

Somatostatin Signalling in Neuroendocrine Tumours

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Contributor: Olesja Rogoza

Somatostatin (SST) is a small peptide that exerts inhibitory effects on a wide range of neuroendocrine cells. Due to the fact that somatostatin regulates cell growth and hormone secretion, somatostatin receptors (SSTRs) have become valuable targets for the treatment of different types of neuroendocrine tumours (NETs).

neuroendocrine tumour

somatostatin

somatostatin receptor

somatostatin analogue

1. Introduction

Neuroendocrine tumours (NETs) represent a heterogeneous group of neoplasms and can originate from neuroendocrine cells in any organ of the body ^[1]. For all NETs, overall survival rates are approximately 55% and 45% five and ten years after diagnosis, respectively ^[2]. The classification and clinical picture of each NET differs based on the organ of origin; however, all NETs share the expression of somatostatin receptors (SSTRs), which have become valuable targets for somatostatin analogue (SSA) therapy. Symptom management is the most prevailing therapy in patients with functioning NETs.

2. Somatostatin Signalling

Somatostatin (SST), also known as the somatotropin release-inhibiting factor (SRIF) or growth hormone-inhibiting hormone (GHIH), is a cyclic peptide that exerts inhibitory effects on the endocrine and exocrine hormone secretion ^{[3][4]}. The growth hormone (GH), prolactin (PRL), thyrotropin (TSH), cholecystokinin, gastric inhibitory peptide, neurotensin, motilin, gastrin, secretin, glucagon, insulin, pancreatic polypeptide, and cytokines in immune cells are all inhibited by SST ^{[3][5]}. The effects of SST on exocrine hormones include the suppression of amylase secretion from salivary glands; the inhibition of hydrochloric acid, pepsinogen, and intrinsic factors in the gastrointestinal mucosa; the reduced secretion of pancreatic enzymes and bicarbonate, and the reduced secretion of bile from the liver. SST also prevents the absorption of glucose, fat, and amino acids, helps to regulate gastrointestinal motility by delaying late gastric emptying, weakens gallbladder contractions, and lengthens small intestinal transit time. SST also reduces the time between migrating motor complexes and accelerates early stomach emptying. Immunoglobulin production and lymphocyte proliferation have both been found to be inhibited by SST in lymphoid tissues ^[5].

SST is produced in many locations of the body, primarily in the pancreas, gastrointestinal (GI) tract, central nervous system (CNS), and hypothalamus ^[6]. Both isoforms of SST (SST-14 and SST-28) are derived from a 116-amino

acid precursor protein, known as pre-prosomatostatin, which is cleaved into 92-amino acid prosomatostatin. To generate SST-14 and SST-28, prosomatostatin undergoes C-terminal post-translational processing, which results in the production of a predominant 14-amino acid molecule as well as a larger, N-terminally extended 28-amino acid form (**Figure 1**) [7][8]. While the shortest isoform is secreted mainly from the β -cells of the pancreas, the SST-28 is the product of GI cells [9][10]. SST-14 has wide-ranging effects, including the inhibition of GH, TSH, and corticotropin (ACTH) within the pituitary, as well as the inhibition of glucagon and insulin in the pancreas [11]. SST-28 refers to the endogenous pro-form of SST, which regulates the inhibition of the hormones previously mentioned in the context of SST-14 [12]. SST-28 is known to be more potent than SST-14 with respect to its effect on GH, PRL, insulin, glucagon, TSH, and gonadotropins (LH and FSH) secretion [13]. It is estimated that 65% of the circulating SST is produced and secreted by the D-cells of the GI tract, 30% is produced by the CNS (hypothalamus and amygdala), and the remaining 5% is produced by pancreatic β -cells [7][14]. Both SST active forms are stored in secretory granules and have a short (~ 1 min) bioactive half-life time ($t_{1/2}$) once released into the circulation [3][10].

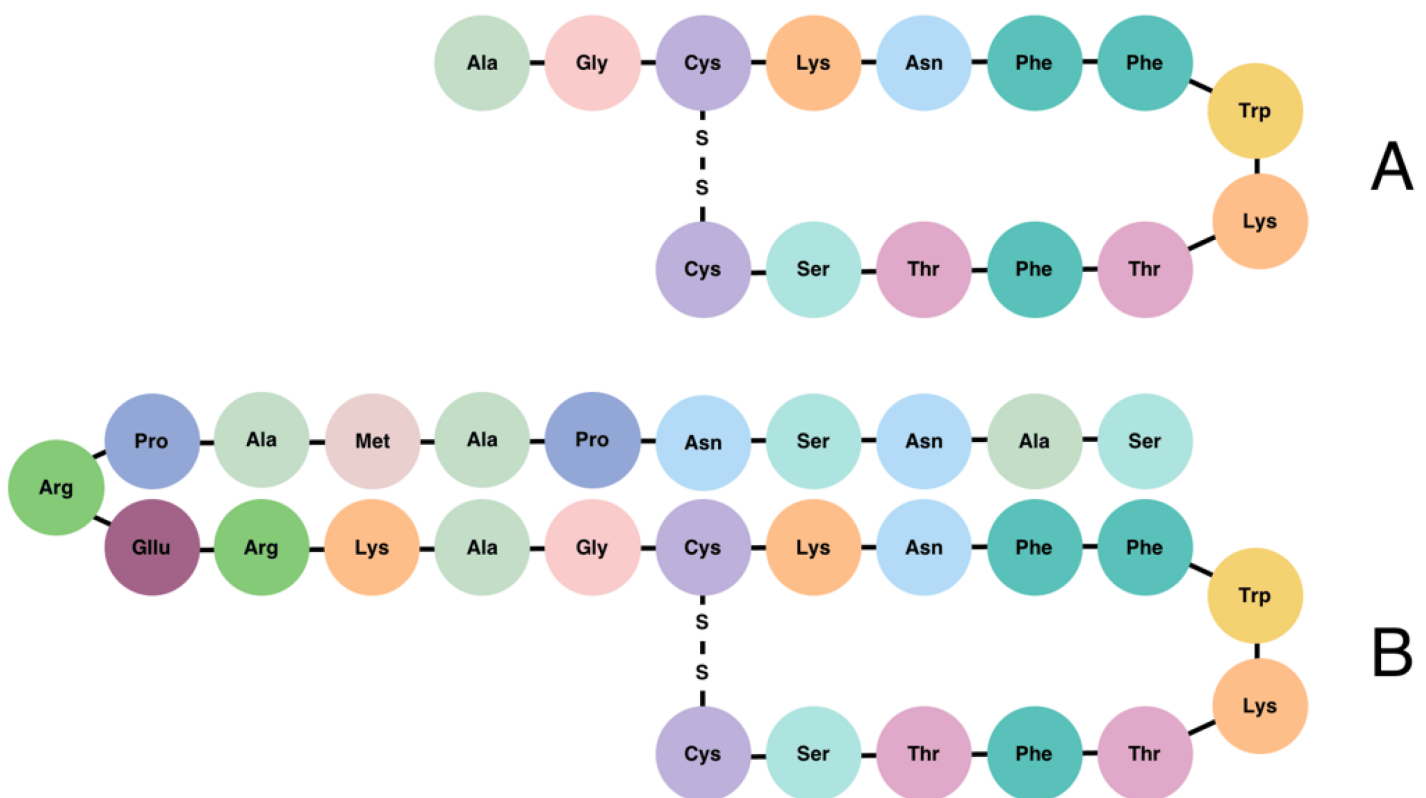


Figure 1. Structure of somatostatin-14 (A) and somatostatin-28 (B).

The activity of SST is mediated by its binding to five subtypes of SSTRs, each encoded by five different genes segregated on chromosomes 14, 17, 22, 20, and 16, respectively [15]. The SST receptor subtypes (SSTR1 through SSTR5) share signalling pathways and structural features [16]. Two isoforms of SSTR2 exist (SSTR2A and SSTR2B), and are produced via alternative splicing [17][18]. These variants of SSTR2 differ in the length of their C-terminal cytoplasmic tails as well as their ability to couple to adenylyl cyclase; as a result, SSTR2A and SSTR2B may activate alternative signal transduction pathways [19][20]. SSTRs belong to the superfamily of G-protein-coupled receptors (GPCRs) and play a crucial role in vertebrate development, metabolism, and growth [21]. GPCRs

represent the largest family of human membrane proteins, characterized by a core of seven transmembrane helices that are connected by three extracellular loops (ECLs) and an amino terminus [15][22]. The activation of SSTRs usually results in the inhibition of adenylyl cyclase and the reduction in intracellular Ca^{2+} , which result in the inhibition of cell proliferation and the secretion of signalling molecules [23][24]. Firstly, SST activates the SSTR which interacts with the G protein, consisting of α -, β -, and γ -subunits, thereby modulating several downstream second messenger systems. The α -subunit reduces the affinity for guanosine diphosphate (GDP), and because the concentration of guanosine triphosphate (GTP) is higher in the cytoplasm, GDP is, thus, replaced by GTP. Thereafter, the $\text{G}\alpha$ protein dissociates from the receptor and subunit complex and modulates the activity of several intracellular pathways [15].

SSTRs are expressed throughout many tissues of the body, including the hypothalamus and pituitary, GI tract peripheral organs, and pancreas, as well as kidneys, thyroid, lungs, and immune cells. Moreover, SSTR expression has been reported in numerous types of tumours [15]. In the GI tract, SST regulates the release of gastric acid by a negative feedback mechanism of paracrine effects. The feedback pathway involves stomach D-cell SST release in response to direct stimulation by gastrin, and this indirectly inhibits further gastric release from G-cells [25]. Within the hypothalamus, SST indicates the inhibition of GH, LH, and TSH release from the pituitary [26]. SST binds to the β -cells of the pancreas to inhibit voltage-gated calcium channels, resulting in the suppression of the early insulin response to glucose and, thus, downmodulating the storage of energy in adipose tissue [27]. SST suppresses several immune functions, such as lymphocyte proliferation, immunoglobulin production, and the release of proinflammatory cytokines such as interferon- γ (IFN γ) and interleukin-8 (IL-8) [28][29]. The effect of SST under physiological conditions is partially determined by the types of SSTRs expressed on the tissue's surface[6]. For instance, SSTR2 and SSTR5 have been reported as the most abundantly expressed receptors. Both show inhibitory effects on GH and ACTH within the pituitary gland, on insulin, within the β -cells of the pancreas, and on glucagon-like peptide 1 (GLP-1), IFN- γ , and reduce the secretion of gastric acid [16][24][30]. SSTR2 is extensively expressed in pulmonary endocrine tumours, including typical and atypical carcinoids and non-endocrine lung cancers such as adenocarcinoma and small cell lung cancer [31]. Receptor expression profiles differ between patients and even between tumours within the same patient. SSTR2 is expressed in about 80% of GI tract and pancreatic endocrine tumours according to Reubi and colleagues [32]. Among the tumours, SSTR2A is the most commonly expressed receptor subtype. The expression of SSTR2A has been reported in gastrinomas, insulinomas, gliomas, medulloblastomas, paragangliomas, and neuroblastomas [33][34]. Neuroblastomas are the most common malignancy among children. These types of tumours are typically associated with a high expression of SSTR1 and SSTR2, which usually indicates a good prognosis for patients [35]. SSTR2A correlates with the overall survival rate in patients with medullary thyroid carcinoma and is considered as a favourable prognostic marker in stage IV patients [36]. The activation of SSTR1 shows antiseecretory effects on the GH, PRL, and calcitonin, whereas SSTR3 regulates antiproliferative signalling and induces apoptosis in several cell types [30][37]. The role of SSTR4 remains mostly unknown, but it may be linked to the inflammation of the intestine. SSTR4 has been identified as a key player in the inflammatory effects exerted by SST, either through the direct targeting of inflammatory cells or via the indirect modification of cells that synthesize and release pro-inflammatory mediators [38]. Pro-inflammatory mediators are released from capsaicin-sensitive sensory nerve endings during inflammation.

These mediators primarily include tachykinins (substance P and neurokinin A) and the calcitonin gene-related peptide, which may be involved in the sympathetic reflex inhibition of GI propulsion, ultimately initiating an inflammatory cascade [38][39]. The expression of SSTR4 has also been detected in the lungs, heart, and placenta [16].

Expression levels of SSTRs have been reported in the majority of NETs and non-neuroendocrine tumour types, including pancreatic NETs (PanNETs), pituitary NETs (PitNETs), and gastroenteropancreatic NETs (GEP-NETs), as well as hepatocellular carcinoma and breast cancer [23][40][41][42]. Since SSTRs are located on the surface of tumour cells, they have the potential to serve as diagnostic markers and be used for SSA treatment strategies [38].

3. Neuroendocrine Tumours

NETs are a heterogeneous group of generally slow-growing neoplasms of epithelial origin with variable clinical prognoses and behaviour [43][44]. NETs, not to be confused with neuroendocrine carcinomas (NECs), are believed to originate from hormonally programmed neuroendocrine precursor cells that undergo tumourigenic mutational events. For this reason, NETs mostly consist of well-differentiated neuroendocrine cells. Normally, neuroendocrine cells can be either diffusely distributed in the mucosal membrane, as in the case in the digestive system, or they can form organised cell clusters or organs of endocrine function, such as pancreatic islets or the pituitary gland [1]. Neuroendocrine cells are widely distributed in the human body and, for this reason, NETs can occur in virtually any location. However, NETs occur most commonly in the GI tract, pancreas, and lungs [45].

NETs are generally subdivided by their proliferative activity using the mitotic and/or Ki67 index. G1 NETs are classified by <2 mitoses/10 high-power fields and a Ki-67 index of <3%, G2 NETs are classified by 2–20 mitoses/10 high-power fields or a Ki-67 index of 3–20%. Well-differentiated G3 NETs are classified by >20 mitoses/10 high-power fields or a Ki-67 index of >20%, and poorly differentiated G3 NECs are classified by >20 mitoses/10 high-power fields or Ki-67 and expression alterations of p53 and Rb1 [1][46][47][47]. Further classification depends on tumour location and functionality, and it is not uniform across different centres.

Due to their hormonal origin, NETs can synthesise and secrete cell-type-specific peptide hormones and neuroamines, and, therefore, are characterised as functioning NETs [48]. For example, PitNETs can additionally secrete GH, PRL, or other pituitary hormones, thereby elevating hormone concentrations in the circulation, leading to hormonal dysregulations and characteristic clinical syndromes [49][50]. About 60–90% of PanNETs are non-functioning and do not show significant symptoms. Functioning PanNETs are uncommon and are usually associated with the increased secretion of various hormones, including insulin, gastrin, ghrelin, vasoactive intestinal peptide (VIP), glucagon, and SST [51]. Most GEP-NETs are non-functioning and present moderately late; in turn, functioning tumours cause distinct clinical syndromes resulting from the production of various bioactive peptides or amines. For instance, active gastric NETs (GNETs) are known to secrete histamine, yet the duodenum produces secretin, gastrin, gastric inhibitory polypeptide, and motilin [52]. Furthermore, NETs have the capacity to modify secreted hormones and peptides at the genetic level. For example, gastrin may appear in five different forms in the circulation, due to different splice variants in NETs [53]. Non-functioning NETs are not associated with

specific hormonal changes or clinical syndromes. As a result, non-functioning NETs are usually diagnosed in the later stages after the occurrence of symptoms related to tumour mass effects or metastases [49][50]. The liver is the most common site of NET metastasis. Due to improved diagnostic tools and an increase in early diagnosis, the majority of cases at the time of diagnosis are graded as G1; most of these are non-metastatic, but only by a small margin [54].

Biochemical and tissue markers in GEP-NETs are applied for diagnostic, prognostic, and predictive intentions [51][55]. Chromogranin A (CgA) is considered to be one of the most implemented biomarkers in the diagnosis and prognosis of NETs. Despite an overall diagnostic sensitivity of 73% and a specificity of 95%, the use of CgA as a biomarker for NETs has gradually declined in recent years. The accuracy of CgA can vary largely based on the type of NET and it can be falsely elevated in the presence of various conditions, such as atrophic gastritis and liver disease, or in cases involving treatment with proton pump inhibitors [56][57][58][59][60]. Other general markers, including the Neuron-Specific Enolase (NSE) and pancreatic polypeptide (PP), are mainly elevated in poorly differentiated NETs and non-functioning NETs, respectively [55]. The serotonin metabolite 5-hydroxy indole acetic acid (5HIAA) can be measured in urine or blood plasma and is used as a diagnostic and follow-up marker for patients with midgut NETs. However, the specificity of 5HIAA is influenced by the fact that its hypersecretion has also been observed in patients with carcinoid syndrome [61][62][63]. Circulating biomarkers, such as gastrin, insulin, glucagon, SST, and VIP, are specific PanNET biochemical markers used for diagnosis and treatment monitoring [64]. Several novel biomarkers have been discovered to improve the early diagnosis and monitoring of NETs, including programmed death ligand-1 and glucose transporters type 1 within lung NETs (Lu-NETs) and PanNETs, as well as survivin, an inhibitor of apoptosis, in Lu-NETs, PanNETs, and GI-NETs [65]. Circulating tumour cells (CTCs) are a relatively novel biomarker for NETs; the elevation of CTCs is measured based on the expression of the epithelial cell adhesion marker [66][67]. The absence of CTCs strongly correlates with 5HIAA and liver metastases extension, indicating disease progression. Therefore, the absence of CTCs may be considered as a prognostic biomarker [67]. Despite promising results of existing research, additional data and evidence in this regard remain sparse. Further studies are necessary to convincingly demonstrate the clinical usefulness of CTCs as a biomarker for NETs.

Although NETs are mostly sporadic, they can be associated with multiple inherited syndromes, including multiple endocrine neoplasia (MEN) types 1, 2, and 4, as well as Von Hippel–Lindau syndrome, neurofibromatosis 1 (NF1), and tuberous sclerosis. These syndromes are caused by dysregulating mutations in oncogenes, proto-oncogenes, tumour suppressors, or cell cycle regulator genes. As a result, these dysregulations can cause cell tumourous growth, among other symptoms [53][68].

NETs are extensively vascularised tumours. They typically have an increased expression of vascular endothelial growth factor (VEGF) and VEGF receptor (VEGFR) subtypes [46]. Interestingly, VEGF expression has been observed to be higher in well-differentiated NETs, compared to poorer differentiated counterparts. The intratumoural vessel density in NETs is approximately 10-fold higher as compared with carcinomas, which elevates not only NET growth, but also the release of secretory products into the bloodstream [69].

4. Somatostatin Signalling in NET Development and Prognostics

Somatostatin signalling is involved in many cell regulatory circuits that can inhibit tumourigenesis. Therefore, shifts in SST signal transduction pathways can significantly contribute to NET development within an affected tissue. The binding of SST to SSTR inhibits the activity of adenylyl cyclase, downregulating the concentration of the second messenger cAMP and following intracellular calcium, leading to a decreased hormone secretion [70][71]. This is particularly important in hormone-producing NETs, where SSA treatment can help to normalise adverse effects of excessive hormone levels in the body. SST signals are also important cell cycle regulators; a ligand binding to SSTR activates protein tyrosine phosphatases SHP-1 and SHP-2, leading to a decreased cell proliferation via the upregulation of cell cycle inhibitors p27 and p21, as well as the inhibition of PI3K/AKT and MAPK, thereby attenuating cell division [16][70]. This property could indicate the possibility to regulate other tumour growth through targeting the SST signalling pathway, especially since SSTRs are expressed also in breast, thyroid, prostate cancer tissues, glioma, hepatocellular carcinoma, and other tumours [72]. Other hallmarks of tumourigenesis, such as angiogenesis and cell migration, are also regulated by SST signalling. The VEGF platelet-derived growth factor (PDGF), insulin-like growth factor, and basic fibroblast growth factor have been shown to enhance the neovascularization and cell growth of tumours [73][74][75][76]. On a cell signalling and functional level, SST and SSTR significantly inhibit hormonal secretion, cell cycle progression, angiogenesis, and cell migration. However, the role of SST signalling and SSTR in NET development, the response to SSA, and prognosis highly depends upon SSTR distribution in different tumour types and additional intrinsic factors of specific tumours [40].

Many studies have assessed the expression of SSTRs in different tumours. The techniques used in these studies include PCR-based methods, immunohistochemistry (IHC), and somatostatin receptor scintigraphy (SRS), each of which has specific advantages and drawbacks [77][78][79][80][81][82][83][84][85]. PCR-based expression evaluation methods remain cost effective, easy to perform, and are scalable. This method is also easily interpreted without highly sophisticated professional experience or background, compared to IHC and imaging. PCR gives bulk representative values for tumour tissue expression levels. However, in several studies, good concordance has been demonstrated between RT-PCR and IHC data [79][86]. On the other hand, IHC and imaging allow for a more precise evaluation of expression levels. However, these techniques are more costly and are highly dependent on available equipment and professional expertise. In IHC studies, the antibodies used for the evaluation can affect the obtained results [87][88]. Nonetheless, previous reports have successfully reported on the expression of SSTR1, SSTR2A, SSTR3, SSTR4, and SSTR5. In studies where all SSTRs have been assessed simultaneously, it has been demonstrated that SSTR4 is not expressed or is expressed in lower levels in NETs compared to other SSTRs [79][80][86]. The most expressed receptor subtypes are SSTR2A and SSTR5, following by a slightly lower abundance of SSTR3 and SSTR1 [79][80][86][89]. However, this information is still highly dependent upon the tumour type and methods used for the estimation of the expression level. Aside from the methodological differences described above, the subgrouping or classification of tumour types and preoperative SSA treatment can have a significant impact on the obtained results, which can hamper the generalisation of these findings in overarching conclusion.

In many studies, all NET types are analysed together, which is understandable given the rarity of these tumours. However, this can bias the results, since tumour development in specific tissue types causes intrinsic functional differences in tumour cells originating from specific cell types. Additionally, in many reports, the preoperative status of SSA is different; some studies include only SSA-treated patients, whereas others include both SSA-treated and naive cases without properly adjusting for the potential therapeutic impact. It has been shown that SSA has the ability to downregulate SSTR expression, which means that an SSA pre-treatment can significantly affect SSTR expression [82][83].

Nonetheless, it has been widely proven that a higher SSTR expression [90] is characteristic of well-differentiated NETs with tumour grades G1 or G2 [42][84][91]. Additionally, several reports have shown that NET patients with a higher tumour SSTR expression have improved survival [42][77][92][93]. Intriguingly, the better prognosis is also observed in those studies where subjects did not receive SSA therapy or only a small fraction of patients were treated with SSA [42][92][93]. This raises the question of how native SSTR expression without SSA therapy might contribute to better outcomes for NET patients. One plausible answer could be that an SSTR, in the absence of exogenous SSA, still receives endogenous somatostatin signals and this slows the tumour progression. It has been demonstrated that pancreatic NET metastases express lower levels of somatostatin, and the knockdown of somatostatin in pancreatic NET cell lines increases metabolic activity, viability, and growth [94].

In addition to providing prognostic insight on NET development, SSTR expression could also serve as a molecular determinant for predicting the SSA response for personalized therapy choices. This approach has been widely discussed for pituitary NETs, where SSTR expression levels are widely correlated with SSA treatment efficacy [95][96]. Other intrinsic tumour components such as genetic predisposition and somatic variation, expression pattern alterations and cellular patterns of dense or sparse granulation can be linked to the SSA response [97][98]. Recently, specific miRNA subtypes have also been shown to be dysregulated by SSA treatment or even downregulate SSTR, promoting tumour progression and indicating the presence of other crucial molecular markers in NETs [99].

The heterodimerization of SSTRs with dopamine receptors has also been widely demonstrated and has the potential to significantly affect NET pathophysiology and prognostics [100]. This has led to the development of chimeric somatostatin–dopamine agonists that could more effectively inhibit tumour progression [101]. Although the first generation of these chimeric compounds demonstrated promising results in preclinical studies, results from human studies were disappointing [100][102][103]. Currently, the second generation of chimeric agonists is under investigation and has shown positive effects both in cell lines and in healthy human trials [104][105]. Research in the field of chimeric somatostatin–dopamine agonists could bring additional improved therapeutic options for NET patients in the future.

Additionally, in recent years, epigenetic regulation in NETs has been implicated as a major tumorigenesis mechanism. For example, it has been demonstrated that the treatment of pancreatic NET cell lines treated with epigenetic modulators can result in the redifferentiation of human primary PanNETs. The upregulation of SSTR expression was observed in these studies, indicating that SSTR expression can be regulated by epigenetic tumour development mechanisms [106][107]. Specifically, valproic acid was used to upregulate SSTR2 expression and

provide further benefit to SSTR-targeted therapies [108]. Other epigenetic agonists have been demonstrated to inhibit cell proliferation, reduce the progression and metastasis-forming capacity, induce apoptosis, and promote cytotoxic effects in various NET cell lines [109][110]. So far, despite promising evidence in preclinical settings, clinical trials have not confirmed the benefits in patient outcomes. Eight patients have showed that valproic acid has neutral to moderate effects, with an overall good tolerance to the treatment [111]. However, 15 patients with metastatic NETs was demonstrated that the histone deacetylase inhibitor depsipeptide was cardiotoxic [112]. In a separate study of 15 patients receiving Panobinostat, no significant benefits were demonstrated [113]. Taken together, it was demonstrated that a further investigation of epigenetic agents is needed to determine the best strategy for improving NET control.

Additionally, in some studies, combination therapy using SSA with mTOR inhibitors showed some promising results. Overall, SSTR and somatostatin signalling is an important molecular factor that can affect the pathophysiology of NETs and should be considered as a target for SSA therapies for NET treatment.

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