IGCS19-0361

228 FACTORS ASSOCIATED WITH LYMPHEDEMA AFTER TREATMENT FOR UTERINE CERVICAL NEOPLASMS: A SYSTEMATIC REVIEW

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Objectives Realize a systematic literature review of studies that identified factors associated with lymphedema after treatment for uterine cervical neoplasms.

Methods A systematic review of the literature was performed according to the PRISMA guidelines. Eligible studies were identified through the databases Medline (via PubMed), LILACS, Scopus and Web of Science. For the search, we used descriptors, keywords and synonyms for: uterine cervical neoplasms, lymphedema and outcomes of interest (incidence, prevalence, frequency, occurrence, morbidity, risk factors and prognosis). We included cross-sectional, retrospective or prospective cohort studies, or case-control studies, published in the English, Portuguese or Spanish languages, with frequency data and risk factors for lymphedema after uterine cervical neoplasms treatment.

Results Fifteen studies were included in the review. The risk factors for lymphedema included adjuvant radiotherapy, removal of circumflex iliac lymph nodes, retroperitoneal closure, open surgical procedure, cellulitis, post-surgery lymphocytes, BMI $\geq$ 25 kg/m^2, pelvic and para-aortic lymphadenectomy.

Conclusions The different delineations and methodologies employed by the authors make it difficult to compare them and may interfere with the frequency and risk factors associated with lymphedema. There is no consensus on the best method used in the diagnosis of lymphedema and the risk factors are mainly associated with cancer treatment and obesity.

IGCS19-0371

229 GENETIC HETEROGENEITY OF OVARIAN SEX CORD-STROMAL TUMORS

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Objectives Sertoli-Leydig and granulosa cell tumors are sex cord-stromal tumors of the ovary that primarily impact young women. Adult-type granulosa cell tumors (aGCTs) are characterized by pathognomonic somatic *FOXL2* mutations, whilst 30–60% of Sertoli-Leydig cell tumors (SLCTs) harbor *DICER1* mutations. A comprehensive assessment of the repertoire of genomic alterations of sex cord-stromal tumors has yet to be performed.

Methods Primary SLCTs (n=2), juvenile (j)GCTs (n=2) and a primary and matched mixed SLCT/aGCT recurrence (n=2) were subjected to whole-exome sequencing. Somatic mutations and copy number alterations were defined using state-of-the-art bioinformatics algorithms.

Results Ovarian sex cord-stromal tumors displayed a low mutational burden, with a median of 22 (range 13–82) somatic mutations. Mutational analysis revealed the presence of a *DICER1* p.R293lfs*4 frameshift mutation in the pure SLCT. A *FOXL2* p.C134W hotpot mutation was identified in the primary and recurrent mixed SLCT/aGCT; in addition, *LAMA5*, *ZNF837*, and *HCFC1* missense mutations and an *UBR2* splice-site mutation were present only in the mixed recurrence but absent in the primary mixed SLCT/aGCT. Neither of the two jGCTs harbored *FOXL2* or *DICER1* mutations, and none of the identified somatic mutations and copy number alterations were shared between the two jGCTs. jGCT1 harbored *GATA4* p.L281M/Q missense mutations and copy number gains of chromosomes 4 and 8, whereas jGCT2 displayed *a TOPAZ1* p.K335R missense mutation and chromosome 12 and 18 gains.

Conclusions Sex cord-stromal tumors are a genetically heterogeneous group of rare ovarian neoplasms. Larger studies to assess whether jGCTs harbor recurrent genetic/epigenetic alterations are warranted.

IGCS19-0217

230 REFERRAL PATTERNS AND UPTAKE OF RISK REDUCING SURGERY FOR NON-BRCA GENES ASSOCIATED WITH INCREASED RISK OF EPITHELIAL OVARIAN CANCER

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Objectives To identify referral patterns and uptake of risk reducing surgery (RRS) in patients with non-*BRCA* genes associated with an increased risk of epithelial ovarian cancer.

Methods A chart review of patients with mutations in *MLH1, MSH2, EPCAM, MSH6, PMS2, RAD51C/D, BRIP1* was conducted from 2015–2018. Patients with *BRCA1/2* and variants of uncertain significance were excluded; *MSH6 and PMS2* were included (though recent change to insufficient evidence). Primary outcomes of interest were referral to a gynecologic oncologist and the uptake of RRS.

Results Of 78 patients, 18 had undergone surgical management for treatment of cancer prior to genetic testing and were excluded. The majority of the patients (41 of 60, 68%) with non-*BRCA* actionable mutations were associated with Lynch Syndrome (LS). Of these patients, 23 of 60 (56%) were seen by gynecologic oncologists. Twenty of 41 (49%) underwent RRS. Excluding the *MSH6* and *PMS2* patients, 9 of 21 (43%) of patients with LS underwent RRS.

Among patients with the non-*BRCA* and non-LS associated genes (*RAD51C, RAD51D, BRIP1*) the most common reason for testing was family history of cancer (10 of 19). Fifteen of 19 were referred to a gynecologic oncologist; all patients with *BRIP1* mutation were referred, while 70% of those with *RAD51/D* were referred. Among this subset of patients, 9/19 (47%) patients underwent RRS; the remaining patients were screened with surveillance ultrasounds and/or CA-125.

Conclusions Two-thirds of patients with non-*BRCA* genes associated with increased risk of ovarian cancer were referred to gynecologic oncologists, with a 48% of uptake or RRS.

IGCS19-0639

231 RISK FACTORS FOR LYMPH NODES INVOLVEMENT IN OBESE WOMEN WITH ENDOMETRIAL CARCINOMAS

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Objectives To assess risk factors for lymph node involvement in patients with endometrial cancer and a body-mass index (BMI) $\geq$30 kg/m^2.

Methods A retrospective analysis was performed of obese patients diagnosed with endometrial carcinoma between 2007 and 2015, treated in a single center in Montreal. Preoperative variables evaluated were age, BMI, parity, and preoperative ASA score, grade, CA-125 and histology. Odds ratios (OR) and hazard ratios (HR) and their respective 95% confidence intervals (95%CI) were calculated using multivariable logistic regression and Cox proportional hazard models.

Results The study included 230 women with BMI >30, 223 (97.0%) had complete staging. Pelvic lymph node involvement was detected in 26 patients (11.3%). Sentinel node detection and pelvic lymph node dissection decreased with increasing BMI (adjusted OR 0.86, 95% CI 0.76–0.97 and 0.76, 95%CI 0.59–0.96, respectively, per 1 kg/m^2 increment). Pelvic lymph node involvement was inversely correlated with BMI (adjusted OR 0.88, 95% CI 0.79–0.99) and present in 16/85 (18.8%), 6/56 (10.7%), and 4/82 (4.9%) of patients with a BMI of 30.0–34.9, 35.0–39.9, and $\geq$40.0 kg/m^2, respectively. Preoperative CA-125 was associated with lymph node involvement (adjusted OR 2.77, 95%CI 1.62–4.73, per quartile increment). During a median follow-up of 72 months, a higher BMI was not associated with worse recurrence-free survival (adjusted HR 1.04, 95%CI 0.98–1.10), disease-specific survival (adjusted HR 0.97, 95%CI 0.88–1.06), or overall survival (adjusted HR 0.92, 95% CI 0.84–0.99).

Conclusions Pelvic lymph node dissection might be omitted in selected cases of morbidly obese patients with failed sentinel nodes mapping and a low CA-125.

IGCS19-0642

232 SURGICAL WAIT TIME MIGHT IMPACT SURVIVAL IN SELECTED PATIENTS WITH ENDOMETRIAL CARCINOMA

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Objectives To determine whether surgical wait time impacts survival in patients with endometrial cancer (EC).

Methods A retrospective analysis was performed, including all patients diagnosed with EC between 2008 and 2015 treated in a single centre in Montreal. Associations between surgery wait times and other variables were calculated using univariable linear regression models. In survival analysis, Cox proportional hazard models were used to calculate hazard ratios (HR); covariates included age, BMI, year of diagnosis, ECOG score, and tumor histology, grade and stage at surgery.

Results The study included 358 patients with median follow-up of 5.9 years, categorized into four groups based on their wait time: 89, 87, 91, and 91 women with a median wait time of 37 days (8–49), 62 days (50–70), 91 days (71–103), and 91 days (104–869), respectively. Increased surgical wait time was associated with lymph-vascular space invasion and distant metastases. A surgery delay of 71 days or more (median) did not result in significantly worse overall (p=0.54) or EC specific survival (p=0.27), while known prognostic variables such as stage and grade at surgery did (p<0.05). In a subgroup analyses, patients with grade II tumors who had more than 71 days between biopsy and surgery (n=51) had significantly (P=0.037) more EC-related mortality (5-year cancer-specific survival 83.9%, versus 100% for those with surgery within 70 days). Similarly, surgery delay had impact on overall survival also in patients with BMI>30 (HR 1.43, 95% CI 1.00–2.03).

Conclusions While surgery delay might predict outcome in specific subgroups, biological tumor determinants seems more important for survival outcome.

IGCS19-0304

233 CLINICAL NEXT-GENERATION SEQUENCING PIPELINE FOR BRCA MUTATIONS PROVIDES TRACEBACK TO THE FAMILIES OF DECEASED OVARIAN CANCER PATIENTS

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Objectives Advances in Next Generation Sequencing (NGS) allow for multiple gene analysis in an efficient, cost-effective manner. Deceased ovarian cancer patients untested for germline BRCA mutations represent a missed opportunity for clinicians to prevent future cancers in their surviving relatives. Families of this lost cohort can benefit through Traceback initiatives. We sought to validate our London Health Sciences custom Hereditary Cancer Panel using formalin fixed paraffin embedded (FFPE) tumor samples to assess BRCA 1/2 status in a cohort of high grade serous ovarian cancer (HGSC) patients.

Methods FFPE samples from 150 deceased HGSC patients were assessed using an Illumina MiSeq sequencer with a mean coverage of 1000x and average minimum coverage of 700x when 24 samples were tested per run. Validation of a subset of identified variants was then undertaken using Sanger and Multiplex Ligation-dependent Probe Amplication (MLPA).