Three Biomarkers Identified from Serum Proteomic Analysis for the Detection of Early Stage Ovarian Cancer

Zhen Zhang,1 Robert C. Bast, Jr.,2 Yinhua Yu,2 Jinong Li,1 Lori J. Sokoll,1 Alex J. Rai,1 Jason M. Rosenzweig,1 Bonnie Cameron,1 Young Y. Wang,1 Xiao-Ying Meng,3 Andrew Berchuck,4 Carolien van Haften-Day,5 Neville F. Hacker,5 Henk W. A. de Bruijn,6 Ate G. J. van der Zee,6 Ian J. Jacobs,7 Eric T. Fung,3 and Daniel W. Chan1

1Department of Pathology, Biomarker Discovery Center, Johns Hopkins Medical Institutions, Baltimore, Maryland; 2M. D. Anderson Cancer Center, Houston, Texas; 3Ciphergen Biosystems, Inc., Fremont, California; 4Duke University Medical Center, Durham, North Carolina; 5The Royal Hospital for Women, Randwick, New South Wales, Australia; 6University Hospital Groningen, Groningen, the Netherlands; and 7Bart’s and The London, Queen Mary’s School of Medicine, London, United Kingdom

INTRODUCTION

Despite progress in cancer therapy, ovarian cancer mortality has remained virtually unchanged over the past two decades (1). Annually in the United States alone, ~23,000 women are diagnosed with the disease and almost 14,000 women die from it (1). Given our knowledge about the steep survival gradient relative to the stage at which the disease is diagnosed, it is reasonable to suggest that early detection remains the most promising approach to improve the long-term survival of ovarian cancer patients.

The relatively low prevalence (40 out of 100,000) of ovarian cancer among postmenopausal women in the general population, the lack of a clearly defined precursor lesion, and the high cost and possible complications associated with surgical confirmatory procedures have placed stringent requirements on any test intended for general population screening. Currently, none of the existing serum markers, such as CA125, CA 72–4, or macrophage colony-stimulating factor, can be used individually for screening (2). Longitudinal studies are under way in Europe, Japan, and the United States to evaluate screening strategies using CA125 and/or transvaginal sonography (3–5) and their impact on overall cancer mortality (6). Preliminary results have shown encouraging evidence of a survival benefit among patients diagnosed through a screening regimen (3).

Reports from retrospective studies have shown that multivariate predictive models combining existing tumor markers improve cancer detection (7, 8). Recent advances in genomic and proteomic profiling technology have made it possible to apply computational methods to detect changes in protein expressions and their association to disease conditions, thereby hastening the identification of novel markers that may contribute to multimarker combinations with better diagnostic performance (9–13).

In this study, we hypothesized that comparison of protein expressions of serum specimens from patients with early stage ovarian cancer with those from healthy women could lead to the discovery of candidate biomarkers for the detection of early stage ovarian cancer. To ensure that the discovered biomarkers are truly associated with ovarian cancer rather than the result of biases in samples, profiling data of specimens from multiple institutions were used for cross-comparison and independent validation. We additionally determined the protein identities of the discovered biomarkers to allow for additional validation with independent methods and as a first step toward understanding the pathways in which they may function.

MATERIALS AND METHODS

Samples. The study involved a retrospective sample of 645 serum specimens. All were collected with institutional approval. Proteomic profiles were obtained from 503 specimens collected at four medical centers (M. D. Anderson Cancer Center, Duke University Medical Center, Groningen University Hospital, the Netherlands, and the Royal Hospital for Women, Australia). Among them, the cancer group consisted of 65 patients with stages I/II invasive epithelial ovarian cancer, 88 patients with stages III/IV invasive epithelial ovarian cancer, 28 patients with borderline tumors, and 14 patients with recurrent disease, all optimally staged by pathologists based on Fédération Internationale des Gynécologues et Obstétristes criteria. Among the stages I/II invasive cases, 20 were serous, 17 were mucinous, 15 were endometrioid, 8 were clear cell, 1 was carcinosarcoma, and 4 were mixed epithelial carcinoma. The samples also included 166 patients with benign pelvic masses and 142 healthy donors as controls. All of the samples were collected before the day of surgery or treatment, stored at ~70°C, and thawed immediately before assay. CA125 levels had been obtained previously using a CA125 radioimmunoassay (Centocor). The clinical characteristics and age distribution of the proteomic profiling study population are summarized in Table 1.

In addition to the 503 specimens for proteomic profiling, 142 independent, archived serum specimens collected for routine clinical laboratory testing at the Johns Hopkins Medical Institutions were tested for levels of the identified biomarkers for which an immunoassay test was available. The sample included 41 healthy women, 41 patients with late-stage ovarian cancer, and groups of 20 patients each with breast, colon, and prostate cancers. All of the samples were processed promptly after collection and stored at 2–8°C for a maximum of
Bioinformatics Analysis. The unified maximum separability analysis algorithm implemented in the software ProPeak (3Z Informatics) was used to analyze the peak intensity data and to select a subset of informative peaks. The unified maximum separability analysis incorporates information from the traditional multivariate statistical classification methods into the support vector machine algorithm (16) to provide a robust approach to analyzing high-dimensional expression data (12, 17–19). Bootstrap was also applied to help to identify peaks with a consistently high discriminatory power over multiple resampled subpopulations.

Protein Identification. The discovered biomarkers were purified according to their biochemical properties using a series of protein separation procedures including anion exchange, size exclusion, and reverse-phase chromatography followed by SDS-PAGE separation. To monitor the purification process, healthy control samples were processed in parallel with the ovarian cancer samples. During each of the iterations, the new fractions were profiled on the same type of ProteinChip arrays used for discovery to monitor the presence or absence of the biomarkers of interest. The purified biomarkers were excised and digested with trypsin before being spotted onto NP20 ProteinChip arrays and read in a PBSII ProteinChip reader. The masses of the proteolytic fragments were used for database searching with the ProFound algorithm. For confirmation, the NP20 arrays containing the proteolytic fragments were analyzed by collision-induced dissociation using a Q-STAR MS/MS instrument (Applied Biosystems/MDSc Sciex) equipped with a PCI 1000 ProteinChip Interface (Ciphergen Biosystems).

Multivariate Predictive Models. The profiling data from the two sites used for biomarker discovery were combined and then divided randomly into a training set and a test set for the derivation and testing of nonlinear multivariate predictive models using nonlinear unified maximum separability analysis. The derived models were then additionally evaluated, in the same way as the individual biomarkers, on the independent validation data that were not involved in biomarker discovery or model construction.

Statistical Analysis. The performance of the identified biomarkers in detecting early stage ovarian cancer from healthy controls was evaluated by descriptive statistics, Mann-Whitney U test or Kruskal-Wallis test, and receiver operating characteristic curves (ROCKIT; University of Chicago, Chicago, IL; Ref. 20). Performance of the nonlinear multivariate predictive models was compared with performance of the CA125 assay alone by receiver operating characteristic analysis and estimated sensitivity and specificity. All of the statistical analyses were performed using Statistica 6.1 (Statsoft).

RESULTS

Biomarker Discovery and Identification. Three potential biomarkers were discovered. Two of them were peaks from fraction pH 4 at m/z 12,828 and 28,043, both down-regulated in the cancer group, and the third was from fraction pH 9/flow through at m/z 3,272,
up-regulated in the cancer group. All bound to the IMAC3-Cu (immobilized metal affinity chromatography array charged with copper ions) ProteinChip array (representative spectra in Fig. 2).

The \( m/z \) 28,043 peak was purified and identified as apolipoprotein A1 (z score 2.38 using the ProFound algorithm; 59% coverage). Three peptides were sequenced by tandem mass spectrometry and confirmed this finding. The \( m/z \) 12,828 peak was puriﬁed and identified as a form of transthyretin (prealbumin; z-score 2.19; 91% coverage). One of the peptides was sequenced by tandem mass spectrometry and conﬁrmed this ﬁnding. The \( m/z \) 12,828 peak copuriﬁed with a much more abundant \( m/z \) 13,900 peak, which was also identiﬁed as transthyretin. Immunoprecipitation and tandem mass spectrometry additionally determined that a truncated form of transthyretin lacking the NH2-terminal 10 amino acids corresponded to the \( m/z \) 12,828 peak. The \( m/z \) 3,272 peak was puriﬁed from the pooled serum of ovarian cancer patients and its sequence was determined to be MNFRPGVLSSRQLGLPGPPDVPDQAAYHPF, a fragment spanning amino acids 660–689 of human inter/trypsin inhibitor, heavy chain H4 (PK-120). This result was conﬁrmed by the analysis of pepsin digestion products of the marker.

**Discriminatory Power of Individual Biomarkers.** Table 2 provides the descriptive statistics (mean ± SD, median) and results from statistical tests of these three biomarkers between healthy controls and ovarian cancer patients of different stage groups in the combined discovery sets and in the independent validation set. Within the discovery sets, the expression levels of the three biomarkers were statistically signiﬁcantly different between the healthy controls and the early stage ovarian cancer patients (\( P < 0.000001 \) for all of the three markers). With the independent validation set, the two biomarkers at \( m/z \) 12,828 and \( m/z \) 28,043 retained their statistically discriminatory power in detecting stage I/II ovarian cancer (\( P < 0.000001 \) and \( P < 0.000008 \), respectively). However, the biomarker at \( m/z \) 3,272, with its large within-group variances, had only a marginal effect in separating healthy controls from epithelial ovarian cancer. In Table 3, the distributions of the biomarkers are compared among subgroups of the cancer samples based on stages, histological subtypes, and age.

Fig. 3, A–D, compares the discriminatory power of the individual biomarkers with that of CA125, using receiver operating characteristic analysis on data from patients with early stage ovarian cancer and healthy controls. CA125 and \( m/z \) 12,828 performed comparably on both the discovery and independent validation sets, whereas the other two markers had a lower area-under-curve than CA125 in one or both data sets. However, the estimated correlations among the three biomarkers and CA125 were low (data not shown), suggesting the possibility that they were complementary to each other and that a multivariate approach might outperform the single assay of CA125.

Because 27% of the samples in the healthy controls were from women age 50 or older compared with 61% of those in the early stage ovarian cancer group, we were concerned that these markers might reﬂect age-related changes. However, the differences between the early stage cancer samples and the healthy controls in the discovery data sets remained statistically signiﬁcant in a multiple regression after adjusting for difference in age (\( P = 0.000001 \) for \( m/z \) 12,828 and \( m/z \) 3,272; and \( P = 0.0174 \) for \( m/z \) 28,043). In a stratified analysis, there were no appreciable differences in biomarker values between cancer patients of age ≥50 years and those below 50 years (Table 3). Previous population-based studies have shown that levels of apolipoprotein A1 actually increase slightly with age (21, 22).

**Multivariate Predictive Models.** The two data sets used for biomarker discovery were merged and then randomly divided into a training set and a test set. The training set had 28 ovarian cancer cases...
and 33 healthy controls, whereas the test set consisted of 29 cancer cases and 46 controls. The training and test data sets retained only the peak intensity values of the three discovered biomarkers and CA125 test results.

Two multivariate predictive models were constructed. The first used only the three biomarkers as its input and the second used the three biomarkers along with the CA125 level. Panels E–H in Fig. 3 compare the overall diagnostic performance of the two models with that of CA125 using receiver operating characteristic analysis, among which are the superimposed views of both the empirical and fitted receiver operating characteristic curves estimated using the healthy control samples against all of the stage I/II epithelial ovarian cancer samples (Fig. 3G) or the invasive stage I/II epithelial ovarian cancer samples (Fig. 3H) in the independent validation data set.

Using cutoffs that maximized the sum of sensitivity and specificity on the training data, these models were applied to the test data and the independent validation data (Table 4). For discrimination between healthy controls and stages I/II invasive ovarian cancer in the independent validation set, the multivariate model using the three biomarkers and CA125, at a sensitivity of 83% (95% CI, 61–95%), had a specificity of 94% (95% CI, 85–98%). This is statistically significantly better than CA125 at the same sensitivity of 83% (with a cutoff of 11 units/ml), which yielded a specificity of only 52% (95% CI, 39–65%). On the other hand, CA125 at the cutoff of 35 units/ml had a specificity of 97% (95% CI, 89–100%) and a corresponding sensitivity of 65% (95% CI, 43–84%). At the same fixed specificity, the multivariate model using the three biomarkers and CA125 resulted in a sensitivity of 74% (95% CI, 52–90%). The difference, however, is not statistically significant, partially because of the few stage I/II invasive cases in the independent validation set. Table 4 also lists in detail the estimated sensitivities or specificities for individual diagnostic groups in the training set, test set, and independent validation set.

It should be noted that the biomarkers, with the exception of m/z 3,272, as well as the two predictive models were moderately capable of differentiating stages I/II invasive cancer from benign cases in the independent validation set ($P = 0.002$ and 0.09 for m/z 12,828 and 28,043, respectively; and $P = 0.02$ and 0.03 for models without CA125 and with CA125, respectively).

**Evaluation Using Immunoassays.** The 142 archived specimens from the Johns Hopkins Medical Institutions were analyzed for apo-
lipoprotein A1 using a turbidimetric immunoassay performed in a microtiter plate format (Wako Chemical USA) and for transthyretin using a particle enhanced turbidimetric immunoassay performed on the Dimension RxL Instrument (Dade-Behring; Table 5). The serum levels of CA125 were up-regulated among the 41 patients with late-stage ovarian cancer and healthy women revealed three biomarkers of which the discriminatory power was confirmed with samples from multiple institutions through cross-validation and independent validation. Combined with CA125 in a multivariate predictive model, these biomarkers improve significantly on the specificity of CA125 alone although maintaining a relatively high sensitivity. Two of the markers were also evaluated using immunoassays. Although the immunoassay for transthyretin was not specific for the particulate trunctated form that corresponds to the m/z 12,828 peak, the results corroborated the findings from the surface-enhanced laser desorption/ ionization mass spectrum data and provided preliminary analysis of tumor site specificity of these two markers.

Results from receiver operating characteristic curve analysis (Fig. 3, G and H) show that at a fixed high sensitivity, the predictive models, with or without CA125 as one of its inputs, had a much-improved specificity over that of CA125 alone. However, when the models were compared with CA125 at a fixed high specificity, the improvement in sensitivity was more moderate and tended to diminish as specificity approached 98% and above. The level of analytical variability in peak intensity measurement relative to the few early stage ovarian cancer cases in the independent validation set made it difficult to evaluate in a statistically meaningful way the diagnostic performance of the individual biomarkers or the multivariate models at extreme specificity or sensitivity values. The differences in area-under-curve in detecting stage III invasive cancer from healthy controls were not statistically significant for the independent validation set. Given the fairly large absolute differences

**DISCUSSION**

Differential analysis of serum protein profiles from patients with early stage ovarian cancer and healthy women revealed three biomarkers the discriminatory power of which was confirmed with samples from multiple institutions through cross-validation and independent validation. Combined with CA125 in a multivariate predictive model, these biomarkers improve significantly on the specificity of CA125 alone although maintaining a relatively high sensitivity. Two of the markers were also evaluated using immunoassays. Although the immunoassay for transthyretin was not specific for the particulate truncated form that corresponds to the m/z 12,828 peak, the results corroborated the findings from the surface-enhanced laser desorption/ionization mass spectrum data and provided preliminary analysis of tumor site specificity of these two markers.

Results from receiver operating characteristic curve analysis (Fig. 3, G and H) show that at a fixed high sensitivity, the predictive models, with or without CA125 as one of its inputs, had a much-improved specificity over that of CA125 alone. However, when the models were compared with CA125 at a fixed high specificity, the improvement in sensitivity was more moderate and tended to diminish as specificity approached 98% and above. The level of analytical variability in peak intensity measurement relative to the few early stage ovarian cancer cases in the independent validation set made it difficult to evaluate in a statistically meaningful way the diagnostic performance of the individual biomarkers or the multivariate models at extreme specificity or sensitivity values.

The differences in area-under-curve in detecting stage III invasive cancer from healthy controls were not statistically significant for the independent validation set. Given the fairly large absolute differences
in area-under-curve, a likely reason would be the relatively few stage I/II invasive cases available.

Serum levels of CA125 have been used widely for distinguishing benign from malignant pelvic masses and for monitoring the clinical course of patients with ovarian cancer. However, CA125 is elevated in only about half of stage I/II ovarian cancer patients (23). Lowering the cutoff of CA125 would increase its sensitivity in detecting stage I/II cancer but result in many false positives in patients with benign conditions as well as in healthy women. The improvement in sensitivity by the multivariate models to detect early stage cancer also increased the false-positive rate among patients with benign pelvic masses, but unlike with CA125, it did not lead to appreciable concomitant loss of specificity among healthy women. At a sensitivity of 83% and specificity of 94%, the current multivariate model by itself is not suitable for general population screening. However, in a two-stage approach with a combination of a serum test followed by sonography, a high specificity might be reached at an acceptable total cost.

The identified biomarkers have been characterized generally as acute-phase reactants. The down-regulation of transthyretin and apolipoprotein A1 in ovarian cancer patients suggests the possibility that they are byproducts of the host response to the tumor. Although recent data have supported the concept that inflammation is a critical component of tumor progression (24), such acute-phase reactants may still represent only epiphenomena because of the presence of tumor and may not be specific to a particular type of cancer (25, 26). In this study, with preliminary data from immunoassays analysis, we were able to verify that the levels of apolipoprotein A1 were not altered in the serum of breast or colon cancer patients and the levels of transthyretin were not altered in the serum of breast or prostate cancer patients.

Fig. 3. Comparison of receiver operating characteristic curves between CA125 and three discovered biomarkers (A–D) and the two multivariate predictive models (E–H). For A–D, (1) CA125; (2) m/z 12,828; (3) m/z 28,043; and (4) m/z 3,272. For E–H, CA125; multivariate model using the three biomarkers; and multivariate model using the three biomarkers and CA125. G–H, the fitted receiver operating characteristic curves are superimposed by the empirical receiver operating characteristic curves. *, Part of biomarker discovery set. Epithelial ovarian cancer included both invasive and borderline tumors. Panels G and H: vertical and horizontal dashed lines correspond to 90% specificity and 83% sensitivity, respectively.
have been shown to be decreased in approximately one-third of ovarian cancer by oligonucleotide array analysis (31) and malignant transformation of ovarian epithelium (29, 30). In addition, the identified proteins have been shown to be associated with an increased rate of cancer.

Mass spectrometry technological platforms, but rather reflects the limitation of the mass spectrometry-based proteomic profiling (36, 37).

The carboxyl portion of inter-α trypsin inhibitor, heavy chain H4, from which the m/z 3,272 biomarker is derived, has been shown to be a substrate for plasma kallikrein (33, 34). The fragment that we identified as a biomarker differs from the postulated fragment derived from cleavage by plasma kallikrein, suggesting a different protease is responsible for the generation of this biomarker. Kallikrein proteases consist of plasma kallikrein and tissue kallikreins, which have overlapping substrate specificity (35). The tissue kallikreins are products of a large multigene family that includes prostate specific antigen (hK3), a tumor marker for prostate cancer. Gene expression of seven of the tissue kallikreins has been found to be up-regulated in ovarian cancer patients, and expression of hK6, hK10, and hK11 has been shown to be increased in >50% of patients with ovarian cancer (36, 37).

The identified proteins associated with the three biomarkers are all of high abundance in serum and are unlikely to be released by tumor cells. This limitation has been pointed out previously as being common among studies using mass spectrometry-based proteomic profiling (25, 26, 38). However, this is not purely a limitation of the mass spectrometry technological platforms, but rather reflects the limitation of high throughput sample preprocessing technologies that would allow us to examine subsets of the serum proteome without introducing additional significant analytical variability. The use of sample prefractionation in addition to multiple array surfaces in this study is a first attempt in surface-enhanced laser desorption/ionization mass spectrometry-based clinical proteomics for biomarker discovery.

Two of the markers found in this study are cleavage products of precursor proteins and present in the serum at a fraction of the concentrations of their corresponding full-length proteins. Neither of these truncation products has been reported previously, indicating that they are new candidate markers. These markers may be the product of cleavage by one or more proteases, including plasma kallikrein, tissue kallikreins, matrix metalloproteases, or prostasin, a trypsin-like serine protease that was reported recently to be increased in cases of ovarian cancer (39). The proteases that generate these markers may themselves act as markers that can be combined with those discovered here in a predictive model. More generally, these results support the increasing body of evidence indicating alterations in the balance of protease and protease inhibitor activity in the serum and tissue of patients with cancer (40, 41). Preliminary results from additional immunoprecipitation pull-down analysis suggest that the forms and relative frequencies of posttranslational modifications of inter-α trypsin inhibitor, heavy chain H4 and transthyretin may be associated with the ovarian cancer disease status (data not shown).

The use of proteomics to identify potential biomarkers has been explored previously for the detection of a number of cancers including prostate (13, 42–44), colon (45), bladder (46), breast (12), and ovarian (9, 17). For example, Petricoin et al. reported the use of self-organizing map coupled with genetic algorithm to search through raw mass spectrum data for informative variables and to form clusters of train.

Table 4  Comparison of distributions of serum levels of CA125 and the discovered biomarkers among 142 archived samples for independent validation using immunoassays for apolipoprotein A1 and transthyretin

<table>
<thead>
<tr>
<th>Group by stage</th>
<th>Healthy control</th>
<th>Benign pelvic mass</th>
<th>Epithelial ovarian cancer</th>
<th>Stages I/II invasive cancer</th>
<th>All stages I/II cancer</th>
<th>Stage III/IV invasive cancer</th>
<th>Recurrent</th>
<th>Stage III/IV borderline tumor</th>
<th>Stages III/IV borderline tumor</th>
</tr>
</thead>
<tbody>
<tr>
<td>Training set</td>
<td>CA125 at cutoff = 35 units/ml</td>
<td>97 (32/33)</td>
<td>68 (19/28)</td>
<td>64 (14/22)</td>
<td>67 (18/27)</td>
<td>100 (1/1)</td>
<td>80 (4/5)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Model with three markers</td>
<td>89 (29/33)</td>
<td>89 (25/28)</td>
<td>86 (19/22)</td>
<td>89 (24/27)</td>
<td>100 (1/1)</td>
<td>100 (5/5)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Model with three markers + CA125</td>
<td>97 (32/33)</td>
<td>100 (28/28)</td>
<td>100 (22/22)</td>
<td>100 (27/27)</td>
<td>100 (1/1)</td>
<td>100 (5/5)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Test set</td>
<td>CA125 at cutoff = 35 units/ml</td>
<td>98 (45/46)</td>
<td>66 (19/29)</td>
<td>70 (14/20)</td>
<td>64 (18/28)</td>
<td>100 (1/1)</td>
<td>50 (4/8)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Model with three markers</td>
<td>91 (42/46)</td>
<td>83 (24/29)</td>
<td>75 (15/20)</td>
<td>82 (23/28)</td>
<td>100 (1/1)</td>
<td>100 (8/8)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Model with three markers + CA125</td>
<td>98 (45/46)</td>
<td>86 (25/29)</td>
<td>80 (16/20)</td>
<td>86 (24/28)</td>
<td>100 (1/1)</td>
<td>100 (8/8)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Independent validation set</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fixed specificity for healthy controls</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CA125 at cutoff = 35 units/ml</td>
<td>97 (61/63)</td>
<td>76 (126/166)</td>
<td>77 (106/138)</td>
<td>65 (15/23)</td>
<td>54 (19/35)</td>
<td>87 (75/86)</td>
<td>79 (11/14)</td>
<td>33 (4/12)</td>
<td>33 (1/3)</td>
</tr>
<tr>
<td>Model with three markers</td>
<td>97 (61/63)</td>
<td>52 (86/166)</td>
<td>78 (107/138)</td>
<td>74 (17/23)</td>
<td>74 (26/35)</td>
<td>81 (70/86)</td>
<td>71 (10/14)</td>
<td>75 (9/12)</td>
<td>33 (1/3)</td>
</tr>
<tr>
<td>Model with three markers + CA125</td>
<td>97 (61/63)</td>
<td>45 (75/166)</td>
<td>78 (108/138)</td>
<td>74 (17/23)</td>
<td>66 (23/35)</td>
<td>85 (73/86)</td>
<td>79 (11/14)</td>
<td>50 (6/12)</td>
<td>33 (1/3)</td>
</tr>
<tr>
<td>Fixed sensitivity for stage III invasive cancer</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CA125 at cutoff = 11 units/ml</td>
<td>52 (33/63)</td>
<td>32 (53/166)</td>
<td>88 (122/138)</td>
<td>83 (19/23)</td>
<td>74 (26/25)</td>
<td>94 (81/86)</td>
<td>93 (13/14)</td>
<td>58 (7/12)</td>
<td>67 (2/3)</td>
</tr>
<tr>
<td>Model with three markers</td>
<td>89 (56/63)</td>
<td>58 (138/166)</td>
<td>82 (113/138)</td>
<td>83 (19/23)</td>
<td>80 (28/35)</td>
<td>86 (74/86)</td>
<td>71 (10/14)</td>
<td>75 (9/12)</td>
<td>33 (1/3)</td>
</tr>
<tr>
<td>Model with three markers + CA125</td>
<td>94 (59/63)</td>
<td>35 (58/166)</td>
<td>82 (113/138)</td>
<td>83 (19/23)</td>
<td>71 (25/35)</td>
<td>87 (75/86)</td>
<td>86 (12/14)</td>
<td>50 (6/12)</td>
<td>33 (1/3)</td>
</tr>
</tbody>
</table>

* All stage III invasive cancer included stage I/II invasive epithelial ovarian cancer and stage I/II borderline tumor.
† 95% confidence intervals for CA125 at cutoff = 11 units/ml, model with three markers, and model with three marker + CA125 were 39.5–65%, 78.95%, and 85.98%, respectively.

Table 5  Comparison of distributions of serum levels of CA125 and the discovered biomarkers among 142 archived samples for independent validation using immunoassays for apolipoprotein A1 and transthyretin

<table>
<thead>
<tr>
<th>Diagnostic groups</th>
<th>n</th>
<th>Age mean ± SD</th>
<th>CA125 (units/ml)</th>
<th>P</th>
<th>Apolipoprotein A1 (mg/dl)</th>
<th>P</th>
<th>Transthyretin (mg/dl)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Healthy control</td>
<td>41</td>
<td>35 ± 10</td>
<td>17.9 ± 23.0(10.2)</td>
<td>0.000000</td>
<td>152.8 ± 28.1(154.3)</td>
<td>0.0004</td>
<td>267.1 ± 5.8(25.1)</td>
<td>0.0005</td>
</tr>
<tr>
<td>Stage III/IV ovarian cancer</td>
<td>41</td>
<td>59 ± 11</td>
<td>2387.9 ± 4723.3(4286.6)</td>
<td>0.000000</td>
<td>121.5 ± 41.9(123.9)</td>
<td>0.0004</td>
<td>19.8 ± 7.1(18.7)</td>
<td>0.0005</td>
</tr>
<tr>
<td>Breast cancer</td>
<td>20</td>
<td>53 ± 14</td>
<td>13.4 ± 13.0(7.9)</td>
<td>0.39</td>
<td>154.4 ± 31.8(145.9)</td>
<td>0.77</td>
<td>26.8 ± 4.8(26.4)</td>
<td>0.51</td>
</tr>
<tr>
<td>Colon cancer</td>
<td>20</td>
<td>70 ± 15</td>
<td>17.0 ± 14.2(10.9)</td>
<td>0.86</td>
<td>144.2 ± 39.7(149.5)</td>
<td>0.69</td>
<td>22.4 ± 5.1(22.8)</td>
<td>0.01</td>
</tr>
<tr>
<td>Prostate cancer</td>
<td>20</td>
<td>57 ± 7</td>
<td>13.1 ± 21.2(7.6)</td>
<td>0.07</td>
<td>138.2 ± 21.2(136.1)</td>
<td>0.02</td>
<td>27.8 ± 7.8(29.8)</td>
<td>0.22</td>
</tr>
</tbody>
</table>

* P estimated by Mann-Whitney U test.
ing samples as the basis of a predictive model. More recently, Kozak et al. (47) reported several panels of selected surface-enhanced laser desorption/ionization peaks for the detection of ovarian cancer. A number of these peaks and their expression patterns are consistent with those from our current or previous results (17).

Biomarker discovery using clinical proteomics involves the simultaneous analysis of expression levels of many proteins measured on a relatively few clinical samples. The difficulty in statistical analysis is complicated additionally by the possibility of nondisease-related biases and variability in data from preanalytical and analytical variables and within-group heterogeneity associated with clinical samples. A major concern has always been whether the discovered biomarkers and the derived multivariate models are truly associated with the disease process. Recent reports examined and highlighted the danger of such issues (26, 38, 48). The current study had a number of features that were designed to alleviate the impact of these factors. First, only the intensities of detectable peaks were used in analysis, which in general are less sensitive to mass shift in raw spectrum data, and the discovered biomarkers are more likely to have an identifiable biological identity. Second, biomarker discovery and construction of predictive models were done in two separate stages. During the discovery stage, only linear models were used to evaluate the informativeness of individual peaks. The bootstrap resampling was used to additionally ensure that the peak selection results are robust among multiple subpopulations. It was only after a small group of biomarkers had been selected and individually validated across the multiple data sets that the more complicated nonlinear unified maximum separability analysis predictive models were derived to combine the multiple markers. It would have been difficult to explain and validate the exact roles of individual inputs if we had started the peak selection directly with a complex nonlinear model using raw spectrum data. Third, in this study, the data sets from multiple sites were used separately to cross-validate discoveries from other data sets and to detect systemic biases in data such as those because of differences in preanalytical sample processing procedures. This differs significantly from the approaches in which data from multiple sites are pooled together and then divided through randomization into (artificially made) identically distributed training and test data sets. Considering the high cost associated with post discovery validation, however, we believe that the conservative approach that we used is more close to the real clinical environment and appropriate for biomarker discovery through expression profiling. Finally, the identification of the discovered biomarkers allowed additional confirmation through immunoassay tests. Previous studies have illustrated the benefits of combining multiple markers and the longitudinal use of tumor markers in the detection of ovarian cancers (8, 49, 50). New biomarkers derived from proteomic approaches for identification of serum biomarkers to detect breast cancer. Clin Chem 2002;48:1296–304.


REFERENCES


### Three Biomarkers Identified from Serum Proteomic Analysis for the Detection of Early Stage Ovarian Cancer

Zhen Zhang, Robert C. Bast, Jr., Yinhua Yu, et al.

*Cancer Res* 2004;64:5882-5890.

| Updated version | Access the most recent version of this article at: [http://cancerres.aacrjournals.org/content/64/16/5882](http://cancerres.aacrjournals.org/content/64/16/5882) |

| Cited articles | This article cites 47 articles, 18 of which you can access for free at: [http://cancerres.aacrjournals.org/content/64/16/5882.full.html#ref-list-1](http://cancerres.aacrjournals.org/content/64/16/5882.full.html#ref-list-1) |

| Citing articles | This article has been cited by 81 HighWire-hosted articles. Access the articles at: [http://cancerres.aacrjournals.org/content/64/16/5882.full.html#related-urls](http://cancerres.aacrjournals.org/content/64/16/5882.full.html#related-urls) |

| E-mail alerts | Sign up to receive free email-alerts related to this article or journal. |

| Reprints and Subscriptions | To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org. |

| Permissions | To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org. |