HHS Public Access

Author manuscript

Transl Cancer Res. Author manuscript; available in PMC 2016 September 19.

Published in final edited form as:

Transl Cancer Res. 2016 August ; 5(Suppl 2): S243–S247.

Actionable Intelligence Provided by Pancreatic Cancer Genomic Landscape: Are Targets for Curative Therapy On The Map?

Nathan A. Berger, MD

Departments Medicine, Biochemistry and Genomic Sciences, Case Comprehensive Cancer Center, Case Western Reserve University School of Medicine

Pancreatic Ductal Adenocarcinoma (PDAC) is a devastating disease with severely debilitating comorbidities and dismal prognosis. In 2015, the worldwide incidence of new cases was estimated to be 367,000, and approximately 359,000 were expected to die from this disease (1). In the Western world, it is the 4th leading cause of cancer deaths (1). Overall survival for newly diagnosed PDAC is usually measured in months and while modest improvements have been made in 1 year survival, now estimated at 20% overall; 5 year survival remains less than 10%. Two problems that contribute to this dismal survival are (1) that PDAC is most commonly diagnosed when it is beyond cure by surgical resection and (2) there is a general lack of effective systemic chemotherapy (1).

In a recent tour-de-force integrated genomic, epigenomic and transcriptomic analysis of 456 annotated PDAC tumors, an international group of investigators, reported the most comprehensive and up-to-date PDAC molecular landscape (2) providing actionable intelligence that should spur multiple new approaches to better understand the epidemiologic development of PDAC, potentially lead to earlier diagnostic assays, certainly provide the basis for more rational development of therapeutic agents and approaches and define more precise criteria for stratifying and evaluating clinical trials. Primarily treatment naive PDAC tumors, obtained by the Australian Pancreatic Cancer Genome Initiative as part of the International Cancer Genome Consortium, were analyzed by a combination of whole-genome and deep-exome sequencing, gene copy number analysis, RNA expression profiling and methylation analysis, revealing 23,578 high confidence coding mutations and another 21,208 high confidence genome rearrangements, from which 32 recurrently mutated genes were identified that aggregated into 10 molecular pathways (Table 1). Based on unsupervised RNA expression analysis, these tumors were divided into 4 subtypes termed 1) Squamous; 2) Pancreatic Progenitor; 3) Immunogenic and 4) Aberrantly Differentiated Endocrine Exocrine (ADEX). These 4 subtypes could be differentiated by transcription networks representing distinct biological processes. The genomically determined subtypes had different histopathologic characteristics and they were associated with prognostic differences with the squamous subtype showing the worst median survival, 13.3 months, compared to 25.6 months for pancreatic progenitor, 23.7 months for ADEX and 30 months for immunogenic (p=0.0302) (2).

Contact Information: Nathan A. Berger, MD, 10900 Euclid Avenue, Cleveland OH 44106-4971, Phone: 216-368-4084, nab@case.edu.

The Squamous Subtype, so named because, although it is a subtype of adenocarcinoma, its upregulated gene pattern is composed of networks involved in squamous differentiation, including Myc activation, TP63ΔN transcriptional targets, inflammation, hypoxia, metabolic reprogramming, autophagy and also activated EGF signaling, all of which are commonly noted in other squamous subtypes of breast, bladder, lung and head and neck cancers. Many of the genes overexpressed in the squamous subtype were found to be downregulated in the other three subtypes. Of particular interest was the demonstration in the squamous subtype of epigenetic regulation characterized by hypomethylation and downregulation of genes that govern pancreatic endodermal determination (2).

The Pancreatic Progenitor Subtype was primarily defined by transcription factors that determine early embryonic pancreatic ductal exocrine and endocrine fate and are linked to maturity onset diabetes of the young. This class also notable for increased expression of genes regulating fatty acid oxidation, steroid hormone metabolism and O-linked mucin glycosylation (2).

The ADEX Subtype was identified by transcription networks that characterize later, more mature stages of exocrine and endocrine pancreatic differentiation as well as those associated with maturity onset diabetes. Tumors of the ADEX subtype were also noted to have distinct methylation patterns (2).

The Immunogenic Subtype was reported as being similar to the pancreatic progenitor subtype but uniquely defined by expression of genes characterizing a significant immune cell infiltrate including both B and T cells. Also noted in some of the immunogenic subtype tumors was upregulation of the CTLA4 and PD1 immune suppression pathways which were associated with the poorest survival (2).

This monumental achievement is a testimonial to big team science, to the value of international cooperation in science and a tribute to the multitude of funding agencies that supported this initiative. Since all the specimens were collected in Australia, the possibility exists that the findings and/or their percentage distributions may reflect unique epidemiologic characteristics or exposures of that population. Thus these observations may be modified or confirmed as the cohort is expanded, especially to include populations where differences may exist in ethnic composition or in some of the major risk factors for PDAC including tobacco use, obesity and diabetes (1). While the current results need to be extended to other population groups, this comprehensive genomic landscape presents a vast trove of data that provides us with unprecedented insights into the operational processes of this tumor. We are now challenged to most effectively use this information in our efforts to defeat PDAC.

Obviously, a major challenge in the war against pancreatic cancer is the identification and optimal application of effective therapies. Extensive studies have been conducted to develop therapeutic approaches to control PDAC, based on anti-metabolic and cytotoxic agents, alone and in combination, by targeted-precision therapy and more recently, by immunotherapy. While many of these approaches were empiric, we now have the unique opportunity to pursue therapeutic strategies based on a more rational and comprehensive

understanding of PDAC molecular processes. Before addressing these approaches it is worth noting that since the four different molecular based subtypes appear to have different prognosis, it would initially be useful to identify a genomic signature for each, to prospectively evaluate survival and to stratify patients for clinical trials.

Two antimetabolites, 5 Fluorouracil (5 FU) and Gemcitabine, which as single agents have modest palliative effects, but negligible survival benefits measured in months, serve as the basis for empirically designed combination chemotherapy regimens with statistically significant but still marginally meaningful clinical benefits. Combining Gemcitabine with the Epidermal Growth Factor Receptor Tyrosine Kinase Inhibitor, Erlotinib has been reported to improve median survival from 5.91 months with Gemcitabine alone to 6.24 months for the combination (3). Combining 5 FU in the FOLFIRINOX regimen (Folinic Acid, 5 FU, Irinotecan and Oxaloplatin), has been reported to improve median overall survival from 4.4 months for 5FU alone to 24 months with the combination (4). More recent studies suggest that Gemcitabine in combination with nanoparticle albumin bound paclitaxel may increase median overall survival to 8.5 months (5). In addition, studies with Gemcitabine plus Capecitebine have shown improved overall response rates with combination 19.1 vs 12.4% but only slight increase in median overall survival, 7.1months for combination vs 6.2 months for Gemcitabine alone (6). In another study, patients with good Karnofsky performance scores, receiving the Gemcitabine-Capecitebine combination showed median overall survival 10.1 vs. 7.4 months compared to Gemcitabine alone (7). While each of these combinations provide a statistically significant increase in survival, the overall prognosis remains grim. Moreover, given the recent demonstration, in malignancies such as lung cancer, of the apparent impact of genomic subtypes on survival, it must be considered that molecular based stratification might significantly alter survival statistics.

Beyond empiric approaches to single agents and their combinations, rational-precision approaches have targeted some of the major mutated oncogene and tumor suppressor drivers in PDAC, including K-RAS, TP53, CDKN2A and SMAD4 (1, 5, 8, 9). However, despite their high frequency of mutation in PDAC (Table 1), and numerous attempts at drug development, no agents have been identified to interfere with these oncogenes and tumor suppressors in a clinically useful manner, causing them to be generally regarded as “undruggable” targets. Nonetheless, the expanded array of recurrent pathways and genetic aberrations identified in this new study (Table 1) should provide an abundance of novel targets for development of strategic agents (2).

We have previously noted, tumors frequently have multiple growth promoting pathways, that interact at numerous levels (10). As a result, attempts to block any single pathway with a specific inhibitor may be bypassed by extensive networks of crosstalk, feedback loops and collateral signaling through alternative pathways. Such pathways have been proposed to contribute to the overall PDAC resistance to targeted therapies (1). Moreover, the newly reported multitude of pathways indicated by RNA expression analysis (2) provides strong support that this phenomenon of collateral escape routes is operational in these PDAC tumors and is likely to contribute to their therapeutic resistance. At the same time, documentation of these genomic aberrations and expression pathways, should provide the

basis for rational development of strategic approaches to simultaneously blockade multiple pathways.

Because of the multiple collateral growth, metabolic and resistance pathways, new agents may be identified that will interfere with a single pathway but not stop tumor growth, whereas rational development of combinations to block collateral pathways may be required to halt progression of PDAC tumors. For example, simultaneous targeting of mutant K-RAS along with multiple parallel and downstream pathways such as Insulin Growth Factor 1, MAPK, AKT, Hepatocyte Growth Factor Receptor, NOTCH and Hypoxia Inducible Factor 1α may provide effective strategies to alter metabolism, and disrupt alternate bypass and resistance pathways (1, 5, 11). Similar approaches have been effectively applied to sensitize B-RAF mutant tumors with intrinsic or acquired resistance to the tyrosine kinase inhibitor Vemurafenib (12–14). This approach has the potential to develop agents that interfere with targets at the molecular level but whose ability to halt tumor growth may not be evident until collateral pathways are simultaneously inhibited. Thus, this approach may require simultaneous testing in patients of combinations that have been shown to work in combination in model systems but whose efficacy cannot be shown in traditional single agent clinical trials.

The differences in the chromatin methylation and gene expression patterns identified in the PDAC subtypes suggest differences in epigenetic regulation, that may be subtype specific, contribute to overall resistance, and may be exploitable from a therapeutic viewpoint. This possibility indicates the importance of 1) more fully characterizing the epigenetic landmarks of PDAC, 2) identifying the PDAC expression pathways regulated by epigenetic control, 3) screening epigenetic modifiers (15) to identify those that control growth promoting, chemotherapy resistance and other metabolic pathways, 4) identify epigenetic signatures to predict subtypes and patients likely to respond and 5) conduct clinical trials of epigenetic modifiers alone and in combination with cytotoxic or targeted agents in patients stratified according to genomic and epigenomic signatures (16) (17). Recent studies have in fact shown antitumor efficacy in model PDAC systems for epigenetic targeted agents, including the histone deacetylase (HDAC) inhibitor SAHA, and JQ1, an inhibitor of bromodomain and etraterminal (BET) protein binding to chromatin (18).

Immunotherapy provides an important alternative to chemotherapy and radiation since it attempts to harness a different set of antitumor mechanisms including antibody and cell mediated cytotoxicity (19). In addition, immunotherapy usually has a different set of host toxicities. Recent studies of immunotherapy for solid tumors have focused on the development of strategies to recruit host immune cells to recognize and destroy tumor cells bearing tumor specific antigens and also to use anti checkpoint blockade agents to reduce tumor immunosuppressive effects (20, 21). These agents have been shown to be successful in immune active tumors, characterized by infiltration of increased CD8 + T Cells but not in immune quiescent tumors which lack these cells (22). Melanoma, non small cell lung cancer, colorectal cancer and renal cell cancer fall into the category of immune active tumors showing promising responses to immune checkpoint blockade inhibitors (22). Unfortunately, pancreatic cancer appears to be an immune quiescent tumor, limiting its response to such agents (22). However, the new genomic classification of PDAC (2) suggests that the

immunogenic subtype may be an appropriate group on which to focus these therapies since it already has an immune cell infiltrate. Moreover, since this tumor subtype is reported to show worse survival when it overexpresses CTLA-4 and/orPD-1 (2), patients with these expression patterns may constitute a unique PDAC subgroup for clinical trials with anti-CTLA4, anti PD-1 and anti PD-L1 antibodies. In terms of focusing this immune approach on the immunogenic subtype or PDAC, it is interesting to note that the anti PD-1 agent Pembrolizumab has shown significant antitumor activity in colorectal cancer (CRC) with mismatch – repair deficiency, but not in CRC that is mismatch - repair proficient (23). This study has important relevance for several reasons. First, it clearly shows that highly specific targeted therapies are likely to have their efficacy manifest in subgroups of tumors with selected markers and pathways. Second, these studies showed that efficacy occurred in mismatch repair deficient tumors which contain a mean of 1782 somatic mutations compared to 73 in the mismatch repair proficient tumors, providing the basis for generation of multiple immunogenic neo-antigens. Third, the sensitive tumors showed an abundance of CB8+ lymphocyte infiltrates supporting the proposal that immune therapies are most likely to work in tumors already showing a major lymphocytic infiltrate.

Vaccine based strategies are being implemented to increase many immune effector cells to improve tumor infiltration and focus their immunotoxic effects on tumor destruction. Mesothelin has emerged as a tumor antigen with early promise for PDAC targeted vaccines (22, 24). The repertoire of mutated oncogenes and tumor suppressors now identified in PDAC (Table 1) should provide an expanded array of neo antigens, unique to tumors and not present in normal tissues, to serve as targets for vaccine development ((2) Bailey et al 2016). Since many of these mutated genes are present at early, premalignant stages of pancreatic tumor development and before immunosuppressive mechanisms develop (25), it is possible, that once shown to be effective, these vaccines may even be useful to treat PDAC precursors on a preventive basis.

In conclusion, it is worth noting that since single modality therapies such as chemotherapy, radiation therapy and immunotherapy have shown minimal efficacy, it will most likely require combinations of these approaches to improve responsiveness. Focused on its newly defined genomic landscape, we now have a host of actionable intelligence to understand the command and control mechanisms of PDAC, the pathways it uses to escape our therapeutic interventions and the basis to begin its systematic eradication.

Acknowledgments

NAB was supported in part by NIH, National Cancer Institute GI SPORE P50 CA150964

References

1. Kleeff J, Korc M, Apte M, La Vecchia C, Johnson CD, Biankin AV, et al. Pancreatic cancer. Nature reviews Disease primers. 2016; 2:16022.
2. Bailey P, Chang DK, Nones K, Johns AL, Patch AM, Gingras MC, et al. Genomic analyses identify molecular subtypes of pancreatic cancer. Nature. 2016; 531(7592):47–52. [PubMed: 26909576]
3. Kelley RK, Ko AH. Erlotinib in the treatment of advanced pancreatic cancer. Biologics: targets & therapy. 2008; 2(1):83–95. [PubMed: 19707431]

4. Suker M, Beumer BR, Sadot E, Marthey L, Faris JE, Mellon EA, et al. FOLFIRINOX for locally advanced pancreatic cancer: a systematic review and patient-level meta-analysis. The Lancet Oncology. 2016; 17(6):801–10. [PubMed: 27160474]
5. Kleger A, Perkhofer L, Seufferlein T. Smarter drugs emerging in pancreatic cancer therapy. Annals of oncology: official journal of the European Society for Medical Oncology/ESMO. 2014; 25(7): 1260–70. [PubMed: 24631947]
6. Cunningham D, Chau I, Stocken DD, Valle JW, Smith D, Steward W, et al. Phase III randomized comparison of gemcitabine versus gemcitabine plus capecitabine in patients with advanced pancreatic cancer. J Clin Oncol. 2009; 27(33):5513–8. [PubMed: 19858379]
7. Herrmann R, Bodoky G, Ruhstaller T, Glimelius B, Bajetta E, Schuller J, et al. Gemcitabine plus capecitabine compared with gemcitabine alone in advanced pancreatic cancer: a randomized, multicenter, phase III trial of the Swiss Group for Clinical Cancer Research and the Central European Cooperative Oncology Group. J Clin Oncol. 2007; 25(16):2212–7. [PubMed: 17538165]
8. Eser S, Schnieke A, Schneider G, Saur D. Oncogenic KRAS signalling in pancreatic cancer. Br J Cancer. 2014; 111(5):817–22. [PubMed: 24755884]
9. Tang SC, Chen YC. Novel therapeutic targets for pancreatic cancer. World journal of gastroenterology. 2014; 20(31):10825–44. [PubMed: 25152585]
10. Hursting SD, Digiovanni J, Dannenberg AJ, Azrad M, Leroith D, Demark-Wahnefried W, et al. Obesity, energy balance, and cancer: new opportunities for prevention. Cancer prevention research (Philadelphia, Pa). 2012; 5(11):1260–72.
11. Holohan C, Van Schaeybroeck S, Longley DB, Johnston PG. Cancer drug resistance: an evolving paradigm. Nature reviews Cancer. 2013; 13(10):714–26. [PubMed: 24060863]
12. Kang HB, Fan J, Lin R, Elf S, Ji Q, Zhao L, et al. Metabolic Rewiring by Oncogenic BRAF V600E Links Ketogenesis Pathway to BRAF-MEK1 Signaling. Molecular cell. 2015; 59(3):345–58. [PubMed: 26145173]
13. Broady R, Yu J, Chow V, Tantiworawit A, Kang C, Berg K, et al. Cutaneous GVHD is associated with the expansion of tissue-localized Th1 and not Th17 cells. Blood. 2010; 116(25):5748–51. [PubMed: 20864580]
14. Baudy AR, Dogan T, Flores-Mercado JE, Hoeflich KP, Su F, van Bruggen N, et al. FDG-PET is a good biomarker of both early response and acquired resistance in BRAFV600 mutant melanomas treated with vemurafenib and the MEK inhibitor GDC-0973. EJNMMI research. 2012; 2(1):22. [PubMed: 22651703]
15. Valdespino V, Valdespino PM. Potential of epigenetic therapies in the management of solid tumors. Cancer management and research. 2015; 7:241–51. [PubMed: 26346546]
16. Dawson MA, Kouzarides T. Cancer epigenetics: from mechanism to therapy. Cell. 2012; 150(1): 12–27. [PubMed: 22770212]
17. Campbell RM, Tummino PJ. Cancer epigenetics drug discovery and development: the challenge of hitting the mark. J Clin Invest. 2014; 124(1):64–9. [PubMed: 24382391]
18. Mazur PK, Herner A, Mello SS, Wirth M, Hausmann S, Sanchez-Rivera FJ, et al. Combined inhibition of BET family proteins and histone deacetylases as a potential epigenetics-based therapy for pancreatic ductal adenocarcinoma. 2015; 21(10):1163–71.
19. Laheru D, Jaffee EM. Immunotherapy for pancreatic cancer - science driving clinical progress. Nature reviews Cancer. 2005; 5(6):459–67. [PubMed: 15905855]
20. Postow MA, Callahan MK, Wolchok JD. Immune Checkpoint Blockade in Cancer Therapy. J Clin Oncol. 2015; 33(17):1974–82. [PubMed: 25605845]
21. Soares KC, Rucki AA, Wu AA, Olino K, Xiao Q, Chai Y, et al. PD-1/PD-L1 blockade together with vaccine therapy facilitates effector T-cell infiltration into pancreatic tumors. Journal of immunotherapy (Hagerstown, Md: 1997). 2015; 38(1):1–11.
22. Foley K, Kim V, Jaffee E, Zheng L. Current progress in immunotherapy for pancreatic cancer. Cancer Lett. 2015
23. Le DT, Uram JN, Wang H, Bartlett BR, Kemberling H, Eyring AD, et al. PD-1 Blockade in Tumors with Mismatch-Repair Deficiency. N Engl J Med. 2015; 372(26):2509–20. [PubMed: 26028255]

24. Lutz ER, Kinkead H, Jaffee EM, Zheng L. Priming the pancreatic cancer tumor microenvironment for checkpoint-inhibitor immunotherapy. Oncoimmunology. 2014; 3(11):e962401. [PubMed: 25941589]

25. Keenan B, Jaffee EM. Immunotherapy in preneoplastic disease: targeting early procarcinogenic inflammatory changes that lead to immune suppression and tumor tolerance. Ann N Y Acad Sci. 2013; 1284:12–6. [PubMed: 23651188]

Table 1

Significant Recurrent Pathway and Genetic Alterations in Pancreatic Ductal Adenocarcinoma.

Altered Pathways	**Altered Genes**	**% Tumors Showing Abnormality**
KRAS Activation	KRAS, MAPK4	92%
Cell Cycle, GI/S Checkpoint Disruption	TP53, CDKN2A, TP53BP2	78%
TGF Beta Signaling	SMAD3, SMAD4, TGF, TGPBR1, TGFBR2, ACVR1B and ACVR2A	47%
Chromatin Modification	KDM6A, SETD2, ASCOM Complex members MLL2 and MLL3	24%
DNA Repair	BRCA1, BRCA2, ATM, PALB2, SATF2	17% *
RNA Processing	SF3B1, U2AF1, RBM10	16%
SWI/SNF Complex	ARID1A, ARID1B, PBRM1 and SMARCA4	14%
WNT Signaling	RNF43, MAPK2, TLE4	5%
ROBO SLIT Axonal Guidance	ROBO1, ROBO2, SLIT2, MYCBP2	5%
NOTCH Signaling	JAG1, NF2, BCORL9, FBXWT	–

Data for Table 1 abstracted from (Bailey, Chang, Nones). Percent abnormality ROBO SLIT from (Biankin Waddell, Kassahn).

* 17% Tumor with abnormal DNA repair genes noted to be 5% Germline, 12% Somatic.