Evaluation of Apolipoprotein A1 and Posttranslationally Modified Forms of Transthyretin as Biomarkers for Ovarian Cancer Detection in an Independent Study Population

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Abstract

Background: Although overall 5-year survival rates for ovarian cancer are poor (10-30%), stage I/IIa patients have a 95% 5-year survival. New biomarkers that improve the diagnostic performance of existing tumor markers are critically needed. A previous study by Zhang et al. reported identification and validation of three biomarkers using proteomic profiling that together improved early-stage ovarian cancer detection. Methods: To evaluate these markers in an independent study population, postdiagnostic/pretreatment serum samples were collected from women hospitalized at the Mayo Clinic from 1980 to 1989 as part of the National Cancer Institute Immunodiagnostic Serum Bank. Sera from 42 women with ovarian cancer, 65 with benign tumors, and 76 with digestive diseases were included in this study. Levels of various posttranslationally forms of transthyretin and apolipoprotein A1 were measured in addition to CA125. Results: Mean levels of five of the six forms of transthyretin were significantly lower in cases than in controls. The specificity of a model including transthyretin and apolipoprotein A1 alone was high [96.5%; 95% confidence interval (95% CI), 91.9-98.8%] but sensitivity was low (52.4%; 95% CI, 36.4-68.0%). A class prediction algorithm using all seven markers, CA125, and age maintained high specificity (94.3%; 95% CI, 89.1-97.5%) but had higher sensitivity (78.6%; 95% CI, 63.2-89.7%). Conclusions: We were able to replicate the findings reported by Zhang et al. in an independently conducted blinded study. These results provide some evidence that including age of patient and these markers in a model may improve specificity, especially when CA125 levels are ≥35 units/mL. Influences of sample handling, subject characteristics, and other covariates on biomarker levels require further consideration in discovery and replication or validation studies. (Cancer Epidemiol Biomarkers Prev 2006;15(9):1641–6)

Introduction

Recent advances in proteomic profiling technologies have made it possible to associate changes in protein expression with disease conditions, allowing the identification of biomarkers that can be combined to generate a multimarker panel to improve disease diagnosis. In particular, there have been several attempts to use serum proteins for the detection of early-stage ovarian cancer (1-4). In ovarian cancer, more than two thirds of cases are detected at an advanced stage, resulting in poor overall 5-year survival rates of 10% to 30% (5). This is in stark contrast to stage I/IIa patients with 95% 5-year survival (5). Longitudinal studies are under way in Europe, Japan, and the United States to evaluate screening strategies using CA125 and/or transvaginal sonography and their effect on overall cancer mortality. Although it is not known whether a survival benefit will be observed among patients diagnosed early through a screening regimen, the existing serum markers such as CA125, CA 72-4, and macrophage colony stimulating factor do not have adequate sensitivity or specificity to be used as screening tools (6). Proteomic technologies have been used to search for new biomarkers that may improve the diagnostic performance of existing markers.

In one study, Zhang et al. (2) reported using surface-enhanced laser desorption/ionization time-of-flight mass spectrometry (SELDI-TOF-MS) to identify three biomarkers that simultaneously improved the detection of early-stage ovarian cancer, in particular test specificity. Subsequently, quantitative chromatographic assays were developed for biomarkers identified at mass to charge ratios (m/z) 28,043 (apolipoprotein A1), 12,828 (a truncated form of transthyretin), and 3,272 (a fragment of inter-α-trypsin inhibitor IV). These three markers were found to differentiate ovarian cancer cases from healthy women with higher accuracy than CA125 alone. Applied to an independent validation sample set of sera from early-stage ovarian cancer cases and healthy controls, the sensitivity of a multivariable model combining the three biomarkers and CA125 at a matched specificity of 97% [95% confidence interval (95% CI), 89-100%] was 74% (95% CI, 52-90%), a small improvement over that of CA125 alone (65%; 95% CI, 43-84%; ref. 2). When compared at a fixed sensitivity of 83% (95% CI, 61-95%), the specificity of the model including CA125 and the proteomic biomarkers (94%; 95% CI, 85-98%) was significantly better than that of CA125 alone (52%; 95% CI, 39-65%).

To evaluate the discriminatory power of these markers, we measured them in an independent study population using a newly developed chromatographic SELDI-TOF-MS–based assay for quantification. We analyzed postdiagnostic/
pretreatment serum samples collected from women hospital-
ized with ovarian cancer, benign ovarian tumors, and digestive
disorders (hematia and gallstones) at the Mayo Clinic and
stored at the National Cancer Institute Immunodiagnostic
Serum Bank for apolipoprotein A1 and posttranslationally
modified forms of transthyretin because these biomarkers
could significantly discriminate ovarian cancer cases from
controls (2). Cautioned by a number of recent articles that have
called into question the reproducibility and relevance of
reported proteomic biomarkers in cancer detection (6-9), and
the absence of positive validation studies in the literature, we
aimed to carefully address several previously raised points of
criticism in our analysis, including sources of marker
variability among noncancer controls.

Materials and Methods

Patient Population. Serum samples (n = 238) were selected
from subjects whose blood was collected at the Mayo Clinic
between 1980 and 1989 (10). Once collected, samples were
shipped to the National Cancer Institute Immunodiagnostic
Serum Bank (Rockville, MD) and stored at −70 °C to −76 °C
until use. The National Cancer Institute Immunodiagnosis
Serum Bank contains −70 °C cryopreserved sera collected
between 1980 and 1989 from Mayo Clinic patients diagnosed
with a wide variety of malignant, benign, and nonneoplastic
conditions (10). For the present study, sera were selected from
all available samples from women with malignant (n = 45) or
benign (n = 71) ovarian tumors, and from 122 female controls
with abdominal hernias (ICD-9CM codes 553.1-553.3) or
gallstones (ICD-9CM codes 574.1-574.4), frequency matched
for age to cases. Information available on all subjects included
age of patient at diagnosis, smoking status (never, past current,
number of packs per day, years of smoking), ICD code for
disease as well as the draw date and number of freeze-thaws
for serum samples. Histologic subtype was known for all
malignant and benign tumors. Stage and grade were provided
for all cases. Six individuals whose serum samples were
previously thawed and refrozen ≥1 times were excluded from
analyses. Two cases were excluded for divergent histology
(one diagnosed with mesothelioma and another with signet
ring cell carcinoma) and one benign tumor was excluded for
early age at diagnosis (3 years). Therefore, the final analyses
included 42 ovarian cancer cases, 65 women with benign
tumors, and 122 noncancer control digestive diseases.

Laboratory Methods

Materials. Sinapinic acid (5-mg vial; Ciphergen, Fremont,
CA); sample denaturation buffer (Ciphergen); OMAC-30 array
(Ciphergen); Bioprocessor (Ciphergen); Q10 ProteinChip
Array (Ciphergen), human prealbumin, purified (Biodesign
International Saco, ME), and apolipoprotein A1 calibrators
(K-ASSAY, Kamiya Biomedical, Seattle, WA).

Assays for Transthyretin and Apolipoprotein A1. To quantita-
tively measure and compare apolipoprotein A1 and posttrans-
lationally modified forms of transthyretin concentrations in
patient sera, a SELDI-TOF-MS Protein Chip array chromato-
graphic assay was developed for each marker. The following
procedures were done on a Tecan Aquarius-96 robotic
workstation. Assays were run in triplicate. For apolipoprotein
A1, IMAC ProteinChip Arrays were precharged with 50 μL of
50 mmol/L CuSO4 for 10 minutes, washed four times with
deionized water, and then equilibrated with IMAC binding/
washing buffer [50 mmol/L sodium phosphate, 250 mmol/L
NaCl (pH 6.0)], twice each for 5 minutes. Five microliters of
sample were denatured with 7.5 μL of sample
denaturation buffer [9 mol/L urea, 2% CHAPS 50 mmol/L
Tris-HCl (pH 9.0)] for 20 minutes on a shaker at room
temperature. The spots were washed thrice with 150 μL of the
binding/washing buffer, pipetting up and down 10 times for
each wash. The spots were then rinsed twice with 150 μL of
water. Excess water was aspirated and the spots allowed to
air-dry for 10 minutes. To each spot, 1 μL of sinapinic acid
matrix dissolved in 50% acetonitrile/0.5% trifluoroacetic acid
in water at a concentration of 12.5 mg/mL was deposited.
After allowing the spots to air-dry for 10 minutes, matrix was added
again. The SELDI-based chromatographic assay for tran-
sthyretin was done using the anion exchange Q10 ProteinChip
Array as previously described (11). A set of transthyretin
calibrators (purified human prealbumin was reconstituted in
binding/washing buffer) and a set of apolipoprotein A1
calibrators were used to monitor assay performance and assay
linearity. Calibrants (representing serial dilutions of tran-
sthyretin and apolipoprotein A1) were treated exactly as serum
samples. In the experimental runs, each cassette incorporated
one set of calibrators with the remaining samples.

Data Acquisition. The arrays were read in a PCS4000
ProteinChip Reader, a time-lag focusing, linear laser desorp-
tion/ionization-time-of-flight mass spectrometer. The instru-
ments were internally calibrated on a daily basis. All spectra
were acquired in the positive-ion mode. Time-lag focus mass
was set at 14,000 Da for transthyretin and 28,000 Da for
apolipoprotein A1. Sampling rate was set at 800 MHz. Ions
were extracted using 3.4-kV ion extraction pulse and acceler-
ated to final velocity using 25-kV acceleration potential. The
system employed a pulsed nitrogen laser at repetition rate of

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Figure 1. A. Posttranslationally modified transthyretin peaks
quantitated on a Q10 ProteinChip Array. B. Apolipoprotein A1
peaks quantitated on an IMAC ProteinChip Array.
20 Hz. Laser pulse energy of 1,500 to 2,000 nJ was delivered into a 100-µm diameter area, and this illuminated area was rastered across a 2-mm diameter sample spot. An automated analytic protocol was used to control the data acquisition process in most of the sample analysis. Each spectrum was an average of at least 1,000 laser shots and externally calibrated against a mixture of known peptides or proteins.

**Data Processing.** Raw data obtained from the PCS4000 ProteinChip Reader were first smoothed by a fixed-width moving average filter of 25 data points, and then a convex hull baseline subtraction algorithm was applied to the smoothed data. Data were then internally normalized using total ion current with the Ciphergen Express 3.0 software. Six peaks corresponding to transthyretin biomarkers, including a truncated form (T1; m/z 12,852), unmodified (T2; m/z 13,773), and four posttranslationally modified forms [sulfonated (T3; +SO2H; m/z 13,857), cysteinylated (T4; Cys; m/z 13,893), cysteinylated and glysinylated (T5; +Cys-Gly; m/z 13,933), and glutathionylated (T6; +Glut; m/z 14,111)], were manually labeled and their intensity recorded from the Q10 ProteinChip Array data while blinded to disease status (Fig. 1A). A peak corresponding to serum apolipoprotein A1 located at m/z 28,107 (A1) was manually selected and its intensity recorded from the IMAC array data (Fig. 1B).

**Immunoassay Protein Analyses.** CA125 levels (units/mL) were obtained using an Elecsys 1010 immunoassay analyzer (Roche Diagnostics, Indianapolis, IN). Transthyretin levels (mg/mL) were obtained using an immunoprecipitation procedure (immunoturbidimetric assay; Pacific Biometrics, Seattle, WA). Samples were mixed with a polymeric enhancer and antiserum. A calibration curve was constructed from a series of five standards with known transthyretin concentrations. A Logit/Log plot was constructed and unknown values are determined by interpolation. Samples from quality control pools were assayed in each analytic run and results were compared with standards with known transthyretin concentrations. A Logit/Log plot was constructed and unknown values are determined by interpolation. Samples from quality control pools were assayed in each analytic run and results were compared with standards with known transthyretin concentrations.

**Results**

The mean storage time was shorter for patients with benign and malignant ovarian tumors compared with digestive disease controls (mean storage time, 17, 17, and 21 years, respectively). Using the chromatographic assay data from all 122 controls, we observed that protein levels decreased significantly with storage time for unmodified (T2; P = 0.008) and cysteinylated (T4; P = 0.05) transthyretin. To minimize bias in detection of protein levels that were negatively associated with storage time in addition to cancer status, the analysis of the biomarker data was limited to include only samples collected from 1983 to 1989, thereby decreasing the mean years in storage among control samples to 20.0 ± 1.2 years (Table 1). Only marker T4 (+Cys) remained significantly decreased with storage time after restriction of analysis to samples collected in 1983 or later. Among controls, age of patient at sample collection influenced levels for the truncated (T1; P = 0.01) form of transthyretin in models adjusted for years in storage.

The clinical characteristics and age distribution of subjects included in the final study analysis are presented in Table 1. Cancer cases and controls were similar with respect to age.
due to frequency matching on age. Benign ovarian tumor patients were younger than cases or digestive disease controls ($P < 0.0001$). The majority of serum samples from women with benign tumors and ovarian malignancies were collected between 1986 and 1989 (89% and 95%, respectively) whereas 66% of digestive disease control samples were collected before 1986 (data not shown). More women with benign tumors reported currently and ever smoking cigarettes. Smoking prevalence did not statistically differ between benign tumors and digestive disease controls. Protein markers T1 to T6 were significantly lower compared with digestive disease ($P < 0.0001$, t-test) or benign tumor controls ($P = 0.0002$, t-test). Serum transthyretin levels did not significantly differ between digestive disease and benign tumor controls ($P = 0.6$). CA125 concentration (<35 versus ≥35 units/mL) was a significant predictor of cancer status, although 25% of women with benign disease and 9% of controls also had levels ≥35 units/mL. Among cancer cases, most women (79%) were diagnosed with advanced-stage disease whereas 21% were diagnosed with stage I/II cancer. CA125 level did not differ by tumor stage or grade (data not shown).

The frequencies of ovarian cancer and benign tumor histologic subtypes in the final analysis are presented in Table 2. Serous cystadenocarcinoma was the major tumor histologic subtype in this study (~40%). Benign ovarian tumor patients had tumors of both epithelial and stromal origin.

In Table 3, Spearman correlation coefficients between markers quantified with the chromatographic and immunoassay were presented separately for ovarian cancer cases, benign ovarian tumor, and digestive disease controls. In each group, the rank of the transthyretin protein levels measured with the immunoassay was correlated with those of the posttranslationally modified forms of transthyretin (T2-T6) and apolipoprotein A1 biomarkers, with the exception of truncated transthyretin (T1) and CA125. CA125 levels were correlated with most biomarkers among cases, with the exception of markers T1 (correlation = 0.25, $P = 0.11$) and T3 (correlation = −0.36, $P = 0.18$). CA125 was not associated with levels of any other biomarker among benign tumor or digestive disease controls.

In Table 4, the unadjusted least squares mean and SE estimates of serum protein levels were given separately for cancer cases, benign tumor, and digestive disease controls. Only CA125 and T1 were higher in cases compared with controls. Protein markers T2 to T6 and apolipoprotein A1 were lower in cases. The mean levels of CA125, total transthyretin, and protein markers T1 to T6 were significantly different between case, benign tumor, and control groups in a model adjusted for age quartile and storage time indicator. Protein markers T1 to T3 decreased and apolipoprotein A1 increased significantly with age of patient (data not shown). Serum CA125 and transthyretin protein levels were not associated with smoking status, age of patient, or sample storage time (data not shown).

In Table 5, the cross-validated sensitivity and specificity estimates for three prediction models are presented for the $K$-nearest neighbor algorithm with $K = 2$. Model 1 included age of patient in quartiles and an indicator variable for CA125 (<35 versus ≥35 units/mL). Model 2 included age of patient in quartiles and protein biomarker levels measured using the chromatographic assay. Model 3 was the most comprehensive and included age in quartiles, the CA125 indicator variable, and all protein biomarkers measured with the chromatographic assay. Sensitivity and specificity estimates to predict cancer/noncancer status were done by combining all noncancer subgroups. Models 1 and 3 were the most sensitive to predict cancer/noncancer status [73.8% (95% CI, 58.0-86.1%) and 78.6% (95% CI, 63.2-89.7%), respectively]. Model 2 had the

### Table 2. Histologic subtypes of ovarian benign disease and cancer

<table>
<thead>
<tr>
<th>Histologic subtypes of benign tumors</th>
<th>N (%)</th>
<th>Histologic subtypes of ovarian cancer cases</th>
<th>N (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adenofibroma, NOS</td>
<td>5 (7.7)</td>
<td>Adenocarcinoma, NOS</td>
<td>7 (16.7)</td>
</tr>
<tr>
<td>Brenner tumor, NOS</td>
<td>1 (1.5)</td>
<td>Adenosquamous carcinoma</td>
<td>1 (2.4)</td>
</tr>
<tr>
<td>Cystadenoma, NOS</td>
<td>1 (1.5)</td>
<td>Brenner Tumor malignant</td>
<td>1 (2.4)</td>
</tr>
<tr>
<td>Dermoid cystadenoma, NOS</td>
<td>9 (13.8)</td>
<td>Carcinoma, NOS</td>
<td>2 (4.8)</td>
</tr>
<tr>
<td>Fibroma, NOS</td>
<td>5 (7.7)</td>
<td>Carcinoma, anaplastic, NOS</td>
<td>1 (2.4)</td>
</tr>
<tr>
<td>Leiomyoma, NOS</td>
<td>1 (1.5)</td>
<td>Clear cell adenocarcinoma, NOS</td>
<td>1 (2.4)</td>
</tr>
<tr>
<td>Mucinous cystadenoma, NOS</td>
<td>9 (13.8)</td>
<td>Endometrioid carcinoma</td>
<td>3 (7.1)</td>
</tr>
<tr>
<td>Papillary cystadenoma, NOS</td>
<td>1 (1.5)</td>
<td>Mucinous cystadenocarcinoma, NOS</td>
<td>3 (7.1)</td>
</tr>
<tr>
<td>Serous adenofibroma</td>
<td>5 (7.7)</td>
<td>Mullerian mixed tumor</td>
<td>1 (2.4)</td>
</tr>
<tr>
<td>Serous cystadenoma, NOS</td>
<td>8 (12.5)</td>
<td>Papillary adenocarcinoma, NOS</td>
<td>3 (7.1)</td>
</tr>
<tr>
<td>Teratoma, benign</td>
<td>16 (24.6)</td>
<td>Papillary mucinous cystadenocarcinoma</td>
<td>2 (4.8)</td>
</tr>
<tr>
<td>Thecoma</td>
<td>3 (4.6)</td>
<td>Papillary serous cystadenocarcinoma</td>
<td>10 (23.8)</td>
</tr>
<tr>
<td>Missing</td>
<td>1 (1.5)</td>
<td>Serous cystadenocarcinoma, NOS</td>
<td>7 (16.7)</td>
</tr>
<tr>
<td>Total</td>
<td>65 (100)</td>
<td>Total</td>
<td>42 (100)</td>
</tr>
</tbody>
</table>

### Table 3. Correlation of transthyretin and CA125 immunoassay levels with apolipoprotein A1 and posttranslationally modified forms of transthyretin by disease status

<table>
<thead>
<tr>
<th>CA125 level (units/mL), correlation coefficient* ($P$)</th>
<th>Transthyretin level (mg/mL), correlation coefficient* ($P$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CA125 (units/mL)</td>
<td>CA125 level</td>
</tr>
<tr>
<td>------------------</td>
<td>-------------</td>
</tr>
<tr>
<td></td>
<td>1.00</td>
</tr>
<tr>
<td></td>
<td>T1-m/z</td>
</tr>
<tr>
<td></td>
<td>T2-m/z</td>
</tr>
<tr>
<td></td>
<td>T3-m/z</td>
</tr>
<tr>
<td></td>
<td>T4-m/z</td>
</tr>
<tr>
<td></td>
<td>T5-m/z</td>
</tr>
<tr>
<td></td>
<td>T6-m/z</td>
</tr>
<tr>
<td></td>
<td>A1-m/z</td>
</tr>
</tbody>
</table>

* Spearman rank correlation coefficient.

**Immunohistochemical measurement.
Discussion

The primary purpose of this work was to reproduce findings presented in Zhang et al. (2) in an independent study population. As in the previous report, differential analysis of protein profiles was conducted using serum samples collected postdiagnosis/pretreatment from ovarian cancer patients and women with benign ovarian tumors. When examined individually, levels of posttranslationally modified forms of transthyretin and apolipoprotein A1 were significantly lower in cancer cases compared with controls; however, these proteins are not specific to ovarian cancer. Serum transthyretin levels decrease rapidly in response to malnutrition and injury and elevated levels have been observed in patients taking medications and with Hodgkin’s disease (18). Apolipoprotein levels reflect HDL protein concentration differences observed among healthy controls but are also influenced by other possible confounders such as age, alcohol intake, hormone use, sex, race, body mass index, and coronary artery disease (19, 20). CA125 protein is often elevated during menstruation and pregnancy, with endometriosis, and decreases with age (21). Like transthyretin and apolipoprotein A1, other biomarkers identified through

Table 4. Least squares mean estimates for patient status by cancer marker

<table>
<thead>
<tr>
<th>Biomarkers</th>
<th>Control</th>
<th>Unadjusted model mean (SD)</th>
<th>Case</th>
<th>P-adjusted* model</th>
</tr>
</thead>
<tbody>
<tr>
<td>CA125(units/mL)</td>
<td>20.5 (19.3)</td>
<td>29.9 (32.7)</td>
<td>1,563.9 (3,350.0)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Transthyretin(m/z)</td>
<td>294.8 (76.6)</td>
<td>287.1 (73.8)</td>
<td>221.9 (89.1)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>T1-12,852*</td>
<td>2.8 (0.8)</td>
<td>2.8 (0.6)</td>
<td>3.6 (1.5)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>T2-13,773*</td>
<td>9.3 (4.3)</td>
<td>9.6 (4.2)</td>
<td>7.3 (4.3)</td>
<td>0.001</td>
</tr>
<tr>
<td>T3-13,857*</td>
<td>5.6 (1.8)</td>
<td>6.1 (1.8)</td>
<td>4.5 (2.2)</td>
<td>0.002</td>
</tr>
<tr>
<td>T4-13,893*</td>
<td>18.8 (6.2)</td>
<td>17.0 (6.2)</td>
<td>15.5 (8.3)</td>
<td>0.0001</td>
</tr>
<tr>
<td>T5-13,933*</td>
<td>6.8 (2.3)</td>
<td>7.2 (2.9)</td>
<td>5.4 (2.6)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>T6-14,111*</td>
<td>4.4 (0.9)</td>
<td>4.5 (1.0)</td>
<td>3.7 (1.5)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Apolipoprotein A1(m/z)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A1-28,107</td>
<td>9.3 (4.3)</td>
<td>8.2 (3.3)</td>
<td>8.3 (3.1)</td>
<td>0.32</td>
</tr>
</tbody>
</table>

*Significance of group differences in model adjusted for age quartile and storage time indicator variable.

Table 5. Cross-validated sensitivity and specificity estimates for various prediction models using the K-nearest neighbor algorithm with K = 2 (proteomic markers, when included into a model, were log transformed)

<table>
<thead>
<tr>
<th>Sensitivity and specificity (95% CI)* to discriminate cancer from noncancer</th>
<th>Stage I/II specificity</th>
<th>Stage III/IV specificity</th>
<th>Specificity benign tumors</th>
<th>Sensitivity CA125 ≥35 units/mL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total sensitivity</td>
<td>Total specificity</td>
<td>Stage I/II sensitivity</td>
<td>Stage III/IV specificity</td>
<td>Specificity benign tumors</td>
</tr>
<tr>
<td>Model 1*</td>
<td>31/42 (73.8%; 58.0-86.1%)</td>
<td>133/141 (94.3%; 89.1-97.5%)</td>
<td>3/9 (33.3%; 7.5-70.1%)</td>
<td>28/33 (84.9%; 68.1-94.9%)</td>
</tr>
<tr>
<td>Model 2*</td>
<td>22/42 (52.4%; 36.4-68.0%)</td>
<td>136/141 (96.5%; 91.9-98.8%)</td>
<td>3/9 (33.3%; 7.5-70.1%)</td>
<td>19/33 (57.6%; 39.2-74.5%)</td>
</tr>
<tr>
<td>Model 3*</td>
<td>33/42 (78.6%; 65.2-89.7%)</td>
<td>133/141 (94.3%; 89.1-97.5%)</td>
<td>5/9 (55.6%; 21.2-86.3%)</td>
<td>28/33 (84.9%; 68.1-94.9%)</td>
</tr>
</tbody>
</table>


*Exact binomial confidence intervals.

1Model 1: CA125 <35, ≥35, and age in quartiles.

2Model 2: all proteomic markers (T1-T6, ApoA1) and age in quartiles.

3Model 3: CA125 <35, ≥35, all proteomic markers (T1-T6, ApoA1), and age in quartiles.
“omic” technologies that are potentially able to differentiate healthy controls from ovarian cancer patients are also found in controls, associated with other disease states, and are considered to be markers of the host metabolic response to cancer rather than specific to the cancer itself (2, 4, 11, 22-24). The major challenge of developing an ovarian cancer detection test is that it must be highly specific to avoid detection of numerous false positives. This requirement and the fact that many markers are not specific to ovarian cancer underscore the need to understand how they are associated with sample processing and handling and other patient characteristics, in addition to their significance in pathogenesis. In this study, we examined associations between all markers and available information on subjects, including age at diagnosis, smoking status, ICD disease code, as well as draw date and number of freeze thaws per sample. It was necessary to include age quartile in all models because it was positively associated with apolipoprotein A1, inversely associated with T1 to T3, and smoking status, ICD disease code, as well as draw date.

When used alone, these markers improved detection of controls with CA125 levels ≥35 units/mL but poor at identifying cases with late-stage cancers. The addition CA125 as a dichotomous variable to the model increased sensitivity to detect high-stage cancers; however, the added specificity was lost.

This is one of the first studies to independently evaluate findings previously reported in ovarian cancer early detection using the SELDI-TOF-MS platform. Two recent editorials pointed to the important role of assessing potential sources of bias in design and conduct and also the effect of chance on data interpretations (7, 25). Several important lessons have been learned through the design and analysis of this study that might be considered in future investigations to reduce ongoing concerns over data validity and improve chances of reproducibility: (a) Convenience samples should be avoided for biomarker discovery or validation until the relationship between the biomarker and diseases in sample handling, processing, storage, and common confounding variables is understood. Ignoring such factors in study design and analysis will decrease any chance of future validation. In contrast to common practice in early phases of biomarker identification and validation, we promote using prospectively collected samples and including comparison groups that are frequency matched to cases and well characterized for possible confounders. Such samples are not generally easy to obtain. (b) Inclusion of a clinically relevant comparison group, in addition to healthy population controls, may be needed to improve understanding of the biomarker performance in future testing populations. (c) When relationships between biomarkers and potential confounders are not well understood, it may be advisable to restrict the samples rather than attempt to eliminate biases by statistical modeling. In biomarker discovery studies, many questions can be addressed in small carefully designed studies to minimize possible sources of variability. Once biomarkers are identified, control samples can be used to identify relationships with possible confounding variables. Whereas ideally one restricts samples in the design phase, sometimes it is necessary to contend with them in the analysis. The major factor biasing our results was length of sample storage time. Because the digestive disease control serum samples were stored longer than those from ovarian cancer cases or benign ovarian tumor controls, the protein levels of two markers would have decreased with storage time, biasing the comparisons between cases and digestive disease controls toward the null. We thus restricted the analysis to samples collected 1983 or later, eliminating the storage artifact for all markers except T4. Analyses comparing benign ovarian tumor and cancer cases were not susceptible to this bias because samples from both groups were collected and stored over a similar time period.

In conclusion, the specificity of a model that included measurements of posttranslationally modified forms of transthyretin, apolipoprotein A1, and age of patient was as high as models that included CA125 and age but sensitivity was lower. When used alone, these markers improved detection of controls with CA125 levels ≥35 units/mL but lost sensitivity to identify late-stage cases. In general, influences of sample storage conditions, subject characteristics, and other covariates on biomarker levels require further consideration in discovery and replication studies.

References
Evaluation of Apolipoprotein A1 and Posttranslationally Modified Forms of Transthyretin as Biomarkers for Ovarian Cancer Detection in an Independent Study Population
