

Hereditary neuroendocrine tumors of the gastroenteropancreatic system

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Abstract Approximately 5–10% of neuroendocrine tumors (NETs) of the gastroenteropancreatic system (GEP) have a hereditary background. The known inherited syndromes include multiple endocrine neoplasia type 1, neurofibromatosis type 1, von Hippel–Lindau disease, and the tuberous sclerosis complex. This review discusses for each of these syndromes the: (1) involved genes and specific types of mutations, (2) disease prevalence and penetrance, (3) affected neuroendocrine tissues and related clinical syndromes, (4) special morphological features of NETs and their putative precursor lesions. In addition, GEP-NETs clustering in individual families or associated with other malignancies without known genetic background are discussed.

Keywords Neuroendocrine tumors · Pancreas · Gut · Hereditary syndromes · Multiple endocrine neoplasia type 1 · Neurofibromatosis · Tuberous sclerosis complex · von Hippel–Lindau disease · Gastrinoma · Insulinoma

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Introduction

Hereditary cancer susceptibility is more frequent and variable in tumors of endocrine organs than in any other category of human neoplasms. Often, a variety of endocrine and nonendocrine tissues are involved, resulting in complex clinical syndromes.

In the digestive tract, approximately 5–10% of neuroendocrine tumors (NETs) have a hereditary background. Inherited tumor syndromes include multiple endocrine neoplasia type 1 (MEN1), neurofibromatosis type 1 (NF1), von Hippel–Lindau disease (VHL), and the tuberous sclerosis complex (TSC). In this article, we focus for each of these syndromes on: (1) the involved genes and specific types of mutations, (2) the disease prevalence and penetrance, (3) the affected neuroendocrine tissues and the related clinical syndromes, and (4) the morphological features of the respective NETs and their putative precursor lesions. In addition, suspected hereditary backgrounds [e.g., association with other malignancies, familial clustering of gastroenteropancreatic system (GEP)-NETs] are discussed.

Multiple endocrine neoplasia type 1

MEN1 is an autosomal-dominant disorder characterized by multifocal endocrine tumors affecting the anterior pituitary, parathyroids, stomach, duodenum, pancreas, adrenal cortex, thymus, and lungs. In addition, various uncommon tumoral lesions may occur in the skin, central nervous system, and soft tissues [12, 57].

The *MEN1* gene is localized on chromosome 11q13 and consists of 10 exons spanning approximately 9 kb of genomic sequence and encoding a 68-kDa protein of 610 amino acids, named menin [12, 15, 57] (Table 1). Menin is

Table 1 Genetic and clinicopathological features of MEN1 and NF1

	MEN1	NF1
Function	Tumor suppressor gene	Tumor suppressor gene
Chromosomal location	11q13	17q11.2
Gene structure	10 exons (~9 kb)	>50 exons (~300 kb)
Protein	Menin (610 amino acids)	Neurofibromin (2,818 amino acids)
Mode of inheritance	Autosomal-dominant (10% de novo)	Autosomal-dominant
Prevalence	~1:20,000–1:40,000	~1:2,000–1:5,000
Penetrance	>95% (at age 50)	~100% (in childhood)
Diagnosis	According to WHO clinical criteria (genetic testing of family members recommended)	According to WHO clinical criteria (genetic testing not recommended)
Intestinal tract		
NETs	Multiple duodenal gastrinomas	Duodenal NETs (somatostatin)
Penetrance	20–60%	~1%
Functional activity	Zollinger–Ellison syndrome	No
Malignancy	Early metastases	~20% metastases
Pancreas		
NETs	Macrotumors and microadenomatosis	Somatostatin/insulin-producing NETs or functionally active insulinomas (case reports)
Penetrance	30–70% (>90% microadenomas)	
Functional activity	Nonfunctioning>insulinoma>PETs with ectopic hormone production	
Malignancy	<10% metastases	<20% metastases
Other GEP tumors	ECL cell tumors (associated with ZES) Esophageal leiomyomas (rare)	GIST (often multiple) Neurofibroma
Tumors or endocrine hyperfunction outside the GEP	Primary hyperparathyroidism, anterior pituitary adenoma, adrenocortical tumor, thymic and bronchial NET, cutaneous lipoma and angiofibroma	<i>Cafe au lait</i> macules, neurofibroma, plexiform neurofibroma, MPNST, pheochromocytoma, optic/brain stem gliomas, bone lesions, renal artery stenosis, congenital glaucoma

NETs Neuroendocrine tumors, GEP gastroenteropancreatic system, MEN1 multiple endocrine neoplasia type 1, WdNEC well-differentiated neuroendocrine carcinoma (defined by presence of lymph node metastases or infiltrative growth in the outer smooth muscle layers), ECL enterochromaffin-like, PETs pancreatic endocrine tumors, ZES Zollinger–Ellison syndrome, NF1 neurofibromatosis type 1, GIST gastrointestinal stroma tumor, MPNST malignant peripheral nerve sheath tumor

a cell cycle-regulated nuclear protein. Menin is assumed to play an important role in pathways controlling cell growth and differentiation during embryogenesis and postnatal life. To date, menin has been shown to interact with numerous proteins involved in regulation of transcription, DNA replication, mitosis, apoptosis, genome integrity, growth factor signaling pathways, and extracellular matrix organization [12, 57]. However, it remains still unresolved why MEN1 mutations affect primarily endocrine tissues.

The prevalence of the MEN1 syndrome has been estimated to be between 1:20,000 and 1:40,000. In approximately 10% of patients, MEN1 germline mutations arise de novo without any family history [8, 12, 15] (Table 1). The MEN1 germline mutations are found spread over the entire exonic and intronic sequences and are not clustered in hotspots. Approximately 60% are truncating mutations, either frameshift (~40%) or nonsense (~20%) mutations; 20% are missense mutations; 10% are in-frame deletions or insertions, and about 10% are intronic and splice-site mutations. Large germline deletions encompassing the whole MEN1 locus have also been detected [12, 14, 15].

A stringent genotype/phenotype relation correlation could not be demonstrated. Among patients meeting the clinical criteria of a MEN1 syndrome, approximately 10% have no identifiable mutations [43]. Most MEN1-associated tumors show somatic loss of the wild-type allele (loss of heterozygosity; LOH) on chromosome 11q13, consistent with the role of MEN1 as a tumor suppressor gene [6, 26, 54, 66].

Twenty to 60% of MEN1 patients suffer from a Zollinger–Ellison syndrome (ZES), characterized by elevated fasting gastrin serum levels, a positive secretin stimulation test, and clinical symptoms such as recurrent peptic ulcer disease, gastroesophageal reflux disease, and occasionally, diarrhea [44, 87]. The gastrinomas observed in MEN1 are almost exclusively localized in the duodenum (Table 1). They are multiple and are associated with multifocal gastrin cell hyperplasia and tiny gastrin-producing microtumors. Despite their small size of 0.3 to 5 mm, the gastrinomas tend to metastasize to regional lymph nodes [3, 4, 67]. In addition, the duodenum harbors multiple tiny somatostatin cell neoplasms and multifocal somatostatin cell hyperplasia [6] (Fig. 1). Recently, molecular studies have

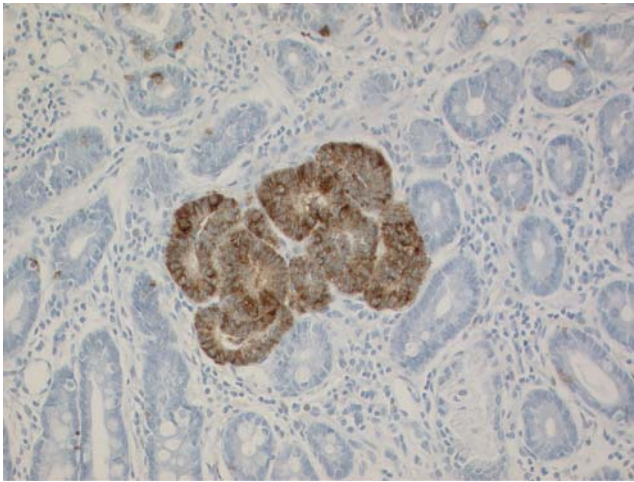


Fig. 1 Linear hyperplasia of somatostatin cells in the duodenal mucosa of a MEN1 patient with ZES

allowed the separation from hyperplastic and neoplastic lesions. LOH of the *MEN1* locus was found in approximately 50% of MEN1-associated duodenal NETs [6]. Allelic loss was detected in tumors as small as 300 μ m (gastrin) and 400 μ m (somatostatin) in diameter, which therefore represent true neoplasms. In contrast, hyperplastic gastrin and somatostatin cells lacked LOH on chromosome 11q13. These findings suggested that although the hyperplastic cells were hyperproliferative and carried the *MEN1* germline mutation, they had not yet assumed the neoplastic genotype characterized by the loss of the *MEN1* wild-type allele.

In addition to duodenal NETs, MEN1 patients with ZES may show multiple gastric NETs of the enterochromaffin-like (ECL) cells (Fig. 2). These tumors occur in a hypertrophic oxyntic mucosa and are associated with an ECL cell hyperplasia, which can be visualized using antisera against the ECL cell-specific marker vesicular monoamine transporter 2 [25] (Fig. 3). They are probably induced by both the *MEN1* germline mutation and the trophic effect of hypergastrinemia. Metastases of these ECL



Fig. 2 Cut surface of a gastric specimen from a MEN1 patient with ZES, showing multiple small tumors in the mucosa and submucosa

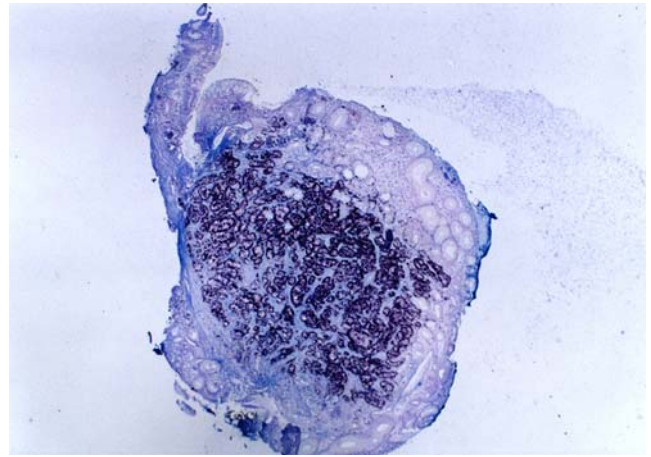


Fig. 3 Polypectomy specimen showing a small benign ECL cell tumor in a MEN1 patient with ZES (immunostaining for the vesicular monoamine transporter 2)

cell tumors are rare, and tumor-related deaths are the exception [9, 10, 12].

Pancreatic NETs lead to symptoms in 30–75% of MEN1 patients [12] and up to 10% of all pancreatic NETs may be associated with a MEN1 syndrome [57]. In a recent study on surgical specimens of the pancreas from MEN1 patients in more than 90% of the cases, numerous microadenomas (i.e., up to 5 mm in diameter) were found [5], a condition that has been called pancreatic microadenomatosis. Although this finding is a hallmark for MEN1, it is not MEN1 specific, as recently, pancreatic microadenomatosis characterized by multiple glucagon-producing or multiple insulin-producing microadenomas was described in several patients who had no evidence of MEN1 or any other known hereditary syndrome [5].

In MEN1 patients, the pancreatic microadenomas are typically multihormonal and are often associated with one or more macrotumors (diameter >5 mm; Fig. 4) [12, 42,

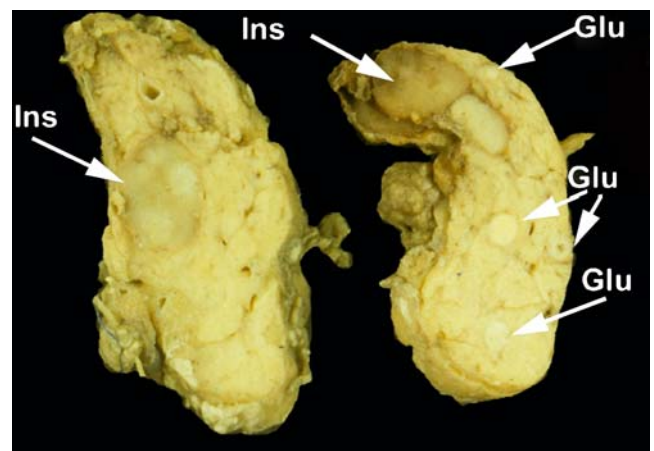


Fig. 4 Pancreatic specimen from a MEN1 patient showing two insulin-positive (*Ins*) macrotumors and four glucagon-positive (*Glu*) microadenomas

77]. The microadenomas in MEN1 are characterized, irrespective of their size (i.e., less than 200 μm), by the following features: (1) frequent expression of glucagon and/or pancreatic polypeptide, (2) trabecular growth pattern, and (3) a distinct stromal component [5, 42, 77]. Their neoplastic nature was demonstrated by LOH of the MEN1 gene [66, 82]. The MEN1-associated macrotumors (≥ 5 mm) also frequently express glucagon and pancreatic polypeptide or, rarely, somatostatin. In all these cases, the patients do not have a hormonal syndrome. However, if one of the macrotumors produces insulin, the patient presents with a hyperinsulinemic hypoglycemia syndrome. This is seen in approximately 10–25% of the cases. Only exceptionally, there are macrotumors that express hormones such as gastrin, vasoactive intestinal polypeptide, or growth hormone releasing hormone, which then may give rise to the respective hormonal syndromes. Regarding MEN1 patients with ZES, this implies that, with all likelihood, the source of hypergastrinemia is not a pancreatic gastrinoma but multiple duodenal gastrinomas.

Recently, forerunners of microadenomas were identified in the MEN1 pancreas, which have been called monohormonal islet-like endocrine cell clusters [66]. In addition, single irregularly shaped and enlarged islets with an increased number of glucagon cells were found. However, in contrast to the monohormonal islet-like endocrine cell clusters, the cells of the glucagon-cell-rich islets show retention of heterozygosity of the *MEN1* gene and are therefore still nonneoplastic in nature.

In summary, the MEN1 syndrome is characterized by multiple endocrine duodenal and pancreatic NETs expressing several peptide hormones, but preferentially either gastrin or somatostatin (duodenum) or glucagon or pancreatic polypeptide (pancreas). The duodenal NETs are associated with multifocal gastrin and somatostatin cell hyperplasia that can be considered precursor lesions. In the pancreas, the islets with hyperplastic glucagon cells are probably the precursors from which microadenomas evolve. Similar precursor changes have so far not been observed in the usually solitary nonhereditary NETs [6].

Neurofibromatosis type 1

NF1 (i.e., von Recklinghausen disease) shows an autosomal-dominant inheritance and a high penetrance: In almost all patients, there is sufficient evidence of the disorder to allow diagnosis in childhood [27]. The condition is characterized by neurofibromas, *Café au lait* patches of the skin, and bone dysplasia. Neurofibromas occur widely throughout the body, but affect mainly the skin. Other tumors are optic nerve and brain stem gliomas, pheochromocytomas, and malignant nerve sheath tumors [27] (Table 1). Gastro-

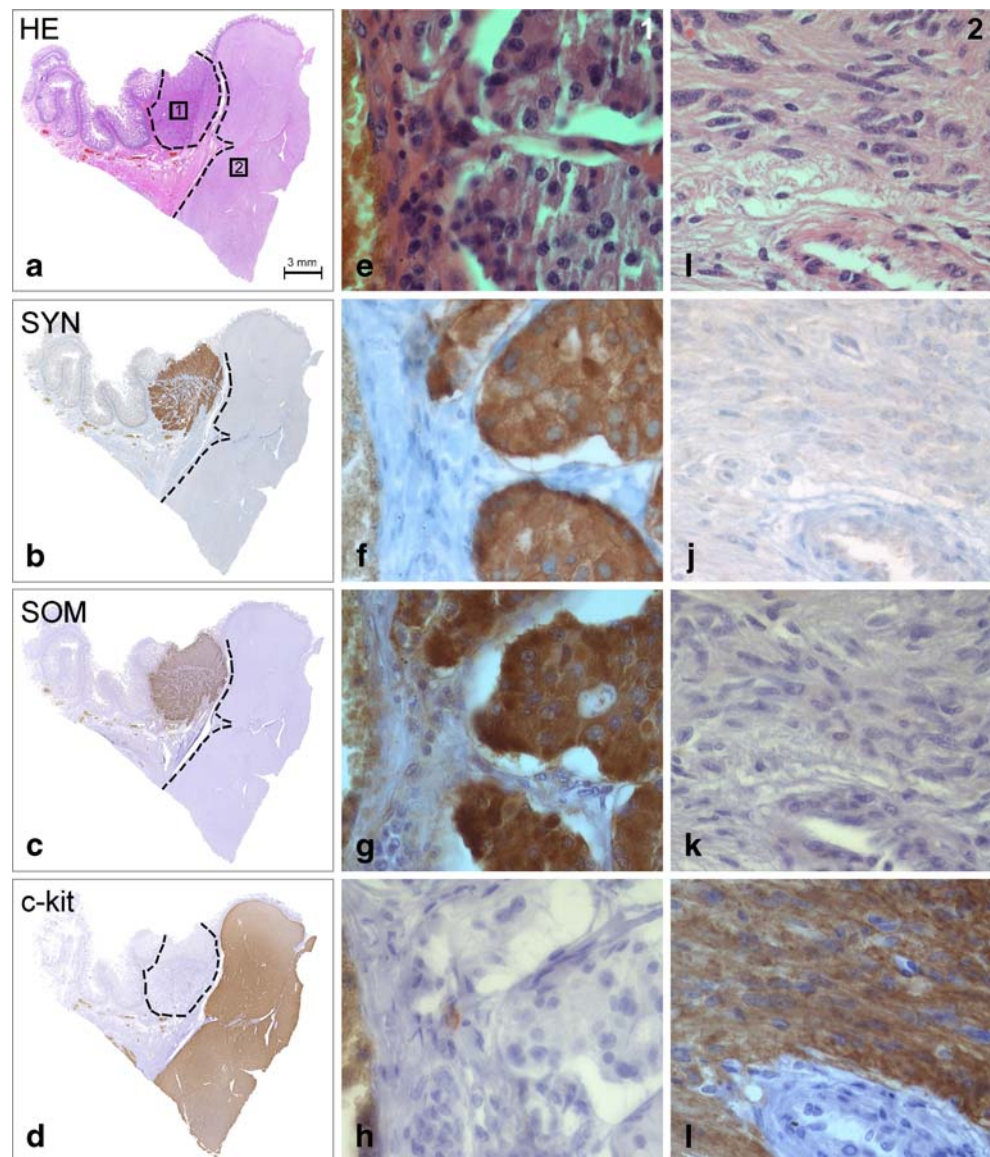
enteropancreatic NETs are rare and occur in 1% of the NF1 patients. They typically arise in the duodenum [23].

The *NF1* gene is localized on chromosome 17q11.2 and consists of more than 50 exons spanning approximately 300 kb of genomic sequence and encoding a 327-kDa protein of 2,818 amino acids, called neurofibromin [81]. Neurofibromin acts as a negative regulator of the ras-related G-proteins by increasing Ras GTPase activity, and thereby, functions at multiple levels: transcription, cell proliferation, cytoskeletal microtubule assembly. Mice that are homozygous for an NF1 mutation fail to develop the normal structure of heart and various neuroectodermal tissues and die in utero [27, 86]. Neurofibromin has been referred to as a tumor suppressor, as malignant peripheral nerve sheath tumors in NF1 patients display LOH of the NF1 gene [27].

Mutation screening is costly and not recommended clinically because of the size of the gene (50 exons) and the fact that the clinical manifestations are so characteristic. Mutations have been identified throughout the *NF1* gene; most mutations are protein-truncating mutations, consisting of nonsense, frameshift, and splice-site mutations. Five to 10% of patients have large deletions, often involving the whole gene, that are easily detectable by fluorescence in situ hybridization [36]. Large deletions of the NF1 gene have been correlated with a greater neurofibroma burden, as well as dysmorphic features, greater mental retardation, and a higher risk of developing malignant peripheral nerve sheath tumors [27]. Except for large deletions, genotype–phenotype correlations have not been described.

Our knowledge about the incidence, histopathology, biology, and functional activity of NF1-associated intestinal NETs is based on reports of single cases or small series of patients and reviews [22, 23, 75, 76]. Most of the GEP-NETs arise in the ampullary region of the duodenum and show glandular structures containing PAS-positive psammoma bodies. Immunohistochemically, they consistently express somatostatin and synaptophysin, but rarely chromogranin A. An association with the so-called somatostatinoma syndrome [i.e., markedly elevated somatostatin levels in the plasma and/or tumor, diabetes mellitus of recent onset, hypochlorhydria, gallbladder disease (cholelithiasis), diarrhea and steatorrhea, anemia, and weight loss] [24] has yet not been described. The clinical symptoms are caused by the site of the tumors, i.e., the ampulla, and lead to obstructive jaundice, intestinal obstruction, and/or bleeding. In our series of 82 duodenal NETs, we identified 15 somatostatin-producing NETs (SOM-NETs), 3 of them associated with the NF1 syndrome (Fig. 5). None of these tumors was associated with a somatostatinoma syndrome. Therefore, the high rate of NF1-associated SOM-NETs reviewed by Soga and Yakuwa [74] could not be confirmed in our series. Precursor lesions of NF1-associated SOM-NETs have not been identified. NF1-associated SOM-NETs

Fig. 5 Simultaneous occurrences of SOM-NET and GIST in a patient with the NF1 syndrome. Whole section scan (a–d) and high magnification of the SOM-NET (e–h) showing strong immunoreactivity for synaptophysin (SYN, f) and somatostatin (SOM, g) but not for c-kit (h). High magnification of the GIST (i–l) showing absence of synaptophysin (j) and somatostatin (k) but strong expression of the c-kit antigen (l)



may be associated with gastrointestinal stroma tumors (Fig. 5). In addition, gangliocytic paragangliomas and ampullary adenocarcinomas have been reported; however, it remains unclear whether these tumors are coincidental or due to the NF1 germline mutations.

Metastases have been described in 27% of SOM-NETs, mainly to the lymph nodes. They appear to be less aggressive than their sporadically occurring duodenal and pancreatic counterparts [35]. A tumor size of more than 2 cm and infiltration of the outer smooth muscle layers increase the risk of metastases ([76] and personal observations). In addition, a few cases of pancreatic NETs have been described in patients with the NF1 syndrome. These were somatostatin-producing NETs or insulinomas [29, 73, 74]. In our series of 541 non-MEN1-associated pancreatic NETs, we identified 19 somatostatin-producing NETs, none of them associated with NF1, and 162 insulinomas, one of

them in a patient with NF1. In this patient, the tumor was proven to lack expression of the wild-type NF1 allele, providing strong evidence that there is indeed a close relationship between NF1 and the development of this insulinoma [65].

von Hippel–Lindau syndrome

VHL is a dominantly inherited familial cancer syndrome caused by germline mutations in the *VHL* tumor suppressor gene. VHL disease shows marked phenotypic variability and age-dependent penetrance [55, 84] (Table 2).

The VHL gene is localized on chromosome 3p25 and consists of three exons encoding two VHL transcripts. The major transcript (isoform I) represents all three exons, whereas exon 2 is absent from isoform II. They encode two

Table 2 Genetic and clinicopathological features of VHL and TSC

	VHL	TSC
Function	Tumor suppressor gene	Tumor suppressor gene
Chromosomal location	3p25	TSC1 9q34 TSC2 16p13.3
Gene structure	3 exons	TSC1 23 exons TSC2 42 exons
Protein	pVHL30 (~28–30 kDa) pVHL19 (~18–19 kDa)	TSC1 Hamartin (~140 kDa) TSC2 Tuberin (~200 kDa)
Mode of inheritance	Autosomal-dominant (~20% de novo)	Autosomal-dominant (~two thirds de novo)
Prevalence	~1:36,000	~1:10,000
Penetrance	~50% (at age 50) >95% (at age 60)	~100%
Diagnosis	According to WHO clinical criteria (genetic testing recommended)	According to clinical and radiological criteria
Intestinal tract		
NETs	Not described	Not described
Penetrance		
Functional activity		
Malignancy		
Pancreas		
NETs	Clear cell type	Insulin->somatostatin-producing
Penetrance	5–17%	<1%
Functional activity	Nonfunctioning	Insulinoma
Malignancy	10–20% metastases	n.d.
Other GEP tumors	Pancreatic microcystic adenoma or benign serous cysts	Hamartomatous rectal polyps
Tumors/lesions or endocrine	Pheochromocytoma, parasympathetic paraganglioma, renal cell carcinoma (clear cell), CNS	Hamartomatous tubers in cerebral cortex and subependymal nodules, giant cell astrocytomas, ocular retinal astrocytic hamartoma, cardiac rhabdomyoma, angiomyolipomas (kidney/liver), hypopigmented skin macules, shagreen patches, ungual and gingival fibromas, multiple renal cysts, pulmonary lymphangioleiomyomatosis, bone cysts
hyperfunction outside the GEP	hemangioblastoma, retinal angioma, papillary cystadenoma epididymis, papillary cystadenoma mesosalpinx, endolymphatic sac tumor, capillary hemangioblastoma and cysts at various locations, hyperparathyroidism	

NETs Neuroendocrine tumors, GEP gastroenteropancreatic system, VHL von Hippel–Lindau syndrome, CNS central nervous system, TSC tuberous sclerosis complex, n.d. not enough data

gene products: a full-length 213-amino-acid protein (pVHL30; ~28–30 kDa) and a shorter protein (pVHL19; ~18–19 kDa). The *VHL* gene product has multiple functions, the best characterized of which is the role of pVHL in regulating proteolytic degradation of the subunits of the HIF transcription factors. In addition, there is strong evidence that pVHL targets other proteins for polyubiquitination [18, 48, 53, 55]. VHL-associated tumors such as renal clear cell carcinoma, hemangioblastoma, and pheochromocytoma are highly vascular and overexpress a wide range of hypoxia-inducible mRNAs, including vascular endothelial growth factor (VEGF) and VEGF receptor. A variety of VHL mutations have been described. Large genomic deletions account for up to 40% of all mutations, and the rest are divided approximately equally between intragenic missense mutations and protein-truncating mutations (nonsense, frameshift insertions and deletions, splice-site mutations). Germline VHL mutations have been

characterized in >500 patients and have provided a wealth of data for genotype–phenotype correlations. VHL mutations may cause (1) VHL diseases, (2) isolated familial pheochromocytoma (VHL disease type 2C), and (3) autosomal recessively inherited polycythemia due to homozygous missense mutations [17, 19, 55, 69, 84].

Although pancreatic involvement in VHL is very common (50–77%), the majority of lesions are cysts. These are rarely of clinical significance, and impairment of pancreatic function is uncommon. Hemangioblastoma occurs rarely in the pancreas of VHL patients [34, 55, 62].

The prevalence of pancreatic NETs in VHL patients has been reported at frequencies of 5–17%. VHL-associated NETs are usually confined to the pancreas and show a solid, trabecular, and/or glandular architecture. In approximately 30–50% of VHL patients, the tumors are multiple. Most of them reveal clear-cell cytology. Immunohistochemically, they are positive for general neuroendocrine

markers (chromogranin A and synaptophysin). A minor subset of tumor cells may be immunoreactive for pancreatic polypeptide, glucagon, somatostatin, or insulin. Clinically, however, almost all of the tumors are functionally inactive and are usually detected by routine radiological assessment of the abdomen in VHL patients [1, 51, 52, 54, 55]. Almost all VHL-related pancreatic NETs reveal LOH of the VHL gene locus on chromosome 3p25, supporting the concept that the VHL gene product acts as a tumor suppressor [54]. Although VHL-related tumors are often multifocal, precursor lesions were not identified in a systematic analysis of 14 patients [54]. VHL-related pancreatic NETs grow slowly. As with other NETs, the risk of malignancy seems to be directly proportional to the diameter of the tumor. In the largest reported series of 30 patients, the median size of the tumor in patients with no metastases was 2 cm ($n=25$) compared to 5 cm for those with metastases ($n=5$) [51].

Tuberous sclerosis complex

Tuberous sclerosis is an autosomal-dominant genetic disorder with a prevalence of 1:10,000 and a disease penetrance of approximately 100%. TSC is a multisystem disorder exhibiting a wide range of manifestations characterized by hamartomatous lesions in the brain, skin, eyes, heart, lungs, and kidneys (Table 2). Epilepsy, mental retardation, and autism are often present. A few cases of pancreatic NETs have been described in patients with TSC. TSC is caused by inactivating mutations in either the *TSC1* gene at 9q34 or the *TSC2* gene at 16p13.3 encoding the proteins hamartin (~140 kDa) and tuberlin (~200 kDa), which form a complex that affects cell growth, differentiation, and proliferation [70, 71, 78, 85] (Table 2). The diagnosis of TSC is usually based on the clinical and radiological findings. Two thirds of the cases result from new dominant mutations. Clinical manifestations may vary, but there is no well-documented report on nonpenetrance.

The TSC1/TSC2 dimer mediates a key step in the phosphoinositide 3-kinase signaling pathway. Thereby, the TSC1/TSC2 complex is involved in the regulation of the activity of mTOR, a master controller of protein translation, integrating information on growth stimuli, cellular energy levels, nutrient availability, hypoxia, and cell growth [47, 49, 68, 79].

Mutations of the TSC1 and TSC2 genes were detected throughout the genes, with some clustering but no striking hotspots, and include inactivating nonsense, frameshift, and splice-site mutations. For TSC2, additionally in-frame deletions and large deletions involving the adjacent PKD1 gene have been reported. Somatic mosaicism occurs in a minority of patients with TSC and seems to be associated with a milder phenotype. Several studies showed that

sporadic TSC2 mutations tend to be associated with a more severe phenotype than sporadic mutations of the TSC1 gene [20, 39, 46, 50]. Among patients meeting the clinical criteria of TSC, 15–20% have no identifiable mutations. These persons generally have milder clinical disease [20, 72]. Somatic mutations often involving large deletions spanning the gene (LOH) account for the majority of tumors occurring in TSC, following Knudsen's two-hit paradigm for tumor suppressor genes [30, 31, 85].

Pancreatic NETs have rarely been described in adults with TSC [21, 28, 33, 38, 41, 80]. In a case report analyzing a 6-year-old child with a de novo mutation of the TSC2 gene, who suffered from an endocrinologically silent malignant pancreatic NET, 16p13 LOH and absence of tuberlin protein expression from the tumor were demonstrated [28]. These findings provide evidence for a role of tuberlin in the pathogenesis of pancreatic NETs. Based on the small series of reported cases, pancreatic TSC-associated pancreatic NETs are insulinomas or endocrinologically silent. Some of them are malignant. Interestingly, in a postmortem series of nine TSC patients, one 21-year-old woman was found to have an incidental nonfunctioning pancreatic NET in association with multiple endocrine adenomas of the pituitary gland, adrenal, and parathyroid glands [38].

GEP-NETs with suspected hereditary background

Data regarding an association of GEP-NETs with other malignancies are limited. In the older literature, several studies indicated that patients with intestinal NETs are at increased risk for developing another primary malignancy [11, 45, 61]. Chen et al. [16] postulated that intestinal adenocarcinomas and intestinal NETs might have common endogenous or environmental risk factors. Kothari and Mangla [45] found that 36% of patients with ileal NETs (carcinoids) had an associated malignancy. However, these results could not be confirmed by two large population studies that included 1,029 and 245 patients from Denmark and the USA, respectively, and failed to confirm a general excess cancer risk in patients with GEP-NETs [7, 83].

Case reports described ileal and rectal NETs in first-degree relatives without any evidence of a known inherited disease [2, 56, 60, 64]. These observations were also confirmed in a large study including 245 patients with intestinal NETs in which 3.7% of patients had at least one first-degree relative with the same malignancy [7]. This rate was found to be much higher than age-adjusted incidence rates for intestinal endocrine tumors ($p<0.00001$ small bowel; $p=0.008$ large intestine). The findings of this study were confirmed by a nationwide epidemiological study from Sweden including 1,933 offspring and 4,713 parents with endocrine tumors at various sites [37]. Similar findings

were reported in four families suffering from lung NETs [63]. None of these studies identified environmental risk factors, which suggests a genetic background for the familial clustering of intestinal NETs that remains to be analyzed in detail.

Further clustering of intestinal NETs was very well established in patients with inflammatory bowel disease [13, 32, 58]. In addition, some case reports described GEP-NETs in patients suffering from familial adenomatous polyposis [40, 59]. However, for both conditions, it remains to be clarified whether and how a hereditary predisposition exists.

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Conflict of interest statement We declare that we have no conflict of interest.

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