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Update on Familial Pancreatic Cancer+

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Introduction

It has been suggested that ~10% of pancreatic cancer has a familial basis [1, 2]. Individuals with a family history of pancreatic cancer have an increased risk of developing both pancreatic and extrapancreatic malignancies, and an individual's risk of developing pancreatic cancer can now be quantified based on their family cancer history [1, 3, 4].

While some of the aggregation of pancreatic cancer in families is due to chance, and some to shared environmental exposures such as cigarette smoking, it is now clear that much of this aggregation has a genetic basis [5]. Several of the genes responsible for the familial clustering of pancreatic cancer have been discovered. For example, germline mutations in the *BRCA2* gene cause familial breast cancer, and individuals with germline *BRCA2* gene mutations have an approximately 3.5-fold increased risk of pancreatic cancer [6–12]. Germline mutations in the *p16*/*CDKN2A* gene cause the Familial Atypical Multiple Mole Melanoma (FAMMM) syndrome, and these individuals have a 13 to 37-fold increased risk of pancreatic cancer [10, 13–23]. Inherited mutations in the *STK11* gene cause the Peutz-Jeghers syndrome, and individuals with Peutz-Jeghers have a 130-fold increased risk of pancreatic cancer [24–30]. The discovery of these familial pancreatic cancer genes has helped identify cellular pathways important for the development of pancreatic cancer, it has provided a basis for genetic counseling of individuals with a family history of pancreatic cancer, and it has established a foundation for prioritizing patients for screening for early pre-invasive disease [21, 29, 31–33]. In

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addition, the discovery of familial pancreatic cancer genes has also lead to the development of gene-specific therapies as demonstrated by the remarkable sensitivity of pancreatic cancers harboring mutations in the *BRCA2* gene to Poly[ADP-ribose] polymerase (PARP) inhibitors and to mitomycin C [34–41].

The field of familial pancreatic cancer is getting even more exciting as we enter the era of whole genome sequencing. For example, this year the *PALB2* gene was discovered to be a familial pancreatic cancer susceptibility gene through complete, unbiased, sequencing of all of the protein-coding genes in a *single* patient's cancer [42, 43]. As the speed of "next generation" sequencing technologies rises and the costs fall, we can foresee the discovery of a number of new familial pancreatic cancer genes in the coming years.

The known genetic syndromes account for less than 20% of the observed familial aggregation of pancreatic cancer, and the discovery of additional familial pancreatic cancer genes remains one of the most exciting opportunities in pancreatic cancer research [1, 2]. As these genes are discovered, the challenge will be to use these scientific breakthroughs to improve clinical care.

Using Family History to Assess Cancer Risk

As the recognition that pancreatic cancer aggregates in families grows, more and more surgeons are being asked by their patients: "*I have a family history of pancreatic cancer, what is my risk of developing cancer?*" A body of evidence-based medicine has been developed to answer this question, and it is clear that individuals with a family history of pancreatic cancer have an increased risk of both pancreatic and of extrapancreatic malignancies [4, 44, 45].

Family History and Pancreatic Cancer

Several large epidemiological studies have established that a family history of pancreatic cancer increases one's risk of developing the disease [4, 44, 46–52]. For example, L. Amundadottir and colleagues correlated the risk of a variety of cancers with family cancer history by linking the Iceland Cancer Registry with the deCODE genealogic database [44]. A first-degree relationship is a parent-child or sibling-sibling relationship, and Amundadottir and colleagues found that Icelanders with a first-degree family relative with pancreatic cancer had a 2.33-fold increased risk of developing pancreatic cancer themselves [44]. Similar observations have been made in a large number of case-control and cohort studies, and it is now clear that having a single close relative with pancreatic cancer doubles one's risk of developing the disease [4, 44, 46–52].

A. Klein and colleagues have extended these analyses by prospectively following thousands of patients with a family history of pancreatic cancer [4]. Klein and colleagues found that individuals with two first-degree relatives with pancreatic cancer have a 6-fold increased risk of developing pancreatic cancer, and individuals with three or more first-degree relatives with pancreatic cancer have a 14 to 32-fold increased risk [4]. Using these and other data, Klein and colleagues have developed a risk prediction tool, called PancPRO, that can be used to quantify an individual's risk of developing pancreatic cancer based on their family history of pancreatic cancer [3]. PancPRO is available for free on-line (http://astor.som.jhmi.edu/BayesMendel/pancpro.html accessed September 1, 2009) and PancPRO can be used to answer the question posed earlier by our hypothetical patient: "*I have a family history of pancreatic cancer, what is my risk of developing cancer?*" Figure 1 illustrates three pedigrees of similar structure but differing family histories of pancreatic cancer. The counselee shown with an arrow in Figure 1A is predicted to have a 3.3 % chance of developing pancreatic cancer by the age of 70 years. This risk increases to ~7% if this patients mother rather than their maternal aunt had history pancreatic cancer (Figure 1B) or if their brother also has a history of pancreatic cancer (Figure 1C)[3]. Without knowing the gene responsible for the

aggregation of pancreatic cancer in a family, clinicians can still provide their patients with quantitative estimates of their absolute lifetime pancreatic cancer risks.

It is also important to put this risk in perspective, as the average patient may be unduly alarmed by relative risks. Pancreatic cancer is a relatively rare disease, averaging 9 per 100,000 per year in the United States [53]. A relative risk of two increases an individual's risk to ~18 per 100,000 per year, less than a fiftieth of one percent per year. This incidence rate increases with age, particularly above the age of 50 culminating in a lifetime risk of developing pancreatic cancer of 1 percent. Contrast this to the risk of a women developing breast cancer. The National Cancer Institute estimates that 12.7 percent of women born in the United States today will develop breast cancer at some time in their lives. Even having a two-fold increased risk of developing pancreatic cancer, the vast majority of patients with a family history of pancreatic cancer will not develop the disease themselves. For this reason it is important to explain both relative and absolute risks to patients.

Family History and Extrapancreatic Malignancies

The risk of cancer is not confined to one organ in most familial cancer syndromes [45, 54, 55]. For example, patients with hereditary nonpolyposis colorectal cancer syndrome have an increased risk of developing cancer of the colorectum, endometrium, ovary, stomach, ureter, renal pelvis, and pancreas [56]. Epidemiologic studies have recently shown that the same is true for familial pancreatic cancer; patients with a family history of pancreatic cancer have an increased risk of extrapancreatic malignancies as well [45, 54, 55]. Wang and colleagues followed families enrolled in the National Familial Pancreas Tumor Registry (http://pathology.jhu.edu/pancreas/nfptr) and found that overall cancer mortality is increased both in the members of sporadic pancreatic cancer kindreds (defined as at least a single pancreatic cancer in the kindred, but not an affected pair of first-degree relatives, Relative Risk [RR] =1.55: 95%, CI 1.39–1.73) and in familial pancreatic cancer kindreds (defined as a family with at least a pair of first-degree relatives with pancreatic cancer, RR=1.41; 95%CI 1.26–1.58) [45]. Relatives of patients with familial pancreatic cancer had an increased risk of dying from breast cancer (RR 1.66, 95% CI=1.15–2.34), ovarian (RR 2.05, 95% CI= 1.10–3.49), and bile duct cancers (RR 2.89, RR= 1.04–6.39) 45.

In addition to the associations identified without knowledge of the gene involved, as noted earlier, several known genetic syndromes increase the risk of both pancreatic and extrapancreatic malignancies (Table 1). For example, individuals with the Peutz-Jeghers syndrome have an increased risk of developing cancers of esophagus, stomach, small intestine, colon, pancreas, breast, lung, ovary and uterus 27, [28]. Similarly, a personal history of young-onset breast cancer with or without a family history of pancreatic cancer (particularly in patients with Ashkenazi Jewish ancestry) could suggest the presence of a familial breast-ovarian cancer syndrome involving one of the breast cancer-related genes (*BRCA1* or *BRCA2*). These genes, particularly *BRCA2*, are associated with a very high risk of breast, ovarian, and prostate cancer and moderate risk for pancreatic cancer [6–12]. Surgeons should be aware that their patients with a strong family history of pancreatic cancer are at higher risk for developing extra-pancreatic malignancies.

Intraductal Papillary Mucinous Neoplasms and Extrapancreatic Neoplasms

It is well-established that intraductal papillary mucinous neoplasms (IPMNs) are precursors to invasive pancreatic cancer, and that patients with an IPMN have an increased risk of developing invasive pancreatic cancer [53]. Patients with a personal history of an IPMN also have an increased risk of developing an extra-pancreatic neoplasm. Excess rates of gastric and colonic epithelial neoplasms have been reported in patients with IPMNs 57–60. This finding suggests

the possibility of a common predisposing genetic susceptibility, but no specific hereditary syndrome linking IPMNs with gastric and colonic neoplasms has been established.

It is now clear that individuals with a family history of pancreatic cancer, as well as those with a personal history of an IPMN, have an increased risk of developing pancreatic and selected extra-pancreatic malignancies. These findings have two immediate implications for surgeons. First, a good family cancer history should be obtained from all patients. Don't just document that a patient has a "family history of cancer," instead carefully document which family members have had cancer, which types of cancer they have had, and how each affected individual is related to the patient. Second, as will be discussed in detail later in this review, knowledge of these increased risks can help guide clinical management.

Familial Pancreatic Cancer Genes

We have handled the question of risk assessment using family cancer history, but it is clear that in most instances an individual's family cancer history is, at best, just a surrogate for gene status, and that determining the specific gene responsible for a given patient's cancer can have significant clinical implications. Our second patient therefore comes to the office and asks "*I have a family history of pancreatic cancer, can I undergo genetic testing, and if so, for which genes*?"

While we believe that this question is often best answered by a trained cancer genetic counselor (see www.nsgc.org to find a local genetic counselor), it is important for surgeons to know the major genes responsible for the familial aggregation of pancreatic cancer (Table 1).

BRCA2 and Other Fanconi Anemia Pathway Genes

BRCA2 is probably the best characterized of all of the familial pancreatic cancer genes. Germline (inherited) mutations in the *BRCA2* gene increase the risk of breast and ovarian cancer, and increase the risk of pancreatic cancer 3.5 to 10-fold [6–12]. While breast cancer develops in most families with a *BRCA2* gene mutation, the absence of a breast cancer in a family should not be used to exclude germline *BRCA2* mutations, as Goggins and colleagues reported that pancreatic cancer can run in *BRCA2* gene mutation-carrying families without an apparent association with breast cancer [8]. Germline *BRCA2* mutations are particularly common in individuals of Ashkenazi Jewish heritage [61–65]. It has been calculated that 1% of the Ashkenazi Jewish population carries a germline *BRCA2* gene mutation, the 6174delT mutation, and these individuals, in addition to an increased risk of breast and ovarian cancer, have a 10-fold increased risk of developing pancreatic cancer [61–65]. Individuals without a Jewish heritage can also carry a germline *BRCA2* gene mutation, but these mutations are more widely distributed throughout the gene and overall it is estimated that only 1 in every 400 to 800 individuals carries a mutation in *BRCA2* [66].

Clinical genetic testing for germline *BRCA2* gene mutations is commercially available through Myriad Genetics (http://www.myriad.com/products/bracanalysis.php). Testing should be considered in patients with a strong family history of pancreatic cancer, especially if the patient or other family members have been diagnosed with bilateral or young age of onset breast or ovarian cancer, and if the individual is of Ashkenazi Jewish heritage. A clinical tool is available to help clinicians identify who would best benefit from genetic testing for *BRCA2* gene mutations (http://astor.som.jhmi.edu/BayesMendel/brcapro.html), but it should be noted that this model does not include pancreatic or prostate cancers as a risk criterion.

The protein product of the *BRCA2* gene functions in the same DNA repair pathway as the Fanconi's anemia proteins to repair DNA cross-linking damage [67]. It should therefore not be surprising that germline mutations in genes coding for other members of the pathway, including

FANC-C and *FANC-G*, have also been linked to the familial clustering of pancreatic cancer [67, 68]. Germline *BRCA1* gene mutations have been reported in only a few patients with familial pancreatic cancer [69–72].

Most recently, the *PALB2* gene has been discovered to be a familial pancreatic cancer gene [42]. The *PALB2* gene codes for a protein that binds to the Brca2 protein and helps to localize Brca2, and possibly also Brca1, to the nucleus [73]. Indeed, "PALB2" stands for "partner and localizer of BRCA2." Jones and colleagues discovered that *PALB2* is a familial pancreatic cancer gene by sequencing all of the genes in a pancreatic cancer from a single patient with familial pancreatic cancer [42]. This remarkable achievement highlights the potential of whole genome sequencing to discover the causes of inherited diseases. The *PALB2* gene finding has been confirmed, and *PALB2* appears to account for 1 to 3% of familial pancreatic cancer [42, 43].

We can take several important lessons from the *BRCA2* gene story. First, as noted earlier, many familial cancer genes do not increase the risk of just one cancer type. Germline *BRCA2* gene mutations increase the risk of breast, ovarian, prostate and pancreatic cancer [6, 66, 74–77]. Once the gene is found in a family, lives can be saved by screening gene carriers for these extrapancreatic neoplasms and, in selected cases, by prophylactic surgery [6, 66, 74–77]. Second, *BRCA2* nicely demonstrates that once a gene is found and its function determined, then genes coding for other members of the same pathway can be screened to see if they also contribute to familial pancreatic cancer. Germline mutations in four members of the Fanconi anemia pathway, *BRCA2*, *FANC-C*, *FANC-G* and *PALB2*, can cause familial pancreatic cancer [42, 43, 67, 68]. Finally, as will be discussed in greater detail later, *BRCA2* gene mutations are a great example of the potential power of gene-specific therapies [34–41].

P16/*CDKN2A* and FAMMM

Germline mutations in the *p16*/*CDKN2A* gene cause about 30 to 40% of FAMMM syndrome, a syndrome characterized my multiple nevi, multiple atypical nevi, and an increased risk of melanoma (Figure 2). Patients with FAMMM due to *p16/CDKN2A* gene mutations also have a 9 to 47-fold increased risk of developing pancreatic cancer [10, 13–23, 78]. For example, de Snoo and colleagues studied 22 families with the *p16*-Leiden founder mutation who had attended a surveillance clinic and found that carriers of the mutation have a 47-fold increased risk of developing pancreatic cancer (RR, 46.6; 95% CI, 24.7–76.4) [17]. Similarly, H. Lynch and colleagues followed eight families with the FAMMM and pancreatic carcinoma in concert with a germline *p16*/*CDKN2A* mutation and reported four incidences of melanoma and pancreatic carcinoma as double primaries in the same individuals [21]. The FAMMM syndrome is important to recognize because lives can be saved by screening at-risk individuals for extrapancreatic neoplasms, in this case atypical nevi and early curable melanomas [79].

STK11 and the Peutz-Jeghers Syndrome

The Peutz-Jeghers syndrome is an autosomal dominant syndrome characterized by melanocytic macules on the lips and buccal mucosa, and hamartomatous polyps of the gastrointestinal tract (Figure 3) [24–30]. In addition to gastrointestinal and breast cancer, patients with the Peutz-Jeghers syndrome have a very high risk of developing pancreatic cancer [24–30]. Indeed, an obligate carrier of the gene developed pancreatic cancer in the kindred first described by Jeghers and colleagues [80]. Hearle and colleagues reported that 80% of *STK11* mutation carriers develop cancer by the age of 60 years [28], and Giardiello and colleagues reported that patients with the syndrome have a remarkable 132-fold increased risk of developing pancreatic cancer (CI= 44, 261) [26, 27]. The very high risk of pancreatic cancer in patients with the Peutz-Jeghers syndrome highlights the clinical need to develop effective screening tests for early curable pancreatic neoplasia in at-risk patients 24–30.

A first step in screening patients with the Peutz-Jeghers syndrome for curable disease will be to characterize the lesions that precede the development of invasive cancer in these patients. Preliminary analyses correlating histopathology with genetics have shown that some patients with Peutz-Jeghers develop intraductal papillary mucinous neoplasms (IPMNs) as the result of their genetic defect [30, 81]. Since IPMNs typically grow to several centimeters in size before they invade, these data suggest that some curable precursor lesions should be detectable and treatable in patients with Peutz-Jeghers.

PRSS1, *SPINK1* and Familial Pancreatitis

Familial pancreatitis, also known as hereditary pancreatitis, is characterized by recurrent episodes of severe acute pancreatitis starting at a young age [82]. Most patients ultimately develop chronic pancreatitis. Germline mutations in the *PRSS1* and *SPINK1* genes have both been shown to cause familial pancreatitis [83–85]. Germline mutations in *PRSS1* lead to an autosomal dominant form of inheritance [85]. Germline mutations in *SPINK1* increase the risk of developing pancreatitis, but the relative risk is small (2–5 fold) and most patients with *SPINK1* mutations never develop pancreatitis [86]. Patients with familial pancreatitis have as high as a 40% lifetime risk of developing pancreatic cancer [87, 88]. As will be discussed in greater detail in the section on therapy, some of these patients elect to have prophylactic pancreatectomy.

Other Genes

Linkage analyses have suggested that chromosome 4q may harbor a pancreatic cancer susceptibility gene, and Pogue-Geile and colleagues have suggested that this gene is palladin (*PALLD*) [89]. Follow-up studies on *PALLD*, have, however, failed to confirm that it is a significant familial pancreatic cancer gene [90–94].

The familial adenomatous polyposis (FAP) syndrome is characterized by the development of greater than 100 adenomatous polyps of the colon [95]. The small bowel can also be affected. It has been suggested that patients with FAP have an increased risk of pancreatic cancer, but some of the apparent increased risk may simple be the result of misclassification of duodenal adenocarcinomas as pancreatic primaries 95.

The hereditary nonpolyposis colorectal cancer syndrome (HNPCC) is characterized by early onset colon cancer, and an increased risk of carcinomas of the endometrium, ovary, bile duct, kidney, bladder, ureter and skin [96]. HNPCC is caused by inherited mutations in one of the DNA mismatch repair genes, including *hMSH2*, *hMLH1*, *hPMS1*, *hPMS2* and *hMSH6*/*GTBP* [1]. There have been several case reports of patients with HNPCC developing pancreatic cancer, but the exact contribution of HNPCC to the familial clustering of pancreatic cancer is poorly defined [1, 97].

While genetic testing may be of benefit to many families, the genetic basis of >80% of the clustering of pancreatic cancer in families remains unknown. Many families with an aggregation of pancreatic cancer may harbor mutations in yet to be identified genes and they will not be found to carry mutations in the above mentioned genes. Mutations in the *BRCA2* gene account for 6–12% of families with at least two pancreatic cancers, *PALB2* 1–3% and the remaining genes account for <1% of familial pancreatic cancer.

Therapeutic Implications

So far in this review we have quantified the risk of pancreatic cancer and we have identified some of the genes responsible for familial pancreatic cancer. We are now ready for a third question from our hypothetical patient: "*I have a germline mutation in a cancer predisposition gene, can this knowledge be used to guide my treatment?*" The answer depends on the patient's specific gene mutation.

Targeting *BRCA2* Gene Mutations

BRCA2-targeted therapies demonstrate that the discovery of a familial pancreatic cancer gene can lead to the development of gene-specific therapies. Pancreatic cancer cell lines harboring biallelic mutations in the *BRCA2* gene are exquisitely sensitive to mitomycin C and to PARP (Poly[ADP-ribose] polymerase) inhibitors in the laboratory [34–41]. These drugs target the very pathway, the repair of DNA cross-linking damage, that is inactivated in *BRCA2* mutant cells [34–41]. Normal cells, with a functional copy of the *BRCA2* gene, can repair the DNA injury caused by these agents, while cancer cells with biallelic inactivating mutations in the *BRCA2* gene do not produce functional Brca2 protein and cannot repair the damage from these agents [34–41]. The cancer cells are killed, while the normal cells survive. These results in the laboratory are now being translated to the clinic and there are already several reports of significant clinical responses in patients with *BRCA2* mutant cancers [34–41]. These findings suggest a scenario in which a patient's genotype can be used to identify the most effective therapy for that patient.

Prophylactic Surgery in Patients with Familial Pancreatitis

The increased risk of cancer in patients with familial pancreatitis is confined to the pancreas, and many patients with familial pancreatitis have severe exocrine and endocrine pancreatic insufficiency [87, 88]. Some of these patients therefore consider prophylactic total pancreatectomy [98–100]. While this surgery will eliminate the patient's very significant risk of developing pancreatic cancer, the benefit of prophylactic surgery has to be weighed against the real risks of total pancreatectomy [101]. The main complication of total pancreatectomy is brittle diabetes and although there is now increasing experience in managing diabetes after total pancreatectomy, there is an increased risk of morbidity and mortality associated with this surgery [98, 99, 101–103]. Some have considered the option of islet autotransplantation, but the "cell of origin" for pancreatic cancer is not known, and the risk of autotransplanting a potential neoplastic cell remains a theoretical concern [98, 99, 101–103].

As more familial pancreatic cancer genes are discovered, we can envision a future in which genetic testing will be used routinely to both determine an individual's risk and to guide therapy should they develop disease.

Screening for Early Neoplasia

Our hypothetical patient, recognizing that an ounce of prevention is worth a pound of cure, next asks: "*I have seen several of my family members die of pancreatic cancer, and I do not want to suffer the same fate. Are any screening tests available?*" The short answer to this question is that, unfortunately there are no clinically proven effective screening tests available for the early detection of pancreatic cancer at this time. Serum CA19-9 levels have been suggested as a possible test, but the assay lacks the sensitivity and specificity needed to screen for pancreatic cancer [104]. There are, however, a number of screening tests being evaluated in clinical trials, and several approaches hold promise.

Recently M. Canto and colleagues studied endoscopic ultrasound (EUS) as a screening test for asymptomatic members of at-risk families [31, 105]. In this trial, called "Cancer of the Pancreas Screening (CAPS)," Canto and colleagues screened asymptomatic patients with a strong family history of pancreatic cancer, as well as asymptomatic patients with the Peutz-Jeghers syndrome [31, 105]. Close to 10% of the asymptomatic individuals screened were found to have a lesion in their pancreas that resulted in surgery [31, 105]. Most of these lesions were IPMNs, and one-fourth of the precursors discovered on screening had significant dysplasia (carcinoma *in situ*), demonstrating that curable precancerous lesions can be detected and treated in asymptomatic at-risk individuals [31, 105–107]. Other groups using either EUS-based or abdominal magnetic resonance imaging (MRI) to screen individuals with multiple affected

family members or germline mutation carriers have also detected and treated IPMNs, pancreatic intraepithelial neoplasia (PanIN), and invasive pancreatic ductal adenocarcinomas [108, 109]. One group in The Netherlands recently reported a low diagnostic yield for screening for pancreatic neoplasia, but the study included subjects in a lower risk population with only two affected relatives 110. Clearly, identifying the correct group to screen is a critical first step in developing an effective screening test.

The screening and surgical resection of early curable neoplasms in at-risk individuals in the CAPS and other similar trials has also provided a unique opportunity for pathologists to study the morphology of unadulterated precursor lesions in individuals with a strong family history of pancreatic cancer [107, 111]. Three observations can be drawn from these morphological studies. First, PanINs are often associated with lobulocentric atrophy (Figure 4) [111]. Although PanIN lesions are small, most are associated with larger areas of lobulocentric atrophy and fibrosis [111]. Second, PanINs in patients with a strong family history of pancreatic cancer are often multifocal 111. As many as 20% of the smaller ducts in some patients contain PanIN lesions 111. Third, the combination of lobulocentric atrophy and multifocality of PanIN often produces grossly appreciable changes in the pancreas, and these changes can be detected by EUS 111–113. While single PanIN lesions are almost always too small to be appreciated grossly, larger PanINs (2–5 mm) can be seen by EUS as anechoic nonseptated lesions, often indistinguishable from saccular dilatations of branch ducts along the main duct or small branch duct IPMNs. Multifocal PanINs together with their multiple foci of associated lobulocentric atrophy produce a mosaic of fibrosis, atrophy and uninvolved parenchyma, changes very similar to chronic pancreatitis [111]. These changes are often detectable by EUS using standard criteria for the diagnosis of chronic pancreatitis, such as heterogeneous parenchyma, multifocal lobularity and dilated main and branch pancreatic ducts 111, 113.

Thus, although there are no clinically proven effective methods to screen at-risk individuals for early pancreatic neoplasia, several EUS-based studies have established that it is possible, in principle, to detect curable pancreatic neoplasms in asymptomatic at-risk patients. As the resolution of imaging improves and as our knowledge of precursor lesions grows, we believe that multifocal PanIN lesions will be detectable in clinical practice.

Future

The coming year will see an explosion in our understanding of familial pancreatic cancer. Next generation sequencing will allow researchers to sequence candidate familial pancreatic cancer genes on a scale unimaginable just a few years ago. In fact, investigators at Johns Hopkins University are planning to sequence the entire coding genomes of a series of patients with familial pancreatic cancer. The resultant flood of information will offer unparalleled opportunities to improve patient care. Investigators at Johns Hopkins have also formed an international screening and surveillance consortium involving 25 countries from North America, Europe, Australia, and Asia. It is hoped that this consortium will define the best methods to assess pancreatic cancer risk, increase our understanding of the natural history of apparently benign precancerous neoplasms, and define the survival benefit, if any, of treating premalignant neoplasms in high-risk individuals.

Surgeons will be at the forefront translating these advances to patient care. Surgical management will not be simply operating to resect a well-defined, but incurable carcinoma. Instead, an integration of clinical history, family cancer history, gene status, imaging and surgical skill will be needed to identify and treat early curable pancreatic neoplasia.

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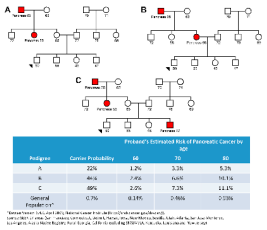

Figure 1. Three Pedigrees with Different Risks of Pancreatic Cancer

The counselee shown with an arrow in Figure 1A is predicted to have a 3.3 % chance of developing pancreatic cancer by the age of 70 years. This risk increases to ~7% if this patients mother rather than their maternal aunt had history pancreatic cancer (Figure 1B) or if their brother also has a history of pancreatic cancer (Figure 1C).

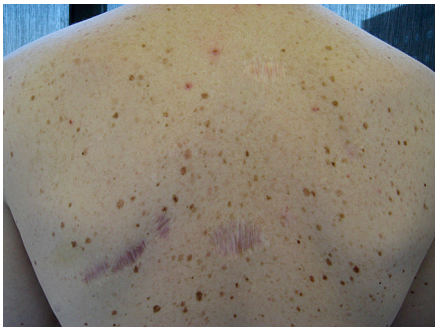

Figure 2. Familial Atypical Multiple Mole Melanoma Syndrome

This patient has multiple melanocytic nevi, some of which were atypical. Note the surgical scars. (Kindly provided by Dr. Rhoda M. Alani)

Figure 3. Peutz-Jeghers Syndrome

This young patient has multiple freckles on his lips. These may fade with age. (Kindly provided by Dr. Francis Giardiello)

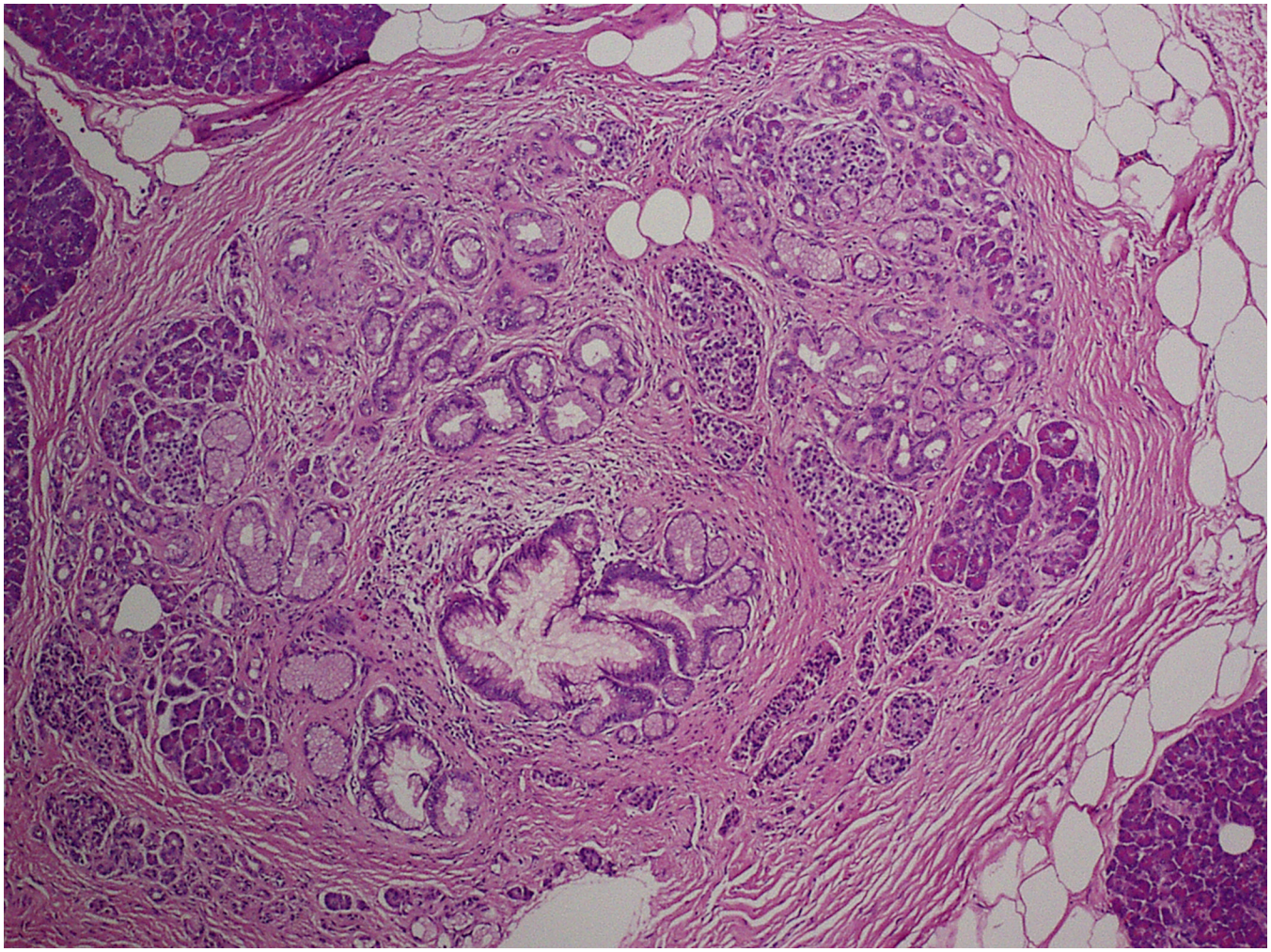

Figure 4. Lobulocentric Atrophy Associated with Pancreatic Intraepithelial Neoplasia lesion
The lobule of pancreatic parenchyma surrounding this small PanIN lesion is remarkable for fibrosis and acinar drop-out.

TABLE 1

Syndromes Associated with Pancreatic Cancer

Genetic Syndrome	Gene(s)	Increased Risk of Pancreatic Cancer	Risk of Pancreatic Cancer by age 70 years	Other Malignancies
No family history	None	RR=1	0.5%	None
Two First-degree Relatives with Pancreatic Cancer	Unknown in most cases	6-fold	3%	Breast, ovarian and bile duct
Hereditary Breast and Ovarian Cancer	*BRCA2*, *FANC-C*, *FANC-G*, *PALB2*	3.5 to 10-fold	2–5%	Breast, ovarian
Familial Atypical Multiple Mole Melanoma Syndrome (FAMMM)	*p16*/*CDKN2A*	9 to 47-fold	5–24%	Melanoma
Three or more First-degree Relatives with Pancreatic Cancer	Unknown in most cases	14 to 32-fold	7–16%	Breast, ovarian and bile duct
Familial Pancreatitis	*PRSS1*, *SPINK1*	50 to 80-fold	25–40%	None
Peutz-Jeghers	*STK11*	132-fold	60%	Small intestine, lung, esophagus, stomach, , breast, lung, uterus, ovary