REVIEW

Neuroendocrine neoplasms: current and potential diagnostic, predictive and prognostic markers

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Introduction

Neuroendocrine neoplasms (NENs) represent a heterogeneous group of rare neoplasms, which originate from enterochromaffin cells that are located throughout the whole body. NENs located in the gastrointestinal tract and pancreas are also referred to as gastroenteropancreatic neuroendocrine neoplasms (GEP-NENs) (Modlin et al. 2008, Xavier et al. 2016). The annual NENs incidence increases over time, although it is not known whether this is a true increase in NEN incidence, the result of increased use of (improved) diagnostic procedures or a combination of both (Xavier et al. 2016, Dasari et al. 2017).

NENs can be divided into ‘functional’ and ‘nonfunctional’ tumors. Functional NENs are able to produce, store and secrete bioactive peptides and can present with specific clinical syndromes related to the biological effects of these substances. Nonfunctional NENs can present with mechanical effects, that is, bowel obstruction or ischemia, but are also frequently discovered by the incidence during diagnostic procedures (Hofland et al. 2018). The clinical course of NENs can be highly variable and includes a spectrum ranging from well-differentiated, indolent growing tumors to...
aggressive, highly proliferative tumors. Around 60–80% of NENS are metastasized when diagnosed (Modlin et al. 2010a). The overall 5-year survival rate of patients with NENS ranges between 35 and 82% in well- to moderately differentiated NENS and between 4 and 38% in poorly differentiated NENS (Pape et al. 2004, Yao et al. 2008).

Survival is specifically determined by several parameters including the localization of the primary tumor (overall 5-year survival: 75.0% for jejunoileal, 42.9% for pancreatic NENS), tumor size, presence of vascular invasion, necrosis, surgical resection margin, metastasis, grade and stage of disease (particularly in G1/G2 NENS with localized, regional and distant disease survival rates of 223, 111 and 33 months have been reported respectively; (Pape et al. 2004, Veenendaal et al. 2006, Gao et al. 2018)). Since several factors are involved in NENS patients’ survival, the use of nomograms that combine clinical, biochemical, histological and therapeutic characteristics has been proposed (Modlin et al. 2010b, Clift et al. 2017). These nomograms are mostly not validated yet and currently not used in clinical practice. Appropriate standardized diagnostic procedures are required to assure early diagnosis, monitor disease progression and guide an optimal treatment (Oberg et al. 2015). An ideal biomarker should have a high sensitivity for the diagnosis of NENS, to predict tumor clinical behavior and for the response to treatment (Turner et al. 2006). To date, only few diagnostic and therapeutic (reflecting treatment response) markers are available with limited performance, but new biomarkers are in development, including peptides/growth factors, DNA/RNA markers and circulating tumor cells. In this review, we describe the currently available and potential future diagnostic, prognostic and therapeutic biomarkers in NEN, with a focus on circulating factors.

Search strategy

We searched the Cochrane Library, MEDLINE and EMBASE up to March 2017. Publications from the past 5 years were predominantly selected. The reference lists of articles identified by this search strategy were screened for relevant publications. Commonly cited and important older publications were also included. Some review articles, but especially original articles, were included.


Currently available biomarkers for NENs

Currently used biochemical markers in NENS are usually hormones or amines secreted by NEN cells, which can be influenced by several factors including co-existent disease(s) and drugs, as shown in Table 1. These biomarkers add to diagnosis, but are insufficient to accurately diagnose NENS, to identify the primary tumor site or to differentiate tumor grading, especially due to sensitivity and specificity issues (Oberg et al. 2015). Despite this, some of them are considered for the diagnosis and follow-up of NENS according to several clinical guidelines as shown in Table 2. In Table 3, a summary of the sensitivity and specificity of currently used biomarkers in NENS is depicted.

Chromogranin A

Chromogranin A (CgA) is a protein expressed in the secretory granules of normal and neoplastic neuroendocrine cell types. It is released with peptide hormones and biogenic amines and is also the precursor for functional neuroendocrine peptides (Eskeland et al. 1996, D’Amico et al. 2014). Several guidelines recommend plasma CgA measurement during diagnosis, treatment and follow-up in GEP-NENS (Table 2). Baseline and serial CgA may predict clinical outcome, prognosis and tumor response (Arnold et al. 2008) and may be indicative for local progression in patients with liver involvement (Bajetta et al. 1999). Additionally, progressive decrease in CgA levels may be observed in patients with extensive metastatic spread and loss of neuroendocrine differentiation (Zatelli et al. 2007).
Table 1  Foods, drugs and other conditions which interfere with the results of current NENs biomarkers (Schwartz 1983, Batterham et al. 2003, Jin et al. 2015, Gut et al. 2016).

<table>
<thead>
<tr>
<th>Current marker</th>
<th>False-positive results</th>
<th>False-negative results</th>
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<tbody>
<tr>
<td>5-HIAA</td>
<td><strong>Foods and drinks:</strong> Fruits (banana, kiwis, avocado, pineapple, plums, tomato, aubergine, figs, grapefruit, melon), red wine, coffee, tea, chocolate, cheese, vegetables (black olives, spinach, broccoli, cauliflower)</td>
<td><strong>Drugs:</strong> Paracetamol, naproxen, phenacetin, fluorouracil, testosterone, methysergide, acetonilide, reserpin, atenolol, pindolol, oxprenolol, ephedrine, diazepam, methocarbamol</td>
</tr>
<tr>
<td>Cg-A</td>
<td><strong>Foods and drinks:</strong> 30–90 min after a meal</td>
<td><strong>Diseases:</strong> Low proliferative, rapidly proliferating and poorly differentiated NENs</td>
</tr>
<tr>
<td>Pancreatic polypeptide</td>
<td><strong>Drugs:</strong> Proton pump inhibitors, histamine type-2 receptor antagonists</td>
<td><strong>Others:</strong> Strenuous exercise before the test</td>
</tr>
<tr>
<td></td>
<td><strong>Diseases:</strong> Atrophic gastritis, pancreatitis, chronic hepatitis, liver cirrhosis, impaired kidney function, chronic heart failure, acute coronary syndrome, untreated hypertension, rheumatoid arthritis, irritable bowel syndrome and inflammatory bowel disease</td>
<td><strong>Others:</strong> Increased age, exercise</td>
</tr>
</tbody>
</table>

However, CgA is elevated in only 60–80% of patients with NENs and has a limited sensitivity of 60–83% and a relatively low specificity, that is, 72–85% (Table 3; Schurmann et al. 1992, Bajetta et al. 1999, Seregni et al. 2001, Stivanello et al. 2001, Nehat et al. 2004, Walter et al. 2012, Duque et al. 2013, Wang et al., 2014, Oberg et al. 2017). Moreover, proton pump inhibitors, atrophic gastritis and impaired kidney function can induce a rise in CgA levels (Ardill & O’Dorisio 2010, Oberg et al. 2017). The combination of CgA with other diagnostic methods, for example, somatostatin receptor scintigraphy, may increase its sensitivity (93%) and specificity (81%) (Kalkner et al. 1995, Cimitan et al. 2003, Namwongprom et al. 2008). Importantly, the sensitivity of CgA depends further on the threshold cut-off (Zatelli et al. 2007, Nolting et al. 2012, Oberg et al. 2017). NEN primary location (Baudin et al. 2001, Tomassetti et al. 2001, Nolting et al. 2012), endocrine-associated syndrome (Modlin et al. 2010a), disease spread, liver metastases (Zatelli et al. 2007, Nikou et al. 2008, Nolting et al. 2012, Walter et al. 2012) and the used assay (Ferrari et al. 2004). Despite its use being described in some clinical guidelines, some recent publications suggest a limited applicability as follow-up marker (Marotta et al. 2018). Importantly, different analytical properties of the CgA kits give different performances, a fact that must be taken into consideration when comparing results from different clinical studies.

Neuron-specific enolase

Neuron-specific enolase (NSE) is a soluble cerebral protein, which provides information on neural, neuroendocrine and paraneuronal cells (Jorgensen et al. 1996). An increase in NSE levels is thought to be related to a high death rate of cells with neuroendocrine differentiation (Bajetta et al. 1999). NSE is probably the most reliable tumor marker in diagnosis, prognosis and follow-up of small-cell lung cancer (SCLC) (Isgro et al. 2015). This marker may be elevated in 38–40% of GEP-NENs patients, in particular, in those with high-grade tumors (Baudin et al. 1998, van Adrichem et al. 2016b). The specificity of NSE is similar to CgA but with lower sensitivity (Table 3; Grouzmann et al. 1990, Nobels et al. 1997, Baudin et al. 1998). NSE levels have been directly associated with tumor differentiation, aggressiveness and size (Baudin et al. 1998, van Adrichem et al. 2016b). Despite its limited sensitivity, NSE is inversely correlated to overall survival (OS) in ENETS TNM stage IV (van Adrichem et al. 2016b) and with shorter progression-free survival (PFS), even if CgA levels are normal (Yao et al. 2011).

N-terminal pro-brain natriuretic peptide

N-terminal pro-brain natriuretic peptide (NT-proBNP) is a peptide produced by myocardial cells in response to electrolyte and fluid balance. Despite it not being a specific NEN marker, its serum concentration is usually elevated in midgut-NENs with a sensitivity of 87% and a specificity of 80% (Oberg et al. 2015, Modlin et al. 2016). NT-proBNP is in particular used for evaluating carcinoid heart disease (CHD), and it has been reported that a cut-off value of 260 pg/mL has a sensitivity of 92% and specificity of 91% (Bhattacharyya et al. 2008). Interestingly, it has been
suggested that patients with elevated NT-proBNP levels combined with increased CgA levels have a worse OS when compared to CgA alone (Korse et al. 2009b, Oberg et al. 2015). Importantly, NT-proBNP is not disease specific; thus, further studies for evaluating its applicability in the progression of CHD are still required (Bhattacharyya et al. 2008).

### 5-hydroxyindoleacetic acid

Serotonin, produced by (midgut) NENs, is the most prominent hormone associated with diarrhea and flushes in carcinoid syndrome. Its metabolite, 5-hydroxyindoleacetic acid (5HIAA), measured in 24-h urine is used as a diagnostic and follow-up marker (Korse et al. 2009a). Urinary (u) 5HIAA levels are not directly related to the severity of symptoms and large fluctuations within an individual have been described (Zuutenhorst & Taal 2005). The specificity of 5HIAA is around 90%, but the reported sensitivity is 35–68% in patients with NENs (Bajetta et al. 1999, Zandee et al. 2016, Oberg et al. 2017). 5HIAA is mainly used as an indicator of hypersecretory activity in patients with NENs, especially in midgut NENs (Bajetta et al. 1999). Its prognostic value, however, is limited. Some studies have related higher urinary SHIAA levels with mortality (Janson et al. 1997), but these results were not reproduced by other studies (Korse et al. 2009a, Zandee et al. 2016). Its combination with other markers also failed to predict OS and for this reason 5HIAA determination is only recommended to assess carcinoid syndrome (Bhattacharyya et al. 2008).

### Pancreatic peptide

Pancreatic peptide (PP) is a non-specific marker in NENs (Landry et al. 2014). Around 63% of pancreatic NENs (PNENs) and 18–53% of primary gastrointestinal NENs show increased PP levels (Panzuto et al. 2004). Its determination does not seem to increase the diagnostic performance of other markers like CgA, but changes above 50% in PP serum levels seem to correlate with tumor increase on imaging (Walter et al. 2012).
potential novel circulating and tissue biomarkers for diagnosis, prognosis and therapy response prediction, as well as their relation with tumor localization, is shown in Fig. 2. Herein we describe the potential applicability of novel peptides/growth factors, DNA, RNA and therapeutic markers for NENs, in particular, circulating biomarkers.

**Peptides and growth factors**

Several peptides and growth factors (Table 4) have been studied for a (potential) role as biomarker in NENs and may (1) help to localize primary tumors (e.g. progastrin-releasing peptide in lung NENs, connective tissue growth factor (CCN2), paraneoplastic Ma antigen 2, DcR3, TFF3 and midkine in small intestine NENs (Bergestuen et al. 2010, Korse et al. 2011, Oberg et al. 2015, Edfeldt et al. 2017)); (2) predict the outcome in functioning NENs (e.g. α-Internexin in insulinomas (Schimack et al. 2012, Liu et al. 2014)) or predict early complications in patients with CHD (CCN2 (Bergestuen et al. 2010)) and (3) add information to that provided by other circulating/tissue markers for treatment response evaluation and outcome prediction (e.g. pro-GRP and CgA for predicting outcome/therapeutic response in lung carcinoids; α-Internexin in combination with Ki67 for aggressiveness prediction in insulinomas (Grabowski et al. 2005, Korse et al. 2011, Fotouhi et al. 2016, Fujino et al. 2016) or as part of multianalytes tests (Edfeldt et al. 2017)).

Although imaging markers are not described in this review, it is important to mention that some peptides may be useful to correlate with imaging techniques. For instance, glucose transporter 1 (GLUT1) expression information to that provided by other circulating/tissue markers for treatment response evaluation and outcome prediction (e.g. pro-GRP and CgA for predicting outcome/therapeutic response in lung carcinoids; α-Internexin in combination with Ki67 for aggressiveness prediction in insulinomas (Grabowski et al. 2005, Korse et al. 2011, Fotouhi et al. 2016, Fujino et al. 2016) or as part of multianalytes tests (Edfeldt et al. 2017)).

![Fig. 2](https://erc.bioscientifica.com)

**Table 3** Sensitivity and specificity of current and novel neuroendocrine biomarkers.

<table>
<thead>
<tr>
<th>Tumor marker</th>
<th>Primary tumor location</th>
<th>Sensitivity (%)</th>
<th>Specificity (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Neuron-specific enolase (Baudin et al. 1998, Bajetta et al. 1999, Oberg et al. 2015)</td>
<td>Non-specific</td>
<td>33</td>
<td>73</td>
</tr>
<tr>
<td>NT-proBNP (Oberg et al. 2015, Modlin et al. 2016)</td>
<td>Midgut (non-specific for CHD)</td>
<td>87</td>
<td>80</td>
</tr>
<tr>
<td>Pro-GRP (Korse et al. 2011)</td>
<td>Lung</td>
<td>43</td>
<td>99</td>
</tr>
<tr>
<td>PNMA2 (Cui et al. 2010)</td>
<td>SB-NENs</td>
<td>46–50</td>
<td>NDA</td>
</tr>
<tr>
<td>DCR (Edfeldt et al. 2017)</td>
<td>SB-NENs</td>
<td>AUC: 0.74</td>
<td></td>
</tr>
<tr>
<td>TFF3 (Edfeldt et al. 2017)</td>
<td>SB-NENs</td>
<td>AUC: 0.72</td>
<td></td>
</tr>
<tr>
<td>Midkine (Edfeldt et al. 2017)</td>
<td>SB-NENs</td>
<td>AUC: 0.71</td>
<td></td>
</tr>
<tr>
<td>Multitranscript genes (Modlin et al. 2013, Kidd et al. 2015, Bodei et al. 2016)</td>
<td>GEP-NENs</td>
<td>75–98</td>
<td></td>
</tr>
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AUC, area under the curve; NDA, no data available.
18-fluorodeoxyglucose (FDG) uptake at FDG-positron emission tomography (PET) scans (Binderup et al. 2013). GLUT-1 expression may serve as an additional marker for aggressiveness of NENs and may add to a more accurate grading (Binderup et al. 2013).

Although some of these peptides have been suggested as promising biomarkers, most of them are non-specific. In addition, their applicability is limited, due to their sensitivity and specificity (Table 3) and the absence of appropriate cut-off levels. In addition, some of them have been described only in single retrospective studies; thus, further validation in larger and longitudinal cohorts is still required. A summary of potential peptide/growth factors markers for NENs is described in Table 4.

**Genetic and epigenetic markers**

Generally, tissue and circulating tumor DNA markers may provide information on the genetic characteristics of the tumor which may result in better prediction of clinical
outcome and could aid in clinical decision making (Modlin et al. 2014b). The possibility of performing liquid biopsies is expected to anticipate malignancy of solid lesions in a non-invasive way, but it is still necessary to optimize the detection technique, analysis and interpretation.

An example of a tissue DNA prognostic marker for NENs involves alternative lengthening of telomeres (ALT). A telomerase-independent mechanism to avoid the chromosome end replication was suggested in tumor cells, and in this context, ALT was reported in liver metastasis of NENs (Dogeas et al. 2014). In PNENs, whole-exome sequencing studies have demonstrated that inactivating mutually exclusive mutations in X-linked transcriptional regulator (ATRX) and death domain-associated protein 6 (DAXX) genes (Jiao et al. 2011) are associated with the ALT (Heaphy et al. 2011, Schwartzentruber et al. 2012). However, results on its relationship with clinical features are inconclusive and in some cases contradictory. In this sense, ALT-positive PNENs have been associated with larger tumor size, grading, vascular/perineural invasion and metastasis (Marinoni et al. 2014, Kim et al. 2017). In addition, an increased risk of recurrence and decreased OS has been reported in ALT-positive NEN metastasis (Marinoni et al. 2014, Kim et al. 2017). In contrast, other authors found an association with better clinical outcomes (Jiao et al. 2011, Dogeas et al. 2014) including metastatic disease (Kim et al. 2017). Since it is possible to determine ALT, ATRX and DAXX using fine-needle biopsies, the potential role as a marker in NENs is an area of active research.

### Table 4 Peptides and growth factors as novel markers in NENs.

<table>
<thead>
<tr>
<th>Peptide/growth factor</th>
<th>Function</th>
<th>Potential role as marker in NENs</th>
</tr>
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<tbody>
<tr>
<td>Progastrin-releasing peptide (proGRP)</td>
<td>Precursor of gastrin-releasing peptide, a neuropeptide hormone widely distributed throughout the gastrointestinal and pulmonary tract (McDonald et al. 1979)</td>
<td>Primary tumor localization in patients with a metastatic NEN of unknown origin. Complementary marker to CgA in lung NEN for treatment response evaluation and survival (Korse et al. 2011, 2015)</td>
</tr>
<tr>
<td>Connective tissue growth factor for carcinoid heart disease (CCN2)</td>
<td>CCN2 is an early gene product of the CCN family of matricellular proteins, which are involved in cell proliferation, angiogenesis, tumorigenesis and wound healing. It may be involved in the pathogenesis of carcinoid heart disease (Holbourn et al. 2008, Bergestuen et al. 2010)</td>
<td>Independent predictor of both reduced right ventricular function and rightsided valve regurgitation (its plasma levels are inversely related to right ventricular function levels) Early predictor of cardiac fibrosis (Bergestuen et al. 2010)</td>
</tr>
<tr>
<td>Paraneoplastic Ma antigen 2 (PNMA2)</td>
<td>Antineuronal antibodies identified as markers of neurological paraneoplastic syndromes (Schuller et al. 2005)</td>
<td>Allows the identification of almost 50% of SB-NENs at the primary stage of the disease Correlation with disease progression and recurrence free survival (Cui et al. 2010)</td>
</tr>
<tr>
<td>Glucose transporters type 1 (GLUT-1)</td>
<td>Mediates the transport of glucose across the cellular membrane and are commonly overexpressed in tumors, probably related with higher metabolism and cell growth (Clavo et al. 1995)</td>
<td>Predictive marker to chemotherapy response(Hu et al. 2010, Wu et al. 2015)</td>
</tr>
<tr>
<td>DcR3</td>
<td>Regulates cytokines which influence tumor growth and reduce apoptotic stimuli (Lin &amp; Hsieh 2011)</td>
<td></td>
</tr>
<tr>
<td>TFF3</td>
<td>Protects and repairs epithelial surfaces Enhances migration, angiogenesis, and inhibits apoptosis (Vestergaard et al. 2010, Casado et al. 2012, Huang et al. 2013)</td>
<td>Higher concentrations have been correlated to reduced survival (Edfeldt et al. 2017)</td>
</tr>
<tr>
<td>Midkine</td>
<td>Promotes tumor cells migration, angiogenesis and reduces apoptosis (Jones 2014)</td>
<td></td>
</tr>
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aspiration (FNA), they may be used as minimally invasive prognostic markers in NENs (VandenBussche et al. 2017), but their clinical significance should still be evaluated in detail.

Additionally, whole-genome sequencing in NENs allow the identification of genomic events related with tumor pathogenesis. In this sense, germline deleterious mutations affecting DNA damage repair in PNENs have been described (in the base-excision-repair MUTYH gene or the homologous recombination gene BRCA2) (Scarpa et al. 2017). Furthermore, mutations in genes involved in chromatin remodeling, DNA repair and mTOR signaling may also play a role in PNEN pathogenesis (Scarpa et al. 2017). Several publications have also shown chromosome losses affecting genes related to DNA repair or damage checkpoints (VHL, MEN1, ATM, PTEN) in PNENs (Capurso et al. 2012, Scarpa et al. 2017). In this sense, most recent reviews describe genetic alterations that are consistently related with the loss of MEN1 function, the activation of the PI3K/mTOR pathway, changes in chromatin remodeling and telomeres alteration (Mafficini & Scarpa 2018).

Importantly, somatic mutations and deletions have also been described in midgut NENs, specifically in the cyclin-dependent kinase inhibitor gene CDKN1B. This finding suggests that the p21/p27/p57 family, which is involved in the cell cycle, may also be involved in the pathogenesis of small-bowel NENs (Francis et al. 2013). Genetic alterations in PNENs are extensively reviewed in a recent publication by Stevenson and colleagues (Stevenson et al. 2018).

Cell-free DNA (cfDNA) from liquid biopsies may become a biomarker in NENs, although to date, no studies have been published yet on the detection of cfDNA in NENs. cfDNA generally contains identical genetic defects as the primary tumor (Diaz & Bardelli 2014), is released after apoptosis (Francis & Stein 2015) and can be detected in serum (Marzese et al. 2013, Rothe et al. 2014). The analysis of cfDNA may be useful for early detection of (residual or recurrent) disease, to monitor tumor burden, to assess molecular heterogeneity and to predict PFS (Francis & Stein 2015), especially in adenocarcinomas (Francis & Stein 2015). Measurement of cfDNA might be a promising tool in NENs, but needs further investigation (Rizzo & Meyer 2018). The ultimate aim of cfDNA assessment would be to add to or replace tissue biopsies (Khan et al. 2013, Sikora et al. 2015). Prerequisites for cfDNA analysis are sufficient tumoral DNA release and the presence of tumor-related mutations to identify tumor DNA. These conditions may only be present in a subset of NEN patients, thereby limiting the applicability of cfDNA measurement. Further study is needed to determine the potential role of cfDNA analysis in NEN.

A summary of genetic markers in NENs is shown in Fig. 3.

**RNA markers**

RNA markers are novel and potentially promising minimally invasive markers used for diagnostic purpose and/or to identify the therapeutic targets of NENs. Specifically, the identification of circulating target gene miRNAs using PCR amplification has been used for determining stage, prognosis, recurrence or new metastasis in several cancers (van’t Veer et al. 2002, Frederiksen et al. 2003, Hess et al. 2006). Blood circulating- and tumor tissue-transcripts from GEP- and bronchopulmonary NENs are highly correlated (Cwikla et al. 2015, Kidd et al. 2015). Modlin et al. have developed a PCR-based molecular test using 51 genes for identifying GEP-NENs (Modlin et al. 2013). For this so-called NETest, a score, based on tissue and peripheral blood transcriptomes, was developed (Modlin et al. 2013) as a prognostic and follow-up tool for NENs (Modlin et al. 2013, 2014a, 2015, Kidd et al. 2015). NETest results were shown to differentiate progressive disease (Kidd et al. 2015) and predict tumor response to somatostatin analogs (SSAs) (Cwikla et al. 2015). Further prospective validation of this test is awaited.

Additionally, dysregulated miRNAs have been correlated with diagnosis, staging, progression, prognosis and therapeutic response in several tumors, including NENs (Di Leva & Croce 2013). miRNAs are endogenous, small (19–25 nucleotides), non-coding RNAs that regulate post-transcriptional gene expression by binding to mRNA molecules, and they probably modulate the expression of at least one-third of protein-coding genes (Demes et al. 2016). miRNAs have the capacity to target different genes implicated in the same pathway and/or in interacting pathways, allowing for the possibility of developing directed therapies that could silence several tumor pathways (Reddy 2015).

Specific patterns of miRNA expression may distinguish tumor tissue from normal tissue and acinar tumors from PNENs (Roldo et al. 2006, Vicentini et al. 2014). Some miRNAs are upregulated in PNENs (miR-140, miR-210), small-bowel (SB-)NENs (miR-96, miR-182, miR-183, miR-196a, miR-200a) and lung carcinoids (mMR-34a) (Li et al. 2013, Demes et al. 2016). Also, the downregulation of miRNA-133a, miRNA-1 and miRNA-143-3p has been demonstrated in metastasis when compared to the
As prognostic marker, miRNA levels have been correlated with Ki-67 (Thorns et al. 2014, Arvidsson et al. 2018), degree of malignancy (e.g. miR-21 in PNENs; miR-13/miR-204-5p in SB-NENs) (Demes et al. 2016, Arvidsson et al. 2018) and OS (e.g. the downregulation of miR-375 in SB-NENs (Arvidsson et al. 2018)).

miRNAs may also be used for therapeutic goals, for example, inhibition of oncogenic miRNA expression or the introduction of a tumor suppressor miRNA (Vicentini et al. 2014). However, the currently available technology is not robust enough to support diagnostic or therapeutic use of miRNAs yet (Oberg et al. 2016). Furthermore, dysregulation of miRNAs is not tumor specific and the absence of cut-off levels for differentiating tissue and tumor subtypes, the lack of reproducibility in other NEN cohorts and the difficulties in their interpretation, currently limit their clinical application. Further studies are required to evaluate the application of miRNAs as clinical and therapeutic markers in NENs. This issue is extensively reviewed in recent publications (Zatelli et al. 2017, Zimmermann et al. 2018, Rizzo & Meyer 2018, Panarelli et al. 2019).

Potential novel diagnostic-therapeutic biomarkers

Some (potential) circulating and tissue therapeutic markers are available in NENs. To a certain extent, the currently available markers CgA and NSE can be used for treatment monitoring. Variations in serum CgA levels after treatment with SSAs and PRRT have been reported. Specifically, decreased CgA in stable/responsive tumors has been observed (Caplin et al. 2014, van der Zwan et al. 2015), but serum CgA may also increase (>20%) due to radiation-induced cell damage or lysis after the first cycle of PRRT. In the latter case, this increase was followed by declined levels usually after 12 weeks (Brabander et al. 2017). Furthermore, tumor shrinkage has been associated with CgA or NSE response after treating patients with everolimus (increased PFS in patients with early CgA/NSE response) (Li et al. 2011). However, specific cut-off values to define response to different treatment modalities have not been determined yet and novel/specific therapeutic biomarkers are still required. A summary of clinical applicability of novel biomarkers in NENs is presented in Table 5.

Somatostatin receptor expression

Somatostatin receptor (SST) expression by NENs, in particular subtype 2, is used for imaging to diagnose and stage NENs (Wong et al. 2012) and is considered to have therapeutic implications for treatment with SSAs and PRRT with radiolabeled somatostatin analogs as Lutetium-177- or Yttrium-90-coupled analogs (Kwekkeboom et al. 2010, Strosberg et al. 2017). SST expression as imaging marker is not described in this review, but it has been comprehensively evaluated in several publications (de Herder et al. 2006, Kwekkeboom et al. 2010, Kunikowska et al. 2017, Bodei & Weber 2018, Hope et al. 2018).
SST can also be evaluated in NEN tissue samples using immunohistochemistry and qPCR (Fig. 4; Righi et al. 2010, Mizutani et al. 2012, Lambertini et al. 2013, Kanakis et al. 2015, Herrera-Martinez et al. 2017, 2018). SST expression may help to differentiate normal and tumor tissue in lung carcinoids and GEP-NENs and has been related to vascular/nerve invasion and metastasis (Herrera-Martinez et al. 2017, 2018). The tumor SST expression profile may also be helpful for predicting treatment response (Reubi et al. 2010, Righi et al. 2010), especially in aggressive cases (Righi et al. 2010). On the other hand, the immunohistochemical assessment of NEN tissue expression of SST subtype 2 had no additional value compared to the uptake on the OctreoScan in predicting tumor response after PRRT (Korner et al. 2012, Bison et al. 2014, van Adrichem et al. 2016a). The tumoral expression of SST3 and SST5 may also be a relevant marker supporting the potential benefit of novel SSAs. Truncated isoforms of SST can also be expressed by NENs, and their presence is associated with aggressive features (Sampedro-Nunez et al. 2016). Unfortunately, results are based on retrospective heterogeneous cohorts, which may limit the reproducibility. Additionally, in some of the above indicated studies, SST expression by qPCR was determined in formalin-fixed paraffin embedded tumors, which may affect the expression profile in some samples (Sampedro-Nunez et al. 2016, Herrera-Martinez et al. 2017, 2018).

O-6-methylguanine-DNA methyltransferase (MGMT)

An example of a tissue DNA therapeutic marker for NENs is the methylation pattern of the DNA repair enzyme O-6-methylguanine-DNA methyltransferase (MGMT). Several agents have antitumor effects by inducing DNA methylation at the O6 position of guanine, resulting in apoptosis and tumor cell death (Liu & Gerson 2006). Those lesions can be restored by MGMT, reduction of which may increase the sensitivity of tumor cells to alklylation-induced DNA damage (Christmann et al. 2011). The methylation of MGMT promoter and loss of MGMT protein expression have been reported in GEP-NENs (Walter et al. 2015). Decreased MGMT expression has been associated to tumor sensitivity to alkylant-based chemotherapy agents, for example, temozolomide, alone or in combination therapy (Gerson 2002). In PNENs, absence of MGMT is more common compared to intestinal or lung carcinoids, which explains the better treatment response in PNENs to temozolomide (Kulke et al. 2009, Schmitt et al. 2014).

Further, a ‘hypermethylator’ phenotype, which is characterized by the presence of a high number of methylated genes, has been associated with more progressive disease and shorter survival (Walter et al. 2015), whereas this association was not found in well-differentiated PNENs (Raj et al. 2017). The predictive value of MGMT status for treatment response in NENs will be evaluated in clinical trials with alkylating agents (NCT03217097).

### Molecular biomarkers for treatment with tyrosine kinase inhibitors (TKIs)

In patients with advanced, well-differentiated, progressive PNENs, sunitinib can induce tumor stabilization and improve PFS. Currently, sunitinib is used for progressive disease, but its combination with SSAs, chemotherapeutic agents or neo-adjuvant or adjuvant therapy in earlier stages of resectable PNENs has also been proposed (Delbaldo et al. 2012, Mateo et al. 2012). The possibility to peripherally measure monoanlytes directly related to

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**Table 5** Clinical applicability of potential new biomarkers in NENs.

<table>
<thead>
<tr>
<th>Clinical diagnosis</th>
<th>Therapeutic role</th>
<th>Function</th>
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<tbody>
<tr>
<td>ALT</td>
<td>ALT(?)</td>
<td>Prognostic role</td>
</tr>
<tr>
<td>cfDNA*</td>
<td>SST expression</td>
<td>ALT* Somatic/germline mutations*</td>
</tr>
<tr>
<td>microRNAs***</td>
<td>MGMT</td>
<td>cfDNA*</td>
</tr>
<tr>
<td>SST expression</td>
<td>VEGF</td>
<td>microRNAs***</td>
</tr>
<tr>
<td>PI GF (?)</td>
<td>IL-8 (?)</td>
<td>SST expression***</td>
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<tr>
<td>proGRP</td>
<td>PD-1/PD-L1</td>
<td>MGMT**</td>
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<tr>
<td>CCN2</td>
<td>XIAP</td>
<td>EGFR**</td>
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<td>PNMA2</td>
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<td>VEGF*</td>
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<td>DcR3</td>
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<td>IL-8***</td>
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<td></td>
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<td>(SDF)-1α**</td>
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<td>proGR P with CgA*</td>
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<td>CCN2*</td>
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<td>PNMA2*</td>
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<td></td>
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<td>á-Internexin*</td>
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<td></td>
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<td>GLUT-1*</td>
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<tr>
<td></td>
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<td>DcR3, TFF3, midkine***</td>
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</tbody>
</table>

* Disease course predictor; ** Intervention outcome predictor; *** Disease and treatment predictor.

ALT, alternative lengthening of telomeres; CCN2, connective tissue growth factor for carcinoid heart disease; cfDNA, cell-free DNA; CTCs, circulating tumor cells; EGFR, epidermal growth factor receptor; GLUT-1, glucose transporters type 1; IL-8, interleukin-8; MGMT, O-6-methylguanine-DNA methyltransferase; PD-1, programmed death-1; PD-1, programmed death ligand 1; PI GF, placental growth factor; PNMA2, paraneoplastic Ma antigen 2; proGR P, progastrin-releasing peptide; SDF-1α, stromal cell-derived factor-1α; SST, somatostatin receptor; VEGF, vascular endothelial growth factor; XIAP, X-linked inhibitor of apoptosis.
Vascular endothelial growth factor receptor
Vascular endothelial growth factor (VEGF) is the most important regulatory factor of tumor angiogenesis and has been related to cell survival, growth and metastasis (Niu & Chen 2010). VEGF may be determined in tumor and in FNA samples (Angelescu et al. 2013). In general, well-differentiated GEP-NENs express high levels of VEGF and its transmembrane receptors (VEFGR-1, VEFGR-2, VEGFR-3) (Pavel et al. 2005), which can be detected in peripheral blood (Mateo et al. 2012). In this context, a worse clinical course has been reported in NENs with increased VEGF expression (Terris et al. 1998, Pavel et al. 2005, Zhang et al. 2007, Yao et al. 2011). Immunohistochemical and molecular expression of VEGFR-1/-2 has been reported in over 50% of GEP-NENs (La Rosa et al. 2003, Angelescu et al. 2013) without being directly related to tumor malignancy (La Rosa et al. 2003).

Some relations between VEGFR and patient outcome have been described; specifically, low VEGFR-1 levels have been related to longer PFS (Yao et al. 2012), high baseline VEGFR-2 levels to decreased OS in PNENs (Zurita et al. 2015) and low VEGFR-3 levels to longer PFS/OS in carcinoid patients (Zurita et al. 2015). Increased VEGF concentrations accompanied by decreased VEGFR-2 and VEGFR-3 levels have been reported after treatment with sunitinib (Deprimo et al. 2007), but their levels returned to baseline during the off-treatment period (Zurita et al. 2015). Unfortunately, VEGFRs are not tumor specific; additionally, cut-off levels are also necessary to predict outcome. The applicability of VEGFR-1 as a therapeutic predictive marker is currently considered in clinical trials (pazopanib in advanced NENs, NCT01280201), but further studies are still required.

Interleukin-8
Interleukin-8 (IL-8) has proangiogenic, mitogenic and motogenic effects through the activation of the receptors CXCR1 and CXCR2 (Mateo et al. 2012). PNENs overexpress not only IL-8 but also its receptor CXCR2 (Tecimer et al. 2000, Hussain et al. 2010). IL-8 seems to be increased in progressive NENs, while lower IL-8 baseline levels have been associated with longer survival (Pavel et al. 2005). Patients with SB-NENs and lower IL-8 levels were shown to have a worse clinical course (Hussain et al. 2010). Increased IL-8 levels may be associated with shorter progression-free survival (Bosch et al. 2013), and IL-8 levels may be used to evaluate treatment efficacy (Diaz et al. 2015). Treatment with erlotinib (Zhu et al. 2015) or gefitinib (Lu et al. 2017) are associated with increased sensitivity to the TKIs erlotinib and gefitinib overexpressed in non–small-cell lung cancer and an increased sensitivity to the TKIs erlotinib and gefitinib has been reported when the EGFR-1 domain of the EGFR has somatic mutations (Lv et al. 2009). EGFR expression by immunohistochemistry was demonstrated in 21–28% of typical carcinoids, 25–57% of atypical lung carcinoids (Rusch et al. 1996, Rickman et al. 2009) and in 40–96% of NENs, while its gene amplification by fluorescent in situ hybridization was observed in 55% of cases (Srivastava et al. 2001, Shah et al. 2006, Rickman et al. 2009, Gilbert et al. 2010). In addition, activating EGFR mutations have been described in NENs and may be associated with improved treatment response (Costanzo et al. 2013, Aroldi et al. 2014). Importantly, EGFR mutations are rare in GEP-NENs, and their clinical relevance may be limited as compared with other tumors including lung adenocarcinoma (Park et al. 2016). The specific clinical significance of the expression of EGFR, however, is still to be determined.

Epidermal growth factor receptor
The epidermal growth factor receptor (EGFR) is overexpressed in non–small-cell lung cancer and an increased sensitivity to the TKIs erlotinib and gefitinib has been reported when the tyrosine kinase domain of the EGFR has somatic mutations (Pazee et al. 2004). EGFR expression by immunohistochemistry was demonstrated in 21–28% of typical carcinoids, 25–57% of atypical lung carcinoids (Rusch et al. 1996, Rickman et al. 2009) and in 40–96% of NENs, while its gene amplification by fluorescent in situ hybridization was observed in 55% of cases (Srivastava et al. 2001, Shah et al. 2006, Rickman et al. 2009, Gilbert et al. 2010). In addition, activating EGFR mutations have been described in NENs and may be associated with improved treatment response (Costanzo et al. 2013, Aroldi et al. 2014). Importantly, EGFR mutations are rare in GEP-NENs, and their clinical relevance may be limited as compared with other tumors including lung adenocarcinoma (Park et al. 2016). The specific clinical significance of the expression of EGFR, however, is still to be determined.

the drug mechanism of action represents an important approach to predict treatment response; in this sense, some molecular biomarkers have been examined in the last years.
have disease stabilization or clinical response to sunitinib (Bello et al. 2006). It has also been hypothesized that monitoring IL-8 in plasma during sunitinib treatment could be useful to predict drug resistance (Huang et al. 2010), but this needs further investigation.

**Stromal cell-derived factor (SDF)-1α**

SDF-1α plays a role in cell migration, proliferation, survival and angiogenesis (Mateo et al. 2012) and is the natural ligand of CXCR4. CXCR4 has been reported in several cancer types (Balkwill 2004), seems to be involved in tumor progression, metastasis, hypoxia adaptation and stem cell survival (Kaemmerer et al. 2015) and may serve as a marker of tumor activity and progression (Zurita et al. 2015). SDF-1α expression seems to be increased in PNEs compared to other NENs and is inversely correlated with time to disease progression (Zurita et al. 2015). In addition, it has been described as a circulating biomarker associated with tumor response to sunitinib (Antonuzzo et al. 2013). Arvidsson and collaborators described downregulation of SDF-1α and upregulation of CXCR4 in hypoxic carcinoid cells with consequently higher cell migration, probably due to the activation of the mitogen-activated protein kinase pathway. Based on this, a putative role in antiangiogenic drugs resistance was also suggested, and SDF-1α may serve as a therapeutic target (Arvidsson et al. 2010).

**Circulating tumor, endothelial and white cells**

Circulating tumor cells (CTCs) have been widely used in several tumors as peripheral blood tumor markers (Cristofanilli et al. 2005, Cohen et al. 2008, Resel Folkersma et al. 2012). The identification of cellular expression of the epithelial cell adhesion molecule (EpCAM) allowed the determination of CTCs in NENs (Modlin et al. 2016), in which a threshold of 1 CTC (similarly to breast cancer) was demonstrated (Khan et al. 2011). CTCs have been associated with higher tumor grade and burden, increased circulating CgA, Ki67 index and worse PFS and OS in grade 1–2 NENs (Khan et al. 2011, 2013). Measurement and molecular characterization of CTCs may be helpful to stratify patients for specific therapies in the future (Khan et al 2011, Zatelli et al. 2017). However, the sensitivity of CTCs varies according to the NEN type, and CTCs are not specific for any subgroup of tumors (Oberg et al. 2015).

Additionally, circulating endothelial cells (CECs) were also described in NENs, specifically two different subpopulations: endothelial precursors derived from the bone marrow (CEPs) and mature CECs (Nolan et al. 2007). Increased circulating CECs have been related to vessel damage during antiangiogenic treatment and consequently with a longer PFS (Beaudry et al. 2005). Theoretically, CEPs should decrease after anti-VEGF therapy (Kalka et al. 2000); but in contrast, decreased CECs and stable CEPs were observed in NENs after the first cycle of treatment with sunitinib (Zurita et al. 2015).

Moreover, myeloid cells have been related to angiogenesis, disease progression, metastasis and the expression of some receptors related with the VEGF and SDF-1α pathways in other tumors (Fernandez Pujol et al. 2000, Condeelis & Pollard 2006). Zurita et al. described decreased CD14+ monocytes expressing VEGFR-1 and CXCR4 in NENs treated with sunitinib. It has been postulated that possible relations exist between specific monocyte subpopulations and drug pharmacodynamics, which would be useful as a treatment response predictor (Zurita et al. 2015). Because of the heterogeneity of the included patient samples (grading, previous treatments and origin of primary tumor), results remain controversial (Antonuzzo et al. 2013). Currently, there is no consensus for supporting the use of CTCs or CECs as an indicator of tumor burden or parameter of treatment response in NENs (Oberg et al. 2016). Further prospective, longitudinal studies in this field are still required. A summary of current tumor biomarkers for TKIs is shown in Fig. 5.

**Molecular biomarkers for mTOR pathway inhibitors**

Increased PFS has been described in patients with advanced metastatic PNEs treated with the mTOR pathway inhibitor everolimus (Yao et al. 2010, Pavel et al. 2011). Although the combination of everolimus and SSAs does not seem to increase OS, the heterogeneity of the included patients makes these results inconclusive (Pavel et al. 2017). Based on this, it would be valuable to develop markers that could early identify those patients who may benefit from everolimus alone or in combination with SSAs.

In this sense, placental growth factor (PlGF) has been related to angiogenesis, tumor burden, presence of metastases and survival (Carmeliet et al. 2001, Fischer et al. 2008) and is thought to reflect the activation of AKT and ERK pathways (Parr et al. 2005, Fischer et al. 2008, Wei et al. 2009). Elevated levels of circulating PlGF have been demonstrated in PNEs, with increasing levels from grade 1 to grade 3 tumors (Hilfenhaus et al. 2013). Decreased circulating PlGF was observed after treatment with everolimus in the RADIANT-III study (Hilfenhaus et al. 2013). PlGF levels reflect tumor aggressiveness.
Figure 5
Therapeutic markers: molecular biomarkers for tyrosine kinase and mTOR inhibitors. Blue arrows represent the effect of the mTOR inhibitor everolimus and red arrows the effect of the tyrosine kinase inhibitor sunitinib. Molecular markers are presented in blue. Response to sunitinib has been related to decreased SDF1, IL-8, VEGFR 2-3, CD14 monocytes expressing VEGFR, decreased CEPs, increased CECs and probably decreased PlGF. Response to everolimus has been related to decreased PlGF and VEGFR2. Factors related to progression-free survival (PFS) and OS are also shown. CECs, circulating endothelial cells; CPECs, circulating endothelial precursors derived from the bone marrow; CXCR 1,2,4, chemokine family receptor 1,2,4; IL-8, interleukin-8; PlGF, placental growth factor; SDF-1α, stromal cell-derived factor 1α; TSC 1-2, tuberous sclerosis complex 1-2; VEGF, vascular endothelial growth factor; VEGFR 1–3, vascular endothelial growth factor receptor 1–3.
(Hilfenhaus et al. 2013), whereas others studies suggest that PIGF may also induce the formation of vascular networks that are hypersensitive to anti-VEGF therapy (Hedlund et al. 2013). Tumor-derived PIGF was postulated to become a potential predictive marker of anti-VEGF therapy (Hedlund et al. 2013).

As previously described for TKIs markers, midgut NENs and PNENs overexpress VEGF and its receptors (Christofori et al. 1995, Terris et al. 1998, La Rosa et al. 2003). In the RADIANT-III trial, a significantly progressive reduction in VEGFR-2 was observed after treatment with everolimus (Yao et al. 2012), but the specific clinical relevance and applicability in NENs must still be determined.

In addition, it has been suggested that mTOR-directed therapies may be more effective in tumors with tuberous sclerosis complex 1 (TSC1) somatic mutation, which acts as a regulator of mTOR pathway activation (Iyer et al. 2012). TSC is an autosomal dominant multisystem disorder caused by mutations of two tumor suppressor genes, TSC1 and TSC2, which encode for hamartin and tuberin, respectively. The interaction between these proteins is critical for cell growth and proliferation (Dworakowska & Grossman 2009). Additionally, mutations in TSC2 have been described in PNENs with more aggressive features and progressive disease (Bombardieri et al. 2013). A schematic overview of current tumor biomarkers for mTOR inhibitors and TKIs is shown in Fig. 5.

**Biomarkers for immune therapy**

Programmed death-1 (PD-1) is expressed on T-, B- and myeloid cells and downregulates the activation of T-cells in tumors. The programmed death ligand 1 (PD-L1) and PD-1 are overexpressed in tumor-infiltrating lymphocytes in several types of cancer (Dong et al. 1999, Freeman et al. 2000, Lyford-Pike et al. 2013, He et al. 2015). PD-1 and PD-L1 induce lymphocyte apoptosis and cytokine secretion, which is crucial in tumor immunosuppression (Fan et al. 2016).

Initially, PD-L1 was described in SCLC (Schultheis et al. 2015), in lung typical-atypical carcinoids and in large cell neuroendocrine carcinoma (Tsuruoka et al. 2017). Subsequently, its presence was described and related with clinical features in other NENs; specifically, PD-L1 has been correlated with tumor stage and histological type in PNENs, as well as with worse survival (Fan et al. 2016). In GEP-NENs, PD-L1 has been related with more proliferative and aggressive tumors (Ghebeh et al. 2006, 2007, Sabatier et al. 2015, Kim et al. 2016), probably related to a higher immunogenicity in proliferative tumor cells (Kim et al. 2016). Despite PDL-1 and tumor grading being associated in GEP-NENs, no specific relation with the site of origin has been established (Kim et al. 2016). Some studies have reported an antitumor effect by drugs targeting PD-1 (nivolumab and pembrolizumab) and PD-L1 (MPDL3280A and BMS- 936559) (Ohaegbulam et al. 2015), especially in non-SCLC, which seems to be correlated to PD-L1 overexpression in the tumor (Powles et al. 2014). Unfortunately, the applicability in well-differentiated NENs seems to be limited, however. Further studies are required, especially focusing in the relation of PD-L1 expression and response rate in poorly differentiated NENs and carcinomas (Roberts et al. 2017).

**Conclusions and future directions**

The currently available biomarkers for NENs have important limitations, and there is an unmet need for accurate biomarkers that can be used for NEN diagnosis, prognosis and follow-up, therapy stratification and evaluation of treatment response. Currently, several prospective trials are evaluating the effect of novel therapeutic strategies in NENs (**)Yt-labeled microspheres, lenvatinib, palbociclib, tremelimumab, bevacizumab, temozolomide, pasireotide, PDR001) and most trials include the evaluation of treatment-related follow-up markers. To date, these new biomarkers include peptides/growth factors, DNA/RNA markers and CTCs.

Circulating markers, as well as, low-invasive techniques for early diagnosis (of disease and related complications) would be valuable to identify a personalized therapeutic sequence and follow-up. Circulating/tissue markers that could predict treatment response could assist to improve treatment-induced PFS. Finally, the combination of markers that enable to better predict the course of the disease, would also allow for better decision making with regard to the therapeutic strategy with the available different treatment options. In this respect, multianalyte measurement based on tumor genomics seems a promising tool for early outcome stratification and decision making. The development of blood-based analysis and liquid biopsy would represent non-invasive methods for diagnosis and prognosis as well. Additional validation studies will establish the definite role for this test. Other new parameters like cfDNA, miRNAs and CTCs and markers that predict response to TKIs and mTOR inhibitors need further investigation before clinical application is possible. Development and validation of novel biomarkers that improve diagnosis, assessment of tumor load, prediction of disease course,
prognosis and outcome of intervention is still a challenge. In this context, genomics may represent the basis for developing multitranscript biomarkers, additionally, the combination of several markers (that provide multifaceted information), may offer better medical management and use of resources in order to improve diagnosis, treatment, quality of life and survival in NEN patients.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of this review.

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