There were not intraoperative complications Orthotopic ileas reconstruction is a complex technique, but it allows a more anatomical reconstruction, avoids the creation of stoma with less impact on the quality of life. It requires integrity of the sphincter and bladder neck and should be assessed and discussed thoroughly with the patient against other possibilities.
Conclusion* It is essential to balance the radicality of the best surgical result with the least posible impact on quality of life

Our next goal shoud be to obtain the best oncological results and survival with the minimum complications and consequences for our patients.

1131 CARTER DOUBLE-BARRELED WET COLOSTOMY AS A SURGICAL RECONSTRUCTION METHOD AFTER PELVIC EXENTERATION

T Echim*, Z Novák. *National Intitute of Oncology, Budapest, Hungary*

10.1136/ijgc-2021-ESGO.586

Introduction/Background* Carter double-barreled wet colostomy (DBWC) is an innovative technique frequently used for pelvic exenteration. The main advantage of this surgical approach is that it keeps the fecal and urine streams separate, thus avoiding fecal reflux and subsequently reducing the risk of ascending pyelonephritis.
Methodology Our aim was to investigate the impact BDWC on quality of life (QOL) after total pelvic exenteration. In our prospective study, self-reported QOL was assessed with the EuroQol 5 Dimensions (EQ5D) QOL questionnaire.
Result(s)* In 2019, two patients underwent total pelvic exenteration involving BDWC in our Institution. Both patients reported an improved QOL after surgery.
Conclusion* Altogether, our findings support the use of the relatively simple and safe DBWC technique in pelvic tumors. Nevertheless, further large-scale studies are warranted to investigate the impact of DBWC on short- and long-term postoperative outcomes, QOL and survival.

Translational research biomarkers

65 THE PROGNOSTIC SIGNIFICANCE OF EUKARYOTIC TRANSLATION INITIATION FACTORS (EIFS) IN OVARIAN CANCER

[1,2]M Sobočan*, [3]S Sprung, [3]C Schatz, [1,2]J Knez, [2,4]R Kavalar, [2,4]I Takač, [3,5]J Haybaeck. *[1]University Medical Centre Maribor, Division for Gynaecology and Perinatology, Maribor, Slovenia; [2]University of Maribor , Faculty of Medicine, Maribor, Slovenia; [3]Medical University of Innsbruck, Institute of Pathology, Neuropathology and Molecular Pathology, Innsbruck, Austria; [4]University Medical Centre Maribor, Department of Pathology, Maribor, Slovenia; [5]Medical University Graz, Diagnostic and Research Center for Molecular BioMedicine, Department of Neuropathology, Diagnostic and Research Institute of Pathology, Graz, Austria*

10.1136/ijgc-2021-ESGO.587

Introduction/Background* Ovarian cancer represents the most lethal gynaecological cancer. Although treatment options for patients with ovarian cancer have expanded, many patients suffer from disease relapse early after primary treatment. Different targeted therapies based on signalling pathways in ovarian cancer have yielded limited clinical success warranting the evaluation of further biological targets to improve therapy precision. A potential target is the machinery of protein synthesis, facilitated by eukaryotic initiation factors (eIFs). However, little is known about the role of eIFs in ovarian cancer. The aim of this study was to evaluate the role of different eIFs and their correlation to clinical outcome in ovarian cancer patients.
Methodology We performed immunohistochemical staining for the 6 eIF subunits (eIF1A1, eIF2alpha, eIF2G, eIF5A, eIF5B and eIF6) from samples of women diagnosed with epithelial ovarian cancer (EOC) at the University Medical Centre Maribor, Slovenia between January 2009 and December 2014. For all samples, a composite score of density and intensity of expression was calculated. Expression data was assessed in correlation to recurrence free survival (RFS) and overall patient survival (OS). The statistical analysis was performed using the Spearman rank correlation.
Result(s)* The cohort consisted of 75 women with EOC with a mean age of 61.2 years (SD 11.15). Disease specific death occurred in 74% of women (n=56) and disease recurred in 61% (n=47) women. The eIF subunit eIF5A (r_s=-.234, $p<0.043$) was found to be correlated with overall survival and recurrence free survival (r_s=-.247, $p>0.033$) in patients with EOC. An overexpression of eIF5A was significantly correlated with RFS (U=496.5, $p>0.017$) and OS (U=398.0, $p>0.006$).
Conclusion* Further evaluation of the initiation translation cascade in ovarian cancer and specifically the impact the expression of eIF5A has on EOC may be warranted. eIF5A may serve as a prognostic marker in EOC.

174 ANALYSIS OF CONSECUTIVE HIGH-GRADE SEROUS OVARIAN CANCER PATIENTS ALLOWS EFFICIENT CATALOGING OF BRCA1/2 MUTATIONS IN YET UNSTUDIED ETHNIC GROUPS

[1]A Sokolenko, [2]L Sultanova, [2]M Tovgereyeva, [3]E Suleymanov, [1]I Stepanov, [1]E Vasilyeva, [1]E Bakaeva, [1]E Imyanitov*. *[1]N.N. Petrov Institute of Oncology, St.-Petersburg, Russian Federation; [2]Chechen Republican Cancer Center, Grozny, Russian Federation; [3]Ministry of Health of Chechen Republic, Grozny, Russian Federation*

10.1136/ijgc-2021-ESGO.588

Introduction/Background* Approximately 15-30% high-grade serous ovarian carcinomas (HGSOCs) are caused by BRCA1/2 germ-line mutations. BRCA1/2 testing of consecutive HGSOC cases is logistically less complicated than the search for women with other clinical signs of BRCA1/2 syndrome (e.g., family history, young age or emergence of multiple cancers). We reasoned that this would be the most straightforward approach to identify ethnicity-specific mutations and investigated patients of Chechen origin. Chechens are a Northeast Caucasian ethnic group consisting of approximately 2 million people. This community is characterized by carefully preserved national and religious traditions, with a relatively low rate of interethnic marriage, and, consequently, high probability of persistence of founder alleles.
Methodology Coding sequences of *BRCA1, BRCA2, ATM, TP53 and PALB2 genes were analyzed by next generation sequencing*.
Result(s)* We initially included in the study 67 consecutive Chechen patients with HGSOC. Pathogenic BRCA1/2 alleles were detected in 12/67 (18%) HGSOC cases; all 8 women with BRCA1 mutation carried the same pathogenic variant (c.3627_3628delAG), while some genetic diversity was

Int J Gynecol Cancer: first published as 10.1136/ijgc-2021-ESGO.588 on 12 October 2021. Downloaded from http://ijgc.bmj.com/ on April 24, 2024 by guest. Protected by copyright.

observed among BRCA2 heterozygous patients (p.Q3299X: n = 2; c.5345dupA: n = 1; c.7408_7409delTT: n = 1). Given the high frequency of mutations in BRCA1 gene, we added to the study 44 consecutive patients with triple-negative breast cancer. This effort relied on the fact, that BRCA1 is specifically associated with the triple-negative phenotype of breast cancer disease; 3 (7%) additional BRCA1 mutation carriers (c.3627_3628delAG: n = 2; c.1338_1339delAG: n = 1) were revealed. All patients with the BRCA1 c.3627_3628delAG pathogenic variant also carried linked c.1067G>A (p.Q356R) polymorphic substitution; therefore, BRCA1 c.3627_3628delAG is indeed a founder allele, but not a mutational hot spot. In addition to BRCA1/2, one HGSOC patient carried ATM truncating variant (p.Q1171X). There were no instances of PALB2 or TP53 germline alterations.

Conclusion* This is a small-scale study, which resulted in convincing demonstration of a strong founder effect in Chechen women with hereditary breast-ovarian cancer. Genetic testing of non-selected HGSOC patients allows highly efficient analysis of ethnicity-specific spectrum of BRCA1/2 mutations.

319 GYNECOLOGIC MALIGNANCIES IN THE ERA OF PRECISION MEDICINE

M Mantiero*, M Ducceschi, M Bini, S Lopez, M Duca, S Damian, A Ditto, F Martinelli, U Leone Roberti Maggiore, G Bogani, M Signorelli, F Bertolina, V Chiappa, B Paolini, L Agnelli, F Raspagliesi. *Fondazione IRCCS Istituto Nazionale dei Tumori di Milano, Milan, Italy*

10.1136/ijgc-2021-ESGO.589

Introduction/Background* Personalized medicine is replacing the classical one-size-fits-all traditional oncology approaches tailoring the most appropriate therapy for each patient. Molecular and genomic profiling diagnostic tools are implementing patients' journey.

Methodology This is a single centre prospective study performed from January 2020 and April 2021 at Fondazione IRCCS Istituto Nazionale dei Tumori di Milano (Italy). All consecutive, heavily pretreated patients, for whom effective conventional treatments were not available, were enrolled in this study and underwent molecular and genomic profiling via Foundation One CDx test.

Result(s)* Overall, 63 heavily pretreated patients had Foundation One CDx test. We identified 10 patients (16%) with mutation or genetic signatures candidate to use personalized therapy (table 1). Out of 10 patients, 4 are patients affected by cervical, 4 by endometrial and the remnant are affected by ovarian carcinoma. Actually 1 patient is receiving immunotherapy with atezolizumab plus anti-ICOS and 1 is undergoing evaluation in order to start same drugs; 2 patients with ovarian cancer had BRAF/V600E mutations and are ongoing on treatment with trametinib +/- dabrafenib; 2 patients with cervical cancer had PI3KCA mutations and are treating with alpelisib. Furthermore, in 4 patients an actionable mutation was found but standard chemotherapeutic treatment is still ongoing (Table 2).

Immunotherapy and target therapy are administered into the clinical trial or thank to compassionate use.

Conclusion* Molecular and genomic profiling of gynecological malignancies is not clinical practice. We demonstrated that in this population identified alterations, by genetic driver, could help to find a new therapeutically opportunity. This allows to identify predictive biomarkers for target therapies in order to offer new therapeutic prospective for our gynecologic patients.

Abstract 319 Table 1 Global patients

Patients total N (%)	63 (100)
Age median (range)	59 (29-78)
Primary tumor	17 (27)
Ovarian carcinoma	5 (8)
Endometrial carcinoma	33 (52)
Cervical carcinoma	4 (6)
Uterine sarcoma	1 (2) 2 (3)
Vaginal carcinoma	
Bartholin's gland adenocarcinoma	
Target therapy	10 (16)

Abstract 319 Table 2 Molecular characteristics & target therapy

Patient	Age	Pathology	Mutation	Target therapy
1	77	Clear cell endometrial carcinoma	mut. L755S ERBB2	Evaluable for Afatinib
2	67	High grade serous ovarian carcinoma	Mut. V600E BRAF	Ongoing Dabrafenib + trametinib
3	54	Squamous cervical carcinoma	HPV at ISH	Ongoing Atezolizumab + anti ICOS
4	52	Endometrial carcinosarcoma	MSI	Evaluable for Atezolizumab
5	71	Endometrial carcinoma	Mut R88Q PI3KCA	Evaluable for Everolimus + exemestane
6	30	Mucinous cervical adenocarcinoma	splice site (134 +1G>T) PTEN	Evaluable for Everolimus
7	60	Low grade serous ovarian carcinoma	Mut. V600E BRAF	Ongoing Trametinib
8	41	Squamous cervical carcinoma	Mut p.E545K PI3KCA	Ongoing Alpelisib
9	71	Endometrioid Endometrial carcinoma	Mut. Q546P PI3KCA	Evaluable for Alpelisib
10	39	Neuroendocrine cervical cancer	Mut p.E545K PI3KCA	Ongoing Alpelisib

323 CHARACTERISATION OF INTRA-TUMOURAL HETEROGENEITY IN HIGH GRADE SEROUS OVARIAN CANCER

[1]P Cunnea*, [1]E Curry, [2]E Christie, [1]K Nixon, [1]CH Kwok, [1]J Ploski, [2]D Bowtell, [1]C Fotopoulou. *[1]Imperial College London, Hammersmith Campus, London, UK; [2]Peter MacCallum Cancer Centre, Melbourne, Australia*

10.1136/ijgc-2021-ESGO.590

Introduction/Background* High-grade serous ovarian cancer (HGSOC) is typified by extensive genomic instability and intra-tumoural heterogeneity (ITH). The majority of patients relapse and eventually acquire resistance to platinum-based chemotherapy. Diverse mechanisms leading to platinum

Int J Gynecol Cancer: first published as 10.1136/ijgc-2021-ESGO.588 on 12 October 2021. Downloaded from http://ijgc.bmj.com/ on April 24, 2024 by guest. Protected by copyright.