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Mutational Analyses of Multiple Oncogenic Pathways in Intraductal Papillary Mucinous Neoplasms of the Pancreas

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Abstract

Objective—There is much accumulated evidence that *EGFR*, *HER2*, and their downstream signaling pathway members such as *KRAS*, *BRAF*, and *PIK3CA* are strongly implicated in cancer development and progression. Recently, mutations in the kinase domains of *EGFR* and *HER2*, associated with increased sensitivity to tyrosine kinase inhibitors, have been described.

Methods—To evaluate the mutational status of these genes in intraductal papillary mucinous neoplasm (IPMN)/intraductal papillary mucinous carcinoma (IPMC), *EGFR* and *HER2* were analyzed in 36 IPMN/IPMC, and the results were correlated to the mutational status of the *KRAS*, *BRAF*, and *PIK3CA* genes in the samples.

Results—Together, we identified 1 silent mutation of *HER2*, 17 (43%) *KRAS* mutations, 1 (2.7%) *BRAF* mutation, and 4 (11%) mutations of *PIK3CA* in the IPMN/IPMC samples.

Conclusions—The *EGFR* and *ERBB2 (HER2)* mutations are very infrequent in IPMN/IPMC, suggesting the limited possibility of targeting mutated *ERBB2* and *EGFR* for therapy for these lesions. The *KRAS*, *BRAF*, and *PIK3CA*, however, could represent interesting targets for future therapies in these lesions.

Keywords

Her2; EGFR; PIK3CA; KRAS; BRAF; IPMN

Intraductal papillary mucinous neoplasms (IPMNs) of the pancreas are divided into 3 groups based on increasing nuclear and architectural atypia: intraductal papillary mucinous adenoma, intraductal papillary mucinous borderline, and intraductal papillary mucinous

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carcinoma (IPMC).¹ According to the absence or presence of neoplastic cells invading the pancreatic tissue surrounding the involved ducts, IPMCs are separated into invasive and noninvasive types.² Most IPMNs are slow growing and less aggressive compared with conventional, pancreatic ductal adenocarcinoma (PDA). 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%.³⁻⁶ However, invasive IPMN 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.^{3-5,7-9} Reported genetic alterations identified in IPMN include mutations in the KRAS, ¹⁰ TP53, ¹¹ STK11/LKB1,¹² and PIK3CA¹³ genes, as well as loss of heterozygosity of several chromosomal loci.^{12,14} Overexpression of ERBB2 (HER2) has been reported, beginning from the early stage of hyperplasia.¹⁵ The *ERBB* family comprises 4 structurally related receptors: ERBB1 (EGFR). ERBB2 (HER2/neu). ERBB3, and ERBB4. The EGFR kinase domain mutations in lung adenocarcinomas could predict significant clinical responses to orally active epidermal growth factor receptor (EGFR) tyrosine kinase inhibitors.¹⁶⁻¹⁸ Furthermore, 1.6% to 9.8% of lung adenocarcinomas also harbored ERBB2 (HER2) kinase domain mutations.^{19,20} There is much accumulated evidence that EGFR and its family members are strongly implicated in the development and progression of numerous human tumors, including IPMNs, pancreatic intraepithelial neoplasias, and PDA.^{6,15} Downstream members of the EGFR/ERBB2 signaling pathways, including KRAS, BRAF, and PIK3CA are also frequently mutated in human cancers and act as oncogenic proteins.^{16,21,22} Previously, we have reported on KRAS, BRAF, and PIK3CA mutations in IPMN/IPMC.^{13,23} Here, we analyzed mutations in the EGFR and ERBB2 genes in the same cohort and correlated their mutation status to other oncogenic changes.

MATERIALS AND METHODS

Patients and Tissue Samples

Surgical paraffin-embedded primary IPMN/IPMC samples of 38 patients were obtained from the archival tissue collection of the Columbia University Medical Center, approved by the institutional review board of the Columbia University Medical Center, and in accordance with Health Insurance Portability and Accountability Act regulations. We analyzed 8 IPMNs, 23 IPMNs with associated IPMCs, 5 IPMCs, and 2 mucinous cystadenomas (see Table 1 for a more detailed register). Invasive carcinoma was associated with IPMN/IPMC in pancreatic resection, but lesion analyzed did not sample invasive carcinoma.

DNA Samples and Mutation Analysis

Paraffin-embedded tumor samples were reviewed by the same pathologists (H.E.R. and N. T. C.) and microdissected by hand. Genomic DNA was extracted using QIAmp DNA Mini Kit (Qiagen, Valencia, Calif). The *ERBB2 (HER2)* (exon 20), *EGFR* (exons 19 and 21), *KRAS* (exon 1), *BRAF* (exons 11 and 15), and *PIK3CA* (exons 4, 9, and 20) were analyzed by polymerase chain reaction (PCR) amplification of genomic DNA and direct sequencing of the PCR products. Genomic DNA (40 ng per sample) was amplified with primers covering the coding region and the exon/intron boundaries of each exon analyzed. Before sequencing, all PCR products were purified (QIAquick PCR Purification Kit; Qiagen). Sequencing was performed with ABI's 3100 capillary automated sequencers at the DNA core facility of Columbia University Medical Center. All samples found to have a genetic alteration in the target gene were subsequently sequenced in the reverse direction to confirm the mutation. The mutation was further verified by sequencing of a second PCR product derived independently from the original template. Corresponding normal tissues derived

Pancreas. Author manuscript; available in PMC 2014 February 05.

from surrounding nontumorous tissue or from a tumor-free block served as the normal control for each patient.

RESULTS

One sample (2.8%), a borderline IPMN, nuclear grade 2, harbored alterations in 3 different genes: a silent *ERBB2 (HER2)* mutation (A830A), a G12D mutation of *KRAS*, and an exon 9 mutation of *PIK3CA* (W551G) (Fig. 1). Two samples (5.6%) harbored mutations in 2 different genes. In an IPMC without invasion sample (nuclear grade 3), we found a *KRAS* G12V mutation and a nonhotspot mutation in the exon 20 of *PIK3CA* (S1015F). In an IPMC with invasion sample, (nuclear grade 3, differentiation moderate to poor), a *KRAS* G12R and an exon 15 mutation of *BRAF* (S615F) were found coin-hibited. In 16 (44%) of 36 samples, we identified single mutations in only 1 gene: 14 (38.8%) of 36 cases harbored a *KRAS* mutation in exon 1 (4 [33.3%]/12 IPMNs without associated invasive carcinoma [1 nuclear grade 1, 1 nuclear grade 2, and 2 nuclear grade 3] and 10 [41.7%]/24 IPMCs with associated invasive carcinoma [all nuclear grade 3]); 2 (5.5%) of 36 cases showed a single mutation of *PIK3CA* (1 exon 4 mutation in an IPMC with invasion [nuclear grade 3, differentiation moderate] and 1 exon 20 hotspot mutation [H1047R] in an IPMC with invasion [nuclear grade 3, differentiation moderate to poor]) (Table 1). None of the mutations was detected in the matching normal tissues.

To investigate whether oncogenic activation impacts patient survival, we compared IPMC/ invasive cancer patients with any of the 3 oncogenic mutations to those without any mutation. The median survival of patients with mutation(s) is 591 days and of those without any mutation is 488 days in our small collection (Fig. 2). Although a larger study is necessary in the future to obtain a significant P value, our results suggested that patients with any oncogenic mutation may have a better median survival than those without.

DISCUSSION

The discovery of EGFR and ERBB2 (HER2) kinase domain mutations predominantly in lung adenocarcinomas, but also in gastric, ovarian, and brain tumors^{16,19,20,24} led us to analyze their genetic status in IPMN/IPMC. Overexpression of ERBB2 (HER2) in IPMNs has been reported to be 55% in the early stage of hyperplasia to up to 80% in the stage of carcinoma in situ.^{6,15} We identified 1 missense mutation in exon 20 of the *ERBB2 (HER2)* kinase domain at nucleotide 2640 (A830A) and none for EGFR, indicating that mutations of these genes are very infrequent in IPMNs/IPMCs. Downstream members of the EGFR/ ERBB2 signaling pathways, including, KRAS, BRAF, and PIK3CA are frequently mutated in human cancers and act as oncogenic proteins.^{16,21,22} Previous studies have found KRAS mutations in 31% to 86% of IPMNs (47% in the present study, without any correlation to tumor size, stage, or differentiation).^{10,23,25} This is unlike PDA where *KRAS* is mutated at a frequency close to 100%.²⁶ This suggests that in a large percentage of IPMNs/IPMCs, the Ras-Raf-message encrypton key-extracellular signal regulated kinase-mitogen-activated protein kinase pathway might be activated differently, other than by KRAS mutation. We identified 1 somatic BRAF mutation out of 36 cases of IPMN/IPMC examined (2.7%) in an IPMC with invasive carcinoma. Although located at exon 15, the S615F mutation is not the previously described hot-spot mutation at exon 15 (V600E) of the BRAF gene^{21,27} and was found to coexist with a G12R mutation of KRAS in the same sample. BRAF mutations, other than BRAF V600E, have been previously reported to coexist with RAS mutations.^{21,28} *PIK3CA* gene mutations were identified in several human tumors.^{22,29} They predominantly occur within exons 9 and 20, affecting the functionally important helical and kinase domains of the protein,²² and they are oncogenic as shown in the functional studies.^{22,30,31} Although

Pancreas. Author manuscript; available in PMC 2014 February 05.

2 of the 3 mutations in exons 9 and 20 are not hot-spot mutations, they are likely to affect the kinase activity of *PIK3CA*.

Our data show that *EGFR* and *ERBB2 (HER2)* kinase domain mutations are very infrequent in IPMN/IPMC, suggesting the limited possibility of targeting mutated *ERBB2* and *EGFR* for therapy for these lesions. *PIK3CA* is the first gene reported to be mutated in IPMN/ IPMC, but not in PDA.^{13,32} According to our data, *PIK3CA* and *BRAF* gene mutations play an important role in the tumorigenesis of IPMN/IPMC, and in comparison to *KRAS* gene mutations, occur later during their transition to malignancy. They could represent interesting targets for future targeted therapies in IPMC. There is limited treatment option available for IPMN/IPMC patients currently, other than surgery. Our data suggest *KRAS*, *BRAF*, and *PIK3CA* as potential targets for future therapeutic development.

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Schönleben et al.

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Schönleben et al.

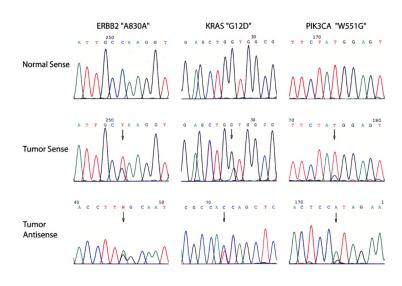


FIGURE 1.

The oncogenic mutation spectrum of patient no. 1. Our data showed that *KRAS*, *BRAF*, and *PIK3CA* mutations can often coexist in the same patient, whereas mutations of *ERBB2* and *EGFR* are rare in IPMN/IPMC.

Schönleben et al.

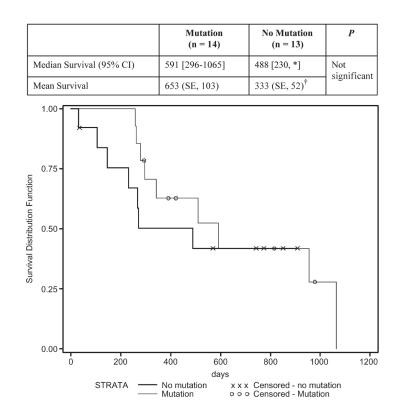


FIGURE 2.

Survival curves of IPMC/invasive carcinoma patients with or without any of the oncogenic mutations. The survival was calculated by the Kaplan-Meier method, and differences in survival between the mutation groups were tested with the log-rank test. Our data suggested that patients with any oncogenic mutation may have a better survival median, although a larger study is needed in the future to obtain a significant *P* value. *The upper limit was a censored observation (i.e., the patient was still alive so that survival time was calculated to the date of last follow-up). †The mean survival time and its SE were underestimated because the largest observation was censored and the estimation was restricted to the largest event time. CI indicates confidence interval.

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TABLE 1

Detailed Patient and Sample Data With Observed Mutations of the Lesions Investigated

| Patient No. | Sex | Age (yrs) | Lesion Analyzed | IPMN Nuclear Grade | Differentiation of Invasive Carcinoma | Location Within Pancreas | Maximum Dimension (cm) [*] | ERBB2 Mutation | <i>KRAS</i> Mutation | <i>BRAF</i> Mutation | <i>PIK3CA</i> Mutation |
|----------------|-----|--------------|--------------------|--------------------------|--|--------------------------------|---|-------------------|-------------------------|-------------------------|---------------------------|
| 1 | Σ | 62 | IPMN/border | 2 | N/A | Body | | A830A | G12D | | W551G |
| 2 | М | 73 | IPMC/inv | б | Moderate | Head/body | 4 | | G12D | | |
| ю | М | 67 | IPMC/inv | б | Moderate | Head | | | GI2V | | |
| 4 | М | 69 | IPMC | б | N/A | Head | 3.5 | | GI2V | | S1015F |
| 5 | Ц | 75 | IPMC/inv | ю | Moderate | Head | 5.5 | | | | T324I |
| 9 | ц | 68 | IPMC/inv | ю | Moderate | Head | 5 | | G12V | | |
| 7 | Σ | 65 | IPMN/border | 7 | $\operatorname{Poor}^{\dot{\tau}}$ | Head | 5 | | | | |
| 8 | Ц | 99 | IPMN/border | 2 | N/A | Unc.proc. | 2 | | G12V | | |
| 6 | М | 84 | IPMC/inv. | ю | Moderate | Head | 5 | | | | |
| 10 | М | 53 | IPMN/aden | 1 | N/A | Head | 3.5 | | GI2V | | |
| 11 | М | 71 | IPMC/inv | 2–3 | N/A | Head | | | | | |
| 12 | Μ | 81 | IPMC | 3 | N/A | Head | 2.5 | | | | |
| 13 | Μ | 63 | IPMC | ю | Moderate/poor † | Head | 2.3 | | | | |
| 14 | М | 99 | IPMC/inv | ю | Moderate/poor | Head | 9 | | | | H1047R |
| 15 | ц | 70 | IPMC/inv | 3 | Moderate/poor | Head/body | 7 | | G12R | S615F | |
| 16 | ц | 70 | IPMC/inv | ю | Moderate | Head | 1.5 | | | | |
| 17 | М | 72 | IPMN/border | 2 | N/A | Head | 0.4 | | | | |
| 18 | ц | 53 | mucin.cystad | 1 | N/A | Head | 3 | | | | |
| 19 | М | 79 | IPMC/inv | ю | Moderate/poor | Head | 6 | | G12R | | |
| 20 | М | 63 | IPMC/inv | 3 | Moderate/poor | Head | 3.5 | | G12R | | |
| 21 | М | LL | IPMN/aden | 1 | N/A | Head/body | 2.2 | | | | |
| 22 | ц | 62 | Mucin.cystad | 1 | N/A | Head | 2 | | | | |
| 23 | М | 41 | IPMC/inv | ю | Moderate/poor | Head | 5 | | | | |
| 24 | М | 71 | IPMC/inv | 3 | Moderate/poor | Head | 1.5 | | | | |
| 25 | Ц | 58 | IPMN/aden | 1 | N/A | Head | 1.5 | | | | |
| 26 | М | 49 | IPMC/inv | ю | Moderate | Head | 4.5 | | | | |
| 27 | Σ | 71 | IPMC/inv | б | Moderate/poor | Head | 5.5 | | G12D | | |

Pancreas. Author manuscript; available in PMC 2014 February 05.

| Patient No. | Sex | Age I (yrs) | Lesion Analyzed | IPMN Nuclear Grade | Differentiation of Invasive Carcinoma | Within Pancreas | Dimension (cm)* | <i>ERBB2</i> Mutation | <i>KRAS</i> Mutation | BRAF I Mutation | <i>PIK3CA</i> Mutation |
|----------------|-----|----------------|--------------------|--------------------------|--|--------------------|--------------------|--------------------------|-------------------------|--------------------|---------------------------|
| 28 | Μ | 74 | IPMC | ŝ | Well [†] | Head/body | Ι | | | | |
| 29 | М | 59 | IPMC | ŝ | $\operatorname{Poor}^{\dagger}$ | Head | 7 | | G12V | | |
| 30 | М | 81 | IPMC/inv | ю | Moderate/poor | Head | 3 | | | | |
| 31 | Ц | 80 | IPMC/inv | б | Moderate/poor | Head | 5 | | G12R | | |
| 32 | Ц | 66 | IPMC/inv | ю | Poor | Head | 3 | | | | |
| 33 | Ц | LL | IPMC/inv | ю | Poor | Head | 3 | | | | |
| 34 | М | 73 | IPMC /inv | 3 | Poor | Head | 5.5 | | G12D | | |
| 35 | Ц | LL | IPMC/inv | ю | Well | Head | 3.2 | | G12D | | |
| 36 | Ц | 61 | IPMC/inv | ю | Well | Head | 1 | | G12D | | |
| 37 | М | 62 | IPMC/inv | б | Moderate | Head | 2.2 | | | | |
| 38 | Ц | 59 | IPMC /inv | 3 | Moderate | Head | 3.4 | | G12D | | |

 $\dot{\tau}_1$ Invasive carcinoma was associated with IPMN/IPMC in pancreatic resection, but lesion analyzed did not sample invasive carcinoma.

F indicates female; IPMN/aden, IPMN adenoma; IPMN/border, IPMN borderline; IPMC/inv, IPMC with invasion; M, male; mucin.cystad, mucinous cystadenomas; N/A, not applicable; —, not available; Unc.proc, uncinate process.