	0
13	p.L790F	1 (10)	1 (9)	0	0	0	0
14	p.V804L/M	0	0	1 (7)	1 (9)	0	0
14	p.I852M	0	0	0	0	0	0
15	p.A883F/T	0	0	0	0	0	0
15	p.S891A	0	0	0	0	0	0
15	p.S904F	0	0	0	0	0	0
16	p.R912P	0	0	0	0	0	0
16	p.M918T	1 (10)	0	2 (13)	1 (9)	5 (25)	0
Total		10 (100)	11 (100)	15 (100)	11 (100)	20 (100)	13 (100)

Due to rounding up, not all sums of the numbers fit.

^aSequence changes classified as pathogenic in the ARUP database July 1, 2016 (30).

^bIncluding series with a minimum of 10 European *RET* families ((25,38,39) excluded), a minimum of exons 10–11 and 13–16 tested ((23,24) excluded), and specifying familial prevalence.

S, single center; M, multicenter; n, number of families.

issues of inter-variability in regards to methods and interpretation of results. However, methods and temporal expansion of *RET* testing were roughly similar in the two major *RET* testing centers, accounting for 94.7% (1499 patients) of the cohort. The remaining 84 patients were tested solely at the Aalborg University Hospital and thus only for the p.C611Y mutation. Of those, 26 were p.C611Y positive, and 45 were related to a p.C611Y patient. This leaves only 13 patients (0.7% of the total cohort) in which a *RET* mutation different from the p.C611Y might have been missed.

To estimate the true number of unrelated MEN2 families, a haplotype or genealogy study would be ideal. However, 24/36 apparently unrelated MEN2 families were defined by thorough clinical work-up. As in other studies, this workup is based on the index patient's recollection and knowledge of the familial history. Thus, possible relations between families carrying similar mutations might have been missed and may cause an overestimation of the number of families.

Codon 611 mutations

In the present study, mutations in codon 611 of exon 10 were the most prevalent accounting for 36% of the 36 families. This appears to be an unusually high prevalence. Numerous other studies did not detect any mutations in codon 611, despite systematic testing of *RET* exon 10 (8–10,16–19,21–26,28,29,39). Most of these are single-center studies, and there might be an expectation of capturing more MEN2 patients in a nationwide study such as the one presented here. However, this does not seem to be the explanation. In fact, in three large European predominantly multicenter series based on a total of 232, 191,

and 97 families, the prevalence of codon 611 mutations was only 0%, 3%, and 1%, respectively (Table 3) (6,7,12,13). The highest prevalence rates reported have been from Portugal (40%), Saudi Arabia (11%), and Iran (9%). However, these reports were based on small mainly single-center studies with a total of 5, 11, and 9 families (20,27,38).

Mutations highly prevalent in other series

An unusually high prevalence of specific *RET* mutations has also been described in other populations (6,7,26,28,29). In Cyprus, eight families were studied, and all carried the p.C618R mutation (28). A Sardinian study of seven families found three kindreds (43%) with the p.V804M mutation (29). In a large Italian multicenter study, 22% and 10% of the families had mutations in codons 804 and 891, respectively (Table 3) (7). A large German study identified codon 790 mutations in 14% of all included families, while a recent Greek study of 58 families found that 36% harbored the p.G533C mutation in exon 8 (Table 3) (6,26).

Results from these studies indicate geographical differences in the distribution of *RET* mutations. On the other hand, if mutations in exon 8 are disregarded in the Greek study, the distribution of mutations would be largely similar to that of other sizeable series where exon 8 was not routinely tested (7,12,13). Also, the high prevalence of codon 804 and 891 mutations in Italy may be caused by an earlier and more extensive testing of exons 14 and 15 compared to other series. A similar explanation for the high prevalence of codon 611 mutations in Denmark seems unlikely, since the traditional *RET* panel included testing of exon 10 from the very beginning (40).

Thus, there seems to be a genuine high prevalence of codon 611 mutations in Denmark. This is supported by the fact that 70% (114/163) of the patients studied carry a codon 611 mutation.

Possible founder effect

Among the 13 apparently unrelated families with codon 611 mutations in the present study, 12 had the p.C611Y mutation. This could indicate a possible founder effect for the p.C611Y mutation. A similar effect has been indicated in other studies (7,26–29,41,42).

In the Mediterranean islands of Cyprus and Sardinia, the authors suggested that a founder effect for the p.C618R and the p.V804M mutation could be explained by geographical isolation (28,29). However, geographical isolation alone does not seem to explain a possible founder effect in Denmark, since its southern border connects the country to Germany and the rest of Continental Europe.

In Greece, the p.G533C mutation was found especially in the southern part of Central Greece and the southeast region of the Peloponnese (26). In Italy, the p.S891A mutation was mainly present in a well-defined northern area. The Italian authors also found a high prevalence of codon 804 mutations, but excluded a founder effect by single-nucleotide polymorphism analysis (7). Only few and very small studies have proven a founder effect of *RET* mutations in mainland areas by haplotype analysis (27,41,42). To elaborate on this question in Denmark, further investigations are planned.

Prevalence of other mutations

Codon 634 mutations have been reported as the most predominant in several European (Table 3) (6–14) and non-European series (Table 4) (17–25). This might be explained by earlier onset of disease and a presentation frequently involving the full-blown MEN2 syndrome (MTC, PHEO, and HPTH). Mutations of codon 634 were the second most frequent alteration found in the present study, accounting for 17% (Table 3).

In the three largest studies to date, the prevalence of the p.V804L/M mutations ranged from 10% to 22% (Table 3) (6,7,12,13). In the present cohort, only one family (3%) was identified with this mutation. Despite testing for mutations in exon 14 since 1996 and 1997 in the two major *RET* testing centers, one center did not test the non-cysteine domains until after 2000. Retesting of patients tested before 2000 was performed but not systematically. Consequently, some patients tested for these mutations between 1996 and 2000 might have been missed, and this may result in a reduced number of families with non-cysteine codon 804 mutations. The distribution of the remaining mutations did not differ largely from that found in the literature.

Conclusion

The distribution of *RET* mutations in Denmark appears to differ from that of other populations. Mutations in codon 611 were by far the most prevalent alterations followed by more frequently reported mutations. This might be due to a possible founder effect for the p.C611Y mutation. However, further studies are needed to find possible explanations for the skewed mutational spectrum in Denmark.

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Author Disclosure Statement

The authors declare that no competing financial interests exist.

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Address correspondence to:
Jes Sloth Mathiesen, MD
Department of ORL Head & Neck Surgery
Odense University Hospital
Sdr. Boulevard 29
DK-5000 Odense C
Denmark

E-mail: jes_mathiesen@yahoo.dk