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PIK3CA, KRAS, and BRAF mutations in intraductal papillary mucinous neoplasm/carcinoma (IPMN/C) of the pancreas

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Abstract

Background and aims—Recent studies have reported high frequencies of somatic mutations in the phosphoinositide-3-kinase catalytic- α (*PIK3CA*) gene in various human tumors. Three hot-spot mutations in the exons 9 and 20 have been proven to activate the Akt signalling pathway. The Raf/MEK/ERK (mitogen-activated protein kinase) signal transduction is an important mediator of a number of cellular fates including growth, proliferation, and survival. The BRAF gene is activated by oncogenic RAS, leading to cooperative effects in cells responding to growth factor signals. Here we evaluate the mutational status of *PIK3CA*, *KRAS*, and *BRAF* in intraductal papillary mucinous neoplasm/carcinoma (IPMN/IPMNC) of the pancreas.

Materials and methods—Exons 1, 4, 5, 6, 7, 9, 12, 18, and 20 of *PIK3CA*, exons 1 of *KRAS*, and exons 5, 11, and 15 of *BRAF* were analyzed in 36 IPMN/IPMC and two mucinous cystadenoma specimens by direct genomic DNA sequencing.

Results—We identified four somatic missense mutations of *PIK3CA* within the 36 IPMN/IPMC specimens (11%). One of the four mutations, H1047R, has been previously reported to be a hot-spot mutation. Furthermore, we found 17 (47%) *KRAS* mutations in exon 1 and one missense mutation (2.7%) in exon 15 of *BRAF*.

Conclusion—This data is the first report of *PIK3CA* mutation in pancreatic cancer and it appears to be the first oncogene to be mutated in IPMN/IPMC but not in conventional ductal

adenocarcinoma of the pancreas. Our data provide evidence that *PIK3CA* and *BRAF* contribute to the tumorigenesis of IPMN/IPMC, but at a lower frequency than *KRAS*.

Keywords

IPMN; IPMC; Pancreas; *PIK3CA*; *KRAS*; *BRAF*; Mutation

Introduction

Intraductal papillary mucinous neoplasms (IPMN) are pancreatic exocrine lesions composed of dilated main or branch ducts lined by mucin producing atypical epithelium, which usually proliferates in a papillary fashion [1]. Based on their increasing architectural and nuclear atypia, IPMN are divided into three groups: intraductal papillary mucinous adenoma (IPMA), borderline IPMN (IPMB), and intraductal papillary mucinous carcinoma (IPMC) [1]. According to the absence or presence of neoplastic cells invading the pancreatic tissue surrounding the involved ducts, IPMC are separated into invasive and noninvasive types [2]. IPMN are precancerous lesions and disclose a progression pattern similar to the “adenoma–carcinoma sequence” in colorectal cancer [3–6]. Most IPMN are slow growing and less aggressive compared with conventional ductal adenocarcinoma. Borderline lesions and carcinoma are accompanied by less atypical lesions in the vicinity, and transition from adenoma to adenocarcinoma has been described. The overall incidence of invasive carcinoma associated with an IPMN is 20% to 40% [7] and invasiveness seems to be the strongest prognostic factor [4]. The prognosis of patients with noninvasive IPMN consisting of adenoma, adenocarcinoma in situ, or minimally invasive adenocarcinoma is excellent, and the 5-year survival rate was reported to be 77% to 100% [4, 8–10]. However, invasive IPMC that macroscopically involves the pancreatic parenchyma comprises 16% to 43% of all IPMN lesions, and the 5-year survival rate for patients with these lesions varied widely from 0% to 64% in several reported series [4, 8, 9, 11–13]. A significant proportion of the patients with completely resected noninvasive IPMN may develop pancreatic adenocarcinoma in the pancreatic remnant and die of disseminated disease. Other studies have also reported recurrences of invasive carcinoma in completely resected noninvasive IPMN [5, 6], some of which demonstrated only moderate dysplasia (borderline IPMN).

Phosphatidylinositol-3 kinases (PI3Ks) constitute a large and complex family of lipid kinases encompassing three classes with multiple subunits and isoforms [14–16]. They play an important role in several cellular functions, such as proliferation, differentiation, chemotaxis, survival, trafficking, and glucose homeostasis [14]. Class IA PI3Ks are heterodimeric proteins composed of a p110 catalytic subunit and a p85 regulatory subunit [17], which can be activated through interaction with phosphotyrosine residues of receptor tyrosine kinases [18, 19] or through the binding of active RAS to the p110 catalytic subunit [16, 19–21]. P85 lacks kinase activity and acts as an adaptor, coupling with the p110 subunit to activate protein tyrosine kinases [22]. Activated PI3Ks phosphorylate the inositol ring 3'-OH group in inositol phospholipids to generate the second messenger phosphatidylinositol-3,4,5-triphosphate (PIP₃) [23], which in turn activates diverse cellular target proteins such as the survival signalling kinase Akt/protein kinase B [14, 15, 24]. A tumorigenic role has been proposed for the *PIK3CA* gene that encodes the catalytic p110 α subunit of phosphatidylinositol 3-kinase belonging to the class IA of PI3Ks [14, 16]. Previously Samuels et al. reported mutations in *PIK3CA* in several tumor types, namely colorectal cancer, gastric cancer, glioblastoma, and breast and lung cancer [25]. Other independent studies in hepatocellular carcinomas, breast carcinomas, lung cancers, ovarian carcinomas, brain tumors, acute leukemias, and head and neck squamous cell carcinomas have since supported and emphasized the oncogenic potential of *PIK3CA* in the development of cancer [26–30]. In the study by Samuels et al. [25], three *PIK3CA*

mutational hot-spots were described and found to affect the helical (exon 9) and catalytic (exon 20) protein domains. Mutations were also described in exons 1, 2, 4, 7, 12, 14 and 18 of *PIK3CA*, but only in a minority of cases [25, 26]. Similar to colon tumors, *PIK3CA* mutations also clustered in the three hot-spot regions (exons 9 and 20) in gastric carcinomas [25, 27, 31]. No *PIK3CA* mutations have been previously reported in IPMN, IPMC, or conventional pancreatic ductal adenocarcinoma [25].

Since the discovery of the role of *RAS* oncogenes in tumorigenesis, an increasing focus has been set to define its oncogenic signal transduction pathway [32]. In trying to understand how Ras proteins transmit extracellular growth signals, the mitogen-activated protein (MAP) kinase pathway has emerged as an important link between membrane-bound Ras proteins and the nucleus [33, 34]. This key Ras effector pathway involves the kinase cascade Raf/MEK/ERK (*MEK*, MAPK/ERK kinase; *ERK*, extracellular signal-related kinase) [35]. Signalling through the MAPK cascade is transduced by guanosine triphosphate loading of Ras leading to the activation of Raf kinase. In mammalian cells, there are three isoforms of *RAF*: *ARAF*, *BRAF*, and *CRAF/RAF1* [36]. Although all three of the Raf isoforms share a common function with respect to MEK phosphorylation, studies have shown that these proteins might be differentially activated by oncogenic Ras [33, 37]. Recently activating *BRAF* mutations, in particular the V600E “hot-spot” mutation in *BRAF*'s exon 15, have been described in about 15% of all human cancers, especially in malignant melanomas, papillary thyroid cancer as well as lung and ovarian cancer [38–43]. Reported genetic alterations in IPMN include mutations in the *KRAS* [44–49], *TP53* [47], and *STK11/LKB1* genes [50, 51] as well as loss of heterozygosity of several chromosomal loci [50, 52]. In addition to these genetic alterations, aberrant DNA methylation may contribute to the inactivation of a subset of tumor-suppressor genes in IPMN [53, 54]. Previous studies have found mutations in the exon 1 of *KRAS* in 31% to 86% of IPMNs [44–49]. Here, we analyzed the status of *PIK3CA*, *KRAS*, and *BRAF* to elucidate a possible role of these genes in the tumorigenesis of IPMN and IPMC.

Materials and methods

Patients and tissue samples

Surgical paraffin-embedded IPMN/IPMC and mucinous cystadenoma samples from 38 patients (female, $n = 14$; male, $n = 24$; median age, 68.1years; range, 41–84years) were obtained from the archival tissue collection of the Columbia University Medical Center. Acquisition of the tissue specimens was approved by the Institutional Review Board of Columbia University Medical Center and performed in accordance with Health Insurance Portability and Accountability Act regulations. In detail, we analyzed three IPMN, adenoma (female, $n = 1$; male, $n = 2$; median age, 62.7years; range, 53–77years), four IPMN, borderline (female, $n = 1$; male, $n = 3$; median age, 66.3years; range, 62–72years), five IPMC without invasion (male, $n = 5$; median age, 69.2years; range, 59–81years), 24 IPMC with invasive carcinoma (male, $n = 14$; female, $n = 10$; median age, 68.9years; range, 41–84years), and two mucinous cystadenomas (female, $n = 2$; median age, 57.5years; range, 53–62years). Thirty-two of these lesions arose in the pancreatic head, one in the uncinate process, four within the transition from pancreatic head to the body, and one within the body. The maximum diameter of the lesions ranged from 0.4 to 7cm (mean, 4.2cm) (for a more detailed register, see Table 1).

DNA samples for mutation analysis

All tissue and genomic DNA samples were handled in an environment free of polymerase chain reaction (PCR) products. All samples were coded, and the investigator was unaware of the patients' clinical data. Paraffin-embedded tumor samples were microdissected to ensure

the highest possible amount of tumor cells. Surrounding nontumorous tissue or tissue derived from a tumor-free block of each patient served as corresponding normal control. Genomic DNA was extracted using the QIAmp DNA Mini Kit (Qiagen, Valencia, CA, USA) according to the manufacturer's instructions for paraffin-embedded tissues. Exons 1, 4, 5, 6, 7, 9, 12, 18, and 20 of *PIK3CA*, exon 1 of *KRAS*, and exons 5, 11, and 15 of *BRAF* were analyzed by PCR amplification of genomic DNA and direct sequencing. Genomic DNA (40ng per sample) was amplified with primers that had been designed to amplify each exon and its exon/intron boundaries of *PIK3CA* [25, 30] the codons 12 and 13 of *KRAS* or each of the three exons and its exon/intron boundaries in the *BRAF* locus [39, 40, 55]. All PCR products were purified (QIAquick PCR Purification Kit; Qiagen, Valencia, CA, USA) prior to sequencing. The PCR primers also served as the sequencing primers. Sequencing was performed with Applied Biosystems' 3100 capillary automated sequencer at the DNA Core Facility of Columbia University Medical Center. Each sample found to have a genetic alteration in the target gene was subsequently sequenced in the reverse direction to confirm the mutation and further verified by sequencing of a second PCR product derived independently from the original template.

Results

In our study, four of the 36 specimens (11%) contained a somatic mutation of the *PIK3CA* gene (Fig. 1 and Table 1) —one in exon 4 (T324I in an IPMC with invasion), one in exon 9 (W551G in an IPMB), and two in exon 20 (S1015F in an IPMC and H1047R in an IPMC with invasion)— whereas the samples showing the W551G and S1015F mutations were also harboring *KRAS* mutations. One of the missense mutations in exon 20 of *PIK3CA*, H1047R, is a previously described hot-spot mutation [25]. The other mutations in exons 4 and 9 are novel. We furthermore identified 17 (47%) mutations within the *KRAS* gene at codon 12 and one mutation (2.7%) in the exon 15 of *BRAF* (S616F in an IPMC with invasion) in the 36 IPMN/IPMC specimens. All mutations were sporadic, since none of the mutations was observed in the matching normal tissues (Fig. 1). Of the 17 samples that harbored *KRAS* mutations, five were IPMN cases without associated invasive carcinoma (5/12 samples, 41.7%) and 12 were IPMC with associated invasive carcinoma (12/24 samples, 50%). The *KRAS* codon 12 mutation was detected in IPMA (1/3), IPMB (2/4), IPMC without invasion (2/5), and IPMC with invasion (12/24) (Table 1). The spectrum of *KRAS* codon 12 mutations was G12D (7/17), G12V (6/17), and G12R (4/17). The exon 15 *BRAF* mutation was found in an IPMC sample with associated invasive carcinoma, which also harbored a *KRAS* (G12R) mutation (Table 1).

Discussion

Recently, much attention has been given to the significance of the *PIK3CA* gene mutations identified in several human tumors. Mutational analysis of the *PIK3CA* gene has revealed that genetic alterations at its locus occur in a wide spectrum of human neoplasms [25–30]. *PIK3CA* mutations preferentially occur in exons 9 and 20 (>75%), affecting the functionally important helical and kinase domains of the protein [25–27, 29, 31]. Functional studies have shown that PI3Ks carrying anyone of the three hot-spot mutations are able to induce transformation in cultures of chicken embryo fibroblasts and that the transforming activity of the mutant is correlated with increased lipid kinase activity and activation of the Akt signaling pathway [25, 56]. Although two of our mutations in exons 9 and 20 are not hot-spot mutations, the mutations are likely to have affected the kinase activity of the PIK3CA protein. The mutation within exon 4, nucleotide 971 C→T, which leads to an alteration of codon 324 ACA (T) → ATA (I), has not been described before. Although the significance of the novel mutation T324I, which belongs to the C2 domain, is unclear, a recent study found that the C2 domain of protein kinase C δ could be a phosphotyrosine-binding domain [57].

Since 7% of *PIK3CA* mutations have been detected within the C2 domain [25], it might be of value to study whether the C2 domain also plays a critical role in *PIK3CA* activity in the future. The frequency of *PIK3CA* mutations has been reported to be 32% in colon cancer, 4–25% in gastric cancer, 8–40% in breast cancer, 5–27% in brain tumors, 4% in lung cancer, and 4–7% in ovarian cancer [25, 28, 31, 58]. Samuels et al. screened 11 pancreatic ductal adenocarcinoma cell lines and found no mutation in the entire coding region of the *PIK3CA* gene [25]. A negative finding was also reported by Gallmeier et al. who examined the exons 9 and 20 of *PIK3CA* for mutation using direct genomic sequencing on the genomic DNA from 91 pancreatic cancer xenografts [59]. In the present study, we report 11% (4/36) of IPMN/IPMC to contain *PIK3CA* mutations. Two of these mutations (W551G and S1015F) were found in IPMN with nuclear grade 3 (IPMC) and nuclear grade 2 (IPMB), respectively, without associated invasive carcinoma. The other two (T324I and H1047R) were observed in IPMC with associated invasive carcinoma. The findings in colorectal cancers indicate that *PIK3CA* mutations generally arise just before or coincident with invasion [25]. Our data show that, in IPMN, mutations of the *PIK3CA* gene seem to be a rather late event on the transition of these lesions to malignancy.

Frequent *KRAS* gene mutations at codon 12 have been reported in several cancers, including those from colonic and pancreatic tissues [60–63]. Previous studies have found *KRAS* mutations, mainly at codon 12 in exon 1, in 31% to 86% of IPMN (47% in our study) [44–49]. The wide variety of the reported frequencies most likely is due to the ongoing better definition of these lesions [1, 64, 65] and might also be dependent on the sensitivity of a chosen screening methodology. In the present study, the distribution of *KRAS* mutation showed a single mutation in all observed cases. *KRAS* mutation is an early event in the tumorigenesis of IPMN—*KRAS* mutation was observed in IPMN; adenoma (1/3) and its mutation frequency remain consistent as IPMN progresses (2/4 in IPMN, borderline; 2/5 in IPMC; and 12/24 in IPMC with invasion). There was no tumor size, gender, or age bias observed associated with *KRAS* mutation. Unlike pancreatic ductal adenocarcinoma where *KRAS* is mutated at a frequency close to 100% [62, 63], 14–69% (53% in our study) of IPMN do not harbor an active *KRAS* mutation. This suggests that a relatively large percentage of IPMN/IPMC might use alternative ways other than *KRAS* mutation to stimulate this Ras-Raf-MEK-ERK-MAP kinase pathway. *BRAF*, a serine/threonine kinase located immediately downstream in Ras signalling, has been examined in a variety of human malignant neoplasms and found to be mutated frequently in malignant melanomas, thyroid cancer, and low-grade ovarian cancer and at lower frequencies in other cancer types [38–40, 42, 55, 66, 67]. Here we report a somatic *BRAF* mutation out of the 36 cases of IPMN/IPMC examined (2.7%). While *BRAF* contributes to the tumorigenesis of IPMN, it is not a frequent event and certainly does not entirely explain the lower mutation rate of *KRAS* in IPMN/IPMC than in pancreatic ductal adenocarcinoma. The *BRAF* mutation occurred at nucleotide 1850, a C to T change at codon 616 of the *BRAF* gene, leading to an amino acid change from serine to phenylalanine (S616F). Although located at exon 15, the S616F mutation is not the previously described hot-spot mutation at exon 15 (V600E) of the *BRAF* gene [38, 39, 55]. This mutation was also found to coexist with a G12R mutation of *KRAS* in the same sample. It has been observed previously in colon and lung cancers that *BRAF* mutations, other than *BRAF* V600E, coexisted with *RAS* mutations [39]. The *BRAF* V600E mutation seems to uncouple cells from their proliferation requirement of *RAS*, and therefore mutation of *RAS* was not detected in any of the tumors carrying *BRAF* V600E mutation [39]. In vitro data indicated that *BRAF* V600E mutants can be further activated by mutant *RAS*, whereas other *BRAF* mutants remain dependent on *RAS* function [39]. A previous study on pancreatic ductal adenocarcinoma revealed that the *BRAF* hot-spot mutation was observed in two of nine tumors retaining wild-type copies of the *KRAS*, *NRAS*, and *HRAS* genes, but none in 72 adenocarcinomas with *KRAS* mutations within exons 11 and 15 [68]. In contrast,

another study found both *KRAS* and *BRAF* V600E mutations coexisting in two cases of pancreatic ductal adenocarcinoma [69]. These two cases did not exhibit different clinicopathological characteristics from pancreatic cancers with *KRAS* mutation alone [69]. The novel S616F mutation observed here is also in the B-Raf activation segment [70], but its functional effect is unknown. Cells with activating mutations in both *KRAS* and *BRAF* had a substantially higher B-Raf kinase activity and ERK 1/2 phosphorylation activities than those with *BRAF* mutation alone [39]. It is possible that tumors with both *BRAF* and *KRAS* mutations have an accelerated course in the development or progression. Together, these observations suggest that different *BRAF* mutations can have distinct transforming potential in tumorigenesis, which would be worthy of further investigations in future studies.

So far, genetic analyses of IPMN have disclosed abnormalities in many of the same genes altered in conventional ductal adenocarcinoma, including mutations of *KRAS* [44], *TP53/p53* [71], and *CDKN2A/p16* genes [72]. In addition, as is true for pancreatic ductal carcinomas, a number of genes, including *CDKN2A/p16*, may be epigenetically inactivated in IPMN through aberrant DNA methylation [53, 54, 73, 74]. The Peutz-Jeghers gene *STK11/LKB1* is inactivated more frequently in IPMN (up to one third) than in ductal adenocarcinoma (4%) [51, 75], and some patients with the Peutz-Jeghers Syndrome develop IPMN [50]. In contrast to ductal adenocarcinomas and pancreatic intraepithelial neoplasia-3 lesions, abnormalities in the *MADH4/SMAD4/DPC4* gene seem to be rare in IPMN [76]. *PIK3CA* is the first gene to be found mutated in IPMN that had not been reported in ductal adenocarcinoma. Although the *BRAF* mutation frequency in IPMN/IPMC is low compared with those observed in malignant melanoma and colon cancers, our data suggest that alteration of the Ras-Raf-MEK-ERK-MAP kinase pathway by *BRAF* mutation together with *RAS* mutation may play an important role in the tumorigenesis of IPMN/IPMC.

Conclusion

In summary, this is the first report of *PIK3CA* mutation in pancreatic cancer and it appears to be the first oncogene to be mutated in IPMN/IPMC and not in conventional ductal adenocarcinoma of the pancreas. Our data provide evidence that oncogenic properties of *PIK3CA* and *BRAF* contribute to the tumorigenesis of IPMN/IPMC, but at a lower frequency than *KRAS*.

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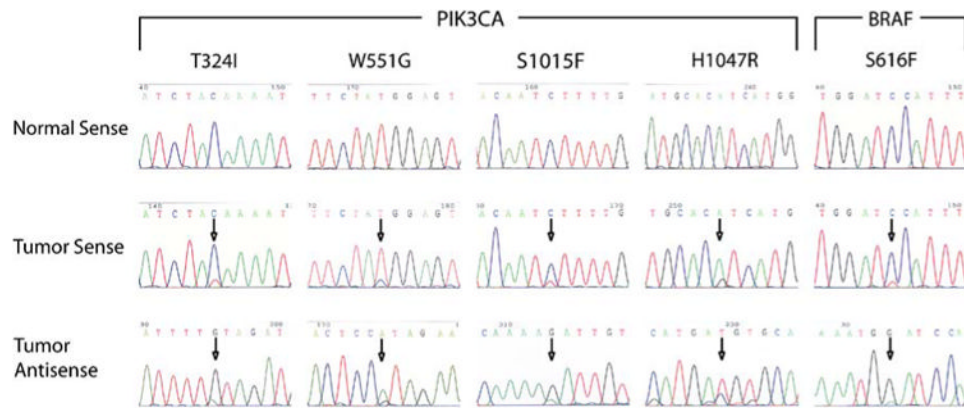


Fig. 1. *PIK3CA* and *BRAF* mutations found in IPMN/IPMC. One of the four *PIK3CA* mutations (H1047R) was a hot-spot mutation. The other mutations were novel. All mutations were confirmed to be somatic

Table 1

Summary of the clinical data and mutation status of the lesion investigated

Case no.	Sex	Age	Lesion analyzed	IPMN nuclear grade	Differentiation of invasive carcinoma	Location within pancreas	Maximum dimension ^a (cm)	PIK3CA mutation	KRAS mutation	BRAF mutation
1	M	62	IPMB	2	N/A	Body	–	W551G	G12D	
2	M	73	IPMC/inv	3	Moderate	Head/body	4		G12D	
3	M	67	IPMC/inv	3	Moderate	Head	–		G12V	
4	M	69	IPMC	3	N/A	Head	3.5	S1015F	G12V	
5	F	75	IPMC/inv	3	Moderate	Head	5.5	T324I	G12V	
6	F	68	IPMC/inv	3	Moderate	Head	5		G12V	
7	M	65	IPMB	2	Poor ^b	Head	5			
8	F	66	IPMB	2	N/A	Uncinate process	2		G12V	
9	M	84	IPMC/inv	3	Moderate	Head	5			
10	M	53	IPMA	1	N/A	Head	3.5		G12V	
11	M	71	IPMC/inv	2–3	N/A	Head	–			
12	M	81	IPMC	3	N/A	Head	2.5			
13	M	63	IPMC	3	Moderate/poor ^b	Head	2.3			
14	M	66	IPMC/inv	3	Moderate/poor	Head	6	HI047R		S616F
15	F	70	IPMC/inv	3	Moderate/poor	Head/body	7		G12R	
16	F	70	IPMC/inv	3	Moderate	Head	1.5			
17	M	72	IPMB	2	N/A	Head	0.4			
18	F	53	mucinous cystadenoma	1	N/A	Head	3			
19	M	79	IPMC/inv	3	Moderate/poor	Head	6		G12R	
20	M	63	IPMC/inv	3	Moderate/poor	Head	3.5		G12R	
21	M	77	IPMA	1	N/A	Head/body	2.2			
22	F	62	mucinous cystadenoma	1	N/A	Head	2			
23	M	41	IPMC/inv	3	Moderate/poor	Head	5			
24	M	71	IPMC/inv	3	Moderate/poor	Head	1.5			
25	F	58	IPMA	1	N/A	Head	1.5			
26	M	49	IPMC/inv	3	Moderate	Head	4.5			
27	M	71	IPMC/inv	3	Moderate/poor	Head	5.5		G12D	
28	M	74	IPMC	3	Well ^b	Head/body	–			
29	M	59	IPMC	3	Poor ^b	Head	7		G12V	
30	M	81	IPMC/inv	3	Moderate/poor	Head	3			

Case no.	Sex	Age	Lesion analyzed	IPMN nuclear grade	Differentiation of invasive carcinoma	Location within pancreas	Maximum dimension ^a (cm)	PIK3CA mutation	KRAS mutation	BRAF mutation
31	F	80	IPMC/inv	3	Moderate/poor	Head	5		G12R	
32	F	66	IPMC/inv	3	Poor	Head	3			
33	F	77	IPMC/inv	3	Poor	Head	3			
34	M	73	IPMC/inv	3	Poor	Head	5.5		G12D	
35	F	77	IPMC/inv	3	Well	Head	3.2		G12D	
36	F	61	IPMC/inv	3	Well	Head	1		G12D	
37	M	62	IPMC/inv	3	Moderate	Head	2.2			
38	F	59	IPMC/inv	3	Moderate	Head	3.4		G12D	

IPMA IPMN adenoma, IPMB IPMN borderline, IPMC/inv IPMC with invasion, N/A not applicable, – not available

^aMaximum tumor size includes both invasive and noninvasive components of tumor.

^bInvasive carcinoma was associated with IPMN/IPMC in pancreatic resection, but the lesion analyzed did not sample invasive carcinoma.