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Validation of biomarkers that complement CA19.9 in detecting early pancreatic cancer

Alison Chan^{1,2,*}, Ioannis Prassas^{1,2,*}, Apostolos Dimitromanolakis², Randall Brand⁴, Stefano Serra^{1,5}, Eleftherios P. Diamandis^{1,2,3}, and Ivan M. Blasutig^{1,3}

¹Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, Canada

²Department of Pathology and Laboratory Medicine, Mount Sinai Hospital, Toronto, ON, Canada

³Department of Clinical Biochemistry, University Health Network, Toronto, ON, Canada

⁴University of Pittsburgh, Division of Gastroenterology, Hepatology & Nutrition, Pittsburgh, PA

⁵Department of Pathology, University Health Network, Toronto, ON, Canada

Abstract

Purpose—Pancreatic ductal adenocarcinoma (PDAC) is a significant cause of cancer mortality. CA19.9, the only tumor marker available to detect and monitor PDAC, is not sufficiently sensitive and specific to consistently differentiate early cancer from benign disease. In this study we aimed to validate recently discovered serum protein biomarkers for the early detection of PDAC and ultimately develop a biomarker panel that could discriminate PDAC from other benign disease better than the existing marker CA19.9.

Patients and Methods—We performed a retrospective blinded evaluation of 400 serum samples collected from individuals recruited on a consecutive basis. The sample population consisted of 250 individuals with PDAC at various stages, 130 individuals with benign conditions and 20 healthy individuals. The serum levels of each biomarker were determined by ELISAs or automated immunoassay.

Results—By randomly splitting matched samples into a training (n=186) and validation (n=214) set we were able to develop and validate a biomarker panel consisting of CA19.9, CA125 and LAMC2 that significantly improved the performance of CA19.9 alone. Improved discrimination was observed in the validation set between all PDAC and benign conditions ($AUC_{CA19.9}=0.80$ versus $AUC_{CA19.9+CA125+LAMC2}=0.87$; $p<0.005$) as well as between early-stage PDAC and benign conditions ($AUC_{CA19.9}=0.69$ versus $AUC_{CA19.9+CA125+LAMC2}=0.76$; $p<0.05$) and between early-stage PDAC and chronic pancreatitis ($AUC_{CA19.9}=0.59$ versus $AUC_{CA19.9+CA125+LAMC2}=0.74$; $p<0.05$).

Corresponding Author: Ivan M. Blasutig, University Health Network, 200 Elizabeth Street, Room 3 EB 362, Toronto, ON, M5G 2C4, Phone: 416-340-4800 ext. 7199, Fax: 416-340-4215, ivan.blasutig@uhn.ca.

*Both authors contributed equally to this work

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Conclusions—The data demonstrate that a serum protein biomarker panel consisting of CA125, CA19.9 and LAMC2 is able to significantly improve upon the performance of CA19.9 alone in detecting PDAC.

Keywords

Pancreatic cancer; early detection; biomarker; phase II validation

Introduction

Pancreatic cancer is the tenth most commonly diagnosed cancer in North America but it ranks fourth in cancer-related deaths (1, 2). In contrast to other major human malignancies (lung, breast, colon and prostate) which have shown notable reductions in mortality rate over the past 30 years, pancreatic cancer has had minimal improvement in patients' survival rate (1). The 5-year survival rate for pancreatic ductal adenocarcinoma (PDAC), the most common form of pancreatic cancer, improves from 2% to 23% if the disease is diagnosed at its localized stage compared to a distant metastatic stage (3). However, the late presentation of disease-specific symptoms often leads to missed or delayed diagnosis of PDAC and at the time of diagnosis approximately 80% of patients harbor aggressive and metastatic disease not suitable for surgical resection, the only potentially curative treatment available (4). These statistics emphasize the urgent clinical need to identify biomarkers that can detect PDAC early.

In terms of diagnosis, there are currently no sufficiently sensitive or specific screening tests for early detection of PDAC. Conventional imaging tools, including computerized tomography (CT) scanning, magnetic resonance imaging (MRI), endoscopic ultrasonography (EUS), and endoscopic retrograde cholangiopancreatography (ERCP) are not sensitive at detecting small premalignant lesions and are relatively costly, time-consuming and invasive (5, 6). On the contrary, serum biomarkers are low cost, minimally invasive and ideal for early diagnosis (7). The current gold-standard serum biomarker CA19.9 is used in the clinic only for disease monitoring and prognosis, has limited sensitivity in PDAC detection due to its absence in Lewis^{a-b-} individuals (5–10% of Caucasian population), is minimally elevated in early premalignant disease and is elevated in other benign conditions and multiple cancer types (2, 8, 9). Taken together, it is critical to discover novel biomarkers to complement CA19.9 in order to improve both its sensitivity and specificity.

In the pursuit of deciphering PDAC biomarkers, we have combined the following approaches: 1) integrative proteomic analysis of cell line conditioned media, pancreatic ascites and pancreatic juice (10, 11); 2) comparative proteomic analysis of PDAC tissues with adjacent benign tissues (12) and 3) bioinformatics analysis of publicly available gene and protein databases for identification of pancreatic-specific proteins (13). Our multiple approaches enabled us to identify numerous biomarker candidates including anterior gradient homolog 2 (AGR2), regenerating islet-derived 1 beta (REG1B), syncollin (SYCN), laminin gamma C (LAMC2) and cancer antigen 125 (CA125), all of which were subsequently validated in over 400 samples (11, 12, 14). (Notably, CA125 was re-

discovered as “CUZD1 protein” (15)). In this study, we took our top 5 candidates: AGR2, REG1B, SYCN, LAMC2 and CA125, and used them to perform a large blinded validation study using 400 patient plasma samples to evaluate their performance, individually and combined, in detecting early stage PDAC.

Methods

Study population

Patients and control subjects were recruited on a consecutive basis from participating investigators in two major hospitals of the University of Pittsburgh Medical Centre (UPMC) system including the UPMC Presbyterian and UPMC Shadyside campus. Subjects with a histologically or CT scan confirmed diagnosis of PDAC or with an abnormal abdominal imaging study (CT, MRI, MRCP and EUS) were eligible for the study. Control subjects with a clinical diagnosis of a pancreas, liver or intestinal condition, or being evaluated for non-pancreatic malignancies were included in the study. Subjects under the age of 18 years old and those without informed consent were excluded. Any patients with a prior history of any other malignancy except non-melanoma skin cancers within ten years of treatment were not included. Healthy controls were eligible volunteers without any pancreatic conditions or malignant diseases.

All samples used in this study were obtained within a four year period from April 2008 to June 2012. Blood was collected in Acid Citrate Dextrose (ACD) anticoagulant vacutainer tubes and plasma samples were processed within 24 hours of blood draw. Blood samples were centrifuged at room temperature for 10 minutes (at $1000 \times g$) to pellet the cells. Immediately following centrifugation, the plasma samples were aliquoted into 1mL cryotubes and stored at -80°C until analysis in October 2012.

A subset of patients was selected from the available subject pool based on desired characteristics (prospective specimen collection, retrospective-blinded-evaluation). A total of 400 blinded plasma samples were obtained and samples within each group were randomly split into a training set ($n=186$) and an independent validation set ($n=214$). Overall, the 400 samples comprised of 20 healthy individuals, 130 benign condition patients, 51 stage 1A, 1B, 150 stage IIB and 49 stage IV PDAC patients. Details about the patient population are shown in Table 1. All samples were collected prior to any treatment following informed consent with an Institutional Review Board approved protocol.

Measurement of markers in blood samples

All samples ($n=400$) were analyzed using ELISA assays on the same day for each candidate, according to the “Standards for the reporting of diagnostic accuracy studies (STARD) initiative” (16) (Supplementary Table 1).

Using commercially available sandwich enzyme-linked immunosorbent assays (ELISA) for AGR2, REG1B, SYCN, and LAMC2 purchased from USCN Life Sciences (Missouri City, TX, USA), the levels of these proteins were measured in duplicates according to the manufacturer’s protocols. CA19.9 levels were measured using the Abbott Architect CA19.9_{XR} immunoassay (Abbott, USA). CA125 values were, first, obtained as “CUZD1

values” from a commercial CUZD1 ELISA kit obtained from USC Life Sciences (Missouri City, TX, USA). When we discovered that this commercial kit was, in fact, measuring CA125, we re-measured all available samples (251/400) with the Abbott Architect CA125 immunoassay (Abbott, USA). As expected, a strong linear $\log_{CA125}/\log_{CUZD1}$ correlation curve was observed (Supplementary Figure 4). CA125 values for the remaining 149 samples (which were depleted) were determined by extrapolation.

Prior to all sample analyses, AGR2, REG1B, SYCN and LAMC2 ELISAs were first tested to optimize the analytical performances, to select appropriate controls (low, medium and high) and the sample dilution factor to be used for each of the ELISA kits. Controls were used to assess the inter-plate variability.

Samples were diluted in assay buffer diluent as follows: 1 in 10 dilution for AGR2, 1 in 10,000 dilution for REG1B, 1 in 20 dilution for SYCN, 1 in 5 dilution for CUZD1 and 1 in 100 dilution for LAMC2. One hundred microliters of diluted sample was incubated in pre-coated ELISA 96-well plates along with standards for 2 hours in 37 °C. After washing the wells, 100 uL of biotin-labeled polyclonal secondary antibody (detection reagent A) was added and incubated for another hour at 37 °C. After washing, 100 uL of avidin-conjugated horseradish peroxidase (detection reagent B) was added and incubated for 30 minutes at 37 °C. After a final washing step, 90 uL of tetramethylbenzidine (TMB) substrate was added to each well and incubated for approximately 10–15 minutes in the dark at 37 °C until the second lowest standard could be distinguished from the blank by a change of colour. 50 uL of stopping solution (sulphuric acid solution) was then added and the absorbance was measured using the Perkin-Elmer Envision 2103 Multilabel Reader at 450 nm wavelength, standardized with a background absorbance at 540 nm.

Inter-plate assay imprecision was assessed across the 12 plates used for each marker using three controls (low, medium and high) (Supplementary Table 2). The coefficient of variation (CV) was calculated for each marker. Overall, LAMC2, AGR2 and SYCN assays demonstrated acceptable reproducibility across 12 plates, with <20% CVs for all controls. REG1B assays were relatively poor, showing medium and high control CVs of 36% and 58% respectively. As an additional quality control step, all samples were analyzed in duplicate to assess the intra-plate variations. The mean and median CVs amongst duplicate samples ranged from 5% to 12% for all markers, which is indicative of good intra-plate performance of the assays (Supplementary Table 2).

Statistical Analysis

Comparisons of levels of markers between groups were performed using the Mann Whitney-Wilcoxon test. Mean level comparisons were performed using a t-test and/or an ANOVA test.

The discriminatory ability of the biomarkers was assessed by building receiver operating characteristic curves (ROC) for individual markers and combined predictors. The diagnostic value of the markers was evaluated based on area under the curve (AUC) and the evaluation of sensitivity and specificity at an optimal cutoff obtained by minimizing the total prediction

error, by the following formula: $\sqrt{(1 - \text{sensitivity})^2 + (1 - \text{specificity})^2}$. Confidence intervals (95%) for areas under the curve and p-value for comparison between related ROC curves were performed using the method described by DeLong (17).

Logistic regression model building

Multi-parametric models explored included logistic regression models using log2-transformed markers (see Supplementary Table 4 for model fit diagnostics), logistic regression models with interaction terms and more advanced non-linear classifiers such as Random Forests and Support Vector Machines (data not shown). Despite its simplicity, the logistic regression model demonstrated the best performance and was chosen as our main model for this paper. Summary of model fitting diagnostics and parameters for our chosen models are shown in Supplementary Tables 4 and 5. FDR adjusted p-values for model comparisons in the training set are shown in Supplementary Table 6. The reduced coefficient models evaluated for diagnostic performance are: (1) $CA19.9 + 1.11 \cdot CA125$, (2) $CA19.9 + 0.202 \cdot LAMC2$, (3) $CA19.9 + 1.13 \cdot CA125 + 0.143 \cdot LAMC2$.

Statistical analysis in the training set was performed while being blinded to clinical annotations of the validation set. Multi-parametric prediction models were built based on the comparison of the benign vs. all PDAC groups in the training set, with p-values adjusted for false discovery rate by the Benjamini-Hochberg procedure (Supplementary Table 6). Once the optimal models were identified, clinical information for the validation samples were unblinded and the model predictions were evaluated. The primary measure for the 3 models was the comparison of the benign vs. all PDAC groups. Hypothesis testing was two-tailed, and p-values of less than 0.05 were considered significant. Statistical analysis was performed in the R environment (version 2.15.2) available from <http://www.R-project.org>. ROC curve analysis and comparisons between ROC curves was performed using the pROC package (18).

Association of markers with age and gender

Pearson correlation was used to evaluate the correlation of markers with age, separately in the healthy and benign groups (Supplementary Table 7). Gender association was evaluated based on a t-test of marker values between males and females (Supplementary Table 7).

Results

Performances of markers in the training and validation sets

As individual markers, the performances of the five candidates were compared to CA19.9 in discriminating benign conditions versus PDAC and healthy controls versus PDAC in both training and validation cohorts (Figures 1, 2, Supplementary Table 3 and Supplementary Figures 1, 2 and 3). As single markers, CA125 and LAMC2 were the most promising of the 5 candidates. Their concentrations were significantly increased in PDAC cases compared to benign controls in both training and validation cohorts ($p < 0.0001$; Figure 1 and Supplementary Table 3). The remaining 3 proteins, AGR2, REG1B and SYCN demonstrated poor discriminatory performances, both individually and as part of a marker panel, and were left out of subsequent analyses (Figure 2, Supplementary Table 3 and

Supplementary Figures 1 and 2). As shown in Table 2, the AUCs for CA19.9 and CA125 in discriminating all benign from all PDAC samples were comparable in the training ($AUC_{CA19.9}=0.85$, $AUC_{CA125}=0.77$) and validation sets ($AUC_{CA19.9}=0.80$, $AUC_{CA125}=0.78$). LAMC2 also showed comparable performance in the training set ($AUC_{LAMC2}=0.81$), however, it demonstrated poorer performance in the validation set ($AUC_{LAMC2}=0.69$). Similarly, in discriminating benign from early stage PDAC, the performance of the 3 markers was comparable in both the training ($AUC_{CA19.9}=0.82$, $AUC_{CA125}=0.78$, $AUC_{LAMC2}=0.73$) and validation sets ($AUC_{CA19.9}=0.69$, $AUC_{CA125}=0.72$, $AUC_{LAMC2}=0.68$). Finally, in discriminating chronic pancreatitis patients from early PDAC patients, both markers had similar performance to CA19.9 in the training ($AUC_{CA19.9}=0.76$, $AUC_{CA125}=0.79$, $AUC_{LAMC2}=0.64$) and validation sets ($AUC_{CA19.9}=0.59$, $AUC_{CA125}=0.75$, $AUC_{LAMC2}=0.69$).

Optimal cutoffs for each marker were obtained by minimizing the total prediction error as described in the methods. Based on the ROC analysis in the training set comparing all PDAC ($n=111$) versus all benign conditions ($n=65$), the optimum diagnostic cutoff for CA19.9 was 20.3 U/mL (sensitivity 77.5%, specificity 83.1%; Table 2). The optimum cutoff for CA125 was 17.9 U/mL (sensitivity 70.3%, specificity 75.4%) and for LAMC2 was 123.2 ng/mL (sensitivity 70.3%, specificity 87.7%).

As expected, CA19.9 displayed strong discriminatory performance in both the training and validation cohorts (Figure 2, Table 2 and Supplementary Figure 2). However, if used at its clinically utilized cutoff (>37 U/mL), a total of 22 out of 130 patients (approximately 17%) with benign disease would be falsely positive for CA19.9 (>37 U/mL), and 75 out 250 (30%) PDAC patients would be missed (false negatives) by this marker. In order to compare the performances of CA19.9 (as a single marker) with the 3-marker panel, multi-parametric models for various combinations of the three proteins (CA19.9, CA125 and LAMC2) were constructed based on the comparison of all PDAC patients versus benign controls in the training set and applied to the blinded validation set. Our proposed panel significantly improved the performance of CA19.9 in the primary measure (benign vs. all PDAC; Table 2 and Figure 3) as well as the secondary measures (Table 2 and Supplementary Figure 3). The power of distinguishing benign conditions from all PDAC cases increased from $AUC_{CA19.9}=0.85$ to $AUC_{CA19.9+CA125+LAMC2}=0.93$ in the training cohort and from $AUC_{CA19.9}=0.80$ to $AUC_{CA19.9+CA125+LAMC2}=0.87$ in the validation cohort ($p<0.005$). Significant improvements were also shown in the validation cohort in discriminating all benign patients from those with early-stage PDAC ($AUC_{CA19.9}=0.69$ versus $AUC_{CA19.9+CA125+LAMC2}=0.76$; $p<0.05$) and in discriminating chronic pancreatitis (CP) cases from early PDAC patients ($AUC_{CA19.9}=0.59$ versus $AUC_{CA19.9+CA125+LAMC2}=0.74$, $p<0.05$). In the last subgroup (CP versus early PDAC), the addition of CA125 alone seems to account for most of the improvement displayed by the panel as the addition of LAMC2 did not add significant diagnostic information (Table 2).

To further investigate the complementarity of CA125 and LAMC2 with CA19.9, we assessed the performance of these two markers (individually or combined) in all PDAC patients that were missed by CA19.9 based on the clinically used threshold of 37 U/mL. As shown in Table 3, CA125 and LAMC2 retained their ability in discriminating benign from

PDAC patients in this subpopulation of PDAC patients lacking elevated CA19.9 in both the training ($AUC_{CA19.9} = 0.59$; $AUC_{CA125+LAMC2} = 0.81$, $p < 0.0001$) and validation cohorts ($AUC_{CA19.9} = 0.54$; $AUC_{CA125+LAMC2} = 0.76$, $p < 0.0001$). Discriminatory ability was also noticed between chronic pancreatitis and early PDAC patients in both the training ($AUC_{CA19.9} = 0.53$; $AUC_{CA125+LAMC2} = 0.84$, $p < 0.0001$) and validation cohorts ($AUC_{CA19.9} = 0.52$; $AUC_{CA125+LAMC2} = 0.73$, $p = 0.01$).

Discussion

Carbohydrate antigen 19.9 (CA19.9) remains the only clinically-used marker for management of PDAC (FDA- approved as a disease monitoring marker). In terms of disease detection, CA19.9 is neither very sensitive (it is elevated mainly in late cancer stages and up to 10% of the population genetically negative) nor specific (elevated in non-pancreatic cancers and several benign conditions). Therefore, the identification of serum markers that could aid in the detection of early-stage PDAC remains a clear unmet need. Our group has utilized various technologies to discover novel PDAC biomarkers and identified 5 proteins (AGR2, REG1B, SYCN, LAMC2 and CA125) that carry significant diagnostic information for the detection of PDAC (10–15). This current study is an extensive blinded validation of these 5 markers, in addition to CA19.9, in a single set of patient samples with a focus on their complementarity in the early detection of PDAC. Our retrospective analysis revealed that CA125 and LAMC2 display strong diagnostic performances as individual serum PDAC markers, but more importantly, our multi-parametric models demonstrated significant complementarity of these two markers with CA19.9, especially in the detection of early stage PDAC (up to stage IIB) from benign conditions (e.g. chronic pancreatitis).

LAMC2 belongs to the laminin family of extracellular matrix glycoproteins, which are major constituents of basement membranes and have been implicated in many tumor-related processes including cell adhesion, migration, differentiation and metastasis. At the gene level, LAMC2 expression has been inversely related to overall patient survival (19). Moreover, LAMC2 overexpression has been proposed as a poor prognostic indicator in late-stage PDAC patients (20). According to the Human Protein Atlas (<http://www.proteinatlas.org/>), LAMC2 demonstrates a very strong positivity in PDAC tissue sections. Furthermore, tissue expression databases, such as BioGPS (<http://biogps.org/#goto=welcome>) and Tiger Expression Database (<http://bioinfo.wilmer.jhu.edu/tiger/>) demonstrate that pancreas is among the main LAMC2-expressing tissues.

CA125 (cancer antigen 125), is a high molecular weight protein that in humans is encoded by the *MUC16* gene. It belongs to the mucin superfamily, many members of which have been tested as candidate markers for a plethora of cancer types. CA125 is primarily known as a useful marker for the clinical management of ovarian cancer; however, accumulating evidence reveals an increased expression of this antigen in the serum of PDAC patients (for example, see (21)).

Recent PDAC-related research suggests that it takes up to a decade before the initial tumor acquires metastatic ability, offering a long window of opportunity for early detection of pancreatic cancer (22, 23). Considering the possibility that no single marker possesses

sufficient sensitivity and specificity for early diagnosis of PDAC, research interest has been shifted into the development of biomarker panels (7, 24, 25). In this study we identify and validate a biomarker panel consisting of CA19.9, CA125 and LAMC2 that is better at detecting PDAC patients than CA19.9 alone, most notably at early disease stages.

The journey for a biomarker from bench to clinic is long and arduous and there remains many obstacles to overcome (26, 27). Independent validation studies, using samples collected and analyzed at multiple centers, will be necessary before this panel can be brought into clinical use. Such studies, as well as investigation of whether these two markers have the ability to complement CA19.9 in prognosis or therapeutic PDAC monitoring are the main focus of our ongoing research.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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List of Abbreviations

AGR2	anterior gradient 2
AUC	area under the curve
CA125	cancer antigen 125
CA19.9	carbohydrate antigen 19.9
CP	chronic pancreatitis
CT	computerized tomography
CUZD1	Cub and zona pellucida-like domains 1
CV	coefficient of variation
ELISA	enzyme-linked immunosorbent assays
ERCP	endoscopic retrograde cholangiopancreatography
EUS	endoscopic ultrasound
LAMC2	laminin gamma C
MRI	magnetic resonance imaging
PDAC	pancreatic ductal adenocarcinoma

REG1B	regenerating islet-derived 1 beta
ROC	receiver operating characteristic
SYCN	syncollin
TMB	tetramethylbenzidine

References

1. Siegel R, Naishadham D, Jemal A. Cancer statistics, 2012. *CA Cancer J Clin.* 2012; 62:10–29. [PubMed: 22237781]
2. Goonetilleke KS, Siriwardena AK. Systematic review of carbohydrate antigen (CA 19-9) as a biochemical marker in the diagnosis of pancreatic cancer. *Eur J Surg Oncol.* 2007; 33:266–270. [PubMed: 17097848]
3. Conrad C, Lillemoe KD. Surgical palliation of pancreatic cancer. *Cancer J.* 2012; 18:577–583. [PubMed: 23187845]
4. Vincent A, Herman J, Schulick R, Hruban RH, Goggins M. Pancreatic cancer. *Lancet.* 2011; 378:607–620. [PubMed: 21620466]
5. Ghaneh P, Costello E, Neoptolemos JP. Biology and management of pancreatic cancer. *Gut.* 2007; 56:1134–1152. [PubMed: 17625148]
6. Hidalgo M. Pancreatic cancer. *N Engl J Med.* 2010; 362:1605–1617. [PubMed: 20427809]
7. Chan A, Diamandis EP, Blasutig IM. Strategies for discovering novel pancreatic cancer biomarkers. *J Proteomics.* 2013; 81:126–134. [PubMed: 23026552]
8. Duffy MJ, Sturgeon C, Lamerz R, Haglund C, Holubec VL, Klapdor R, et al. Tumor markers in pancreatic cancer: a European Group on Tumor Markers (EGTM) status report. *Ann Oncol.* 2010; 21:441–447. [PubMed: 19690057]
9. Locker GY, Hamilton S, Harris J, Jessup JM, Kemeny N, Macdonald JS, et al. ASCO 2006 update of recommendations for the use of tumor markers in gastrointestinal cancer. *J Clin Oncol.* 2006; 24:5313–5327. [PubMed: 17060676]
10. Kosanam H, Makawita S, Judd B, Newman A, Diamandis EP. Mining the malignant ascites proteome for pancreatic cancer biomarkers. *Proteomics.* 2011; 11:4551–4558. [PubMed: 21932441]
11. Makawita S, Smith C, Batruch I, Zheng Y, Ruckert F, Grutzmann R, et al. Integrated proteomic profiling of cell line conditioned media and pancreatic juice for the identification of pancreatic cancer biomarkers. *Mol Cell Proteomics.* 2011; 10:M111. [PubMed: 21653254]
12. Kosanam H, Prassas I, Chrystoja CC, Soleas I, Chan A, Dimitromanolakis A, et al. Laminin, gamma 2 (LAMC2): a promising new putative pancreatic cancer biomarker identified by proteomic analysis of pancreatic adenocarcinoma tissues. *Mol Cell Proteomics.* 2013; 12:2820–2832. [PubMed: 23798558]
13. Prassas I, Chrystoja CC, Makawita S, Diamandis EP. Bioinformatic identification of proteins with tissue-specific expression for biomarker discovery. *BMC Med.* 2012; 10:39. [PubMed: 22515324]
14. Makawita S, Dimitromanolakis A, Soosaipillai A, Soleas I, Chan A, Gallinger S, et al. Validation of four candidate pancreatic cancer serological biomarkers that improve the performance of CA19.9. *BMC Cancer.* 2013; 13:404. [PubMed: 24007603]
15. Prassas I, Brinc D, Farkona S, Leung F, Dimitromanolakis A, Chrystoja CC, et al. False Biomarker Discovery due to Reactivity of a Commercial ELISA for CUZD1 with Cancer Antigen CA125. *Clin Chem.* 2013
16. Bossuyt PM, Reitsma JB, Bruns DE, Gatsonis CA, Glasziou PP, Irwig LM, et al. Towards complete and accurate reporting of studies of diagnostic accuracy: the STARD initiative. *Clin Biochem.* 2003; 36:2–7. [PubMed: 12554053]

17. DeLong ER, DeLong DM, Clarke-Pearson DL. Comparing the areas under two or more correlated receiver operating characteristic curves: a nonparametric approach. *Biometrics*. 1988; 44:837–845. [PubMed: 3203132]
18. Robin X, Turck N, Hainard A, Tiberti N, Lisacek F, Sanchez JC, et al. pROC: an open-source package for R and S+ to analyze and compare ROC curves. *BMC Bioinformatics*. 2011; 12:77. [PubMed: 21414208]
19. Badea L, Herlea V, Dima SO, Dumitrascu T, Popescu I. Combined gene expression analysis of whole-tissue and microdissected pancreatic ductal adenocarcinoma identifies genes specifically overexpressed in tumor epithelia. *Hepatogastroenterology*. 2008; 55:2016–2027. [PubMed: 19260470]
20. Mitsunaga S, Fujii S, Ishii G, Kinoshita T, Hasebe T, Aoyagi K, et al. Nerve invasion distance is dependent on laminin gamma2 in tumors of pancreatic cancer. *Int J Cancer*. 2010; 127:805–819. [PubMed: 20013810]
21. Luo G, Xiao Z, Long J, Liu Z, Liu L, Liu C, et al. CA125 is Superior to CA19-9 in Predicting the Resectability of Pancreatic Cancer. *J Gastrointest Surg*. 2013; 17:2092–2098. [PubMed: 24146342]
22. Campbell PJ, Yachida S, Mudie LJ, Stephens PJ, Pleasance ED, Stebbings LA, et al. The patterns and dynamics of genomic instability in metastatic pancreatic cancer. *Nature*. 2010; 467:1109–1113. [PubMed: 20981101]
23. Yachida S, Jones S, Bozic I, Antal T, Leary R, Fu B, et al. Distant metastasis occurs late during the genetic evolution of pancreatic cancer. *Nature*. 2010; 467:1114–1117. [PubMed: 20981102]
24. Faca VM, Song KS, Wang H, Zhang Q, Krasnoselsky AL, Newcomb LF, et al. A mouse to human search for plasma proteome changes associated with pancreatic tumor development. *PLoS Med*. 2008; 5:e123. [PubMed: 18547137]
25. Brand RE, Nolen BM, Zeh HJ, Allen PJ, Eloubeidi MA, Goldberg M, et al. Serum biomarker panels for the detection of pancreatic cancer. *Clin Cancer Res*. 2011; 17:805–816. [PubMed: 21325298]
26. Pavlou MP, Diamandis EP, Blasutig IM. The long journey of cancer biomarkers from the bench to the clinic. *Clin Chem*. 2013; 59:147–157. [PubMed: 23019307]
27. Diamandis EP. Cancer biomarkers: can we turn recent failures into success? *J Natl Cancer Inst*. 2010; 102:1462–1467. [PubMed: 20705936]

Statement of Translational Relevance

There is a desperate need for accurate early detection of pancreatic cancer. Serum biomarkers represent a relatively non-invasive and cost-effective method for disease detection. For pancreatic cancer, the most widely used marker, CA19.9, lacks the necessary sensitivity and specificity for early detection and is, therefore, only recommended for monitoring response to treatment in patients who had elevated levels prior to treatment. The current study outlines a large blinded analysis of 5 promising serum markers that we have recently identified through several discovery platforms. These markers (single or in combination) were evaluated on their capacity to complement CA19.9 in early pancreatic cancer diagnosis versus other pancreatic benign conditions. Two of these markers (LAMC2 and CA125) significantly improved the performance of CA19.9 in discriminating early pancreatic cancer from other benign diseases. This panel has the potential to allow for earlier detection of pancreatic cancer, which could lead to earlier intervention and better outcomes.

Figure 1. Scatter plots of CA19.9, CA125 and LAMC2 in the training and validation cohorts CA19.9 (A, B), CA125 (C, D) and LAMC2 (E, F) for training and validation cohorts, respectively. Black horizontal lines are medians. PDAC=pancreatic ductal adenocarcinoma. The clinical groups are shown on the x-axis and further described in the text.

Figure 2. Diagnostic performances of CA19.9, CA125, LAMC2, AGR2, SYCN and REG1B for all PDAC patients versus benign patients, as individual markers
Receiver operator characteristics (ROC) curves for CA19.9, CA125, LAMC2, AGR2, SYCN and REG1B for all patients with pancreatic ductal adenocarcinoma (PDAC) versus all benign patients as individual markers in the training cohort (A) and validation cohort (B). The area under the curve (AUC) for each marker is provided along with its associated 95% confidence intervals in brackets.

Figure 3. Complementarity of CA19.9, CA125 and LAMC2 in differentiating all patients with PDAC versus all benign patients

Receiver operator characteristics (ROC) curves for CA19.9, CA125+CA19.9, CA19.9+LAMC2 and CA125+CA19.9+LAMC2 multiple markers models for all patients with pancreatic ductal adenocarcinoma (PDAC) versus all benign patients in the training (A) and validation cohort (B). The area under the curve (AUC) for each marker is provided along with its associated 95% confidence intervals in brackets.

Table 1

Sample characteristics and numbers in training and validation sets.

Sample characteristics	Training	Validation	Total
Healthy control	10	10	20
Acute pancreatitis	6	23	29
Chronic pancreatitis	25	25	50
CBD ¹ stones	19	0	19
Other benign conditions	15	17	32
PDAC, stage IA	4	5	9
PDAC, stage IB	3	5	8
PDAC, stage IIA	17	17	34
PDAC, stage IIB	62	88	150
PDAC, stage IV	25	24	49
Total	186	214	400
Number of females/males	84/101 (1 unknown)	110/104	194/205
Median (mean) age	66.0 (63.0)	64.0 (63.1)	65.0 (63.1)
Smoking history ²	35C/62P/88NE (1 unknown)	43C/70P/74NE (2 unknown)	78C/132P/162NE
Diabetic history ³	53Y/131N (2 unknown)	25Y/189N	78Y/320N

¹ CBD=common bile duct. PDAC=pancreatic ductal adenocarcinoma.² C=current; P=past; NE=never³ Y=yes; N=no

Table 2

Performances of CA19.9, CA125, LAMC2, two- and three- marker models for diagnosis of PDAC¹.

	Training		Validation	
	AUC (95% CI)	Sensitivity (%)	Specificity (%)	AUC (95% CI)
Benign vs all PDAC				
CA19.9	0.85 (0.80–0.91)	77.5	83.1	0.80 (0.74–0.86)
CA125	0.77 (0.70–0.84)	70.3	75.4	0.78 (0.71–0.84)
LAMC2	0.81 (0.75–0.88)	70.3	87.7	0.69 (0.62–0.77)*
CA19.9+CA125	0.90 (0.86–0.94)*	81.1	87.7	0.87 (0.82–0.91)**
CA19.9+LAMC2	0.91 (0.87–0.95)*	82.9	89.2	0.83 (0.77–0.88)
CA19.9+CA125+LAMC2	0.93 (0.89–0.96)**	84.7	89.2	0.87 (0.83–0.92)**
Benign vs early PDAC (stage IA, IB & IIA)				
CA19.9	0.82 (0.69–0.94)	75.0	81.5	0.69 (0.57–0.81)
CA125	0.78 (0.68–0.89)	79.2	72.3	0.72 (0.60–0.84)
LAMC2	0.73 (0.60–0.86)	58.3	89.2	0.68 (0.56–0.80)
CA19.9+ CA125	0.90 (0.83–0.98)	83.3	84.6	0.74 (0.62–0.86)
CA19.9+LAMC2	0.85 (0.74–0.95)	79.2	83.1	0.74 (0.63–0.85)
CA19.9+ CA125+ LAMC2	0.91 (0.83–0.98)	83.3	86.2	0.76 (0.65–0.87)*
CP vs early PDAC (stage IA, IB, IIA)				
CA19.9	0.76 (0.62–0.90)	70.8	68.0	0.59 (0.44–0.75)
CA125	0.79 (0.66–0.92)	70.8	84.0	0.75 (0.62–0.89)
LAMC2	0.74 (0.59–0.88)	58.3	92.0	0.69 (0.54–0.83)
CA19.9+ CA125	0.88 (0.79–0.98)*	83.3	80.0	0.73 (0.59–0.87)*
CA19.9+LAMC2	0.81 (0.68–0.93)	79.2	72.0	0.66 (0.52–0.81)
CA19.9+ CA125+LAMC2	0.88 (0.79–0.98)*	79.2	88.0	0.74 (0.60–0.88)*

¹ PDAC=pancreatic ductal adenocarcinoma. CP=chronic pancreatitis. AUC=area under curve. CI=confidence interval

* p<0.05,

*** p<0.005 in comparison to CA19.9. When used as single markers, the specificity/sensitivity for each protein was estimated based on the following cutoffs: CutoffCA19.9=20.3U/mL, CutoffCA125=17.9U/mL and CutoffLAMC2=123.2 ng/mL

Table 3
Performances of CA125, LAMC2 in diagnosis of CA19.9 negative PDAC¹ patients.

		Training set		Validation set	
		AUC (95% CI)	p-value	AUC (95% CI)	p-value
Benign vs. all PDAC	CA19.9	0.59 (0.46–0.72)	0.2	0.54 (0.41–0.66)	0.5
	CA125	0.73 (0.62–0.84)	0.0003	0.78 (0.67–0.88)	<0.0001
	LAMC2	0.76 (0.65–0.86)	<0.0001	0.64 (0.53–0.76)	0.02
	CA125+LAMC2	0.81 (0.71–0.90)	<0.0001	0.76 (0.66–0.86)	<0.0001
CP vs. early PDAC	CA19.9	0.53 (0.37–0.69)	0.7	0.52 (0.35–0.70)	0.8
	CA125	0.72 (0.58–0.86)	0.007	0.77 (0.64–0.90)	0.002
	LAMC2	0.79 (0.67–0.91)	0.0002	0.62 (0.44–0.79)	0.2
	CA125+LAMC2	0.84 (0.73–0.95)	<0.0001	0.73 (0.57–0.89)	0.01

¹PDAC=pancreatic ductal adenocarcinoma. AUC=area under curve. CI = confidence interval. CP=chronic pancreatitis
p-value are calculated by Wilcoxon test in the comparison between benign and cancer groups.