node mapping 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: 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 LVSIs (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.

EP109/#1527 THE APPLICATION VALUE OF DUAL GENE METHYLATION DETECTION FOR ENDOMETRIAL CANCER IN WOMEN WITH ABNORMAL UTERINE BLEEDING

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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 biomarkers, 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.

Conclusion/Implications Using non-invasive dual gene methylation assay to screen women with suspected endometrial cancer of abnormal uterine bleeding for hysteroscopy may reduce the risk of endometrial cancer and improve the ability of the clinic to perform noninvasive early detection, it also reduces the need for repeated invasive hysteroscopy in women.