Introduction/Background Ovarian cancer ascites is one of the signs of ovarian cancer (OC) metastatization in the peritoneum and is found in patients at the time of diagnosis and in disease relapse. This serous fluid is used for the initial cytopathological diagnosis and is frequently drained from the peritoneal cavity at advanced stages only for symptomatic relief (and is discarded). In the ovarian cancer context, the presence of ascites is a unique opportunity to monitor the tumor kinetics during disease progression without additional invasive procedures. The main aim of this work was to evaluate the potential of this usually discarded biological material to evaluate the expression of proteins associated with therapy resistance in ovarian cancer ascites cells during disease progression.

Methodology We received ascites from OC patients at diagnosis (n=7) and during treatment (n=8). After centrifugation, samples were formalin-fixed and embedded in Histogel before standard histological processing. Next, immunocytochemistry was performed to assess the expression of three biomarkers associated with chemoresistance in ovarian cancer (ALDH1, SOX2, and Pgp).

Results The majority of our samples had a sufficient number of cells to perform a diversity of histological-based techniques and other molecular studies. The expression of cancer stem cell markers ALDH1 and SOX2 was frequently negative. However, SOX2 and ALDH1 were expressed in samples obtained after chemotherapy. Multi-drug resistance marker (Pgp) expression was negative in samples at diagnosis but was found positive, especially in samples from patients with refractory ascites and without clinical response to treatment.

Conclusion The multidimensional potential ovarian cancer ascites as a spontaneous ‘liquid biopsy’ remains underexplored. Our results show that the use of immunocytochemistry to evaluate resistance biomarkers in tumor cells present in ascites drained from patients during treatment has the potential to predict response to treatment.

Introduction/Background It’s very important to identify individuals with high genetic risk of developing cancer for prevention of familial ovarian cancer forms, their follow-up management and timely preventive care. A burdened family history (BFH) of cancer is unquestionable and most important indication for genetic testing. Objective: To assess the BFH in patients with ovarian cancer (OC), fallopian tube carcinoma (FTC), primary peritoneal carcinoma (PPC).

Methodology All women with OC, FTC and PPC, who treated at oncogynecologic department N.N. Alexandrov National Cancer Centre of Belarus between January 2022 and May 2022 were retrospectively identified. The main criteria were serous carcinoma, endometrioid carcinoma and clear cell carcinoma. All patients filled out BFH questionnaires. Analysis of the normality of data distribution was carried out on the basis of the Shapiro-Wilk’s W test. The Mann-Whitney U-test was used to compare two independent samples.

Results A total of 92 patients were analyzed: 81 patients with OC, 9 with FTC, 2 with PPC. The mean was 54.5 years, high grade serous carcinoma was the predominant (87%). The majority of patients were of Belarusian (93.5%). 53 (57.6%) women were in menopause at the time of diagnosis, in premenopause was less (28.3%). Most of the study participants had pregnancies, children, lactation were noted (88.0%, 84.8%, 71.7%, respectively). Only 15.2% of women indicated the use of contraceptives. A BFH was noted in 58 (63.0%) patients, it was absent in 34 (17%) patients. The average age of women with a BFH was 53.2 years, without – 56.7 years. There were no statistically significant differences in the groups of patients without and with a BFH, depending on age, diagnosis, histological variant of the tumor (p>0.05).

Conclusion Presence of burdened family history revealed in most cases (63% patients with OC, FTC, PPC) requires further genetic testing.

Introduction/Background The low response rates to traditional systemic therapies prompts the need for novel therapies in the treatment of LGSC. LGSC tumors have demonstrated a high frequency of mutations in the MAPK cascade, which is targeted by MEKi. The primary objective of this systematic review was to assess the overall response rate (ORR) of LGSC to MEKi.

Methodology Pubmed, EMBASE, Medline and the Cochrane Database were searched from inception to March 2022. Inclusion criteria were studies assessing the treatment of LGSC in the primary or recurrent setting with the use of a MEKi, published in English. Case reports, case series, conference proceedings, in vitro studies and animal studies were excluded. Studies were screened and assessed for eligibility by two independent reviewers (AK, CC), with conflicts resolved by a third reviewer (TZ). Data was extracted using pre-established criteria.