of patients (92.1%) were white. Eighty-four patients (81.4%) had lymph node macrometastases, 12 patients (11.7%) had MM, and 7 patients (6.8%) had ITCs. On univariate analysis, increasing tumor size, cervical involvement, increasing grade, type II histology, African American race, para-aortic involvement, and not using combination chemotherapy/radiation were associated worse survival ($p<0.05$). Predictors of lymph node involvement were increasing tumor size, depth of invasion, grade, and LVSI, but there was no predictor to distinguish MM/ITC from macrometastases. For depth of invasion <50%, size <2cm, no LVSI, there were no macrometastases or MM/ITC seen. Chemotherapy with radiation was the most common adjuvant regimen (chemo+RT - 78%, chemo only – 14%, RT only – 1%, none – 6%). No survival difference was seen in MM/ITC vs macrometastases ($p=0.79$).

Conclusions: The management of MM/ITC is unclear. We report that there is no predictor to distinguish macrometastases versus MM. Treatment, recurrence, and survival patterns did not differ significantly likely due to the majority of patients receiving combination therapy. Continued research is necessary to understand the impact of isolated MM/ITC to inform prospective study for treatment management of isolated MM/ITCs.

doi:10.1016/j.ygyno.2019.03.122

Poster #18

The impact of adjuvant treatment in intermediate risk, Stage I endometrial cancer with somatic CTNNB1 mutation

K.C. Kurnit[a], B. Fellman[a], S.S. Xie[a], J. Bowser[b], G.B. Mills[c], R. Broaddus[a]. [a]*The University of Texas MD Anderson Cancer Center, Houston, TX, USA,* [b]*The University of Texas Health Science Center at Houston, Houston, TX, USA,* [c]*Oregon Health and Science University, Portland, OR, USA*

Objectives: Somatic *CTNNB1* mutations have been associated with worse recurrence-free survival in low grade, early stage endometrial cancer patients. We hypothesized that the use of current adjuvant therapy strategies would improve survival outcomes in *CTNNB1* mutant early stage endometrial cancer patients.

Methods: Patients with Stage I endometrioid endometrial cancer who received care at our institution were included in this study. Demographic and clinical information were obtained by review of the electronic medical record. *CTNNB1* mutation status was determined using either next-generation sequencing panels or focused Sanger sequencing of exon 3 of the *CTNNB1* gene. Comparative statistics were used to compare baseline characteristics, and Kaplan-Meier product limit estimator was used to determine recurrence-free survival (RFS).

Results: 253 Stage I endometrial cancer patients were identified. Of these, 45 (18%) had *CTNNB1* mutations. In patients with low risk endometrial cancer (no LVSI, no or superficial myometrial invasion less than 50% myometrial thickness, grade 1-2) who did not receive adjuvant therapy, *CTNNB1* mutation status was not associated with significantly worse RFS (8.1 vs. 11.3 years, $p=0.64$). However, in patients with deep myometrial invasion and/or LVSI with any histologic grade ($n=71$), the presence of a *CTNNB1* mutation was associated with shorter RFS (2.4 vs 8.5 years, $p = 0.01$). Furthermore, those patients with somatic *CTNNB1* mutations who did not receive adjuvant therapy demonstrated the worst RFS (Table 1). Of the 5 patients with somatic *CTNNB1* mutations who received adjuvant therapy, all received radiation (3 brachytherapy only, 2 pelvic radiation and brachytherapy).

Conclusions: In Stage I endometrioid endometrial cancer patients with intermediate risk factors, treatment of patients whose tumors harbor *CTNNB1* mutations resulted in improved recurrence-free survival. Molecular characteristics including *CTNNB1* mutation status should be incorporated into adjuvant therapy treatment algorithms. Prospective trials such as PORTEC4a can help elucidate which adjuvant therapies are most beneficial.

doi:10.1016/j.ygyno.2019.03.123

Poster #19

Hypermethylation testing to identify Lynch Syndrome in endometrial cancer patients: Is it worth it?

K. Tyrie[a], L. Drury[a], K. Dumas[b], L. Amacker-North[a], K. Warsinske[a], R.W. Naumann[a], D.L. Tait[a], E.K. Crane[a], A.B. Drummey[a], J. Brown[a]. [a]*Levine Cancer Institute, Carolinas Medical Center, Charlotte, NC, USA,* [b]*Greenville Health System, Greenville, SC, USA*

Objectives: To determine if MLH1 promoter hypermethylation (HM) testing of endometrial cancer (EC) is a cost-effective triage strategy for Lynch Syndrome (LS) testing.

Methods: We constructed a decision analysis to compare cost-effectiveness of 3 screening strategies: (1) no immunohistochemistry (IHC) testing, with referral for genetic testing (GT) based on Bethesda criteria (BC) alone; (2) IHC alone with no HM testing, with referral for GT based on BC or abnormal IHC testing; or (3) IHC and reflex HM testing, with referral for GT based on BC or abnormal IHC testing with negative HM. To evaluate the cost associated with each strategy, data from all consecutive patients with primary EC treated by gynecologic oncologists within one system from 2013-2017 were used to populate the model. Pts were identified through the institutional cancer registry and departmental billing records; data was extracted from the medical record. Costs were obtained for each branch point at which reimbursement occurred. Cost/life years (LY) saved and cost/quality-adjusted (QA) LY were calculated for each testing option based on published insurance reimbursement rates, cost data, and institutional reimbursement data. Results were compared using a one-way ANOVA for the three screening strategies.

Results: We identified 1208 eligible pts. In our system, 282 pts had no IHC or HM; 876 pts had IHC but no HM; and 50 had IHC with reflex HM. Of the 282 pts with no IHC or HM, 33% of pts complied with GT when indicated and 1 case of LS was identified. In the second group of 876 pts with IHC but no HM, 698 pts had normal IHC and GT was indicated in 45 of these pts with 0 cases of LS identified. In the 178 pts with abnormal IHC, 100 pts were compliant with GT and 13 cases of LS were identified. In the last group of 50 pts with IHC and reflex HM, 1 had abnormal IHC without HM, and she underwent GT and had LS. Including downstream testing, the cost/case of LS identified with each modality was $4000, $24,178, and $17,000 respectively. The cost/QALY gained in each modality was $3235, $4895 and $3486 respectively. The percentage of pts referred for GT was 22%, 41%, and 22% respectively.

Conclusions: The cost/QALY gained for each of the 3 testing algorithms was acceptable. Although IHC +/- HM was more expensive than no IHC testing, the number of unnecessary GT visits was lower when reflex HM was incorporated. The optimal cost-effective triage strategy to detect LS in pts with EC that preserves the scarce resource of GT appears to be IHC with reflex HM testing.

doi:10.1016/j.ygyno.2019.03.124

Poster #20

Endometrial cancers in BRCA1 or BRCA2 germline mutations carriers

E. Smith, A.D.C. Paula, D. Mandelker, B. Weigelt. *Memorial Sloan Kettering Cancer Center, New York, NY, USA*

Objectives: Bi-allelic alterations in *BRCA1* or *BRCA2* (*BRCA1/2*) are associated with genomic features of homologous recombination DNA (HRD) repair deficiency. We aimed to determine if endometrial cancers (ECs) arising in *BRCA1/2* germline mutation carriers harbor bi-allelic alterations and/or features of HR deficiency.

Methods: EC patients with *BRCA1/2* germline mutations whose tumors were subjected to a) massively parallel sequencing targeting 410 cancer-related genes under an IRB-approved protocol (n=7) and b) whole-exome sequencing (WES) by The Cancer Genome Atlas (n=3) were identified. Sequencing data were analyzed to define somatic mutations, copy number alterations, loss of heterozygosity (LOH) and microsatellite instability (MSI); in cases subjected to WES, genomic features of HRD were assessed.

Results: Of the 10 ECs included, 6 and 4 were from patients with pathogenic *BRCA1* and *BRCA2* germline mutations, respectively. The median age at EC diagnosis was 60 years (range 44-78). The ECs were of various histologic types, including endometrioid (grade II, n=1; grade III, n=5), serous/clear cell (n=2) and carcinosarcoma (n=2). Staging information was available for 8 cases, and ECs presented at all stages (stage I, n=3; stage II, n=1; stage III, n=3; stage IV, n=1). Allele-specific copy number analysis revealed that 5 (83%) and 1 (25%) ECs harbored bi-allelic *BRCA1* and *BRCA2* alterations, respectively, uniformly through LOH of the wild-type allele. All ECs analyzed, irrespective of the presence of mono- or bi-allelic *BRCA1/2* alterations, harbored somatic *TP53* mutations. Of note, one *BRCA1* and one *BRCA2* EC with mono-allelic alterations had a high mutational burden and were MSI-high by MSIsensor. The three ECs subjected to WES harbored *BRCA1* bi-allelic alterations, were of grades II and III endometrioid subtype, and displayed genomic features of HRD, including high large-scale transition scores and a dominant mutational signature 3.

Conclusions: Our findings demonstrate that a small subset of patients with ECs arising in patients with pathogenic germline *BRCA1/2* mutations harbor bi-allelic alterations, and may benefit from HR-directed treatment regimens. Another subset of *BRCA1/2*-associated ECs, however, may be sporadic and MSI-high.

doi:10.1016/j.ygyno.2019.03.125

Poster #21

Clinical outcomes of patients with pole mutated endometrioid endometrial cancer

I.U. Tunnage[b], M. Stasenko[a], C.W. Ashley[a], M. Rubinstein[a], A.J. Latham[a], J.J. Mueller[a], M.M. Leitao Jr[a], C.F. Friedman[a], V. Makker[a], R.A. Soslow[a], B. Weigelt[a], D. DeLair[a], D.M. Hyman[a], C.A. Aghajanian[a], N.R. Abu-Rustum[a], K.A. Cadoo[a]. [a]*Memorial Sloan Kettering Cancer Center, New York, NY, USA,* [b]*Georgetown/Washington Hospital Center, Washington, DC, USA*

Objectives: Data from the selected patients (pts) included in The Cancer Genome Atlas suggested that somatic *POLE*endonuclease domain (END) hotspot mutation (mut) associated endometrioid endometrial cancers (EEC) have a better prognosis. We sought to describe the outcomes of a clinical cohort of pts with this mut profile.

Methods: Pts provided consent to an IRB approved protocol of tumor-normal sequencing via a custom massive parallel sequencing platform (MSK-IMPACT) that identifies somatic genomic alterations in 468 cancer genes. We captured all EEC sequenced 2014 - 2018 with a somatic *POLE* END hot spot muts: A456P, V411L, P286R, F367V. All tumors were assessed for microsatellite instability (MSI) via MSIsensor and had immunohistochemical (IHC) staining for mismatch repair (MMR) proteins. Clinical data was abstracted and descriptive statistics were employed.

Results: 451 EEC tumors were sequenced; 22 had *POLE*- END mut (5%). Primary tumor was sequenced in 19 cases (86%) and recurrent in 3 (14%). 17 (77%) were stage 1, 3 (14%), stage III and 2 (9%) had de novo stage IV tumors. 12 had low- and 10 high-grade tumors (55, 45%, respectively). 21 pts had surgery (95%) and 1 had neoadjuvant chemotherapy then surgery (5%). 16 pts (73%) received adjuvant radiation therapy (RT) with or without chemotherapy, and 6 (27%) stage I, low-grade tumors had no adjuvant therapy.

Tumors had a median of 161 muts (range 39-527). MMR protein IHC were retained in 18 (82%). 1 tumor (5%) had loss of MLH1/PMS2, with MLH1 hypermethylation. 4 (18%) had MSH6 IHC loss, of which, 3 had dual somatic MSH6 muts potentially underpinning the phenotype, 1 had a single MSH6 and single PMS2 mut in addition to the POLE mut. None had Lynch syndrome. MSIscores were obtained: 19 were microsatellite stable (MSS), 2 MSI-high, 2 MSI-indeterminate.

There were 4 recurrences: 2 pts with initial stage I disease, 2 with stage III. All were treated with a combination of surgery, chemotherapy, and RT. After a median follow up of 21 mo, all pts was alive, 3 with evidence of disease.

Conclusions: In this clinical cohort of pts with *POLE* mutant EEC, de novo metastatic disease was noted and recurrences were seen in 4 cases. These tumors are hyper/ultra - mutated phenotype with most being MSS and MMR proficient. Further research is needed to evaluate if *POLE*EDM mutant EEC are susceptible to immunotherapy.

doi:10.1016/j.ygyno.2019.03.126

Poster #22

Postoperative survival analysis of laparotomy vs robotic interval debulking in epithelial ovarian cancer patients following neoadjuvant chemotherapy

S.E. Paraghamian, A. Staley, K. Tucker, Y. Zhang, M. Wang, L.H. Clark. *University of North Carolina at Chapel Hill, Chapel Hill, NC, USA*

Objectives: Neoadjuvant chemotherapy (NACT) is a commonly utilized strategy for primary treatment of advanced epithelial ovarian cancer (EOC) in women with unresectable disease or poor surgical candidates. Minimally invasive surgery offers several advantages, including decreased postoperative morbidity, shorter hospitalization, and faster recovery; however, there are limited published data to demonstrate that these advantages are also balanced by non-inferior survival or improved time to adjuvant chemotherapy. Thus, we sought to assess if there is a difference in time to disease recurrence as well as time to adjuvant chemotherapy in robotic (RA) versus open (OA) interval debulking surgeries (IDS).

Methods: We performed a retrospective review of EOC patients diagnosed and treated with 3-6 cycles of NACT with platinum and taxane chemotherapy followed by IDS from January 2014 through February 2017. Demographic, clinicopathologic, and treatment data were recorded from review of records from a single tertiary care institution. Survival analysis with Kaplan-Meier estimation with Wilcoxon rank test for significance were utilized for statistical assessment.

Results: Forty-seven patients met inclusion criteria from the initial cohort of 207 patients. Thirteen (28%) underwent RA and 34 (72%) underwent OA IDS. In comparing the RA vs OA groups, there were non-significant differences in age (60 vs 64 yrs, $p = 0.23$); rate of Stage IV disease (62% vs 44%, $p = 0.29$); rate of debulking to no gross residual (46% vs 59%, $P = 0.43$); and rate of complete response on preoperative imaging (31% vs 12%, $p = 0.12$). There was no difference in time to disease recurrence in the RA vs OA groups (8.9 vs 7.9 months, $p = 0.7$). There was no difference in time to adjuvant chemotherapy between the two arms (29.7 vs 33.3 days, $p = 0.97$).