Current concepts in RET-related genetics, signaling and therapeutics

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The receptor tyrosine kinase RET is expressed in cell lineages derived from the neural crest and has a key role in regulating cell proliferation, migration, differentiation and survival during embryogenesis. Germline and somatic mutations in \textit{RET} that produce constitutively activated receptors cause the cancer syndrome multiple endocrine neoplasia type 2 and several endocrine and neural-crest-derived tumors, whereas mutations resulting in nonfunctional RET or lower expression of \textit{RET} are found in individuals affected with Hirschsprung disease. This review focuses on the genetics and molecular mechanisms underlying the different inherited human neural-crest-related disorders in which RET dysfunction has a crucial role and discusses RET as a potential therapeutic target.

Introduction

The human gene \textit{RET} is localized on chromosome 10 (10q11.2) and contains 21 exons [1]; alternative splicing generates three isoforms, which contain 51 (RET\textsubscript{51}), 43 (RET\textsubscript{43}) and 9 (RET\textsubscript{9}) amino acids in the carboxyl (C)-terminal tail [2]. RET\textsubscript{51} and RET\textsubscript{9} are the most prevalent and best-characterized isoforms \textit{in vivo}; RET\textsubscript{43} has not yet been characterized. The RET\textsubscript{51} isoform shows the highest transforming and kinase activity \textit{in vitro} [3], and several observations suggest that these isoforms have different tissue-specific effects during embryogenesis [4]. Monoisoformic RET\textsubscript{9} mice are viable and normal, whereas the monoisoformic RET\textsubscript{51} mice (which lack RET\textsubscript{9}) have kidney hypoplasia and lack enteric ganglia from the colon [4].

RET (Figure 1) is the receptor for members of the glial cell-derived neurotrophic factor (GDNF) family of ligands (GFLs); namely GDNF, Neurturin, Persephin and Artemin [5]. To stimulate RET, these GFLs first need to form a complex with their glycosylphosphatidylinositol (GPI)-anchored co-receptor, a member of the GDNF receptor-\alpha family (GFR\alpha\textsubscript{1}–GFR\alpha\textsubscript{4}), after which the GFL–GFR complex activates RET [6,7]. The GFRs differ in their specificity for GFLs (Figure 1).

During embryogenesis, RET is expressed in the developing excretory system, in all lineages of the peripheral nervous system, and in motor and catecholaminergic neurons of the central nervous system [8]. In addition, RET is also expressed in C-cells of the thyroid and tumors originating from these cells, in medullary thyroid carcinomas (MTCs), and in other tumors of neural crest origin such as pheochromocytomas and neuroblastomas [9].

The role of RET in cancers was first described when somatic rearrangements of \textit{RET} (named \textit{RET}/\textit{PTC}) showing constitutive tyrosine kinase activity were found in papillary thyroid carcinomas (PTCs) [10]. These RET/PTC oncoproteins, of which over ten have been described, are all chimeric proteins in which the amino (N)-terminal region of different proteins is fused to the catalytic domain of RET [11]. Subsequently, germline mutations that give rise to constitutively activated RET proteins were discovered as the cause of the cancer syndrome 'multiple endocrine neoplasia type 2' (MEN2) [12]. By contrast, mutations causing loss of function of the RET protein were found to be associated with Hirschsprung disease: a developmental disorder characterized by the absence of enteric ganglia in the intestinal tract [13].

In this review, we focus on current concepts in the genetics and molecular mechanisms underlying the different inherited human neural crest disorders in which RET dysfunction plays a crucial role, and we further discuss new developments in which RET is a therapeutic target.

Wild-type RET activation and signaling

Wild-type RET signaling is crucial for the development of the enteric nervous system (ENS), kidney organogenesis and spermatogenesis [14]. Activation of the tyrosine kinase domain of RET occurs through transient homodimerization induced by the formation of a macromolecular GFL–GFR\alpha–RET complex, which involves lipid rafts (reviewed by Saarma [15]).

Dimerization and activation of wild-type RET result in phosphorylation of its intracellular tyrosine residues, which act as docking sites for various adaptor proteins (Figure 2). For an excellent review that discusses in...
detail the signaling pathways activated by the wild-type RET receptor, we refer to Ichihara et al. [16]. GDNF-independent activation of RET has also been observed on binding of nerve growth factor to the receptor TRKA [17].

Neural crest disorders associated with RET mutations MEN2
Germine missense mutations resulting in constitutive activation of RET cause MEN2, a dominant inherited cancer syndrome that affects neuroendocrine organs [12]. Depending on the tissues affected, three different clinical subtypes can be distinguished.

(i) MEN2A, which is characterized by medullary thyroid carcinoma (MTC) in all affected individuals (100%); pheochromocytoma, a tumor of the adrenal medulla cells (50%); and hyperparathyroidism (15–30%) [18].

(ii) MEN2B, which is also characterized by MTC (100%) and pheochromocytoma (~50%); instead of hyperparathyroidism, affected individuals develop a more complex clinical phenotype including ganglioneuromas on the tongue, lips and eyelids, intestinal ganglioneuromas, thickened cornea nerves and a marfanoid habitus. MEN2B is considered to be the most aggressive subtype of MEN2 with the earliest age of onset [19].

(iii) Familial MTC (FMTC), usually considered to be the third MEN2 subtype, is characterized by the manifestation of only MTC in four or more members of an affected family.

Hirschsprung disease
Hirschsprung disease is a complex genetic disorder characterized by aganglionosis of variable length of the distal gastrointestinal tract. Genetic dissection has led to the identification of ten genes and four loci associated with Hirschsprung susceptibility [20], most of which cause
syndromic Hirschsprung disease (Table 1). Of the genes identified so far, \textit{RET} has been shown to be the most important.

Various \textit{RET} mutations have been identified and correlated with disease phenotype (Figure 3). The functional consequences of the different \textit{RET} mutations have also been characterized [12,21,22] (Table 2). A recent update on all MEN2- and FMTC-associated \textit{RET} mutations identified so far has been provided by Arighi et al. [14]. The \textit{RET} mutations associated with Hirschsprung disease can be classified according to the dysfunctional mechanism of action of the \textit{RET} protein (Figure 4, Table 3).

**Oncogenic RET activation and signaling in MEN2**

Despite the clear correlation between mutations found in MEN2 and their associated phenotypes, the molecular

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**Table 1. Genes involved in (syndromic) Hirschsprung disease**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Map position</th>
<th>Phenotype</th>
<th>Inheritance</th>
</tr>
</thead>
<tbody>
<tr>
<td>\textit{RET}</td>
<td>10q11.2</td>
<td>Non-syndromic</td>
<td>Dominant, incomplete penetrance</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Hirschsprung-MEN2A/FMTC</td>
<td></td>
</tr>
<tr>
<td>\textit{GDNF}</td>
<td>5p13</td>
<td>Non-syndromic</td>
<td>Non-Mendelian</td>
</tr>
<tr>
<td>\textit{Neurturin}</td>
<td>19p13</td>
<td>Non-syndromic</td>
<td>Non-Mendelian</td>
</tr>
<tr>
<td>\textit{EDNRB}</td>
<td>13q22</td>
<td>Shah–Waardenburg</td>
<td>Recessive</td>
</tr>
<tr>
<td>\textit{EDN3}</td>
<td>20q13</td>
<td>Non-syndromic</td>
<td>Dominant (de novo in 80%)</td>
</tr>
<tr>
<td>\textit{SOX10}</td>
<td>22q13</td>
<td>Shah–Waardenburg</td>
<td>Dominant (de novo in 75%)</td>
</tr>
<tr>
<td>\textit{ECE-1}</td>
<td>1p36</td>
<td>Congenital heart malformation</td>
<td>\textit{De novo} dominant</td>
</tr>
<tr>
<td>\textit{ZFHX1B}</td>
<td>2q22</td>
<td>Mowat-Wilson</td>
<td>\textit{De novo} dominant</td>
</tr>
<tr>
<td>\textit{KIAA1279}</td>
<td>10q21.3-q22.1</td>
<td>Goldberg-Shprintzen</td>
<td>Recessive</td>
</tr>
<tr>
<td>\textit{PMX2b}</td>
<td>4p12</td>
<td>Congenital central hypoventilation syndrome (CCHS)</td>
<td>Dominant (de novo in 90%)</td>
</tr>
<tr>
<td>Unknown</td>
<td>3p21</td>
<td>Non-syndromic, S-HSCR</td>
<td>Non-Mendelian</td>
</tr>
<tr>
<td>Unknown</td>
<td>9q31</td>
<td>Non-Syndromic, L-HSCR</td>
<td>Dominant, incomplete penetrance</td>
</tr>
<tr>
<td>Unknown</td>
<td>19q12</td>
<td>Non-syndromic, S-HSCR</td>
<td>Non-Mendelian</td>
</tr>
<tr>
<td>Unknown</td>
<td>16q23</td>
<td>Shah-Waardenburg</td>
<td>Non-Mendelian</td>
</tr>
</tbody>
</table>

\*Reviewed in Ref. [20].

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**Figure 3.** Germline missense mutations in \textit{RET} associated with MEN2 and Hirschsprung disease (HSCR). Shown are the structure of the \textit{RET} mRNA and protein. The codons mutated, the associated clinical entities, and the location of these mutations in relation to the exons and structural domains are indicated.
mechanisms that connect the mutated receptors with their different clinical subtypes are far from understood. Mutations affecting the extracellular cysteine-rich domain of RET result in the replacement of a crucial cysteine residue and the loss of an intramolecular disulfide bond, thereby facilitating the formation of an intermolecular disulfide bond between two (mutated) RET monomers and producing a constitutively activated receptor. Intracellular mutations, associated usually with FMTC and always with MEN2B, signal independently of GDNF as monomeric oncoproteins. These oncoproteins show not only an altered catalytic activity but also an altered substrate specificity because, unlike wild-type RET, they phosphorylate substrates that are usually preferred by cytoplasmic tyrosine kinases such as SRC and ABL [3]. It has been shown, however, that GDNF can further enhance RET activity of most MEN2A proteins and in MEN2B[23–25]. Furthermore, a different pattern of RET receptor autophosphorylation has been found for MEN2A-mutated (RET-MEN2A) and MEN2B-mutated (RET-MEN2B) RET proteins [26,27]. As a consequence, different sets of phosphotyrosine-mediated downstream signaling pathways will be triggered by RET mutants associated with specific disease phenotypes, which might explain the distinct clinical features observed.

This hypothesis has been partially corroborated by several studies over the past few years. For example, Liu et al. [26] have shown that, as compared with wild-type RET, RET-MEN2B mutants lack phosphorylation at Tyr1096, directly leading to a decrease in binding of GRB2 to RET[26]. RET-MEN2B oncoproteins also trigger higher levels of activated PI3K and its downstream signaling molecules [24]. In addition, expression of RET/PTC2-MEN2B, in contrast to that of wild-type RET/PTC2, results in activation of the cytoskeleton protein Paxillin [28]. Furthermore, RET-MEN2B mutants trigger higher activation of Jun N-terminal kinase (JNK) [29]. These data suggest that the high levels of activated AKT and JNK contribute to the MEN2B phenotype. Along the same lines, phosphorylation of Tyr1062 of RET and its association with

### Table 2. Subdivision of RET mutations

<table>
<thead>
<tr>
<th>Phenotype</th>
<th>Codons mutated/position of the mutation</th>
<th>Consequences of the mutation</th>
</tr>
</thead>
<tbody>
<tr>
<td>MEN2</td>
<td>Level 1: C609, E768, L790, Y791, V804, S891</td>
<td>Mild activating RET mutations predisposing to FMTC</td>
</tr>
<tr>
<td></td>
<td>Level 2: C611, C618, C620, C634</td>
<td>Moderate activating RET mutations predisposing to FMTC or MEN2A</td>
</tr>
<tr>
<td></td>
<td>Level 3: A883, M918</td>
<td>Aggressive RET mutations predisposing to MEN2B</td>
</tr>
<tr>
<td>HSCR</td>
<td>Class 1: Mutations in the extracellular domain</td>
<td>Mutations disrupting RET maturation and/or transport to the membrane</td>
</tr>
<tr>
<td></td>
<td>Class 2: C609, C611, C618, C620</td>
<td>Moderate activating RET mutations predisposing to a combination of Hirschsprung disease and FMTC or MEN2A</td>
</tr>
<tr>
<td></td>
<td>Class 3: Mutations in the catalytic domain</td>
<td>Mutations altering the catalytic activity of RET</td>
</tr>
<tr>
<td></td>
<td>Class 4: Mutations surrounding residue Y1062</td>
<td>Mutations interfering with RET substrates binding to this tyrosine</td>
</tr>
<tr>
<td></td>
<td>Class 5: Mutations in regulatory sequences</td>
<td>Changing the expression of the RET gene</td>
</tr>
</tbody>
</table>

*Mutations are subdivided according to the predisposing phenotype, the position in the coding sequence and the consequences of the mutations for the encoded proteins [21–23]. The levels of the MEN2 mutations represent a scale of aggressiveness of the associated phenotype (level 1 represents the least aggressive and level 3 the most aggressive phenotype).
SHC are stronger for RET-MEN2B than for RET-MEN2A mutants, resulting in higher activation of the Ras/ERK and the PI3K/AKT signaling pathways [25]. Also, interestingly, the ligand-induced activation of AKT by wild-type RET is dependent on the localization in lipid rafts, and this regulatory mechanism is bypassed by RET-MEN2A [30].

Finally, we should mention STAT3, a latent transcription factor that is involved in the activation of many cytokine- and growth-factor-inducible genes but that, when aberrantly activated, contributes to cancer development [31]. Transactivation of STAT3 by the RET-MEN2A mutant RETC634R is required for cellular transformation in a process that is independent of JAKs and SRC [32]. By contrast, the FMTC-associated mutants RETY791F and RETS891A implicate SRC and JAKs in constitutive activation of STAT3 [33]. Moreover, Yuan et al. [34] have demonstrated that RET-MEN2B mutants interact with and activate STAT3 more strongly than do RET-MEN2A mutants. These data support previous findings showing that RET-MEN2B mutants are specifically associated with SRC, of which STAT3 is one of the best-characterized targets [35]. Notably, we have found that STAT3 is activated only by gain-of-function MEN2-associated RET mutants, and not by ligand-stimulated wild-type RET (Ivan Plaza-Menacho, unpublished). The different mechanisms of receptor activation by wild-type RET and MEN2-associated RET mutants are shown in Figure 5.

Taken all together, these studies indicate that specific signaling profiles are connected with specific MEN2-associated RET mutations. A better understanding of the molecular mechanisms underlying this cancer
syndrome might ultimately help us to design new therapeutic strategies for this disease.

**Polymorphisms and haplotypes in RET-associated disorders**

Not only do high penetrance germline RET mutations have a key role in disease development, but also RET polymorphisms and haplotypes, containing disease-associated mutations, exist that are believed to be genetic modifiers and might be associated with an increased relative risk for the development of disorders derived from neural crest cells. These polymorphisms might interact with other genetic variants or with disease-associated germline mutations, modulating the disease phenotype or age of onset. How these polymorphisms contribute to disease development is largely unknown, but there are several possibilities: missense polymorphisms might alter the function of the protein, silent (coding) polymorphisms might be involved in aberrant splicing, and noncoding variants could regulate the level of expression. Because polymorphisms are comparatively common in the population, they could bestow a much higher attributable risk on the general population as compared with rare mutations in high-penetrance disease susceptibility genes such as RET.

**MEN2 and FMTC**

It has been suggested that the RET polymorphisms G691S and S904S have a modifier effect on the age of onset of MEN2A [36], and the same has been concluded for the single-nucleotide polymorphism (SNP) L769L in combination with the FMTC germline mutation Y791F [37]. It has also been proposed that the polymorphism G691S might be functional because it probably creates a new phosphorylation site affecting downstream signaling [36], or it might change the secondary structure of RET [38].

**Sporadic MTC**

Several RET polymorphisms have been described in association with sporadic MTC. The SNPs S836S [39,40] and IVS1–126G → T have been found to be overrepresented and associated with the somatic mutation M918T; however, other studies have not confirmed this finding [37,41,42]. A specific haplotype (the so-called ‘CGGATGCCAA haplotype’) containing the SNPs G691S and S904S has proved to be associated with sporadic MTC [38]. Both G691S and S904S has been previously associated with sporadic MTC and MEN2A [36,43].

Interestingly, SNP IVS14–24G → A, which was originally interpreted as a Hirschsprung mutation [44], has now been observed more frequently in sporadic MTC [37]. Another study has found, however, that IVS14–24G → A is not associated with either Hirschsprung or sporadic MTC [45]. Finally, a haplotype with a protective effect for sporadic MTC has been recently identified [38].

**Sporadic pheochromocytoma**

A low-penetrance RET haplotype comprising the wild-type allele at IVS1–126 and IVS1–1463 and a 16-base-pair intron-1 deletion 5’ of these SNPs is strongly associated with and overrepresented in sporadic pheochromocytoma [46]. The significant association between an individual’s age of diagnosis and genotype suggests that the additive effect of the haplotypes can modulate the age of onset of the disease.

In summary, several different RET polymorphisms and haplotypes have been associated with different MEN2-related endocrine tumors. For almost all polymorphisms analyzed however, the data are inconsistent, most probably because of the small sample sizes analyzed. Thus, the significance and mechanism of action of these potential genetic modifiers remain to be demonstrated.

**Hirschsprung disease**

Inactivating coding sequence mutations in RET are responsible for a dominant form of Hirschsprung disease (with incomplete penetrance), and mutations are found in up to 50% of the familial and 15% of the sporadic cases [47]. However, ample evidence indicates that, in addition to coding sequence mutations, noncoding regions of the RET gene also have a chief role in the development of this disease.

This was concluded from association studies on Hirschsprung populations living in The Netherlands, Italy, France, Spain, USA and Hong Kong. The same disease-associated haplotype was observed in the 5’ region of the RET locus in 56–62% individuals of European descent (including Americans) [48–55]. The same haplotype was also present in Asians, although at a much higher frequency (85%) [52,54]. The common haplotype spans a 27-kb region (4 kb of the 5’ UTR, exon 1, intron 1 [23 kb] and exon 2 of RET) and strongly indicates the existence of a regulatory mutation or mutations located either in the promoter region or in intron 1 of RET. In addition, most of the individuals found to carry the Hirschsprung haplotype were homozygous for it. Because individuals who are homozygous for the disease-associated haplotype have a tenfold higher risk of developing the disease than heterozygous carriers, a dose-dependent action of the unknown mutation has been suggested [51].

Several groups have characterized candidate disease-associated polymorphisms [49,55–57]. Two promoter SNPs, rs10900296 and rs10900297 (also named SNP-5G > A and SNP-1A > C, respectively), located just upstream of the RET transcriptional start site, have been shown to reduce RET promoter activity in luciferase reporter assays [49,55], although others have shown that this effect is dependent on the cell lines studied [57].

Two groups have described two closely located SNPs, rs2435357 and rs2506004, in intron 1 as disease-causing candidates on the basis of association studies, functional assays and comparative genomics [52,56]. In particular, the last approach seems to be useful for judging the functional relevance of noncoding mutations, because it shows that the two disease-causing candidates are located in regulatory binding sites, which in turn are in regions that are conserved among different vertebrate species. Furthermore, mutant alleles from rs2435357 and rs2506004 show the highest associated values in affected individuals, and Emison et al. [52] have found that the region containing both of these SNPs reduces promoter activity in reporter assays. In addition, Grice et al. [58] recently generated
LacZ reporter mice that express the MCS+9.7 RET intron 1 region containing both rs2435357 and rs2506004 in the context of the hsp68 promoter. Interestingly, they found that the MCS+9.7 region drives a pattern of LacZ expression that resembles the temporal and spatial expression of RET during embryonic development, which is a good indication of the relevance of this particular region for regulating RET expression. The transcription factor that binds to the sequence studied by Grice et al. [58], however, remains unidentified.

Nevertheless, many affected individuals do not have any (RET) mutations. In these individuals, other disease susceptibility factors must be present in the form of rare noncoding RET mutations or mutations at other loci either in coding or regulatory sequences.

**RET as a central factor in Hirschsprung development**

So far, almost all Hirschsprung-causing mutations are found in genes encoding proteins involved in the RET and endothelin receptor type B (EDNRB) signaling pathways [20]. At first, these two signaling pathways seemed to be completely unrelated. Now, however, growing evidence indicates that these two key signal transduction routes interact directly in the development of the ENS, at both the genetic and the biochemical level [53,59,60]. In a population of Old Order Mennonites, for example, it has been shown that specific alleles of the RET and the EDNRB loci are nonrandomly associated with Hirschsprung disease and are jointly transmitted to individuals much more often than expected [53,61].

To test the functional connection between the RET and EDNRB pathways, McCallion et al. [59] generated intercrossed mice from existing strains, resulting in offspring that were compound heterozygous for a null RET allele (truncating deletion at Lys748) and loss-of-function EDNRB alleles (s, piebald; s', piebald lethal) [59]. It was thought, in particular, that the combination of Ret and Ednrb genotypes (Ret+/Ret', Ednrb+/Ednrb') explained better the Hirschsprung transmission and phenotype observed in humans than did the independent mutants, thereby indicating interactions between the two pathways. McCallion et al. [59] also showed that 100% of the male offspring with this genotype were affected; similarly, all females manifested variable length of an aganglionic colon, although 30% had reduced clinical expression of Hirschsprung disease, which to some extent explains the sex bias observed in humans. Furthermore, compound genotypes did not have strong effects on melanocyte or renal development as compared with isolated genotypes, showing that the interaction of these genes might be specific to ENS development [59].

Work of Barlow et al. [60] in mice has elaborated on the spatial and temporal regulation of neural crest migration and ENS formation by the RET and EDNRB transduction routes. Seventy per cent of double homozygotes for Ret/C0 and Et-3sl (the null allele of the ligand of Ednrb) developed total intestinal aganglionosis, although 30% had reduced clinical expression of Hirschsprung disease, which to some extent explains the sex bias observed in humans. Furthermore, compound genotypes did not have strong effects on melanocyte or renal development as compared with isolated genotypes, showing that the interaction of these genes might be specific to ENS development [59].

**Hirschsprung combined with MEN2**

Mutations of extracellular residues Cys609, Cys611, Cys618 and Cys620, which were primarily thought to be specific for MEN2A and FMTC, have also been identified in individuals with (sporadic) Hirschsprung disease and in MEN2A families in which Hirschsprung sometimes segregates with MEN2A or FMTC [64]. These mutations have a dual impact on RET. On the one hand, they constitutively activate RET through the formation of covalent dimers; and on the other hand, they result in a marked reduction of RET expression at the plasma membrane. This leads to uncontrolled proliferation of thyroid C-cells, as seen in MEN2A and FMTC, and in apoptosis of enteric neurons, as seen in Hirschsprung disease. The reason why C-cells hyperproliferate and enteric neurons undergo apoptosis is probably due to differences in sensitivity to GDNF. MEN2A mutations such as C634R are responsive to GDNF, whereas Hirschsprung–MEN2A and Hirschsprung–FMTC mutations of RET (e.g. C620R) do not respond to GDNF [65]. Insensitivity to GDNF renders cells more prone to apoptosis, and these features are shared by all Hirschsprung-associated mutations of RET [66].

**RET as a therapeutic target**

Using drugs to target various (constitutively activated) tyrosine kinases has been a recent success in the fight against cancer; for example, Herceptin, Imatinib and Gefitinib have been successfully used in breast cancer, gastrointestinal stromal tumors and non-small-cell lung cancers, respectively [67]. This success has directed attention to RET as a possible therapeutic target in MEN2 and FMTC because so far no systematic treatment for individuals with MEN2 is available [68]. All of the crucial steps in the activation and signaling of RET might be subject to specific inhibitors.

The most potent therapeutic drugs are expected to come from tyrosine kinase inhibitors. Imatinib (Glivec or Gleevec) shows inhibitory activity against RET-MEN2A and RET-MEN2B in MTC-derived cell lines and induces degradation of RET; however, the concentrations needed to inhibit cellular proliferation are high [69,70]. Encouraging results have been obtained with another tyrosine kinase inhibitor, BAY43–9006 [71], although resistance might become a problem, as has been previously demonstrated for RET [72].

Another elegant approach to targeting RET might be the inhibition of RET dimer formation. The neutralizing, nuclease-resistant D4 aptamer can bind and inhibit
might contribute to the development of new therapeutic neural crest disorders not only has been a success in the ing the signaling properties and transcriptional regulation give rise to different (inherited) human diseases by alter-
mutations, either alone or as part of a polygenic model, can

In conclusion, RET, one might of course target downstream signaling proteins of (mutant) RET. In summary, the RET receptor represents a potential therapeutic target in the neuroen-
docrine tumors observed in MEN2, in which RET dysfunction has a crucial role.

Conclusions
In conclusion, RET provides an excellent example of how mutations, either alone or as part of a polygenic model, can give rise to different (inherited) human diseases by altering the signaling properties and transcriptional regulation of the protein encoded. Unraveling the genetic and molecular mechanisms underlying the different RET-related neural crest disorders not only has been a success in the history of genetic medicine but also has helped us to understand how these different diseases develop and might contribute to the development of new therapeutic strategies.

Acknowledgements
Supported by grants from the Groningen University Institute for Drug Exploration, The Ubo Emmius Programme of the University of Groningen and the Netherlands Organization for Scientific Research (no. 901–04–225).

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