predictive algorithm, several proteins that might be targeted by miR-152 were examined.
Results Upregulated expression of miR-152 leads to decreased expression of DNMT1 (DNA methyl transferase 1), RICTOR and MET proteins, which are often found deregulated in rather wide spectrum of oncogenic diseases. In addition to DNMT1, the protein level of ERBB3 was also affected by downregulation of CDK12 in various ovarian cancer cells, such as PEO1, COV362 and OVCAR5.
Conclusions We speculate CDK12 participates in DDR machinery by two distinct mechanisms, either by orchestrating transcription of DDR genes or by stabilization of DNMT1 protein by blocking expression of miR-152 targeting DNMT1.

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IGCS19-0638

119 TARGETED SEQUENCING OF HISTOLOGICALLY DEFINED SEROUS ENDOMETRIAL CANCER REFLECTS PROGNOSIS AND CORRELATES WITH PREOPERATIVE BIOPSY

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Objectives Evaluation of the impact of discordant endometrial sampling on the prognosis of patients finally diagnosed with uterine papillary serous carcinoma (UPSC) and analysis of UPSC mutational profile.
Methods Retrospective cohort study comparing outcomes of patients with UPSC preoperatively diagnosed with endometrioid endometrial cancer (EEC) or UPSC. Genes commonly implicated in carcinogenesis were analyzed in a subgroup of 40 patients, using next generation sequencing.
Results 61 patients with UPSC on post-surgical, final pathology were included in the study. Prior to surgery, 15 were diagnosed with EEC (discordant) and 46 were correctly diagnosed with UPSC (concordant). After a median follow-up of 41.6 months [5.4–106.7], a preoperative diagnosis of EEC was associated with better 3-year progression-free survival (100% vs. 60.9%, P=0.003) and longer disease free interval (63.5 versus 15 months, P=0.026) compared to patients with an initial diagnosis of UPSC. Patients with a concordant diagnosis of UPSC were 5 times more likely to progress or die compared to those with a discordant EEC diagnosis (P=0.02, P=0.03, respectively), and their tumors were associated with higher rates of *TP53* (88.9% vs. 61.5%, P=0.04), and a lower rate of *PTEN* (14.8% vs. 38.5%, P=0.09)and *ARID1A* (3.7% vs. 23.1%, P=0.05) mutations.
Conclusions A pre-surgical diagnosis of EEC is associated with improved prognosis in patients with UPSC. Some histologically defined UPSC tumors contain endometrioid-like molecular characteristics that may confer a survival advantage.

IGCS19-0687

120 FACTORS ASSOCIATED WITH EXTENDED SURVIVAL FOR PATIENTS WITH PLATINUM-RESISTANT OVARIAN CANCER (PROC) TREATED WITH MODIFIED VACCINIA ONCOLYTIC VIROTHERAPY (VOV)

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Objectives VIRO-15 phase IB trial (NCT02759588) enrolled 11 patients with PROC, extensive tumor burden, and median 5 prior lines of therapy. We aimed to retrospectively determine factors that predict clinical benefit from VOV monotherapy in PROC.
Methods Patients received a modified VOV (GL-ONC1, Genelux Corp.) intra-peritoneally on two consecutive days. Four patients had apparent clinical benefit with >5 mos progression-free survival (PFS) following virotherapy (A). Seven (B) patients had <5 mo PFS. Comparative analyses included: measures of immune-competence with neutralizing antibody (NA) titers, virus-encoded glucuronidase activity (GA), tumor response by RECIST 1.1, Prognostic Nutritional Index (PNI), circulating tumor cells (CTCs), number of prior platinum and total therapies. Mann-Whitney test, *t*-test, *z*-test were used to evaluate differences between the groups.
Results Following GL-ONC1, the PFS was 10.9±5.1 and 2.4 ±1.1 mos for A vs B ($p< 0.05$). Mean OS for A was 21.7 ±8.2 mos vs 3.6±1.5 mos for B ($p<0.05$). Three A pts are alive, and one with stable disease died at 8-mos from pulmonary embolism. Factors that predicted clinical benefit were: i) PNI [mean 49.0±5.7 vs 42.1±4.3 ($p<0.05$)], ii) Week-5 CA125 values < Week-2 [4/4 vs 0/7 ($p<0.01$)], iii) absence of CTC [3/4 vs 1/7 pts ($p<0.05$)].
Conclusions Factors associated with clinical benefit post GL-ONC1 monotherapy in PROC include higher PNI, absence of CTCs, and Week-5 CA125 less than Week-2 levels. In the absence of these factors, cytotoxic therapy should be considered by Week-6 following GL-ONC1. Three patients are currently alive at 22.8–28.2 mos, following additional therapies.

IGCS19-0562

121 ADENOMYOSIS AND ENDOMETRIAL CANCER – IS THERE A RELATIONSHIP OR ONLY A PARTNERSHIP?

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Objectives Adenomyosis (AM) is very often diagnosed in histology slides of endometrioid endometrial adenocarcinoma (EEAC). The combination of EEAC and AM has not been investigated sufficiently. The aim of this study is to evaluate the combination of AM and EEAC in morphological and morphometrical terms and to reflect a possible role of AM in the pathogenesis of EEAC.

Methods A retrospective review of an institutional pathology archive over a five-year-period was performed to identify cases of combined EEAC and AM. 79 cases were identified. Histological slides exhibiting the combination of AM and EAC were digitalised using Aperio Slide scanner and evaluated by using Aperio Morphometry tools. Morphological results were correlated with tumour type, tumour grade and staging and compared with routine AM (RAM) cases. In a next step all histological slides were immunohistochemical examined by different antibodies.
Results The mean distance AM – EEAC was 0,67 ± 0,75 mm, the mean AM gland size was 0,22 ± 0,10 mm, while the mean RAM gland size was 2,31mm. All EAC cases were type 1 EEAC. The majority of AM-EEAC cases were classified as stage pT1a tumours and graded as G1. Immunohistochemical we were able to distinguish betweena p16 positive and p16 negative group.
Conclusions AM in combination with EEAC exhibits a special morphology with small AM glands near the EEAC. Our hypothesis is that Adenomyosis could be involved in the pathogenesis of endometrial cancer or a random incidental finding. Adenomyosis in the p16 negative group could play a rule in carcinogenesis.

IGCS19-0760

122 ANTI-HUMAN PAPILLOMAVIRUS ANTIBODY DETECTION USING RHODAMINE B LABELED L1-HPV-16 DERIVED PEPTIDES

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Objectives To detect differences in anti-HPV antibodies response between young women HPV-vaccinated and unvaccinated using rhodamine-b labeled L1-derived peptides and non-conventional techniques.
Methods The peptides were designed from the epitopes of the virus surface recognized by the antibodies of B cells from HPV-infected. Serum from eight VLP vaccinated women, who have received three doses of immunization (positive controls PC), and serum from eight girls under 14 years of age, who have not had their first intercourse (negative controls NC), were obtained by venipuncture at the faculty of health of Universidad Industrial de Santander and at the university hospital. The fluorescence polarization assays were performed and the polarization readings were made in the microplate reader using a cube of filters for polarization with excitation wavelength of 525 nm and emission at 585 nm. These serum were also tested by Enzyme-linked immunosorbent assay (ELISA).
Results It was found that these designed peptides presented higher reactivity with antibodies from the serum of PC-women than with antibodies from the serum of NC-women with $p < 0.0001$. Six out of eleven peptides derived from three L1-regions were specifically recognized by antibodies present in the serum of HPV-vaccine immunized women as was detected by ELISA. Peptide P-BC in the dot fluorescence assay showed the highest specific reactivity to PC-serum, suggesting that this peptide could be used to detect changes in the antibody response against HPV with this technique.
Conclusions Fluorescent peptides from the L1 protein can be used to detect of antibodies induced by vaccination using different techniques.

IGCS19-0747

123 DIFFERENTIALLY EXPRESSED PROTEINS AMONG NORMAL CERVIX, CERVICAL INTRAEPITHELIAL NEOPLASIA AND CERVICAL SQUAMOUS CELL CARCINOMA

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Objectives To explore the differentially expressed proteins in normal cervix, cervical intraepithelial neoplasia (CIN) and cervical squamous cell carcinoma (CSCC) tissues by differential proteomics technique.
Methods Cervical tissues (including normal cervix, CIN and CSCC) were collected in Department of Gynecologic Oncology of Beijing Obstetrics and Gynecology Hospital. 2-D DIGE) and DeCyder software were used to detect the differentially expressed proteins. MALDI-TOF/TOF MS was used to identify the differentially expressed proteins. WB and IHC were performed to validate the expressions of selected proteins among normal cervix, CIN and CSCC.
Results 46 differentially expressed proteins were differentially expressed among the normal cervix, CIN and CSCC. 26 proteins were successfully identified by MALDI-TOF/TOF MS. S100A9 was the most significantly up-regulated protein. eEF1A1 was the most significantly down-regulated protein. The results of WB showed that with the increase in the severity of cervical lesions, the expression of S100A9 protein was significantly increased among the three groups ($P = 0.010$). IHC showed that protein S100A9 was mainly expressed in the cytoplasm, and its positive expression rate was 20.0% in normal cervix, 70.0% in CIN and 100.0% in CSCC, with a significant difference among them ($P = 0.006$).
Conclusions There are differentially expressed proteins among normal cervix, CIN and CSCC. S100A9, eEF1A1 and PKM2 may become candidate markers for early diagnosis of cervical cancer and new targets for therapy. It also provides a basis for further studies of the mechanism for CIN developing to CSCC.

Breast

IGCS19-0658

124 BREAST CANCER IN YOUNG WOMEN: CLINICO-PATHOLOGICAL FEATURES OF 27 CASES

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Objectives Analyze the clinico-pathological features of breast cancer occuring in young women under 30 years.