EGFR diffuse strong positivity (2+/3+) was significantly related to vascular invasion ($p = 0.038$) in a subgroup of ESCC patients. Statistical trend towards poor outcome was observed in ESCC patients overexpressing EGFR (3+). The HER-2 expression was negative in 14/31 (45.2%) and positive in 17/31 (54.8%), of which 12 (38.7%) were 2+ and 5 (16.1%) were 3+. No significant associations were found among protein expression and clinic-pathological data. Our results revealed a high rate of HER-2 overexpression in the group of ESCC patient with poor disease outcome ($p = 0.019$).
Conclusion: Our data demonstrate the great potential prognostic interest of evaluation EGFR and HER-2 overexpression in ESCC. Protein overexpression of HER-2 (3+) is an indicator of poor prognosis in ESCC patients, although the results should be confirmed in a larger series.

PP73

Differential staining of SPARC across 3 different tumor types treated with nab-paclitaxel

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Background: Overexpression of albumin-binding protein SPARC (Secreted Protein Acidic and Rich in Cysteine) in tumors is generally associated with poor prognosis. SPARC expression in the tumor is complex with many SPARC-expressing components including stroma, fibroblasts, tumor cells, inflammatory cells, normal tissues, nerve, and blood vessels. To define the component responsible for SPARC being a negative prognostic factor, we conducted a comprehensive analysis of SPARC expression across 3 tumor types (breast, melanoma, and pancreas).
Materials and Methods: A series of antibodies were evaluated against SPARC. SPARC IHC was performed in a CLIA approved central laboratory using 2 antibodies with different affinities against SPARC. Detailed pathological evaluation was performed by a board certified pathologist. Score was assigned on scale of 0−3, with 3 being positive. Breakdown of the various components was performed to include: tumor, blood vessels, fibroblast, acellular stroma, inflammatory cells, and normal anatomy. Clinical samples for these analyses came from three clinical trials with nab-paclitaxel: 1) metastatic pancreatic cancer, 2) unresectable stage IV melanoma, and 3) neoadjuvant breast cancer.
Results: Two epitopes were defined during the evaluation of all anti-SPARC antibodies, with one preferentially expressed on fibroblasts (antibody 1) and one preferentially expressed on tumor cells (antibody 2). The profile of SPARC staining was distinct for each tumor type. For pancreatic cancer, SPARC positive staining by antibody 1 and antibody 2 respectively was 10/36 vs 7/36 for tumor cells, and 18/29 vs 5/29 for fibroblasts. For melanoma, SPARC positive staining by antibody 1 and antibody 2 respectively was 30/41 vs 20/41 for tumor cells, and 19/33 vs 14/33 for fibroblasts. For breast cancer, SPARC positive staining by antibody 1 and antibody 2 respectively was 22/76 vs 27/76 for tumor cells, and 60/77 vs 20/77 for fibroblasts. This same epitope on fibroblasts was found on blood vessel endothelial cells. Preliminary data from 3 clinical trials including pancreatic, melanoma, and neoadjuvant breast cancer suggest that positive SPARC expression may correlate with response to nab-paclitaxel.
Conclusion: SPARC expression profiles across the various components in patient tumors were examined for 3 tumor types: pancreas, breast, and melanoma. The distinctive SPARC expression profiles suggest that the role of SPARC in each tumor type may be contextually different.

PP48

A proliferation measure integrates the outcome-related information contained in the breast cancer transcriptome

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Background: A number of completely distinct gene expression signatures predict disease-free survival in breast cancer patients. However, the biological variables underlying these signatures remain unclear.
Materials and Methods: We established a signature, called 'super PCNA', composed of genes whose expression follows closely that of proliferation marker PCNA in a compendium of gene expression in normal tissues. We then proposed a method to adjust any microarray data set for the signal embedded in the super PCNA signature. This decovolution procedure removes proliferation-related signals without excluding proliferation genes from the data sets. Next, the prognostic abilities of 32 signatures published in the literature and of 10,000 randomly generated signatures were evaluated in the original and in the super PCNA-deconvolved versions of three breast cancer data sets of 295, 380, and 412 patients, respectively.
Results: Although most published signatures were significant predictors of disease-free survival, 36−64% were not significantly better predictors than random signatures in the original data sets. Deconvolving the proliferation-associated signals out of the data drastically reduced or completely cancelled the predictive abilities of both literature and random signatures. By contrast, substituting PCNA by unrelated genes in the deconvolution process had limited influence on predictors' significance.
Conclusion: Because programs related to proliferation affect ubiquitously the breast cancer transcriptome, most signatures − biologically motivated or random − assess the same proliferation-associated phenotypes and are therefore significant, but equivalent predictors. The study suggests new evaluation standards for cancer outcome predictors.

PP26

Immune response to gastrin-17 is an independent covariate for improved survival in gastrointestinal cancers

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Background: The trophic activity of gastrin has generated significant interest in gastrin as a potential growth factor for tumors arising within the gastrointestinal tract. Polyclonal Antibody Stimulator (PAS), is a novel immune stimulator that elicits antibodies that neutralize and block the proliferative activity of gastrin-17 (G17) and its precursor, glycine extended G17 (gly-G17). Early research with PAS suggested a clinical benefit in patients who mounted an immune response. Data from over 1200 patients with pancreatic, gastric, and colorectal (CRC) cancers were analyzed to define the relationship between immune response and efficacy and to determine the dependence of this effect on several baseline characteristics related to patients' health status.
Materials and Methods: PAS was administered intramuscularly as a monotherapy or in combination therapy as three initial doses, with a booster in some studies. PAS responders were defined by ELISA. The relationships between demographics and baseline disease characteristics and immune response and between immune response and survival were analyzed.
Results: In these studies, PAS responders varied between 52 and 89%. In Stage II−IV pancreatic responder patients, median survival (MS) was 176d and 63d for non responders ($p < 0.002$, log rank). Stage IV pancreatic responder patients had higher MS compared with non-responders (167d vs 104d). Similarly, Stage I−III pancreatic responders had higher MS (179d vs 146d in non-responders). For advanced gastric responder patients who received PAS with cisplatin and 5-FU, MS was 303d compared to 70d for non-responders ($p < 0.001$, log-rank). In Stage IV CRC with PAS alone, PAS responder patients showed better survival (267d) than non-responders (192d). In metastatic CRC responder patients who received PAS with irinotecan, MS was 249d versus 119d for non-responders ($p < 0.001$, log rank). Additional analysis showed that this immune responder survival correlation was independent of any covariates.
Conclusion: Overall, patients who generated antibodies to PAS had a significantly prolonged survival rate compared to those who did not. This effect was independent of various covariates that predicted the health status of the patients at baseline. The survival benefit for antibody responders and the favorable safety profile, indicate that PAS has exciting prospects for an improved anti cancer treatment for various GI cancers.

PP11

Expression differences of proteolytic factors uPA, PAI-1, and seven kallikrein-related peptidases (KLK5, 6, 7, 8, 10, 11, 13) between primary tumor and omentum metastasis impact outcome in advanced ovarian cancer

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Background: Primary tumor levels of serine proteases of the KLK family (kallikrein-related peptidases), as well as the serine protease uPA (urokinase-type plasminogen activator) and its inhibitor PAI-1, are related to disease course in ovarian cancer. Level differentials of these factors between primary and tumor omentum metastasis could thus be associated with the aggressiveness of metastastic processes typical for ovarian cancer.
Materials and Methods: Protein levels of uPA, PAI-1, and seven tissue kallikrein-related peptidases (KLK5, 6, 7, 8, 10, 11, 13) were determined in extracts of primary tumor tissues and corresponding omentum metastases of 54 FIGO stage III/IV ovarian cancer patients. Following radical surgery, 31/54 patients had minimal residual tumor (<10 mm), of whom 18 were optimally debulked (0 mm). Median follow-up in patients still alive at time of analysis was 24.5 months. All patients received postoperative platinum-containing chemotherapy.
Results: Collectively speaking, moderate correlations in protein levels between primary tumor tissues and omentum metastases were seen for