

## Validation of Biomarkers That Complement CA19.9 in Detecting Early Pancreatic Cancer

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### Abstract

**Purpose:** Pancreatic ductal adenocarcinoma (PDAC) is a significant cause of cancer mortality. Carbohydrate antigen 19.9 (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 ( $AUC_{CA19.9} = 0.80$  vs.  $AUC_{CA19.9+CA125+LAMC2} = 0.87$ ;  $P < 0.005$ ) as well as between early-stage PDAC and benign conditions ( $AUC_{CA19.9} = 0.69$  vs.  $AUC_{CA19.9+CA125+LAMC2} = 0.76$ ;  $P < 0.05$ ) and between early-stage PDAC and chronic pancreatitis (CP;  $AUC_{CA19.9} = 0.59$  vs.  $AUC_{CA19.9+CA125+LAMC2} = 0.74$ ;  $P < 0.05$ ).

**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. *Clin Cancer Res*; 20(22); 5787–95. ©2014 AACR.

### 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) that 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 with 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-

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**Note:** Supplementary data for this article are available at Clinical Cancer Research Online (<http://clincancerres.aacrjournals.org/>).

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doi: 10.1158/1078-0432.CCR-14-0289

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### Translational Relevance

There is a desperate need for accurate early detection of pancreatic cancer. Serum biomarkers represent a relatively noninvasive and cost-effective method for disease detection. For pancreatic cancer, the most widely used marker, carbohydrate antigen 19.9 (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 before treatment. The current study outlines a large blinded analysis of five 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.

standard serum biomarker carbohydrate antigen 19.9 (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<sup>a-b-</sup> individuals (5%–10% of Caucasian population), is minimally elevated in early pre-malignant 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 to improve both its sensitivity and specificity.

In the pursuit of deciphering PDAC biomarkers, we have combined the following approaches: (i) integrative proteomic analysis of cell line conditioned media, pancreatic ascites, and pancreatic juice (10, 11); (ii) comparative proteomic analysis of PDAC tissues with adjacent benign tissues (12); and (iii) 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 more than 400 samples (11, 12, 14). (Notably, CA125 was rediscovered as "CUZD1 protein"; ref. 15.) In this study, we took our top five 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.

### Materials and 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; Pittsburgh, PA) 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, magnetic resonance cholangiopancreatography, and EUS) were eligible for the study. Control subjects with a clinical diagnosis of a pancreas, liver, or intestinal condition, or being evaluated for nonpancreatic 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 nonmelanoma skin cancers within 10 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 4-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 1,000  $\times$  g) to pellet the cells. Immediately following centrifugation, the plasma samples were aliquoted into 1 mL cryotubes and stored at  $-80^{\circ}\text{C}$  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 20 healthy individuals, 130 benign condition patients, 51 stage IA and IB, 150 stage IIB, and 49 stage IV PDAC patients. Details about the patient population are shown in Table 1. All samples were collected before 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" (Supplementary Table S1; ref. 16).

Using commercially available sandwich enzyme-linked immunosorbent assays (ELISA) for AGR2, REG1B, SYCN, and LAMC2, purchased from USCN Life Sciences, 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<sub>XR</sub> immunoassay. CA125 values were, first, obtained as "CUZD1 values" from a commercial CUZD1 ELISA kit obtained from USCN Life Sciences. When we discovered that this commercial kit was, in fact, measuring CA125, we remeasured all available samples (251 of 400) with the Abbott Architect CA125 immunoassay. As expected, a strong linear  $\log_{\text{CA125}}/\log_{\text{CUZD1}}$  correlation curve was observed (Supplementary Fig. S4). CA125 values for the remaining 149 samples (which were depleted) were determined by extrapolation.

**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
CP	25	25	50
CBD <sup>a</sup> 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 <sup>b</sup>	35C/62P/88NE (1 unknown)	43C/70P/74NE (2 unknown)	78C/132P/162NE
Diabetic history <sup>c</sup>	53Y/131N (2 unknown)	25Y/189N	78Y/320N

<sup>a</sup>CBD, common bile duct.

<sup>b</sup>C, current; P, past; NE, never.

<sup>c</sup>Y, yes; N, no.

Before all sample analyses, AGR2, REG1B, SYCN, and LAMC2 ELISAs were first tested to optimize the analytic 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 interplate variability.

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

Interplate assay imprecision was assessed across the 12 plates used for each marker using three controls (low, medium, and high; Supplementary Table S2). 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 intraplate variations. The mean and median CVs among duplicate samples ranged from 5% to 12% for all markers, which is indicative of good intraplate performance of the assays (Supplementary Table S2).

### 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 on the basis of 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% CI) for AUCs and *P* value for comparison between related ROC curves were performed using the method described by DeLong and colleagues (17).

### Logistic regression model building

Multiparametric models explored included logistic regression models using log<sub>2</sub>-transformed markers (see Supplementary Table S4 for model fit diagnostics), logistic regression models with interaction terms and more advanced nonlinear classifiers such as Random Forests and Support Vector Machines (data not shown). Despite its

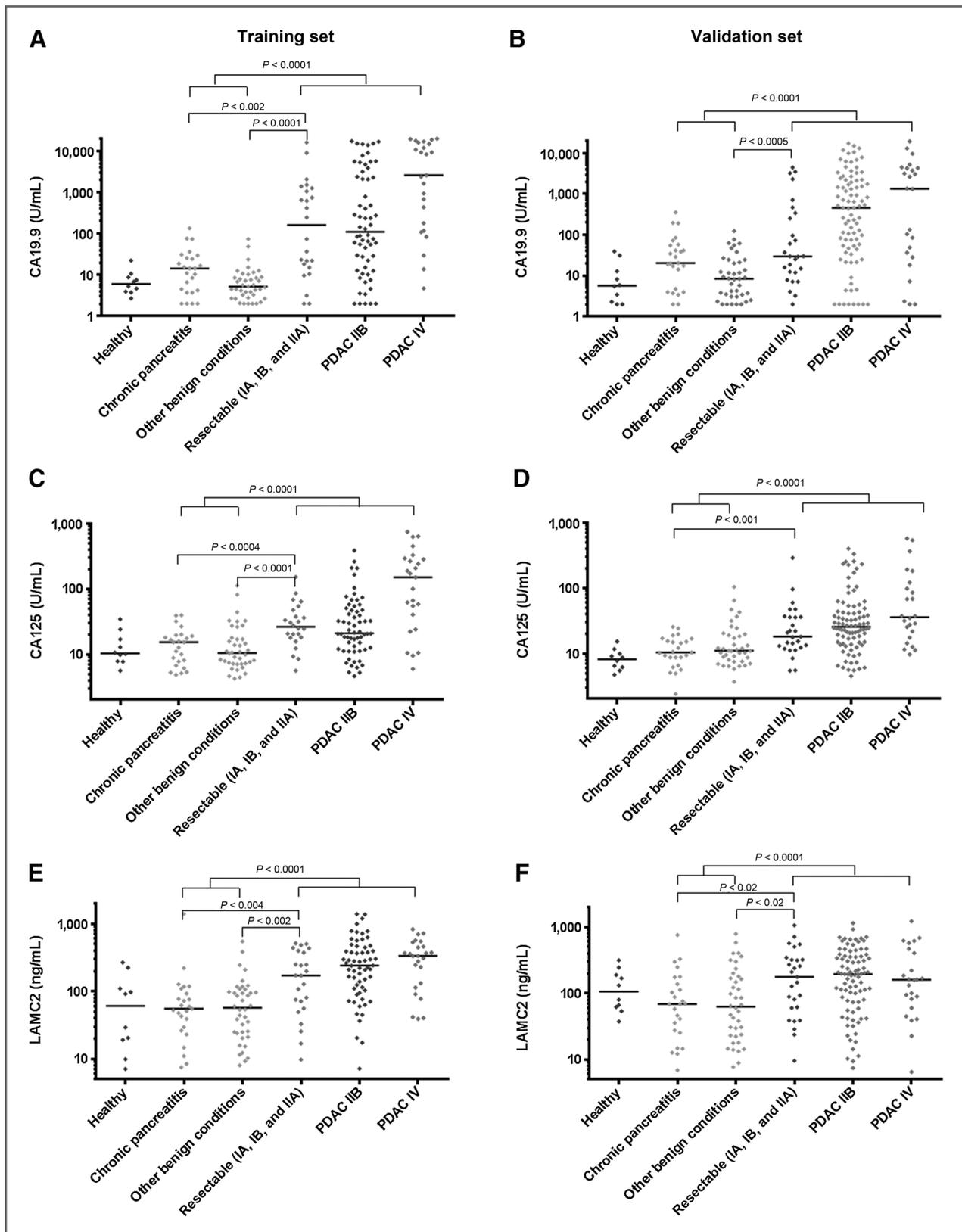
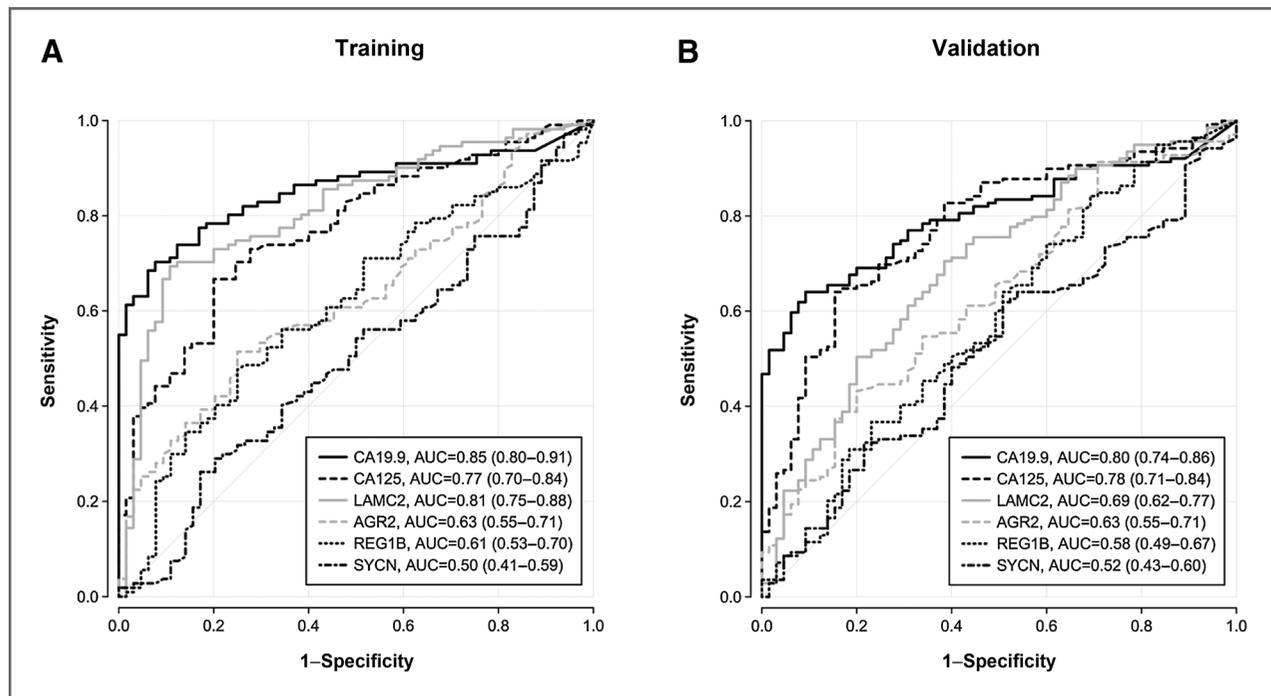


Figure 1. Scatter plots of CA19.9, CA125, and LAMC2 in the training and validation cohorts. CA19.9 (A and B), CA125 (C and D), and LAMC2 (E and F) for training and validation cohorts, respectively. Black horizontal lines are medians. The clinical groups are shown on the x-axis and further described in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



**Figure 2.** Diagnostic performances of CA19.9, CA125, LAMC2, AGR2, SYCN, and REG1B for all patients with PDAC versus benign patients, as individual markers. ROC curves for CA19.9, CA125, LAMC2, AGR2, SYCN, and REG1B for all patients with PDAC versus all benign patients as individual markers in the training cohort (A) and validation cohort (B). The AUC for each marker is provided along with its associated 95% CIs in brackets.

simplicity, the logistic regression model demonstrated the best performance and was chosen as our main model for this article. Summary of model fitting diagnostics and parameters for our chosen models are shown in Supplementary Tables S4 and S5. FDR-adjusted *P*-values for model comparisons in the training set are shown in Supplementary Table S6. The reduced coefficient models evaluated for diagnostic performance are: (i)  $CA19.9 + 1.11 \cdot CA125$ , (ii)  $CA19.9 + 0.202 \cdot LAMC2$ , and (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. Multiparametric prediction models were built based on the comparison of the benign vs. all PDAC groups in the training set, with *P* values adjusted for FDR by the Benjamini–Hochberg procedure (Supplementary Table S6). 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 three 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 S7). Gender association was evaluated on the basis of a *t* test of marker values between males and females (Supplementary Table S7).

## Results

### Performances of markers in the training and validation sets

As individual markers, the performances of the five candidates were compared with CA19.9 in discriminating benign conditions versus PDAC and healthy controls versus PDAC in both training and validation cohorts (Figs. 1 and 2; Supplementary Table S3; Supplementary Figs. S1–S3). As single markers, CA125 and LAMC2 were the most promising of the five candidates. Their concentrations were significantly increased in PDAC cases compared with benign controls in both training and validation cohorts ( $P < 0.0001$ ; Fig. 1 and Supplementary Table S3). The remaining three 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 (Fig. 2; Supplementary Table S3; Supplementary Figs. S1 and S2). 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

**Table 2.** Performances of CA19.9, CA125, LAMC2, two- and three-marker models for diagnosis of PDAC

	Training			Validation		
	AUC (95% CI)	Sensitivity (%)	Specificity (%)	AUC (95% CI)	Sensitivity (%)	Specificity (%)
Benign vs. all PDAC						
CA19.9	0.85 (0.80–0.91)	77.5	83.1	0.80 (0.74–0.86)	69.1	80.0
CA125	0.77 (0.70–0.84)	70.3	75.4	0.78 (0.71–0.84)	70.0	75.4
LAMC2	0.81 (0.75–0.88)	70.3	87.7	0.69 (0.62–0.77) <sup>a</sup>	70.5	61.5
CA19.9 + CA125	0.90 (0.86–0.94) <sup>a</sup>	81.1	87.7	0.87 (0.82–0.91) <sup>b</sup>	74.1	83.1
CA19.9 + LAMC2	0.91 (0.87–0.95) <sup>a</sup>	82.9	89.2	0.83 (0.77–0.88)	72.7	76.9
CA19.9 + CA125 + LAMC2	0.93 (0.89–0.96) <sup>b</sup>	84.7	89.2	0.87 (0.83–0.92) <sup>b</sup>	82.0	73.8
Benign vs. early-stage PDAC (stage IA, IB, and IIA)						
CA19.9	0.82 (0.69–0.94)	75.0	81.5	0.69 (0.57–0.81)	59.3	69.2
CA125	0.78 (0.68–0.89)	79.2	72.3	0.72 (0.60–0.84)	77.8	61.5
LAMC2	0.73 (0.60–0.86)	58.3	89.2	0.68 (0.56–0.80)	66.7	61.5
CA19.9 + CA125	0.90 (0.83–0.98)	83.3	84.6	0.74 (0.62–0.86)	63.0	73.8
CA19.9 + LAMC2	0.85 (0.74–0.95)	79.2	83.1	0.74 (0.63–0.85)	81.5	56.9
CA19.9 + CA125 + LAMC2	0.91 (0.83–0.98)	83.3	86.2	0.76 (0.65–0.87) <sup>a</sup>	77.8	63.1
CP vs. early-stage PDAC (stage IA, IB, and IIA)						
CA19.9	0.76 (0.62–0.90)	70.8	68.0	0.59 (0.44–0.75)	55.6	56.0
CA125	0.79 (0.66–0.92)	70.8	84.0	0.75 (0.62–0.89)	88.9	56.0
LAMC2	0.74 (0.59–0.88)	58.3	92.0	0.69 (0.54–0.83)	66.7	64.0
CA19.9 + CA125	0.88 (0.79–0.98) <sup>a</sup>	83.3	80.0	0.73 (0.59–0.87) <sup>a</sup>	66.7	72.0
CA19.9 + LAMC2	0.81 (0.68–0.93)	79.2	72.0	0.66 (0.52–0.81)	59.3	60.0
CA19.9 + CA125 + LAMC2	0.88 (0.79–0.98) <sup>a</sup>	79.2	88.0	0.74 (0.60–0.88) <sup>a</sup>	74.1	68.0

NOTE: When used as single markers, the specificity/sensitivity for each protein was estimated on the basis of the following cutoffs: Cutoff<sub>CA19.9</sub> = 20.3 U/mL, Cutoff<sub>CA125</sub> = 17.9 U/mL, and Cutoff<sub>LAMC2</sub> = 123.2 ng/mL.

<sup>a</sup>*P* < 0.05 in comparison with CA19.9.

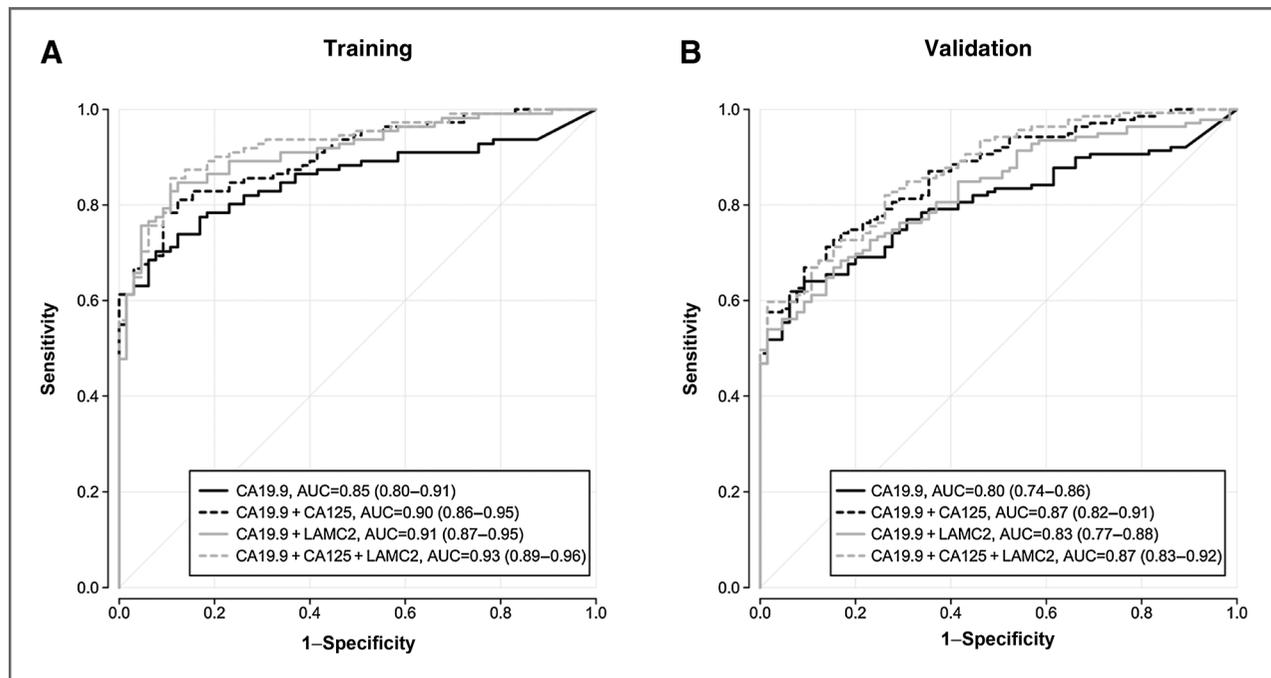
<sup>b</sup>*P* < 0.005 in comparison with CA19.9.

benign from early-stage PDAC, the performance of the three markers was comparable in both the training (AUC<sub>CA19.9</sub> = 0.82; AUC<sub>CA125</sub> = 0.78; AUC<sub>LAMC2</sub> = 0.73) and validation sets (AUC<sub>CA19.9</sub> = 0.69; AUC<sub>CA125</sub> = 0.72; AUC<sub>LAMC2</sub> = 0.68). Finally, in discriminating patients with CP from patients with early-stage PDAC, both markers had similar performance to CA19.9 in the training (AUC<sub>CA19.9</sub> = 0.76; AUC<sub>CA125</sub> = 0.79; AUC<sub>LAMC2</sub> = 0.64) and validation sets (AUC<sub>CA19.9</sub> = 0.59; AUC<sub>CA125</sub> = 0.75; AUC<sub>LAMC2</sub> = 0.69).

Optimal cutoffs for each marker were obtained by minimizing the total prediction error as described in Materials and Methods. On the basis of 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 (Fig. 2; Table 2; Supplementary Fig. S2). However, if used at its clinically used cutoff (>37 U/mL), a total of 22 out of 130 patients (~17%) with benign disease would be falsely

positive for CA19.9 (>37 U/mL), and 75 out of 250 (30%) patients with PDAC would be missed (false negatives) by this marker. To compare the performances of CA19.9 (as a single marker) with the three-marker panel, multiparametric models for various combinations of the three proteins (CA19.9, CA125, and LAMC2) were constructed on the basis of the comparison of all patients with PDAC 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 Fig. 3) as well as the secondary measures (Table 2 and Supplementary Fig. S3). The power of distinguishing benign conditions from all PDAC cases increased from AUC<sub>CA19.9</sub> = 0.85 to AUC<sub>CA19.9+CA125+LAMC2</sub> = 0.93 in the training cohort and from AUC<sub>CA19.9</sub> = 0.80 to AUC<sub>CA19.9+CA125+LAMC2</sub> = 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<sub>CA19.9</sub> = 0.69 vs. AUC<sub>CA19.9+CA125+LAMC2</sub> = 0.76; *P* < 0.05) and in discriminating CP cases from patients with early-stage PDAC (AUC<sub>CA19.9</sub> = 0.59 vs. AUC<sub>CA19.9+CA125+LAMC2</sub> = 0.74, *P* < 0.05). In the last subgroup (CP vs. early-stage PDAC), the addition of CA125



**Figure 3.** Complementarity of CA19.9, CA125, and LAMC2 in differentiating all patients with PDAC versus all benign patients. ROC curves for CA19.9, CA125 + CA19.9, CA19.9 + LAMC2, and CA125 + CA19.9 + LAMC2 multiple markers models for all patients with PDAC versus all benign patients in the training (A) and validation cohort (B). The AUC for each marker is provided along with its associated 95% CIs in brackets.

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 patients with PDAC 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 patients with PDAC in this subpopulation of patients with PDAC 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 patients with CP and early-stage PDAC 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

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

**Table 3.** Performances of CA125, LAMC2 in diagnosis of CA19.9-negative PDAC patients

	Training set		Validation set	
	AUC (95% CI)	P	AUC (95% CI)	P
<b>Benign vs. all PDAC</b>				
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
<b>CP vs. early-stage PDAC</b>				
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

P values are calculated by the Wilcoxon test in the comparison between benign and cancer groups.

very sensitive (it is elevated mainly in late-cancer stages and up to 10% of the population genetically negative) nor specific (elevated in nonpancreatic 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 used various technologies to discover novel PDAC biomarkers and identified five 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 five 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 multiparametric 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., CP).

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 patients with late-stage PDAC (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 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 patients with PDAC (for example, see ref. 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 patients with PDAC 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.

#### Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

#### Disclaimer

The contents of this publication are solely the responsibility of the authors and do not necessarily represent the official views of National Cancer Institute or The University of Texas Health Science Center at San Antonio.

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**Conception and design:** A. Chan, I. Prassas, R. Brand, I.M. Blasutig

**Development of methodology:** I. Prassas

**Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.):** A. Chan, R. Brand

**Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis):** A. Chan, A. Dimitromanolakis, S. Serra

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**Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases):** I. Prassas, S. Serra

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#### Acknowledgments

The authors thank Gerard J. Davis and Abbott Laboratories for providing CA19.9 and CA125 reagents, A. Soosaipillai for assistance with the ELISAs, and Y. Wang for assistance with the automated analyzer. I.M. Blasutig thanks G.C. Leung for her assistance with proofing the article.

#### Grant Support

I.M. Blasutig was supported by The Early Detection Research Network through the National Cancer Institute Grant no. U01 CA086402.

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Received February 11, 2014; revised July 24, 2014; accepted August 2, 2014; published OnlineFirst September 19, 2014.

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# Clinical Cancer Research

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*Clin Cancer Res* 2014;20:5787-5795. Published OnlineFirst September 19, 2014.

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