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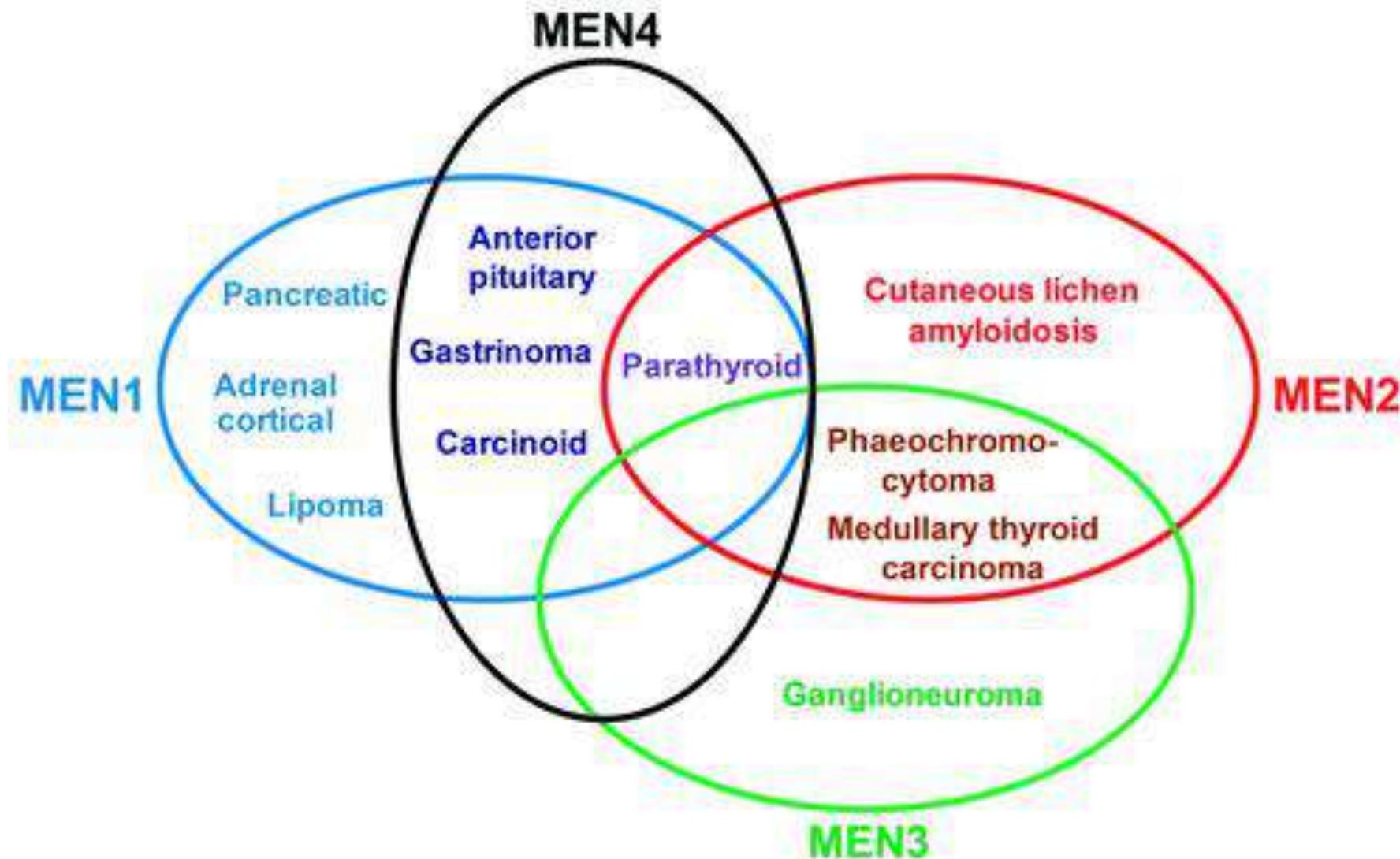
Grupo Español de Oncología Transversal
y Tumores Huérfanos e Infrecuentes

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Sesión 1: Del síndrome Hereditario a la diana *4 de noviembre de 2021 - Formato virtual* terapéutica

Título: Síndrome de Neoplasia Endocrina Múltiple.
Bases moleculares y oportunidades terapéuticas

Ponente: Mercedes Robledo



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MEN TYPE 2 A&B

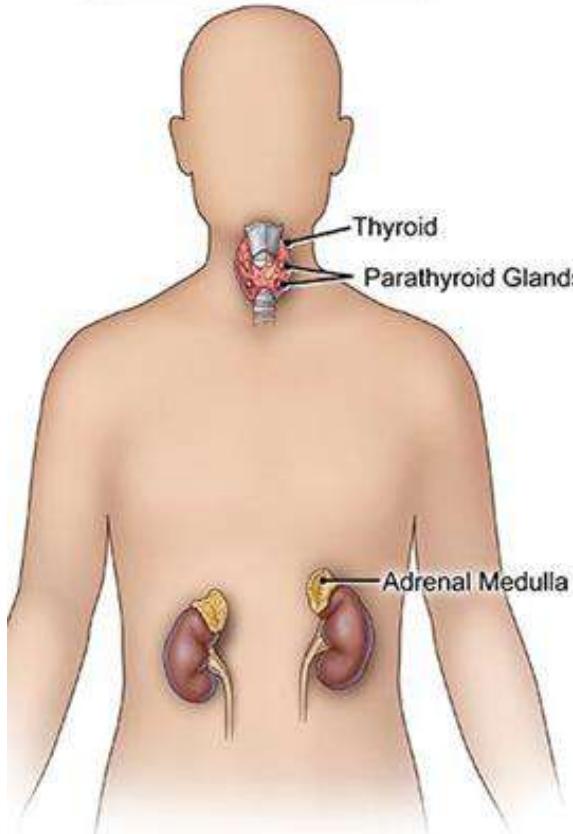


Table 1 Multiple endocrine neoplasia type 2A and type 2B phenotypic characteristics and lifetime risk of development.

	Risk of medullary thyroid carcinoma	Pheochromocytoma	Primary hyperparathyroidism	Other extra-endocrine signs
MEN2A	90–100%	0–50% (risk depends on genotype)	0–20% (risk depends on genotype)	<5% (Hirschsprung disease, Cutaneous lichen amyloidosis)
MEN2B (M918T, A883F, tandem mutations)	100%	50% (risk depends on genotype)	0%	100% Gastrointestinal Ophthalmological Skeletal Manifestations Mucosal neuromas

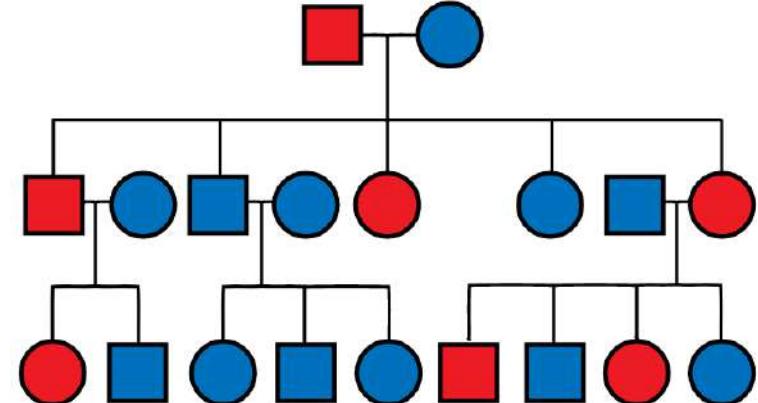
Castinetti F, et al. *Endocr Relat Cancer*. 2018 Feb;25(2):T29-T39.

CMT: 25% hereditary; 75% sporadic

PPGL: 40% hereditary; 40% sporadic; 20% unknown

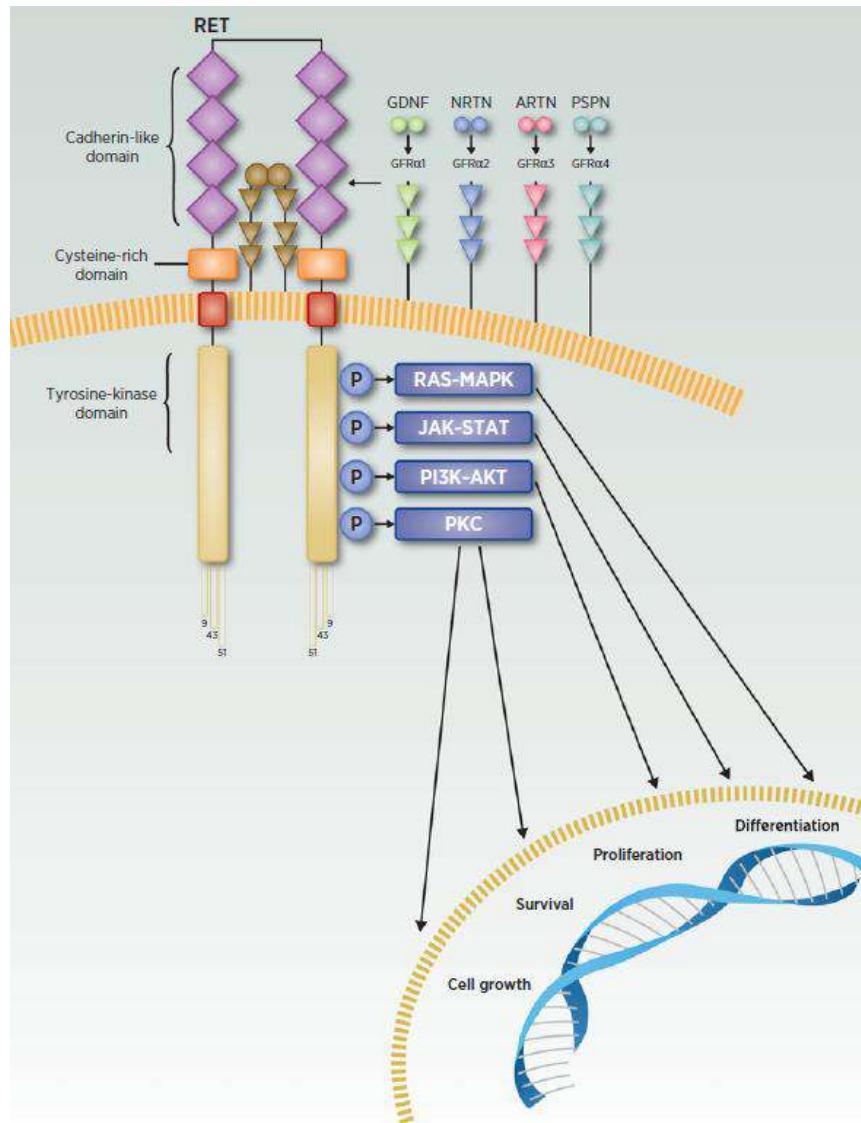
PHPT: 10-15% hereditary

Dominant inheritance



**Caused by germline mutations in *RET*
(rearranged during transfection)**

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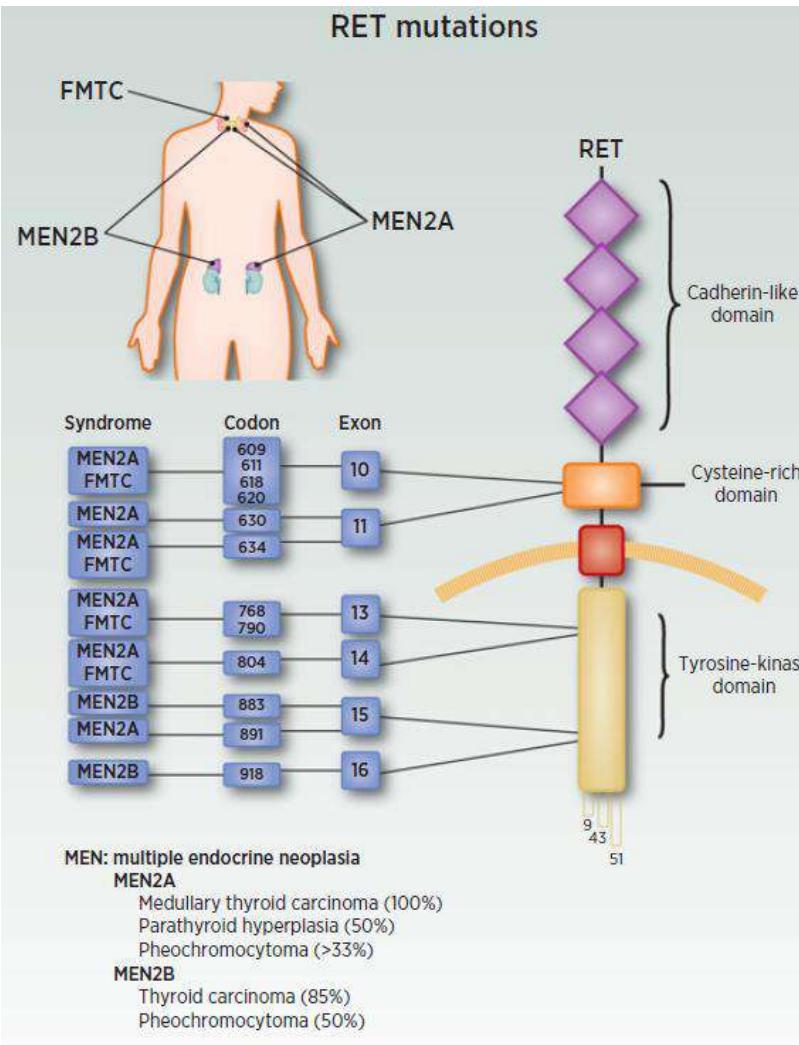


RET (located at chromosome 10q11.21) encodes a TK receptor.

Oncogenic activation mainly in two different ways: (i) chromosomal rearrangement giving rise to chimeric *RET* fusion genes and (ii) **somatic or germline gain-of-function mutations** → constitutive activation of *RET*.

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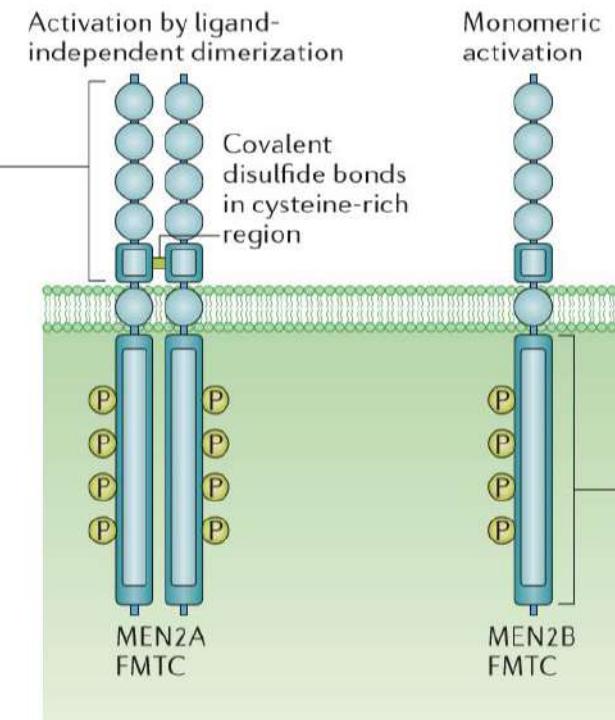
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Mutation effect

b RET nonsynonymous point mutations

Extracellular domain
Exon 8 G533C
Exon 10 C609F/G/R/S/Y C611F/G/S/Y/W C618F/R/S C620F/R/S
Exon 11 C630R/Y D631Y C634F/G/R/S/W/Y K666E



Kinase domain
Exon 13 E768D L790F Y791F
Exon 14 V804M/L Y806C
Exon 15 A883F S891A
Exon 16 M918T

Drilon A, et al. *Nat Rev Clin Oncol.* 2018 Mar;15(3):151-167;

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Risk according to the specific mutation.

RET mutation	Exon	MTC risk level ^a	Incidence of PHEO ^b	Incidence of HPTH ^b	CLA ^c	HD ^c
G533C	8	MOD	+	-	N	N
C609F/G/R/S/Y	10	MOD	+/++	+	N	Y
C611F/G/S/Y/W	10	MOD	+/++	+	N	Y
C618F/R/S	10	MOD	+/++	+	N	Y
CF20F/R/S	10	MOD	+/++	+	N	Y
C630R/Y	11	MOD	+/++	+	N	N
D631Y	11	MOD	+++	-	N	N
C634F/G/R/S/W/Y	11	H	+++	++	Y	N
K666E	11	MOD	+	-	N	N
E768D	13	MOD	-	-	N	N
L790F	13	MOD	+	-	N	N
V804L	14	MOD	+	+	N	N
V804M	14	MOD	+	+	Y	N
A883F	15	H	+++	-	N	N
S891A	15	MOD	+	+	N	N
R912P	16	MOD	-	-	N	N
M918T	16	HST	+++	-	N	N

^aRisk of aggressive MTC: MOD, moderate; H, high; HST, highest; MTC, medullary thyroid carcinoma; PHEO, pheochromocytoma; HPTH, hyperparathyroidism; CLA, cutaneous lichen amyloidosis; HD, Hirschsprung's disease; ^bIncidence of PHEO and HPTH; ^cY, positive occurrence; N, negative occurrence: + = ~10%, ++ = ~0-30%, +++ = ~5-%.

Presymptomatic genetic testing → prophylactic or early interventions before dissemination of the disease.

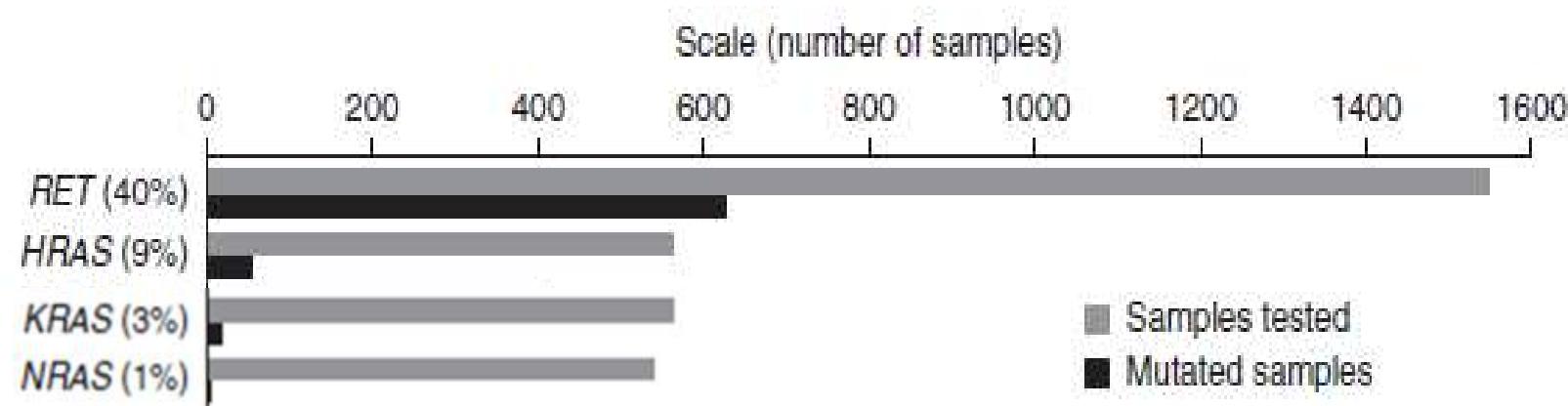


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- 25% of MTC are **hereditary** associated with MEN2 syndrome (*RET* germline mutations).
- The remaining **75%** are classified as **sporadic**: can be related to **RAS or RET somatic mutations (mostly mutually exclusive)**



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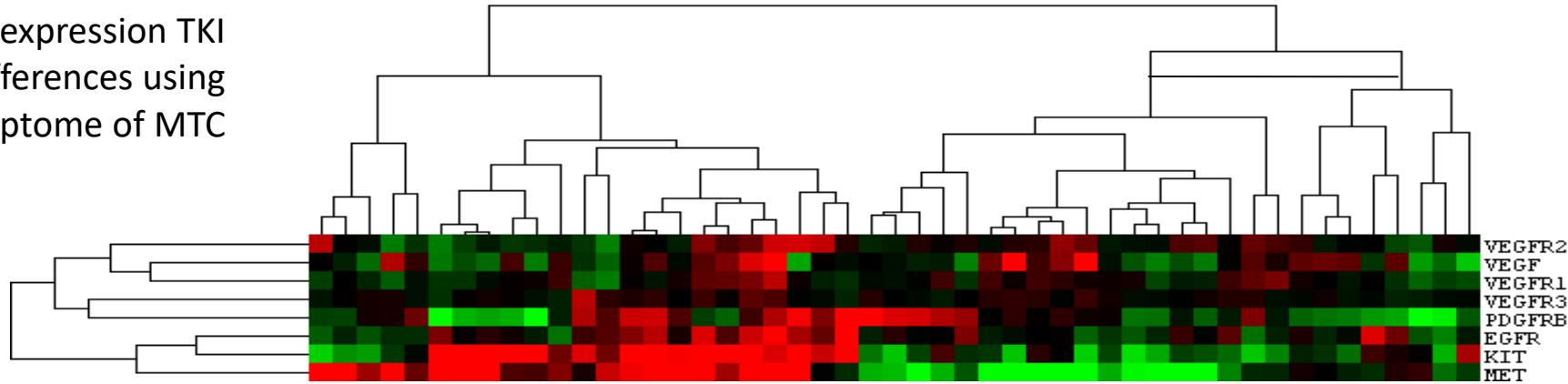
Multikinases inhibitors, originally developed to target conserved regions of other kinases have also shown efficacy against RET.

MKIs	Study phase	All pts	Treatment group	ORR (%) ^a	mPFS (mos.)	mOS (mos.)	TRAEs all grades (%) ^b
Thyroid cancer							
Sorafenib (68)	II	21	Sorafenib	1/15 (6)	17.9	nr	HFSR 19/21 (90) Rash (non-HFSR) 18/21 (86)
Lenvatinib (69)	II	59	Lenvatinib	21/59 (36)	9.0	16.6	Diarrhea 44/59 (75) Proteinuria 35/59 (59)
Sunitinib (70)	II	71	Sunitinib	19/71 (27)	na	na	Asthenia/fatigue 59/71 (83) Mucosal AE 46/71 (65)
Dovitinib (71)	II	40	Dovitinib	8/39 (20)	5.4	nr	Diarrhea 21/39 (54) Anorexia (36)
Motesanib (72)	II	91	Motesanib	2/91 (2)	12	na	Thyroid dysfunctions 76/91 (83) Diarrhea 37/91 (41) Fatigue 37/91 (41)
Vandetanib (66)	III	331	Vandetanib	104/231 (45)	30.5	na	Diarrhea 130/231 (56)
Cabozantinib (64, 65, 67)	III	330	Placebo	13/100 (13)	19.3		Rash 104/231 (45)
			Cabozantinib	58/208 (28)	11.2	26.6	Diarrhea 135/214 (63)
			Placebo	0/104 (0)	4.0	21.1	PPE 107/214 (50)
Mutational subgroups							
			Cabozantinib				
			RET MUT+	32/101 (32)	14	—	
			RET MUT-	7/32 (22)	5.8	—	
			RET M918T+	26/77 (34)	14.2	44.3	
			RET M918T-	14/69 (2)	5.8	20.2	
			Placebo				
			RET M ^{918T+}	—	—	18.9	
			RET M ^{918T-}	—	—	21.5	

Any clue about inter-patient response rate variability?

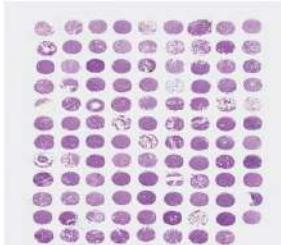
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Exploring expression TKI
receptors differences using
transcriptome of MTC

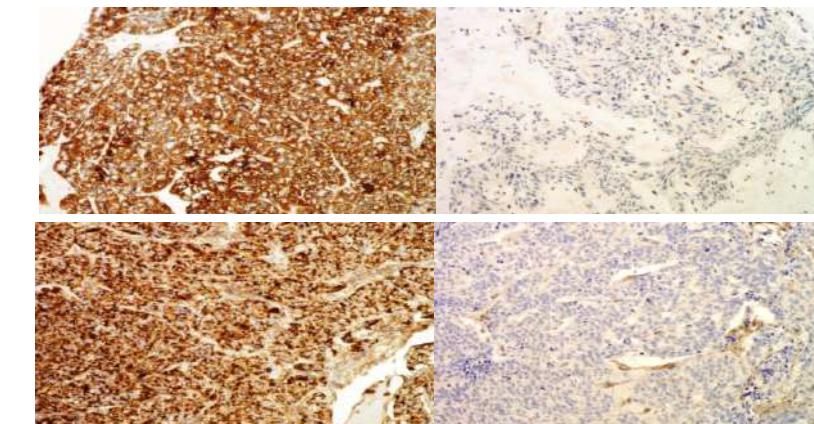


103 primary MTC (genetically characterized)

Tissue arrays



IHC of 8 key proteins



PDGFR-b VEGFR2

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The driver mutation can affect the likelihood of benefiting from a particular TKI therapy

Proteins ^{\$}	RAS vs RET			WT vs RET			WT vs RAS		
	RAS	RET	p-value	WT	RET	p-value	WT	RAS	p-value
VEGF	2/12 (17%)	15/52 (29%)	0.49	9/13 (69%)	15/52 (29%)	0.011	9/13 (69%)	2/12 (17%)	0.0082*
PDGFRB	0/13 (0%)	21/53 (40%)	0.0060*	2/12 (17%)	21/53 (40%)	0.19	2/12 (17%)	0/13 (0%)	0.22
VEGFR1	6/10 (60%)	13/37 (35%)	0.28	6/13 (46%)	13/37 (35%)	0.52	6/13 (46%)	6/10 (60%)	0.68
VEGFR2	4/10 (40%)	22/39 (56%)	0.48	10/13 (77%)	22/39 (56%)	0.19	10/13 (77%)	4/10 (40%)	0.10
VEGFR3	1/14 (7%)	31/53 (59%)	0.00062**	5/12 (42%)	31/53 (59%)	0.35	5/12 (42%)	1/14 (7%)	0.065
MET	0/12 (0%)	12/40 (30%)	0.047	4/14 (29%)	12/40 (30%)	0.99	4/14 (29%)	0/12 (0%)	0.10
RAS vs RET ^{C634}									
Proteins ^{\$}	RAS	RET ^{C634}	p-value	RAS	RET ^{M918T}	p-value			
	2/12 (17%)	6/24 (25%)	0.69	2/12 (17%)	6/16 (38%)	0.40			
VEGF	0/13 (0%)	11/24 (46%)	0.0032*	0/13 (0%)	6/17 (35%)	0.024*			
PDGFRB	6/10 (60%)	3/17 (18%)	0.039*	6/10 (60%)	5/10 (50%)	0.99			
VEGFR1	4/10 (40%)	10/17 (59%)	0.44	4/10 (40%)	6/12 (50%)	0.69			
VEGFR2	1/14 (7%)	16/24 (67%)	0.00037**	1/14 (7%)	10/17 (59%)	0.0067**			
VEGFR3	0/12 (0%)	4/17 (24%)	0.12	0/12 (0%)	5/14 (36%)	0.042			

- **RAS-related MTC do not express MET and PDGFRB.**
- **RET-related express more frequently VEGFR3.**
- **WT MTC express notably more frequently VEGF.**

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To note: **side effects** →

Treatment discontinuation rate was 12% with vandetanib and 16% with cabozantinib,

Dose reduction: 35% of patients treated with vandetanib and 79% with cabozantinib.

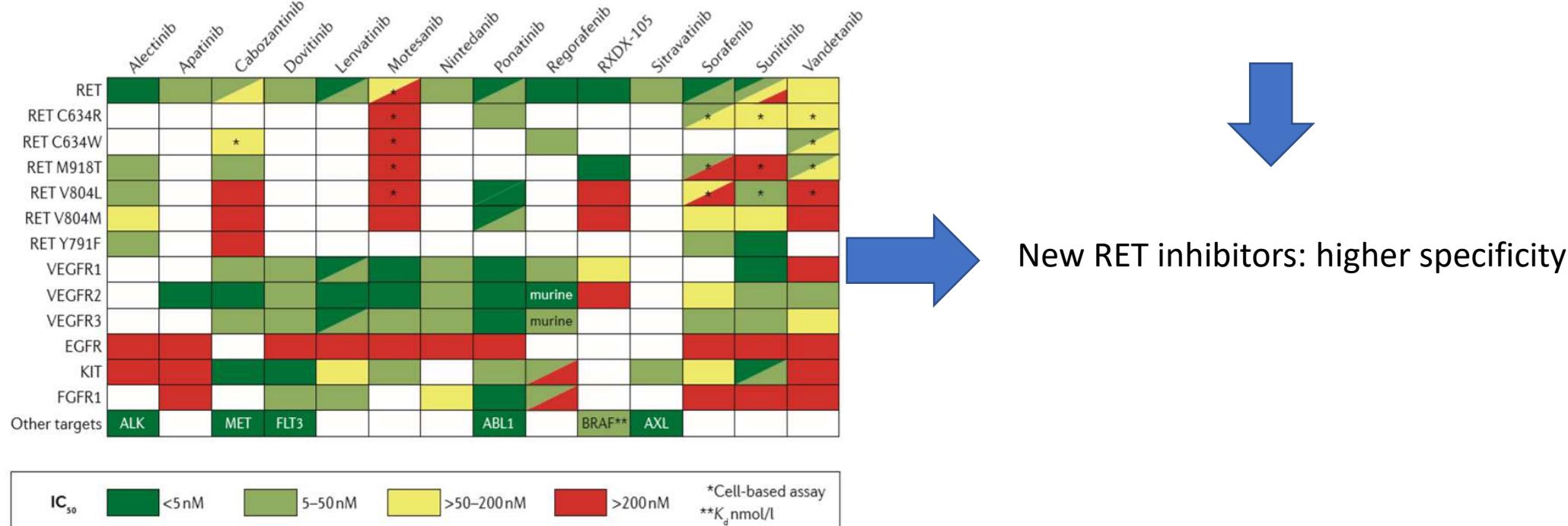


Figure 4 | Multikinase inhibitor activity against RET and other kinases. The half-maximal inhibitory concentration (IC_{50}) of select multikinase inhibitors with varying levels of activity against RET are shown. The various colours represent a range of IC_{50} values, from <5 nM to >200 nM. Unless otherwise indicated, the IC_{50} values shown reflect the results of *in vitro* kinase assays. The presence of two or more colours within a given box indicate different IC_{50} values reported in separate publications. A white box indicates that biochemical data are not currently available.

Efstathiadou ZA, et al. Eur Thyroid J 2021;10:125–139;
 Belli C, et al. Clin Cancer Res. 2020 Dec 1;26(23):6102-6111.
 Drilon A, et al. Nat Rev Clin Oncol. 2018 Mar;15(3):151-167;

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New RET inhibitors, selpercatinib and pralsetinib, might **solve off-target toxicity** problems as they inhibit more potently and selectively both wild-type RET and RET+ cancer cell lines in biochemical assays.

Table 3. Clinical trials with new selective *RET* inhibitors in lung and thyroid cancer.

RET inhibitors	Tumor type	All pts	Fusion or mutation types (%)	ORR (%) ^a	TRAEs all grades (%) ^b
Selpercatinib (73)	Thyroid	226	M918T 129/226 (57) Non-M918T 97/226 (43)	Treatment naïve 64/88 (73) Pretreated 38/55 (69)	nr ^c
Pralsetinib (76)	Thyroid	64	M918T 36/64 (56) Non-M918T 28/64 (44)	18/32 (56)	Hypertension 19/64 (30) Neutropenia 15/64 (23)

RET alterations have become increasingly more relevant in the clinics. These **new *RET* inhibitors** → improved response rates, more durable disease control, and favorable safety profile compared with MKIs (possibly due to the lack of VEGF Inhibition). **But** these two drugs will not be used in *RET*-negative MTCs.

Again → **mechanisms of acquired resistance*** to first-generation selective RET inhibitors is **not yet fully known**

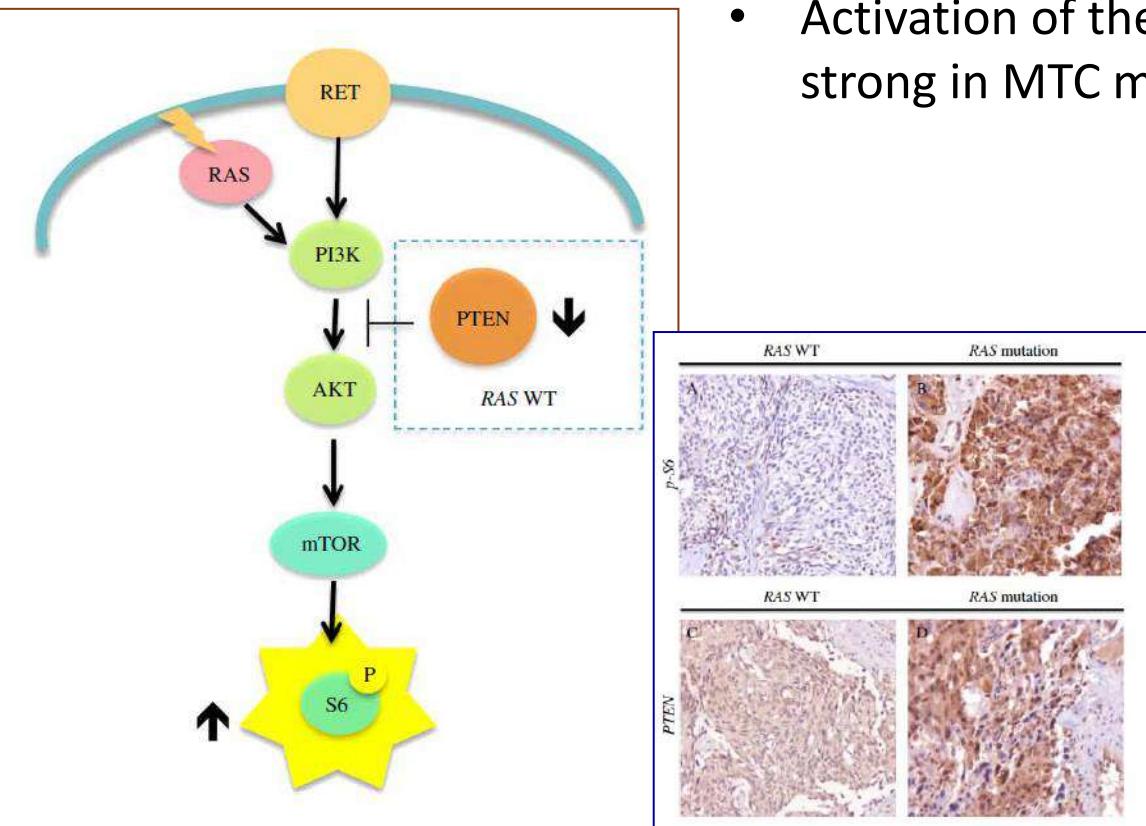


The **next-generation RET inhibitors**: TPX-0046 and BOS172738.

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Alternatives? → Combination therapy based on the biological knowledge

- Activation of the mTOR pathway has been demonstrated in MTC (particularly strong in MTC metastases).



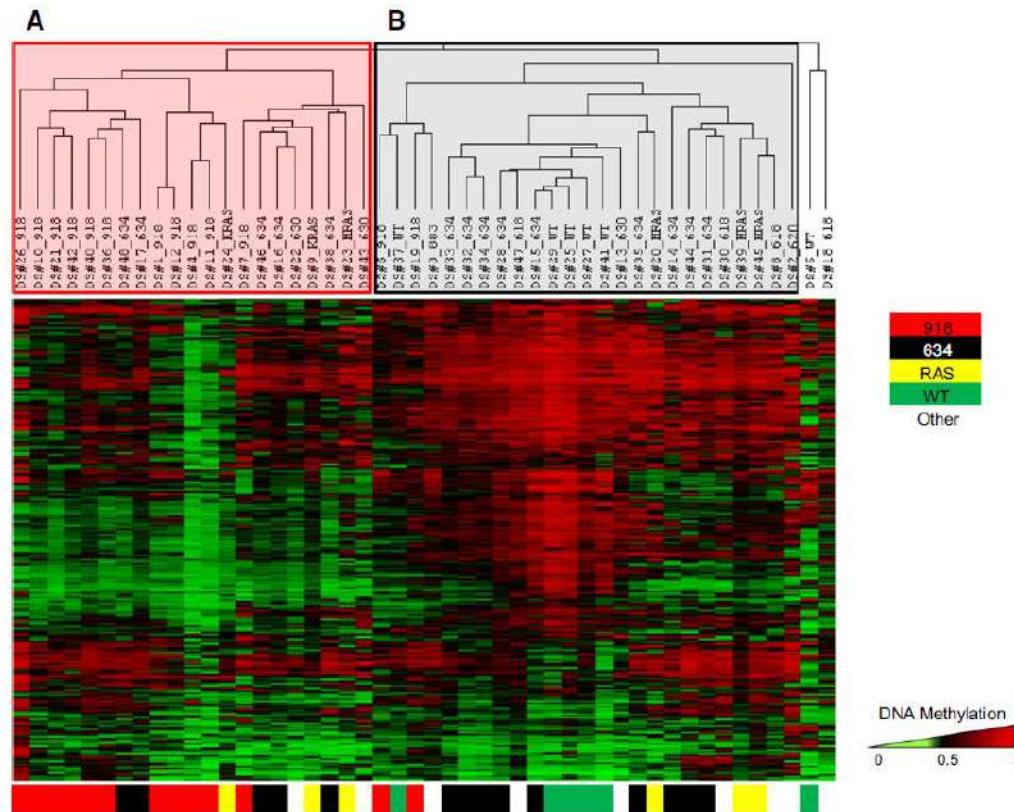
p-S6 high expression in RAS-related MTC vs WT-RAS (P=0.007)

p-S6 expression can be used as indicator of increased metastatic capacity of MTC, as well as a potential predictive biomarker for mTOR inhibitors response.

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Alternatives? → Combination therapy based on the biological knowledge

Based on 48 frozen MTCs genetically characterized



Activation of JAK/STAT signaling pathway linked to p.M918T mutation

Activation of STAT3 is associated with a **worse prognosis** due to its role in uncontrollable proliferation, inflammation and modulation of microenvironment.

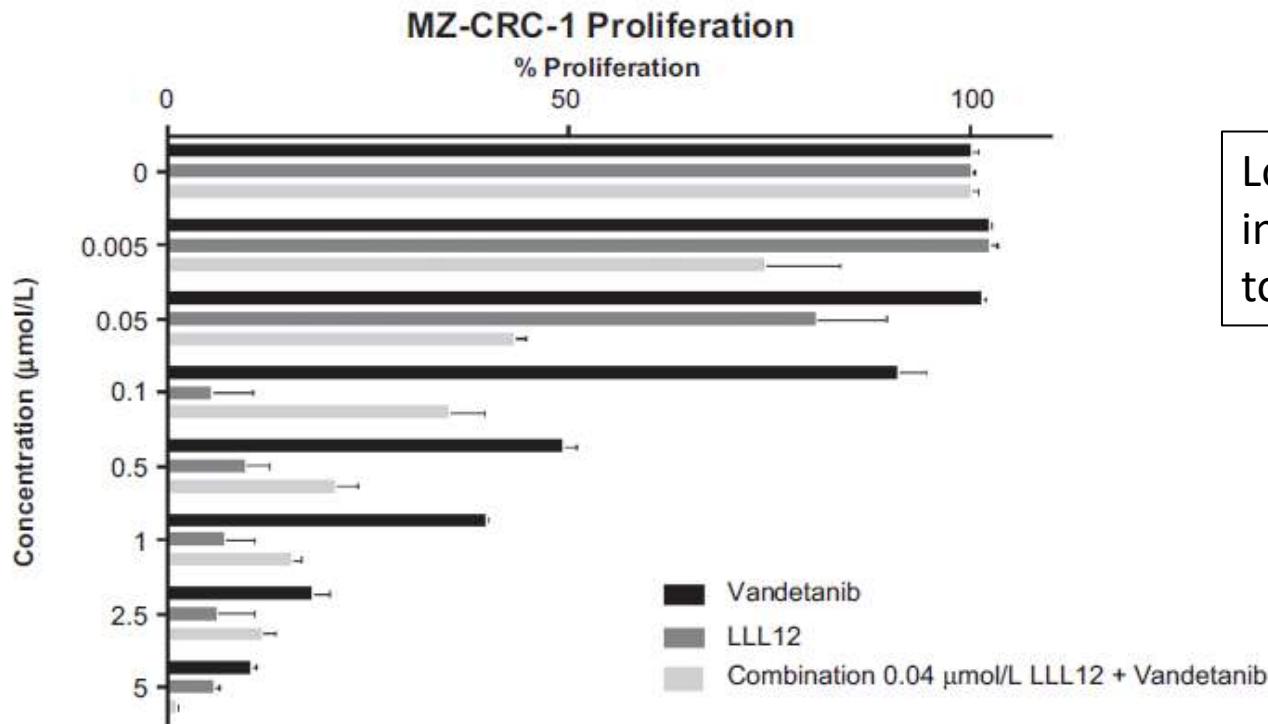
Thus, STAT3 is a very **attractive molecule for targeted therapies**.

Thomas SJ, et al. *Br J Cancer* 2015;113:365–71.

Debnath B, et al. *J Med Chem* 2012; 55:6645–68.

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Our **aim** was to know if this activation could be relevant for treatment response, and then we use STAT3 inhibitors commercially available.



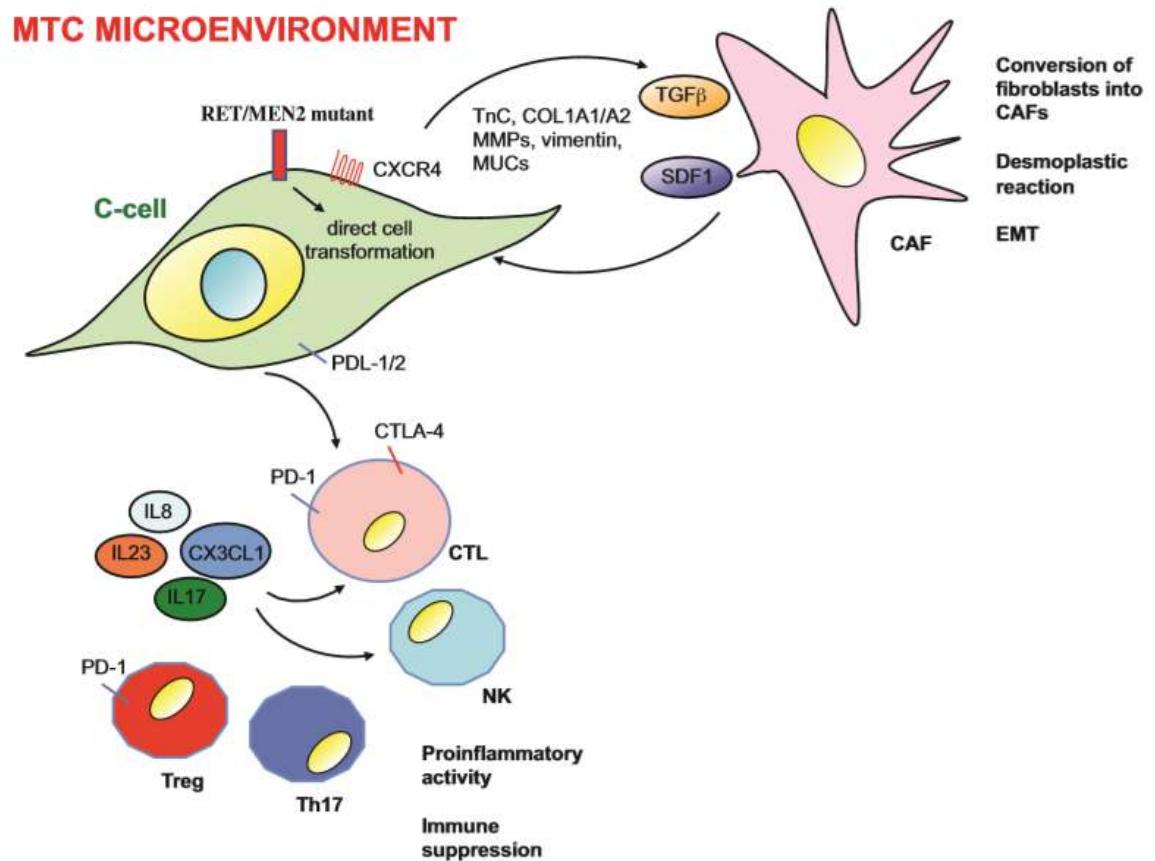
Low doses of the inhibitor of pSTAT3 increased the sensitivity of MTC cells to vandetanib treatment.

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Alternatives? → Combination therapy based on the biological knowledge

Beyond tumor cells → TME.

The activation of the **immune-inflammatory transcriptional program** depends on the signaling pathway activated and thus, **on the mutation**.



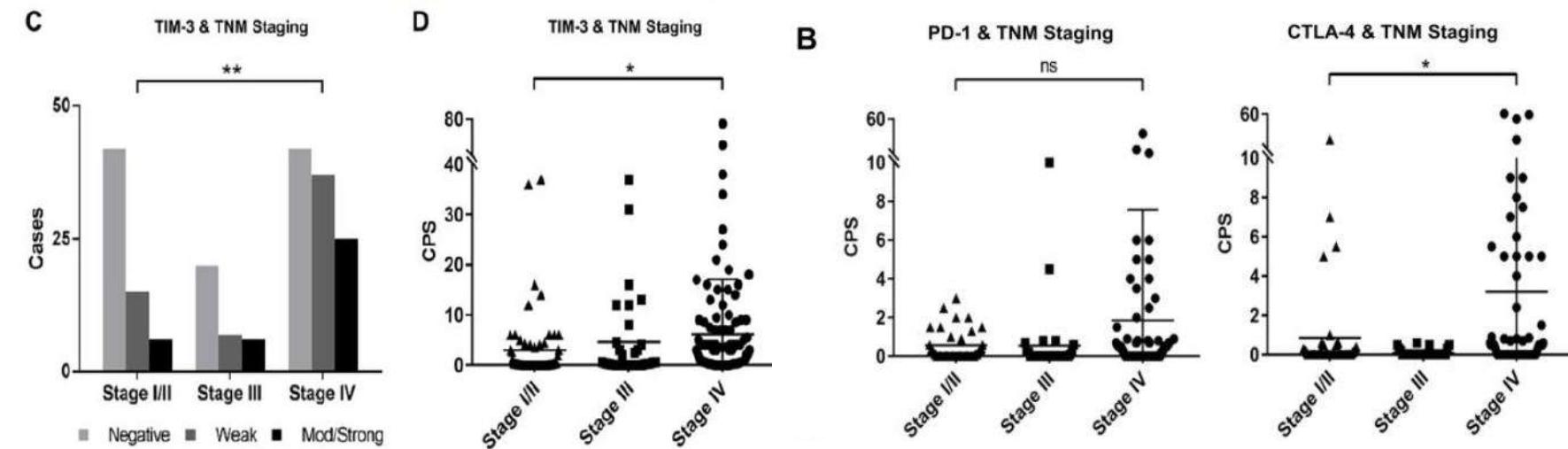
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200 patients were enrolled



tumor-infiltrating leukocytes (TILs),
PD-1, CTLA-4, TIM-3, LAG-3, TIGIT



In the setting of advanced MTCs, single or combined immunotherapy including TIM-3, PD-1/PD-L1 or CTLA-4 blockade may be potential therapeutic approaches



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Lack of **MTKs response is multifactorial** and influenced by the specific target mutation, the off-target inhibition, intrinsic resistance, pathway reactivation, and TME.

The deeper biological knowledge of mechanisms involved in these events will facilitate **combined and personalized treatment**.