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**BRAF Rearrangements and BRAF V600E Mutations Are Seen in a Subset of Pancreatic Carcinomas With Acinar Differentiation**

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- **Context.**—Comprehensive genomic profiling has demonstrated that approximately 20% of pancreatic carcinomas with acinar differentiation harbor potentially targetable BRAF fusions that activate the MAPK pathway.

- **Objectives.**—To validate the above finding by BRAF break-apart fluorescence in situ hybridization (FISH) in a large series of pure acinar cell carcinomas (ACCs), evaluate tumors for the presence of BRAF V600E mutations, and compare clinicopathologic features of tumors with BRAF rearrangements with those without.

- **Design.**—Thirty cases of pure ACC and 6 cases of mixed acinar-neuroendocrine carcinoma (ACC-NEC) were retrieved. A break-apart FISH probe was used to detect BRAF rearrangements. Immunohistochemistry for BRAF V600E was performed.

- **Results.**—BRAF rearrangements by FISH were found in 6 of 36 cases (17%), 5 of which were pure ACC and 1 was a mixed ACC-NEC. Follow-up was available in 29 of 36 (81%). The median survival was 22 months for BRAF-rearranged cases and 16 months for BRAF-intact cases; the 2-year overall survival was 50% for BRAF-rearranged cases and 35% for BRAF-intact cases. No significant clinicopathologic differences were identified in cases with BRAF rearrangement compared with those without BRAF rearrangement. BRAF V600E mutation was identified in 2 of 34 cases (6%), both of which were pure ACC and were BRAF-intact by FISH.

- **Conclusions.**—This study supports the finding that BRAF rearrangements are present in approximately 20% of cases and identified BRAF V600E mutations in approximately 5% of cases. These cases may benefit from targeted therapy.

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recently been examined. In a comprehensive genomic profiling study, approximately 20% of pancreatic ACC cases were shown to harbor recurrent \(\text{BRAF}\) and \(\text{RAF1}\) (\(\text{CRAF}\)) rearrangements. A study by Prall et al confirmed the presence of \(\text{RAF1}\) rearrangements in 5 of 30 pancreatic tumors with acinar differentiation, indicating that the MAPK pathway has a recurrent role in such tumors. In addition, these findings suggest that ACC bearing these alterations may be amenable to \(\text{BRAF}\) and/or MEK inhibition. While survival is improved with surgical management, only a minority of patients respond sustainably to chemotherapy and radiotherapy. This underscores the value of identifying novel recurrent targets for inhibition.

To this end, this study sought to validate the findings of recurrent \(\text{BRAF}\) gene rearrangements with the development and utilization of a custom developed break-apart fluorescence in situ hybridization (FISH) probe, compare clinicopathologic characteristics of ACCs with \(\text{BRAF}\) rearrangements to those without \(\text{BRAF}\) rearrangements and evaluate for \(\text{BRAF}\) V600E mutations in these tumors.

**METHODS**

**Cases**

Thirty cases of pure ACC and 6 cases of mixed ACC-NEC were identified between 1985 and 2016 in adult patients, retrieved from the authors’ institutions. The histologic sections of all cases underwent review by 7 submitting pathologists. The cases comprised 25 partial or total pancreatectomy specimens and 11 biopsy specimens (including primary and metastatic biopsy specimens). A representative tissue block or unstained formalin-fixed, paraffin-embedded tissue sections were selected in each case for ancillary immunohistochemical studies and FISH. Clinical data were extracted from the patients’ medical records.

Immunohistochemistry was performed using commercially available antibodies on a Ventana Benchmark XT using standard laboratory protocols: trypsin (Biodesign, polyclonal), BCL10 (Santa Cruz, clone 331.1) chromogranin A (Ventana, clone LK2H10), synaptophysin (Leica (Novocastra), clone 27G12), keratin 7 (Dako, clone OV-TL 12/30), and \(\text{BRAF}\) V600E (Spring, clone VE1). Cases that were positive for \(\text{BRAF}\) V600E by immunohistochemistry were subjected to a targeted \(\text{BRAF}\) V600E polymerase chain reaction assay using a previously published method.

Mixed ACC-NEC were defined as neoplasms with at least 30% identifiable acinar and neuroendocrine components.

**Interphase Break-Apart FISH**

A break-apart FISH probe was designed to detect \(\text{BRAF}\) rearrangements, including all fusions previously described by comprehensive genomic profiling (Figures 1 and 2), and was tested on all cases.

\(\text{BRAF}\) rearrangement was analyzed with a break-apart FISH probe set. Human bacterial artificial chromosomes flanking the \(\text{BRAF}\) gene region were identified using the University of California Santa Cruz February 2009 Assembly hg19. The 3 \(\text{BRAF}\) clones (RP11-577C22, RP11-96122 and RP4-592F3) were labeled by nick translation with Spectrum Orange dUTP (Abbott Molecular/Vysis Products), and the 5 \(\text{BRAF}\) clones (CTD-2023L14, CTD-2655E10 and RP11-145N8) were labeled with SpectrumGreen dUTP (Abbott Molecular/Vysis Products). Labeled clones were combined to create a dual-color fusion break-apart probe set. The break-apart probe set was applied to individual slides, hybridized, and washed according to the Partially Automated Tissue Reduced Pepsin FISH
protocol. Slide processing was done as previously reported by authors from our group. The slides were analyzed by 2 technologists using standard fluorescence microscopy methods. Each technologist independently scored 50 qualifying tumor nuclei (including both acinar and neuroendocrine tumor cells in mixed cases) for each sample, and the results were reviewed by 2 other authors. A positive BRAF rearrangement constituted at least 10% break-apart nuclei.

**Statistical Analysis**

Data were summarized as frequencies and percentages and medians or means and ranges (as appropriate). Comparisons between the BRAF FISH-positive and FISH-negative cases were performed using Fisher exact tests for categoric variables and with Wilcoxon rank-sum tests for continuous or ordinal variables. Median survival (along with the 95% CI) and the estimated 2-year survival was summarized with the Kaplan-Meier method. All analyses were performed using SAS version 9.4 (SAS Institute Inc., Cary, North Carolina).

**RESULTS**

The cases in this cohort showed a male predilection (26 of 36; 72%). The mean age at diagnosis was 64 years (SD, 12.9). The median maximum tumor dimension in the BRAF-rearranged cohort was 4.5 cm (range, 3–7 cm), and the median maximum tumor dimension in the BRAF-intact cohort was 4.8 cm (range, 1.6–29 cm). The majority of cases displayed a mixture of architectural patterns, including acinar, trabecular, glandular, and solid (Figure 3, A through F). Keratin 7 was positive in 23 of 28 cases (82%) and focally positive in 1 of 28 (4%) for which sufficient material was available for immunohistochemistry.

![Figure 3](image-url)
BRAF Rearrangements

BRAF rearrangements were identified in 6 of 36 cases (17%), 5 of which were pure ACC and 1 of which was a mixed ACC-NEC (Figure 4, A and B). All of our cases demonstrated at least 60% of tumor nuclei showing break-apart signals (range, 66%–98%). The Table shows clinicopathologic comparisons between cases with BRAF rear-

**Figure 4.** Panels demonstrating intact and rearranged BRAF fluorescence in situ hybridization results. A, A normal result with 2 intact copies of the BRAF locus in each nucleus, as depicted by 2 yellow signals or 2 closely positioned red and green signals (orange arrows highlight intact signals). B, BRAF rearrangement with separation of the red and green signals (green arrows highlight split signals).

**Figure 5.** BRAF V600E mutation by immunohistochemistry. This was identified in 2 cases, 1 was confirmed by polymerase chain reaction–based fragment analysis. Both cases were negative for BRAF rearrangement by fluorescence in situ hybridization and were cases of pure acinar cell carcinoma (original magnification ×40).

| Clinicopathologic Feature                          | BRAF Rearranged (n = 6) | BRAF Intact (n = 30) | P Value |
|---------------------------------------------------|-------------------------|---------------------|---------|
| Mean age (range)                                  | 71 (63–78)              | 63 (37–88)          | .14     |
| Sex (M:F)                                         | 1:1                     | 3.3:1               | .32     |
| Tumor location                                    |                         |                     |         |
| Head: 3                                           |                         |                     |         |
| Body: 1                                           |                         |                     |         |
| Body/tail: 1                                      |                         |                     |         |
| Tail: 1                                           |                         |                     |         |
| Median maximum tumor size (range)                 | 4.5 cm (3–7) (6 cases)  | 4.2 cm (1.6–29) (28 cases) | .93 |
| Lymph node metastasisb                            | 3/6                     | 7/21                | .64     |
| Distant metastasisb                               | 0/6                     | 12/26               | .06     |
| Necrosis                                          | 4/6                     | 14/27               | .66     |
| Lymphovascular invasion                           | 6/6                     | 15/27               | .06     |
| Perineural invasion                               | 2/6                     | 6/27                | .62     |
| Median mitoses/10 hpf (range)                    | 2.5 (0–16) (6 cases)    | 9.5 (0–88) (28 cases) | .20 |
| Keratin 7 expression                              | 5/5                     | 18/23               | .64     |
| Available follow-up (No. of deathsc)              | 4 (3)                   | 25 (19)             | .64     |
| Median survival, mo                               | 22 (95% CI: 9.0–NA)     | 16 (95% CI: 9.0–26.0) | .64 |
| 2-year overall survival                           | 50.0% (95% CI: 1.0%–99.0%) | 35.4% (95% CI: 15.8%–55.0%) | .64 |

Abbreviation: NA, not available (data too sparse to estimate upper end of CI).

a Data were collected in available cases; some were consultation cases in which material was returned, and therefore data were unable to be obtained. Chromogranin and synaptophysin-positive cases constituted ≥30% positively staining cells; focally positive cases constituted 10%–29% positively staining cells. Trypsin and CK7-positive cases constituted ≥10% positively staining cells; focally positive cases constituted 5%–9% positively staining cells.

b At diagnosis.

c All deaths were due to disease.
rangement and those without. Cases designated as "BRAF-
rearranged" refer to cases showing rearrangement by FISH, all of which were negative for BRAF V600E by immunohistochemistry.

Follow-up data were available in 29 of 36 of cases (81%). The median survival was 22 months for BRAF-rearranged cases and 16 months for BRAF-intact cases; the 2-year overall survival was 50% for BRAF-rearranged cases and 35% for BRAF-intact cases (Table).

**BRAF V600E**

Two cases were strongly and diffusely positive for BRAF V600E by immunohistochemistry (Figure 5) and negative for BRAF rearrangement by FISH. Both BRAF V600E mutant cases were pure ACC. Confirmatory polymerase chain reaction was successful in 1 case, and was positive for BRAF V600E. The other case failed sequencing due to poor-quality DNA, and there was no residual material from the small biopsy specimen. Both BRAF V600E-positive cases had metastatic disease at presentation, with the survival intervals measuring 8 and 22 months.

**DISCUSSION**

Our study validates the finding that BRAF rearrangements are seen in approximately 10% to 20% of pancreatic carcinomas with acinar differentiation, corroborating findings from both prior comprehensive genomic profiling studies and studies of BRAF rearrangements by FISH.6,12,13 We furthermore identified BRAF V600E mutations that did not co-occur in the cases with BRAF rearrangements. Others have identified BRAF V600 alterations as part of whole-exome sequencing14,15 and genome-wide studies.7 However, BRAF fusions were not detected in the whole-exome sequencing studies. Although the finding of BRAF fusions and BRAF point mutations is not new, there are only few studies on this biomarker with slightly different designs. Further, our study analyzed a relatively large number of cases and compares the clinicopathologic features between BRAF-rearranged tumors and BRAF-intact tumors. In our cohort, no statistically significant clinicopathologic difference was identified between BRAF-rearranged and BRAF-intact tumors.

This is the third study specifically examining BRAF rearrangements in pancreatic neoplasms with acinar differentiation. The first study included 44 pancreatic carcinomas with acinar differentiation, including 16 pure ACCs, 14 mixed ACC-NEC, and other mixed variants. Twenty percent of the tumors demonstrated recurrent BRAF gene rearrangements.8 The most prevalent fusion genes were SNDY-BRAF (50%), followed by HERPUD1-BRAF (18%), which may be amenable to MEK inhibition.8,13 The same group then developed a BRAF break-apart FISH assay.15 The second study by Prall et al19 examined 25 pure ACCs, 2 mixed ACC-NEC, 1 mixed ACC-NET, and 2 pancreaticoblastomas and identified R1F1 rearrangements in 18.3% of cases and BRAF rearrangements in 2 of 28 cases (7%) (exclusive of pancreaticoblastoma), with 1 BRAF-rearranged case also harboring R1F1 rearrangement.

Our study provides a likely therapeutically targetable finding that adds to the data published in the prior studies.8,9,13,14,16,17 BRAF V600E is a targetable alteration in several malignancies, including malignant melanoma,26 hairy cell leukemia,27 and colorectal carcinoma.28 In cancer, BRAF alterations are targetable by BRAF inhibitors, but also may be targeted by MEK inhibition or combined BRAF and MEK inhibition, as these effectors are all part of the MAPK pathway.20,21 This raises the possibility that BRAF inhibition or combination therapy may be effective in acinar cell carcinoma; this merits further study.

The frequency of BRAF rearrangements in our study is similar to that identified by Chmielecki et al26 (20%) and somewhat higher than that identified by Prall et al9 (7%). The low sample sizes of BRAF-rearranged cases likely accounts for these differences. These studies did not report clinicopathologic correlations between BRAF-rearranged tumors and those without BRAF rearrangements, and so comparison in this regard is not possible. Considering the findings of our study along with those of Chmielecki et al26 and Prall et al9 pathogenic alterations involving BRAF or another member of the MAPK pathway underlie a significant subset of cases of ACC and suggests that these cases should be screened for pathogenic alterations in this pathway.

In this study, we developed and tested an efficient and economic FISH probe that can identify potentially targetable gene rearrangements. Currently, transcriptome sequencing for BRAF genetic rearrangements is not widely available and, in most institutions, has not been optimized for the most common biospecimen, formalin-fixed, paraffin-embedded tissue. As such, this FISH probe may be a useful clinical test to determine patients who may benefit from therapy. One advantage of this FISH assay is that it is informative on very small biopsy specimens and can be performed on a single unstained slide, unlike many sophisticated molecular assays. Next-generation sequencing provides the opportunity for a single assay to detect both BRAF gene rearrangements and point mutations, creating efficacy and analytic sensitivity in a cost-effective way. This is because next-generation sequencing can be designed to detect not only point mutations, such as polymerase chain reaction–based assays, but also, using bioinformatics tools, recognize sequence changes that correspond to large structural rearrangements, such as fusions, or in RNA-based next generation sequencing, directly identify the fusion transcripts.

This study design does have a limitation based on use of FISH as the sole methodology. We note that false positives may occur with FISH, such that FISH signals may be disrupted by large genomic changes and not indicate an in-frame functional fusion gene. Therefore, BRAF rearrangements identified by this method do not necessarily indicate the presence of an in-frame fusion oncogene. Nonetheless, the frequency of BRAF rearrangements identified by our methodology accords well with the previously published frequencies of BRAF fusions in other studies.8,9 This suggests that despite this study design limitation, our findings were valid. Our study was also limited by the lack of additional formalin-fixed, paraffin-embedded tissue to molecularly confirm the second study design limitation, our findings were valid. Our study was also limited by the lack of additional formalin-fixed, paraffin-embedded tissue to molecularly confirm the second study design limitation, our findings were valid. Our study was also limited by the lack of additional formalin-fixed, paraffin-embedded tissue to molecularly confirm the second study design limitation, our findings were valid. Our study was also limited by the lack of additional formalin-fixed, paraffin-embedded tissue to molecularly confirm the second study design limitation, our findings were valid. Our study was also limited by the lack of additional formalin-fixed, paraffin-embedded tissue to molecularly confirm the second study design limitation, our findings were valid. Our study was also limited by the lack of additional formalin-fixed, paraffin-embedded tissue to molecularly confirm the second study design limitation, our findings were valid. Our study was also limited by the lack of additional formalin-fixed, paraffin-embedded tissue to molecularly confirm the second study design limitation, our findings were valid. Our study was also limited by the lack of additional formalin-fixed, paraffin-embedded tissue to molecularly confirm the second study design limitation, our findings were valid. Our study was also limited by the lack of additional formalin-fixed, paraffin-embedded tissue to molecularly confirm the second study design limitation, our findings were valid. Our study was also limited by the lack of additional formalin-fixed, paraffin-embedded tissue to molecularly confirm the second study design limitation, our findings were valid.
In conclusion, this series of pancreatic carcinomas with acinar differentiation, which includes the largest series of pure ACCs evaluated to date for BRAF rearrangements by FISH, we confirmed that BRAF rearrangements are present in approximately 20% of these tumors. We discovered that a subset of cases of ACC harbor BRAF V600E mutations, mutually exclusive of BRAF rearrangements. This study adds to the literature that suggests cases of pancreatic ACC should be examined for MAPK abnormalities and studies of therapeutic sensitivity to BRAF and MAPK pathway inhibition are timely.

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