Homeodomain transcription factor NKX2.2 functions in immature cells to control enteroendocrine differentiation and is expressed in gastrointestinal neuroendocrine tumors

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Abstract

The homeodomain transcription factor NKX2.2 is necessary for neuroendocrine (NE) differentiation in the central nervous system and pancreas. NE tumors derived from the gut are defined by their NE phenotype, which is used for diagnosis and contributes to tumorigenicity. We hypothesized that NKX2.2 is important for NE differentiation in normal and neoplastic gut. NKX2.2 and NE marker expression was investigated in the small intestine of embryonic and adult mice using immunofluorescence (IF). To determine the role of NKX2.2 in NE differentiation of the intestine, the phenotype of Nkx2.2 (−/−) mice was examined by IF and real-time (RT)-PCR. NKX2.2 and NE marker expression in human NE tumors of the gut and normal tissues were evaluated by immunohistochemistry and qRT-PCR. NKX2.2 expression was detected in the intervilus/crypt regions of embryonic and adult mouse intestine. Co-expression of Nkx2.2 with neurogenin3 (NEUROG3) and hormones was observed in the adult intestinal crypt compartment, suggesting NKX2.2 functions in NEUROG3-positive endocrine progenitors and newly differentiated endocrine cells. In the intestine of Nkx2.2 (−/−) mice, we found a dramatic reduction in the number of cells producing numerous hormones, such as serotonin, gastrin, cholecystokinin, somatostatin, glucagon-like peptide 1 (GLP-1), and secretin, but an increase in cells producing ghrelin. NKX2.2 was expressed in most (24 of 29) human NE tumors derived from diverse primary sites. We conclude NKX2.2 functions in immature endocrine cells to control NE differentiation in normal intestine and is expressed in most NE tumors of the gut, and is therefore a novel target of diagnosis for patients with gastrointestinal NE tumors.

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Introduction

The incidence of neuroendocrine (NE) – or carcinoid – tumors has increased over the past 25 years, occurring in ~38.5 individuals/million in the USA (Maggard et al. 2004, Modlin et al. 2008). The gastrointestinal (GI) tract is the predominant site of origin for NE tumors, which frequently metastasize. At diagnosis, most patients with GI NE tumors are not candidates
for surgery, the only potentially curative treatment, due to the presence of extensive metastatic disease (Modlin et al. 2008). NE tumors are defined by their NE phenotype, which is used for diagnosis and contributes to tumor-related morbidity and mortality. Detection of the NE marker chromogranin A (CgA) is used to diagnose NE tumors. Serotonin (5-HT) and other mediators cause debilitating symptoms and stimulate NE tumor growth (Ishizuka et al. 1992, von Wichert et al. 2000). Current therapy is ineffective in palliating symptoms long-term and has little activity in shrinking tumors (Nakakura et al. 2007). More effective therapies and earlier diagnosis are needed but require a better understanding of NE tumor biology.

NE tumors are thought to arise from endocrine cells of the gut – the largest endocrine organ in the body (Creutzfeldt 1994). The gut produces more than 100 GI hormones that play important roles in intestinal motility, secretion, inflammation, pain, appetite regulation, and neoplasia (Rehfeld 1998). In the small intestine, endocrine cells and the three other main cell types (enterocytes, goblet cells, and Paneth cells) arise from multipotent stem cells located in the crypt compartment (Schonhoff et al. 2004a). Every 3–4 days, endocrine cells turn over as newly differentiated cells migrate from the crypt to the villus tip and are extruded into the gut lumen.

Very little is known about how a gut stem-cell becomes a hormone-producing endocrine cell. Only a handful of transcription factors are known to regulate NE differentiation in mouse small intestine (Schonhoff et al. 2004a). One factor, neurogenin3 (NEUROG3), initiates NE differentiation in immature cells (Jensen et al. 2000a, Jenny et al. 2002, Lee et al. 2002, Schonhoff et al. 2004b). Subsequent genes that promote formation of hormone-producing cells in the intestine include PAX4, PAX6, and NEUROD1, but other genes are likely to be involved (Schonhoff et al. 2004a). Many of the same transcription factors function during NE differentiation in various contexts, including central nervous system and gut development (Schonhoff et al. 2004a), and in neoplastic tissue (Borges et al. 1997, Nakakura et al. 2001, 2005). For many years, the homeodomain transcription factor NKX2.2 has been known to be important for NE differentiation in the central nervous system and pancreas (Sussel et al. 1998, Briscoe et al. 1999, Cheng et al. 2003, Craven et al. 2004, Pattyn et al. 2004). A recent study showed that a transgenic zebrafish line with EGFP driven by the Nkx2.2a locus identifies endocrine cells in the intestine (Ng et al. 2005). We hypothesized that NKX2.2 is important for NE differentiation in normal and neoplastic gut.

Materials and methods

Animals and human tissues

Nkx2.2 mutant mice were generated, maintained, and genotyped as previously described, according to the regulations of the IACUC at the University of California, San Francisco (Sussel et al. 1998). Human tissue samples were obtained from resection specimens in the UCSF Pathology Department after approval by the Committee on Human Research.

Histology and immunohistochemistry

Tissues were fixed in Z-fix (Anatech, Battle Creek, MI, USA) and processed for paraffin sections (Sussel et al. 1998). The following primary antibodies were used: mouse monoclonal anti-NKX2.2 (Developmental Studies Hybridoma Bank, 1:25; rabbit anti-NEUROG3, 1:2000 (Michael German); rabbit anti-gastrin/cholecystokinin (CCK), which reacts with gastrin and CCK as they share a common carboxy-terminal tetrapeptide sequence that is necessary for bioactivity, (Novocastra, Newcastle, UK), 1:200; goat anti-ghrelin (Santa Cruz, CA, USA), 1:800; rabbit anti-CgA (Immunostar, Hudson, MA, USA), 1:1000; rabbit anti-GLP1 (Peninsula), 1:200; rabbit anti-secretin (Phoenix, Belmont, CA, USA), 1:1000; rabbit anti-serotonin (Immunostar), 1:4000; mouse monoclonal anti-serotonin (Dako, Carpinteria, CA, USA), 1:25; rabbit anti-somatostatin (Dako), 1:200; rabbit anti-cleaved caspase-3 (Cell Signaling, Danvers, MA, USA), 1:125; mouse monoclonal anti-MKI67 (Novocastra), 1:100. Secondary antibodies (Jackson ImmunoResearch) were FITC-conjugated goat anti-mouse and anti-rabbit, 1:200; FITC-conjugated donkey anti-goat and anti-mouse, 1:200; Cy3-conjugated donkey anti-goat, and goat anti-mouse and anti-rabbit, 1:400. Biotinylated secondary antibodies (Vector, Burlingame, CA, USA) were detected with the ABC Elite immunoperoxidase system (Vector). Alcian blue staining of goblet cells was done according to manufacturer’s instructions (Poly Scientific). Enterocyte differentiation was assessed by FITC-conjugated wisteria floribunda agglutinin (WFA) lectin staining (Vector Labs). Slides were imaged on an Axioskop 2 microscope (Zeiss, Thornwood, NY, USA) or on an LSM510 META confocal microscope (Zeiss).

Cell quantitation and data analysis

Multiple sections from the small intestine (duodenum) from at least 3 Nkx2.2 (+/+ ) and Nkx2.2 (−/−) mice were analyzed for each experiment. The number of cells per unit length of intestine was calculated for at least
Results

NKK2.2 is expressed in immature endocrine cells of embryonic and adult mouse small intestine

To first ascertain whether NKK2.2 is involved in gut NE differentiation, we evaluated NKK2.2 expression in embryonic and adult mouse proximal small intestine (duodenum) by immunofluorescent (IF) analysis. The proximal small intestine contains a variety of gut endocrine cell types, which arise from pluripotent stem cells in the intervillus/crypt regions and occupy characteristic locations along the crypt-villus axis (Wilson & Radtke 2006). Endocrine cells in mice can be detected starting on embryonic day (E) 9.5 in the pancreas and on E15.5 in the small intestine (Schwitzgebel et al. 2000, Jenny et al. 2002).

Coincident with the appearance of CgA- and 5-HT-positive cells in the intestine at E15.5, we detected NKK2.2 expression in intervillus regions (Fig. 1D–F). Although, we confirmed NKK2.2 expression in the pancreas at earlier time points (data not shown), we did not observe NKK2.2 expression in the intestine before E15.5 (Fig. 1A–C). NKK2.2 expression was seen at later embryonic time points and persisted in the adult intestine (Fig. 1G–I). In embryonic and adult intestine, NKK2.2 expression was mainly in the intervillus/crypt regions. Infrequently, we detected weak NKK2.2 expression along the villi. These observations suggest that Nkx2.2 is transiently expressed in immature and/or newly differentiated cells.

To determine whether Nkx2.2 is expressed in endocrine progenitors, we costained for NKK2.2 and NEUROG3. Approximately, 80% of NEUROG3-positive endocrine progenitor cells co-expressed NKK2.2 (Fig. 2A–D). Next, we studied the co-expression of NKK2.2 and MKI67, a marker for proliferating cells. We did not observe co-expression of NKK2.2 and MKI67, suggesting NKK2.2-positive cells have exited the cell cycle (Fig. 2E–H).

To determine whether Nkx2.2 is expressed in gut endocrine cells, we performed double IF analysis. The most predominant hormone in the gut is 5-HT, and we observed co-localization of NKK2.2 with 5-HT in the crypt compartment of adult intestine (Fig. 3A). We did not observe NKK2.2 expression in the villus regions, where more differentiated endocrine cells reside, as shown by the cells that were positive for 5-HT but negative for NKK2.2 (Fig. 3A). We also detected co-expression of NKK2.2 with GLP-1 (Fig. 3B), gastrin/CCK (Fig. 3C), and somatostatin (Fig. 3D) in adult intestinal crypts. Consistently, we observed NKK2.2 expression in the crypt compartment but not along the villi. Secretin
expression is known to be restricted to the villus compartment (Aiken et al. 1994); we confirmed this observation and again found NKX2.2 expression only in the crypts (Fig. 3E). Thus, we did not detect any cells that were positive for both Nkx2.2 and secretin. These results suggest that in the adult intestine, NKX2.2 is transiently expressed in newly differentiated endocrine cells that produce serotonin, GLP-1, gastrin/CCK, and somatostatin.

**Nkx2.2** (−/−) mice display defects in intestinal endocrine cell development

To elucidate the role of NKX2.2 in gut endocrine development, we analyzed the proximal small intestine (duodenum) in Nkx2.2 (−/−) mice. Since homozygous mutant animals die within 6 days of birth, we analyzed intestine from embryos at E18.5 (Sussel et al. 1998). At this time point, mutant embryos are viable and gut hormones are present. By routine H&E staining, we did not detect any abnormalities in the appearance of Nkx2.2 (−/−) intestine (data not shown). We first assayed for 5-HT expression by IF analysis because 5-HT is the most abundant gut endocrine cell type. Strikingly, we observed that cells producing 5-HT were absent from the intestine of Nkx2.2 (−/−) mice (Fig. 4A–C). Consistent with this, mRNA levels of tryptophan hydroxylase-1 (Tph1), which catalyzes the rate-limiting step in 5-HT biosynthesis in the gut, were absent in Nkx2.2 (−/−) intestine as assayed by qRT-PCR (Fig. 5B).

In the small intestine, particular endocrine cell types may serve as progenitors for other endocrine cells. For example, Aiken and Roth (1992) postulated that a population of cells that express substance P remain in the crypt and ultimately express 5-HT. They also suggested that another population of upwardly migrating gut endocrine cells sequentially express substance P, 5-HT, and secretin as they move from the crypt to the villus. We therefore examined the expression of tachykinin precursor 1 (Tac1) that encodes for substance P (by RT-PCR) and secretin (by RT-PCR and IF) and observed a marked decrease in the intestine of Nkx2.2 (−/−) compared with wild-type litter mates (Fig. 4G–I, 5A). These findings support a common differentiation pathway involving cells that produce substance P, 5-HT, and secretin.
Aiken et al. (1994) postulated that cells which express secretin might also arise from a distinct differentiation pathway for upwardly migrating cells that express gastrin, CCK, and GLP-1. In support of this postulate, we detected a decrease of cells producing gastrin/CCK and GLP-1 in the intestine of Nkx2.2 (−/−) mice, when compared with their Nkx2.2 (+/+) littermates (Fig. 4D–F). Transcript levels of gastrin, CCK, glucagon, and somatostatin were also decreased in Nkx2.2 (−/−) intestine (Fig. 5A). The glucagon gene encodes for preproglucagon, which undergoes post-translational processing to produce GLP-1, GLP-2, or glucagon (Rehfeld 1998). Therefore, Nkx2.2 is critical for the development of several types of gut endocrine cells.

Nkx2.2 (−/−) mouse intestine does not exhibit defects in proliferation, increased apoptosis, or deviation to other types of gut epithelial cells

Depletion of several gut endocrine cells in Nkx2.2 mutant mice may result from defects in epithelial proliferation, increased apoptosis, or deviation to an alternative cell fate. We did not observe impaired proliferation of Nkx2.2 mutant intestine when it was assessed by MKI67 labeling (WT = 21.3, MUT = 25.9 cells/mm; P = 0.26). When we assayed for cell
death as a cause for decreased gut endocrine populations in Nkx2.2 (-/-) mouse intestine by activated caspase3 staining, we did not detect an increase in apoptosis, which was low in both wild-type and Nkx2.2 mutant mice (WT = 0.84, MUT = 0.10 cells/mm; P = 0.30). We did not observe an increase in goblet cell numbers (WT = 23.6, MUT = 21.2 cells/mm; P = 0.75) in the intestine of Nkx2.2 mutant mice to suggest that endocrine cells adopted a goblet cell fate in the absence of Nkx2.2. Moreover, expression of cryptidin, an early Paneth cell marker, or enterocyte glycoprotein distribution (assessed by FITC-conjugated WFA staining) was not altered in Nkx2.2 mutant intestine (data not shown).

The number of ghrelin-producing cells is increased in Nkx2.2 (-/-) mouse intestine

We observed a marked reduction in endocrine cells in Nkx2.2 (-/-) mouse intestine; however, we found no evidence for a decrease in proliferation, increase in apoptosis, or deviation to an alternative epithelial cell fate to explain the loss of endocrine cells. In the pancreas, Nkx2.2 is required for the differentiation of all β-cells, which produce insulin, as well as some cells that produce glucagon and pancreatic polypeptide (Sussel et al. 1998). In the absence of Nkx2.2, β-cells are replaced by ghrelin-producing cells in the pancreas (Prado et al. 2004, Heller et al. 2005). We therefore investigated whether an increase of ghrelin-producing cells was associated with the depletion of most endocrine cell types in Nkx2.2 mutant intestine. We analyzed the intestine of Nkx2.2 mutant mice and observed a marked increase in the number of ghrelin cells (Fig. 4M–O). Concordant with the detection of increased numbers of ghrelin cells in Nkx2.2 (-/-) intestine, the expression of ghrelin assayed by qRT-PCR was elevated in Nkx2.2 mutant intestine (Fig. 5C). Potential reasons for the difference in magnitude increase in ghrelin cell number and transcript level in Nkx2.2 (-/-) intestine include: 1) Nkx2.2 loss may cause more of an increase in ghrelin transcript level than cell number; 2) differential sensitivity in the detection of ghrelin transcript level and protein by the methods used; and 3) differences in the stability of ghrelin transcript and protein. As in the pancreas (Schwitzgebel et al. 2000), NEUROG3 expression levels in Nkx2.2 (-/-) intestine did not differ from those in wild-type littermates when assayed by IF and qRT-PCR (data not shown). Similar to its role in the pancreas, Nkx2.2 functions to control endocrine cell fate in the intestine.

NKX2.2 expression in normal human gut tissue recapitulates that in mice

Given the importance of Nkx2.2 function in the differentiation of NE cells in the mouse gut, we
evaluated NKX2.2 expression in human gut tissues. Using immunohistochemistry (IHC), we detected strong NKX2.2 expression in the nuclei of islets in normal human adult pancreas (Fig. 6A). As in adult mice (Sussel et al. 1998), we did not observe NKX2.2 expression in pancreatic exocrine tissue. In normal human adult small intestine, NKX2.2 protein is present in cells located in the crypt compartment (Fig. 6B and C). Infrequently, we detected weak NKX2.2 expression in cells located in the villi; however, the intensity of NKX2.2 expression in the villi was always much less than in the crypts. Therefore, the pattern of NKX2.2 expression in normal human adult pancreas and small intestine resembles that found in mice, suggesting a conserved role for NKX2.2 in NE differentiation in mouse and human gut.

**Figure 4** Nkx2.2 regulates enteroendocrine development. Immunofluorescence analysis of duodenal sections of control (A, D, G, J, M) or Nkx2.2 (−/−) (B, E, H, K, N) mouse embryos at E18.5 with the antibodies indicated. In Nkx2.2 (+/+) intestine, 5-HT (A), gastrin/CCK (D), secretin (G), somatostatin (J), and ghrelin (M) are observed in characteristic patterns. There is a near absence of 5-HT (B), gastrin/CCK (E), secretin (H), and somatostatin (K) expression in Nkx2.2 (−/−) intestine. Conversely, ghrelin (N) expression is increased in Nkx2.2 (−/−) intestine. (C, F, I, L, O) Results of immunofluorescence experiments presented quantitatively. The number of hormone-positive cells per mm intestinal length of every fourth section of Nkx2.2 (+/+) (n=3) and Nkx2.2 (−/−) (n=3) intestine was counted. Results represent mean ± S.E.M.

**NKK2.2 expression in human gut NE tumors**

Because conserved pathways of NE differentiation function in normal and neoplastic tissues (Borges et al. 1997, Nakakura et al. 2001), we evaluated NKX2.2 expression in human NE tumors derived from the gut. Using qRT-PCR, we analyzed NKX2.2 expression in matched pairs of normal and tumor samples from patients with well-differentiated NE tumors of the ileum (n=4) and pancreas (n=2). When compared with matched normal ileum samples, NE tumors of the ileum (three primary ileum tumors and one liver metastasis) showed an approximately 20- to 200-fold increase in NKX2.2 expression (Fig. 6O). In addition, we observed about a 9- to 900-fold increase in NKX2.2 expression in pancreas NE tumor samples when
compared with matched normal pancreas tissue (Fig. 6P). These findings indicate that NKX2.2 is expressed in NE tumors derived from the gut, which may reflect utilization of a common pathway of NE differentiation in normal and neoplastic tissues.

To further evaluate NKX2.2 expression in human tumors, we used IHC to detect NKX2.2 protein in a variety of well-differentiated NE tumors found throughout the gut. Overall, we detected nuclear expression of NKX2.2 in 83% (24/29) of human NE tumor samples (Table 1). Specifically, NKX2.2 was present in NE tumors of the stomach (1/1), duodenum (1/1), ampulla of Vater (2/2), pancreas (14/16; Fig. 6D), ileum (5/5; Fig. 6H), and colon (1/1). NKX2.2 was detected in both functioning and non-functioning NE tumors. Interestingly, NKX2.2 was not present in NE tumors of the bronchus (0/3; Fig. 6L).

For the five NE tumor specimens (two pancreas, three bronchus) in which we did not observe NKX2.2 expression by IHC, NE markers (CgA, synaptophysin) and/or hormones were present. Because robust NKX2.2 expression is readily detected by IHC in most human NE tumors from diverse GI primary sites, we conclude that NKX2.2 is a novel GI NE tumor marker.

Discussion

In the present study, we show that the homeodomain transcription factor NKX2.2 functions in immature endocrine cells to control NE differentiation in mouse intestine and is expressed in most human GI NE tumors derived from diverse primary sites. We also show that NKX2.2 is expressed in normal human pancreas and intestine in a similar distribution as in mice, supporting the use of the mouse as a model for studying NE differentiation in the human gut. Together, our findings suggest a conserved role for NKX2.2 in NE differentiation of normal and neoplastic gut.

We are the first to report that NKX2.2 expression is restricted to the intervillus/crypt regions of embryonic and adult mouse intestine, where it is co-expressed in NEUROG3-positive endocrine progenitors and newly differentiated endocrine cells. The presence of NKX2.2 in immature endocrine cells is consistent with our finding that NKX2.2 functions to control endocrine cell fate in the intestine. Our analysis of NKX2.2 (−/−) mouse intestine suggests NKX2.2 functions downstream of Neurog3 to control the development of numerous endocrine cells. In the intestine of NKX2.2 (−/−) mice, Neurog3 expression was unaffected, and we observed a dramatic reduction in the number of cells producing numerous hormones, such as serotonin, gastrin, CCK,
somatostatin, GLP-1, substance P, and secretin, but an increase in cells producing ghrelin. These data suggest that endocrine cells in the intestine arise from a common progenitor and that \textit{Nkx2.2} acts to specify or maintain the expression of numerous hormones.

The study reported herein expands on and is consistent with that of Desai \textit{et al.} (2008). Desai \textit{et al.} (2008) showed that \textit{Nkx2.2} regulates endocrine cell fate in the small intestine and is expressed in glucagon-producing cells. Our study is the first to show that \textit{NKX2.2} expression is restricted to immature endocrine cells located in the intestinal crypts. In particular, we observed that \textit{Nkx2.2} expression is limited to \textit{NEUROG3}-positive endocrine progenitors and newly-differentiated endocrine cells, producing numerous hormones, such as 5-HT, gastrin/CCK, somatostatin, and GLP-1. Importantly, our study reveals several new aspects of \textit{NKX2.2} expression in neoplastic as well as normal gut. We are the first to show \textit{NKX2.2} is expressed in the majority of NE tumors derived from the gut. In particular, \textit{NKX2.2} expression was detected in NE tumors of the stomach, duodenum, ampulla of Vater, pancreas, ileum, and colon. In support of our observations, \textit{NKX2.2} is
present on chromosome 20p11, and amplification of chromosome 20p is a frequent allelic alteration in well-differentiated NE tumors of the gut (Kim et al. 2008). Conserved pathways of NE differentiation function in diverse contexts. In normal tissues, the basic helix-loop-helix transcription factor ASCL1 functions in the development of neurons producing 5-HT, pulmonary NE cells, and thyroid C cells (Blaugrund et al. 1996, Borges et al. 1997, Lanigan et al. 1998, Pattyn et al. 2004). Studies have also suggested ASCL1 regulates the NE phenotype in cancers of many sites: brain, thyroid, lung, prostate, and GI tract (Borges et al. 1997, Hu et al. 2004, Nakakura et al. 2005, Shida et al. 2005, Somasundaram et al. 2005, Kunnimalaiyaan et al. 2006, Rousseau et al. 2006). Evidence also suggests that ASCL1 may promote tumorigenesis (Linnoila et al. 2000, Osada et al. 2005). NKX2.2 functions with ASCL1 in 5-HT neuron development (Briscoe et al. 1999, Cheng et al. 2003, Craven et al. 2004, Pattyn et al. 2004). Recently, NKX2.2 has been shown to promote tumorigenesis in Ewing’s sarcomas (Smith et al. 2006). These previous studies in conjunction with the data presented herein demonstrate that NKX2.2 is involved in both normal and neoplastic development, and it is tempting to speculate that NKX2.2 might act with ASCL1 in these contexts. Transcription factors, such as NKX2.2 and ASCL1, may exhibit dual functions: 1) to regulate NE differentiation and

### Table 1 Immunohistochemical analysis of NKX2.2, CgA, and Syn expression in NE tumors of the gut

<table>
<thead>
<tr>
<th>Primary site</th>
<th>NKX2.2 IHC</th>
<th>CgA IHC</th>
<th>Syn IHC</th>
<th>Functioning/ non-functioning</th>
<th>Hormones/syndrome</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 Stomach</td>
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<td>Positive</td>
<td>Negative</td>
<td>NF</td>
<td>Gastrinoma</td>
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<td>ND</td>
<td>F</td>
<td>5-HT</td>
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<tr>
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<td>4+</td>
<td>Positive</td>
<td>Positive</td>
<td>NF</td>
<td>5-HT</td>
</tr>
<tr>
<td>4 Ampulla</td>
<td>4+</td>
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<td>Positive</td>
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<td>Insulinoma</td>
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<td>Positive</td>
<td>F</td>
<td>Glucagon, VIP</td>
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<td>F</td>
<td>Glucagonoma</td>
</tr>
<tr>
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<td>NF</td>
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<td>Positive</td>
<td>F</td>
<td>Gastrinoma, MEN I</td>
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<td>F</td>
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<td>F</td>
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</tr>
<tr>
<td>27 Bronchus</td>
<td>0</td>
<td>Positive</td>
<td>Positive</td>
<td>F</td>
<td>5-HT</td>
</tr>
<tr>
<td>28 Bronchus</td>
<td>0</td>
<td>Positive</td>
<td>ND</td>
<td>F</td>
<td></td>
</tr>
<tr>
<td>29 Bronchus</td>
<td>0</td>
<td>Positive</td>
<td>Positive</td>
<td>F</td>
<td>5-HT/MEN I (pituitary adenoma, HPT, gastrinoma of pancreas and duodenum)</td>
</tr>
</tbody>
</table>

CgA, chromogranin A; Syn, synaptophysin; IHC, immunohistochemistry; LN, lymph node; NF, non-functioning; F, functioning; MENI, multiple endocrine neoplasia I; HPT, hyperparathyroidism; 5-HT, serotonin; ND, not done.
2) to promote tumorigenesis. Therefore, the study of the determinants of NE differentiation in normal development has the potential to provide important insights into NE tumor biology and vice versa.

Elucidating the transcription factors that maintain the NE phenotype in tumors and their regulation by signaling pathways has the potential to directly impact patient morbidity and mortality. Functioning NE tumors, by definition, produce debilitating symptoms due to the elaboration of hormones (Nakakura & Bergsland 2007, Nakakura et al. 2007, Modlin et al. 2008). Hormones such as serotonin also stimulate NE tumor growth via autocrine and paracrine stimulatory loops (Ishizuka et al. 1992, von Wichert et al. 2000).

We and others have previously shown that Notch signaling inhibits ASC11, NE marker, and hormone expression, as well as growth, in a variety of NE tumors (Kunnimalaiyan et al. 2005, 2006, Nakakura et al. 2005). As a result, pharmacological activators of Notch signaling, such as valproic acid, are being evaluated in clinical trials for patients with advanced NE tumors (Greenblatt et al. 2007a,b). The effect of Notch signaling on NNX2.2 expression in NE tumors is not known; however, in the developing intestine, the absence of the Notch effector, Hes1, leads to increased NNX2.2 expression, suggesting NNX2.2 is a Notch target in normal intestinal epithelium (Jensen et al. 2000b). It is plausible that targeting NNX2.2 in NE tumors might actually worsen the biology by causing dedifferentiation to a poorly differentiated NE carcinoma. Further studies of NNX2.2 and other transcription factors with conserved functions in normal and neoplastic tissues are likely to provide new insights into NE tumor biology that can be exploited to better treat patients.

**Declaration of interest**

There is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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