ATM Mutations in Patients with Hereditary Pancreatic Cancer

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INTRODUCTION

Pancreatic ductal adenocarcinomas carry a dismal prognosis, with fewer than 5% of patients surviving 5 years (1). This disease is particularly tragic when several members of a single family are affected, a situation that occurs in 5% to 10% of cases of pancreatic ductal adenocarcinomas diagnosed in the United States (2). The genes responsible for 85% to 90% of familial pancreatic cancer kindreds, defined

Pancreatic cancers are the fourth most-common cause of cancer-related deaths in the Western world, with >200,000 cases reported in 2010. Although up to 10% of these cases occur in familial patterns, the hereditary basis for predisposition in the vast majority of affected families is unknown. We used next-generation sequencing, including whole-genome and whole-exome analyses, and identified heterozygous, constitutional, ataxia telangiectasia mutated (ATM) gene mutations in 2 kindreds with familial pancreatic cancer. Mutations segregated with disease in both kindreds and tumor analysis demonstrated LOH of the wild-type allele. By using sequence analysis of an additional 166 familial pancreatic cancer probands, we identified 4 additional patients with deleterious mutations in the ATM gene, whereas we identified no deleterious mutations in 190 spouse controls (P = 0.046). When we considered only the mostly severely affected families with 3 or more pancreatic cancer cases, 4 deleterious mutations were found in 87 families (P = 0.009). Our results indicate that inherited ATM mutations play an important role in familial pancreatic cancer predisposition.

SIGNIFICANCE: The genes responsible for the majority of cases of familial pancreatic ductal adenocarcinoma are unknown. We here identify ATM as a predisposition gene for pancreatic ductal adenocarcinoma. Our results have important implications for the management of patients in affected families and illustrate the power of genome-wide sequencing to identify the basis of familial cancer syndromes. Cancer Discovery; 2(1): 41–6. © 2011 AACR.

ABSTRACT

Pancreatic cancers are the fourth most-common cause of cancer-related deaths in the Western world, with >200,000 cases reported in 2010. Although up to 10% of these cases occur in familial patterns, the hereditary basis for predisposition in the vast majority of affected families is unknown. We used next-generation sequencing, including whole-genome and whole-exome analyses, and identified heterozygous, constitutional, ataxia telangiectasia mutated (ATM) gene mutations in 2 kindreds with familial pancreatic cancer. Mutations segregated with disease in both kindreds and tumor analysis demonstrated LOH of the wild-type allele. By using sequence analysis of an additional 166 familial pancreatic cancer probands, we identified 4 additional patients with deleterious mutations in the ATM gene, whereas we identified no deleterious mutations in 190 spouse controls (P = 0.046). When we considered only the mostly severely affected families with 3 or more pancreatic cancer cases, 4 deleterious mutations were found in 87 families (P = 0.009). Our results indicate that inherited ATM mutations play an important role in familial pancreatic cancer predisposition.

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as those with at least 2 affected first-degree relatives, are unknown. In the remaining families, germline mutations of genes, including BRCA2, PALB2, CDKN2A, STK11, and possibly BRCA1, have been identified (2).

Unbiased, genome-wide sequencing can be used to identify familial pancreatic genes, as demonstrated by the finding that PALB2 is a pancreatic cancer susceptibility gene (3). To identify additional familial pancreatic cancer genes, we evaluated the whole-genome sequences of 16 subjects from 6 families and the whole-exome sequences of an additional 22 subjects from 10 families. All families included at least 3 members with pancreatic ductal adenocarcinoma, and DNA was available from at least 2 such members. Families had enrolled into one of the familial pancreatic cancer registries participating in the Pancreatic Cancer Genetic Epidemiology Consortium (National Familial Pancreas Tumor Registry at Johns Hopkins, Mayo Clinic, Dana-Farber Cancer Institute, MD Anderson Cancer Center, Ontario Pancreas Cancer Study, and Karmanos Cancer Center). In this brief report, we present data from 2 families (FPC-A and FPC-B) that harbored inactivating mutations of a putative pancreatic cancer susceptibility gene.

RESULTS

Whole-genome sequencing was applied to 3 members of FPC-A and whole-exome sequencing was applied to 3 members of FPC-B. These efforts produced an average of 113.0 and 7.1 gigabases per sample, resulting in 34-fold and 97-fold distinct coverage of the genome and exome, respectively (Table 1). On average, whole-genome sequencing identified 6,132,376 variants per person, of which 61.6% (3,778,674 variants) matched those deposited in single-nucleotide polymorphism (SNP) databases. Similarly, exome sequencing resulted in an average of 35,440 variants per individual, at least 2 such members. Families had enrolled into one of the familial pancreatic cancer registries participating in the Pancreatic Cancer Genetic Epidemiology Consortium (National Familial Pancreas Tumor Registry at Johns Hopkins, Mayo Clinic, Dana-Farber Cancer Institute, MD Anderson Cancer Center, Ontario Pancreas Cancer Study, and Karmanos Cancer Center). In this brief report, we present data from 2 families (FPC-A and FPC-B) that harbored inactivating mutations of a putative pancreatic cancer susceptibility gene.

that any causative variant would be rare in the general population and therefore heterozygous in an affected individual. In addition, a causative variant would be inactivating and shared among all affected members of a family. We therefore filtered the variants according to the following criteria: (i) variants present in SNP databases were excluded from further analysis; (ii) the fraction of distinct sequence reads containing a variant had to be between 25% and 75% of the total number of distinct sequence reads of the corresponding base (i.e., it had to be heterozygous); (iii) the variant had to be present in all affected members of an affected kindred; and (iv) the variant had to be inactivating, that is, predicted to produce a nonsense mutation, frameshift insertion or deletion, or splice-site alteration (IVS -1 or -2; IVS +1 or +2).

When these filters were used, the 18,503,448 variants initially identified in the sequenced members of families FPC-A and FPC-B were narrowed to 156. Of these 156 variants, most interesting were in ATM because FPC-A and FPC-B family members harbored different heterozygous nonsense variants of this gene (c.8266A>AT; p.K2756X and c.170G>G; p.W57X). The pedigrees of these families are shown in Figure 1. Both of these variants have been reported previously in patients with ataxia-telangiectasia, an autosomal-recessive condition associated with an increased risk of multiple cancer types (4, 5).

To estimate the prevalence of deleterious ATM mutations in patients with familial pancreatic cancer and control subjects, we conventionally sequenced the entire coding region of the ATM gene in an additional 166 familial pancreatic cancer patients and 190 spouse controls (Supplementary Table S1). Patients with pancreatic cancer and control subjects were recruited as part of the National Familial Pancreas Tumor Registry. Of the 166 patients with familial pancreatic cancer, 71 were from kindreds with 3 or more pancreatic cancers. Chromatograms for all variants in ATM were visually inspected. Variants present in the Human Gene Mutation Database (6) were then manually curated and pathogenic alterations previously seen in ataxia-telangiectasia patients were confirmed with Sanger sequencing in a second, independent PCR amplification. Four variants (c.3214G>GT; p.E1072X, c.6095G>G; 42 | CANCER DISCOVERY JANUARY 2012 www.aacrjournals.org

Table 1. Summary data for familial pancreatic cancer families with inactivating ATM variants

<table>
<thead>
<tr>
<th>Type</th>
<th>Family</th>
<th>Individual</th>
<th>Read length</th>
<th>Bases mapped to genome</th>
<th>Bases mapped to exome</th>
<th>Exome bases with &gt;10 reads</th>
<th>Average raw coverage</th>
<th>Effective coverage</th>
<th>Total number of variants</th>
<th>Variants in SNP database</th>
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</thead>
<tbody>
<tr>
<td>Whole-genome</td>
<td>FPC-A</td>
<td>1</td>
<td>100</td>
<td>115,388,854,300</td>
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<td>3,758,900</td>
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<tr>
<td>sequencing</td>
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<td>2</td>
<td>100</td>
<td>110,742,763,000</td>
<td>1,219,892,546</td>
<td>34,328,889</td>
<td>33</td>
<td>94.7%</td>
<td>6,181,369</td>
<td>3,793,150</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3</td>
<td>100</td>
<td>112,771,643,500</td>
<td>1,271,909,140</td>
<td>34,656,841</td>
<td>34</td>
<td>95.1%</td>
<td>6,190,892</td>
<td>3,783,971</td>
</tr>
<tr>
<td>Whole-exome</td>
<td>FPC-B</td>
<td>1</td>
<td>75</td>
<td>8,110,266,675</td>
<td>4,118,378,295</td>
<td>36,458,593</td>
<td>109</td>
<td>97.9%</td>
<td>35,674</td>
<td>19,573</td>
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<tr>
<td>sequencing</td>
<td></td>
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<td>75</td>
<td>7,597,985,850</td>
<td>4,076,171,309</td>
<td>36,560,365</td>
<td>108</td>
<td>98.0%</td>
<td>35,724</td>
<td>19,605</td>
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<tr>
<td></td>
<td></td>
<td>3</td>
<td>75</td>
<td>5,649,542,100</td>
<td>3,778,674</td>
<td>36,067,752</td>
<td>74</td>
<td>97.6%</td>
<td>34,923</td>
<td>19,554</td>
</tr>
</tbody>
</table>
Disease Mutations in Familial Pancreatic Ductal Adenocarcinoma

DISCUSSION

The ATM protein is a serine/threonine kinase involved in DNA double-strand break repair (13, 14). Ataxia-telangiectasia is caused by the inheritance of biallelic deleterious mutations in the ATM gene (13) and occurs in 1/40,000 to 1/300,000 live births. The reported carrier frequency of deleterious ATM variants in the population is 0.5% to 1% (14, 15). Ataxia-telangiectasia is characterized by progressive cerebellar ataxia, oculomotor apraxia, telangiectasias of the conjunctiva and skin, immunodeficiency, sensitivity to ionizing radiation, and an increased rate of malignancies, particularly lymphoma and leukemia (14–16).

Women who carry pathogenic ATM mutations have an increased risk of breast cancer (15–17). However, the role played by ATM mutations in a patient’s susceptibility to breast cancer has proven controversial (18–21). There are no other previous reports of ATM mutations in the germline of patients with pancreatic ductal adenocarcinoma. Similarly, no somatic mutations of ATM have been reported in pancreatic ductal adenocarcinoma. Pancreatic neuroendocrine tumors have little in common with pancreatic ductal adenocarcinoma, and occasionally harbor a somatic mutation of ATM (22). However, these mutations may be passengers because there is no genetic or biochemical evidence indicating that these mutations inactivate the gene product.

In our series of 166 familial pancreatic cancer probands, 2.4% (4/166) carried deleterious ATM mutations. When we considered only families with more than 3 affected members,
we found that 4.6% (4/87) carried deleterious ATM mutations. The evidence that these mutations are functional is unambiguous because we defined deleterious mutations in the most rigorous way possible: only those mutations that are known to cause ataxia-telangiectasia when inherited were considered deleterious. Thus, these mutations cause a recessive disease phenotype in humans under natural conditions. We identified other germline mutations of ATM in the families we studied but could not conclude that they were functionally inactive because they had not been demonstrated to occur in the germline of patients with ataxia-telangiectasia. Future functional studies of these additional mutations may reveal an even greater role for ATM in the susceptibility of pancreatic cancer.

The identification of deleterious ATM mutations in probands has substantial implications for risk assessment and surveillance in other family members. Moreover, because ATM is a key participant in DNA repair, it is possible that new therapeutics based on synthetic lethal interactions can be developed to treat these patients with pancreatic ductal adenocarcinoma, as has been accomplished for patients with BRCA gene mutations (23, 24).

**METHODS**

**Study Participants**

This study was reviewed and approved by the Institutional Review Board of the Johns Hopkins Medical Institutions, and informed consent was obtained from all study participants. Study participants were enrolled into one of the familial pancreatic cancer registries participating in the Pancreatic Cancer Genetic Epidemiology Consortium (National Familial Pancreas Tumor Registry at Johns Hopkins, Mayo Clinic, Dana-Farber Cancer Institute, MD Anderson Cancer Center, Ontario Pancreas Cancer Study, and Karmanos Cancer Center). The Pancreatic Cancer Genetic Epidemiology Consortium and National Familial Pancreas Tumor Registry have been previously described (25, 26).

**Preparation of Genomic DNA**

Genomic DNA from familial pancreatic cancer cases was extracted from peripheral blood lymphocytes (PBL) or Epstein-Barr virus transformed PBLs via use of the QiAamp DNA mini kit (catalog number 51304; QIAGEN, Valencia, CA) according to the manufacturer’s protocol. Similarly, genomic DNA from control individuals was extracted from PBLs with the QiAamp DNA mini kit (catalog number 51304; QIAGEN).

**Preparation of Genomic DNA Libraries and Whole-Genome Sequencing**

A total of 5 to 10 μg of genomic DNA per sample were sequenced with the Illumina GAIIx Genome Analyzer via use of the Illumina Whole (Illumina, San Diego, CA) Genome Fast-Track Sequencing Service to yield 200 (2 × 100) base pairs from the final library fragments. Sequencing reads were analyzed and aligned to human genome hg18 with the Eland algorithm in CASAVA 1.7 software (Illumina). The Database of Single Nucleotide Polymorphisms (National Center for Biotechnology Information) was used in the analysis of whole-genome sequencing data (27).

**Preparation of Genomic DNA Libraries and Whole-Exome Sequencing**

Genomic DNA libraries were prepared with the use of 1.5 to 3 μg of genomic DNA and human exome capture was performed following a modified protocol from Agilent’s SureSelect Paired-End Version 2.0 Human Exome Kit (Agilent, Santa Clara, CA) as previously described (28).

Captured DNA libraries were sequenced with the Illumina GAIIx Genome Analyzer, yielding 150 (2 × 75) base pairs from the final library fragments. Sequencing reads were analyzed and aligned to human genome hg18 with the Eland algorithm in CASAVA 1.7 software (Illumina). The Database of Single Nucleotide Polymorphisms was used in the analysis of whole-exome sequencing data (27).

**Evaluation of ATM in Additional Pancreatic Cancers, Controls, and Tumor Samples**

The coding region of the ATM gene was sequenced in 166 familial pancreatic cancer patients and 190 spouses who served as controls.
ATM Mutations in Familial Pancreatic Ductal Adenocarcinoma

Figure 2. Chromatograms from IV-1 of family FPC-A. A, PBLs of IV-1 demonstrating heterozygosity for the ATM inactivating mutant c.8266A>AT; p.K2756X. B, laser capture microdissected pancreatic tumor of IV-1 showing LOH with retention of the ATM inactivating mutant c.8266A>T; p.K2756X.

PCR amplification and Sanger sequencing were performed following protocols described previously (29) with the primers listed in Supplementary Table S2.

Laser Capture Microdissection and DNA Extraction of Pancreatic Tumor Samples

To identify somatic mutations and copy number changes in patients with germline ATM mutations, primary pancreatic cancer cells (∼1 × 10^5) were meticulously microdissected from frozen sections with the PALM micro-laser system (Carl Zeiss Microimaging Inc.; North America, Thornwood, NY) as previously described (29). Genomic DNA was then extracted with the QIAamp DNA Micro Kit (QIAGEN).

Statistics

Two-tailed P-values were calculated using the Fisher exact test. A P-value < 0.05 was considered significant.

Disclosure of Potential Conflicts of Interest

Under a licensing agreement between Myriad Genetics, Inc., and the Johns Hopkins University, K.W. Kinzler, V.E. Velculescu, B. Vogelstein, A.P. Klein, J.R. Eshleman, R.H. Hruban, and M. Goggins are entitled to a share of royalty received by the University on sales of products related to genes and technologies described in this manuscript. N. Papadopolous, B. Vogelstein, K.W. Kinzler, and V.E. Velculescu are co-founders of Inostics and Personal Genome Diagnostics and are members of their Scientific Advisory Boards. They own stock in Inostics and PGDx, which is subject to certain restrictions under Johns Hopkins University policy. The terms of these arrangements are managed by the Johns Hopkins University in accordance with its conflict-of-interest policies.

Authors’ Contributions


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REFERENCES


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