**Introduction**

The growing adoption of molecular and genomic characterization is changing the current landscape of treatment of endometrial cancer (EC) patients. Using the surrogate molecular classification EC patients are classified in four subgroups: POLE mutated, MMRd/MSI-H, p53 abnormal, and NSMP, respectively. Among those 31 patients, six had postoperative adjuvant therapies, and no recurrence occurred (median follow-up: 10.5 months (seven patients had at least 2-year follow-up)). Forty-one (56.9%) patients were diagnosed with tumors harboring both p53 plus MMRd/MSI-H. Adjuvant therapy was administered in 25/41 patients (60.9%). Four (9.8%) recurrence occurred after a median follow-up of 8.9 months (eleven non-recurring patients had at least 2-year follow-up).

**Conclusion/Implications**

Multiple classifier EC are characterized by a good prognosis. POLE mutation seems confer protection in multiple classifier EC even in case of presence of MMRd/MSI-H and/or p53 abnormality. Prospective studies with long-term follow-up are needed.

**Results**

Charts of 210 EC patients were evaluated. The study population included 178 (85%) and 32 (15%) patients with endometrioid and non-endometrioid EC, respectively. According to conventional pathological uterine characteristics, 94, 46, 41, and 32 were classified as low, intermediate, intermediate-high, and high-risk, respectively. According to molecular classification 10 (5%), 42 (20%), 57 (27%), and 101 (48%) were included in the POLE mutated, p53 abnormal, MMRd/MSI-H, and NSMP, respectively. Overall, 41 (19.5%) patients were detected with positive nodes. Molecular features were not associated with the risk of having nodal metastases (OR: 1.03 (95%CI: 0.21, 5.95; p=0.969) for POLE mutated; OR: 0.788 (95%CI: 0.32, 1.98; p=0.602) for p53 abnormal; OR: 1.14 (95%CI: 0.53, 2.42); p=0.733 for MMRd/MSI-H). At multivariate analysis, only myometrial invasion (OR: 3.33 (95%CI: 1.40,7.80); p=0.006) and LVI (OR: 6.03 (95%CI: 2.56, 15.4); p<0.001) correlated with nodal status. A nomogram evaluating the impact of pathological and molecular features on nodal status was built (C-index 0.78, figure 1).

**Conclusion/Implications**

Our prospective study suggested that molecular features seem not helpful in tailoring the need for nodal dissection in EC. Further external validation is warranted.

**Introduction**

To explore the clinical value of dual gene (CDO1 and CELF4) methylation test for endometrial cancer in women with abnormal uterine bleeding.

**Methods**

From July to June 2022, 216 female patients with abnormal uterine bleeding were enrolled in the gynecologic clinic of Gansu Provincial Woman & Child Medical Center. The exfoliated cervical cells were collected for dual gene methylation detection, and the basic information, tumor biological markers, and endometrial thickness of patients were collected. The clinical statistics of dual gene methylation detection for endometrial cancer in women with abnormal uterine bleeding were analyzed.

**Results**

The following factors were associated with endometrial cancer in univariate analysis: age, BMI, diabetes mellitus, number of births, menopause, CDO1 methylation, and CELF4 methylation (all p < 0.001). Binary logistic regression analysis showed that BMI, diabetes mellitus, menopause, CDO1 methylation, and CELF4 methylation were independent risk factors for endometrial cancer (OR: 4.062, 3.504, 17.484, 20.555, and 66.599, respectively). The dual gene methylation assay had a sensitivity and specificity of >90% and >95%, respectively. The sensitivity and specificity of endometrial thickness by ultrasound and CA125 were <60% and <80%, respectively. Dual gene methylation detection is more sensitive and specific than the current gynecological examination for the detection of endometrial cancer.