7 Neuroendocrine Tumorigenesis

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Before the year 2000, gastroenteropancreatic neuroendocrine tumors (GEP NETs) were not well characterized [\[3](#page-4-0)]. The GEP NET incidence has increased worldwide over the last decades [\[2](#page-3-0), [4\]](#page-4-1). Considering the constantly evolving imaging technology, small asymptomatic lesions in the gut can be identified [[5\]](#page-4-2). NETs are a heterogeneous group found in different locations of the body, e.g., pancreas, foregut, midgut, hindgut, and lung [\[5](#page-4-2), [6\]](#page-4-3). The regional distribution of NETs over the entire body is schematically displayed in Fig. [7.1.](#page-1-0) Gastroenteropancreatic (GEP) NETs are with two thirds the most common primary NETs [[4,](#page-4-1) [7\]](#page-4-4). With one quarter of NETs, they occur in the lung as the second most location [[2\]](#page-3-0).

NETs arise from neuroendocrine-programmed cells, which are found throughout the body and are known to excessively produce and secrete molecules like neuropeptides and biologically active neuramines, such as insulin, serotonin, and somatostatin [\[7](#page-4-4)[–9](#page-4-5)]. An overview of neuroendocrine-programmed cells is displayed in Fig. [7.2.](#page-1-1)

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Fig. 7.1 Overview of NET occurrence in the human body (Adapted of Yao) [[4\]](#page-4-1). NETs are found all over the body; the gastropancreatic system is with 58% the most frequent region, followed by 27% NETs in the lung

Fig. 7.2 Schematic overview of neuroendocrine-programmed cells (Adapted from Tischler and DeLellis) [[10](#page-4-6)]

The classification of neuroendocrine tumors is based on size, tissue invasion, Ki67 index, and mitotic activity, according to the current WHO classification [[5\]](#page-4-2). KI-67 is a proliferation marker and helps to determine tumor grade and prognosis [[11\]](#page-4-7).

There is still no balanced therapy for NETs [[5\]](#page-4-2). Total resection in early stages is unchallenged in curative treatment compared to therapies, such as those with somatostatin analogues, radiotherapy, and chemotherapy, because they are still insufficient [\[4,](#page-4-1) [7,](#page-4-4) [12\]](#page-4-8). Knowledge on how to suppress hypersecretion or neoplastic growth could lead to a new therapeutic and palliative approach [\[13\]](#page-4-9). Due to the lack of mechanistic insights regarding this disease, many whole-genome sequencing approaches on NET patient tissues were initiated in order to identify mutations, which correlate with the development, prediction, or diagnosis of NETs [[14](#page-4-10)]. The most frequent gene alterations in NET patients were found in the following genes: *MEN-1* (encodes menin), *DAXX* (death domain-associated protein), *ATRX* (alpha thalassemia/mental retardation syndrome X linked), and mTOR (mammalian target of rapamycin) with the related pathway members [\[14](#page-4-10)[–17\]](#page-4-11).

7.1 MEN-1

NETs occur either sporadically or as manifestation of a syndrome, like the multiple endocrine neoplasia type 1 (*MEN-1*) syndrome [[16\]](#page-4-12). A germline mutation in the *MEN-1* tumor suppressor gene, located on the chromosome 11q13, causes this autosomal dominantly inherited condition [\[15](#page-4-13), [16\]](#page-4-12). This gene encodes the 610 amino acid nuclear protein menin, which is associated with regulation of transcription, genomic stability, cell division, and cell cycle control [\[10](#page-4-6), [18](#page-4-14)[–20](#page-4-15)]. Over 450 different germline mutations have been identified to date. About two thirds of these mutations are predicted to lead to truncations on the protein [\[18](#page-4-14)]. Either truncations or missense in *Men-1* leads to lower protein levels because of proteolytic degradation via the ubiquitin pathway [[16,](#page-4-12) [21\]](#page-5-0). Mutations in *MEN-1* are associated with a prolonged survival compared to patients without *MEN-1* mutation [\[14](#page-4-10)].

7.2 DAXX/ATRX

Likewise, NET patients with mutations in *DAXX/ATRX* have a better survival rate [\[17](#page-4-11), [22](#page-5-1)]. These mutations affect incorporation of the histone H3.3 complex into telomeres by inducing alternative lengthening of telomeres and chromosomal instability [[17,](#page-4-11) [22\]](#page-5-1).

7.3 mTOR Signaling

Some NET patients were reported to have mutations in the *PTEN*, *PI3K*, and *TSC2*, genes of the mTOR pathway [[14](#page-4-10)]. It seems that these mutations are relevant only for few NET patients because alterations in expression of mTOR pathway members are found in most patients [\[14,](#page-4-10) [23,](#page-5-2) [24\]](#page-5-3). Therefore, whole-genome sequencing of NETs can help to identify patients which would benefit from therapy with mTOR inhibitors [\[14\]](#page-4-10).

Chromosomal instability in NET patients is associated with tumor progression. As the extent of genomic changes seems to correlate with disease stage, indicating alterations accumulate during tumor progression [[10,](#page-4-6) [19\]](#page-4-16).

7.4 Biomarkers of Neuroendocrine Neoplasms

At the beginning of their formation, NETs usually do not show specific symptoms over a long time period. The low proliferation rate of most NETs might be an explanation for this phenomenon [\[25](#page-5-4)]. Due to their origin, NETs secrete different molecules. This might be a way to look for a tumor marker. Four biomarkers for NETs have been established: chromogranin A (CgA), synaptophysin (SYP), neuron-specific enolase (NSE), and urinary 5-hydroxyindole-3-acetic acid (5-HIAA) [[26\]](#page-5-5).

Neuroendocrine cells secrete their products via large dense-core or small synaptic-like vesicles. Those vesicles store proteins like CgA and synaptophysin and therefore serve as markers for neuroendocrine cells [\[11](#page-4-7)]. CgA is a member of the chromogranin family and is often observed to be elevated in serum of patients [\[27](#page-5-6)]. Immunohistochemistry for CgA can confirm the origin in the tissue [\[11](#page-4-7)]. It also seems that CgA is a prognostic marker because it positively correlates with disease progression, liver metastases, and treatment efficiency [\[8](#page-4-17), [11](#page-4-7)].

For the histopathological diagnosis of NETs, CgA and synaptophysin have to be present [\[28](#page-5-7)]. SYP is a calcium-binding integral membrane glycoprotein [[11\]](#page-4-7). It is present in epithelial and neuronal types [[10\]](#page-4-6). SYP is expressed independently from other NET biomarkers [[28\]](#page-5-7).

Neuron-specific enolase (NSE) plays a role in glucose metabolism. This enzyme was shown to be present in thyroid and prostatic carcinoma, neuroblastoma, small cell lung carcinoma, carcinoid, gastropancreatic tumor, and neoplasms with a neuroendocrine differentiation [\[26](#page-5-5), [29](#page-5-8)]. Based on its lacking sensitivity and specificity as biomarker, it is mostly used to confirm the diagnosis or to control the treatment efficacy during follow-up [\[29](#page-5-8)].

Serotonin is one of the most hypersecreted hormones in NETs. 5-Hydroxyindoleacetic acid (5-HIAA) has serotonin as substrate and is excreted via the urine, where high levels of 5-HIAA are detected in patients with NETs [[30,](#page-5-9) [31\]](#page-5-10). Although tryptophan- or serotonin-rich food can elevate 5-HIAA levels, the specificity of this marker is about 88% in NETs [[31\]](#page-5-10).

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