micrometastasis and macrometastasis, respectively, as the largest type of metastasis. MRI and EUS showed comparable sensitivity for tumour size measurement and for the failure to detect parametrial, or macrometastatic LN involvement (table 1). Combining both imaging methods did not increase the outcome (table 1).

Conclusion Pelvic MRI and EUS are equally sensitive methods for assessing clinically relevant parameters in preoperative clinical staging of cervical cancer, including tumour size, parametrial involvement, and macrometastatic nodal involvement.

Disclosures The authors declare no conflict of interest.

Trial registration ClinicalTrials.gov: NCT02494063

Abstract #451 Table 1 Sensitivity of pelvic MRI and EUS in preoperative staging of patients with cervical cancer

		EUS only	MRI only	MRI+EUS	p
Parametrial involvement based on pathology *	Yes	9 (3.6%)	15 (5.0%)	2 (3.1%)	0.687
	No	239 (96.4%)	286 (95.0%)	62 (96.9%)	
Macrometastatic lymph node involvement based on pathology	Yes	18 (6.0%)	19 (5.96%)	4 (5.8%)	0.876
	No	280 (94.0%)	303 (94.04%)	66 (94.2%)	
Tumour size assessment**	<5 mm	231 (77.52%)	242 (75.16%)	51 (72.86%)	0.452
	5–10 mm	33 (11.07%)	35 (10.87%)	7 (10.0%)	
	10–20 mm	23 (7.72%)	35 (10.87%)	10 (14.29%)	
	>20 mm	11 (3.69%)	10 (3.11%)	2 (2.86%)	

*Only patients who underwent parametrectomy.

**Discrepancy between the largest tumour size assessed by preoperative imaging and final pathology.

EUS: expert ultrasound; MRI: magnetic resonance imaging.

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#827 APPLICATION OF PAX1 AND JAM3 GENE METHYLATION DETECTION AS A TRIAGE TOOL FOR CERVICAL CANCER SCREENING IN WOMEN: ANALYSIS OF A SINGLE-CENTER PROSPECTIVE STUDY IN CHINA

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Introduction/Background Currently, cervical cytology and HPV DNA testing are the most widely employed methods. However, these screening approaches possess inherent advantages and limitations that contribute to overdiagnosis or overuse of colposcopy, as over 30% of cases with CIN2, CIN3, and invasive cancers remain indistinguishable through cytology alone.

Methodology A total of 549 participants were enrolled in the study. Cervical brush sampling was performed on all participants to collect cervical exfoliated cells. These cells were then subjected to analysis using liquid-based cytology, HPV testing, and PAX1-JAM3 gene methylation detection (CISPOLY, China). The results obtained were compared with pathological findings.

Results A total of 549 participants were included in this study, encompassing various histological diagnoses across different age groups, including benign abnormalities (n=31), benign/CIN1 (n=321), CIN2 (n=44), CIN3 (n=36), cervical cancer (n=26), postoperative cases (n=28), and other malignant tumors (n=20). When compared to HPV testing (sensitivity: 94.68%, specificity: 9.95%) and liquid-based cytology (LBC) (sensitivity: 89.62%, specificity: 45.5%), dual-gene methylation detection of PAX1-JAM3 exhibited higher sensitivity (92.45%) and specificity (95.16%) for detecting CIN2 across all age groups. For CIN3, the methylation performance demonstrated a sensitivity of 98.39% and a specificity of 86.78%. In the population aged 50 years or older, dual-gene methylation detection exhibited a sensitivity of 100% and a specificity of 93.98% for detecting CIN2, surpassing the lower sensitivity (89.47%) and specificity (14.61%) of HPV testing and LBC (sensitivity: 91.3%, specificity: 54.17%). The misdiagnosis rates for cancer were 0% for PAX1-JAM3 dual-gene methylation detection, 5% for HPV testing, and 7% for LBC among all participants.

Conclusion Our findings demonstrate that gene methylation detection, when compared to HPV testing and cytology, shows promise in cervical cancer screening, particularly for patients with CIN2 or lower. It has the potential to serve as an independent biomarker for accurate cervical cancer diagnosis and triage among the Chinese population.

#864 A NOMOGRAM COMBING MRI AND SERUM INFLAMMATORY BIOMARKERS PREDICTS POSTOPERATIVE VAGINAL INVASION IN IB-IIA STAGE CERVICAL CANCER —— A SINGLE INSTITUTIONAL RETROSPECTIVE STUDY OF 580 PATIENTS

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10.1136/ijgc-2023-ESGO.6

Introduction/Background In cervical cancer (CC), pelvic examination has long been considered the standard method for clinical stage classification. However, it may easily misjudge and bias, including the occult vaginal invasion (VI). Insufficient preoperative assessment of VI often leads to vaginal lesions residues or inferior tumor-free distance during the operation. Recently studies showed MRI has the potential to detect occult tumors. At the same time, serum inflammatory biomarkers have been demonstrated to correlate with the tumor migration in various tumors such as lung cancer, esophageal cancer, and gastric cancer. Combining MRI and inflammatory biomarkers is meaningful to predict occult VI in CC patients with surgical procedures.

Methodology Our study was designed one-center and retrospectively. 580 CC patients with FIGO2018 stages IB-IIA2 were enrolled between January 2013 and December 2021. All patients underwent preoperative MRI and radical hysterectomy. The demographic, bimanual examination, MRI, and laboratory data were analyzed based on logistic regression analysis. Then the nomogram was developed to predict the probability occurrence of postoperative VI.

Results All patients were randomly divided into training set (n = 290) and validating set (n = 290). Parameters including MRI-derived vaginal invasion ($P < 0.018$), clinical vaginal invasion ($P < 0.038$), systemic inflammatory response index (SIRI) ($P < 0.001$), and platelet/albumin ratio (PAR) ($P < 0.013$) were the independent diagnostic factor for

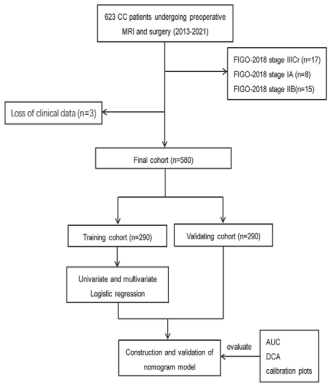

Figure 1. Flow diagram of the study

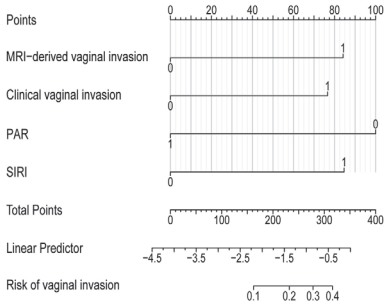

Figure 2. The prediction nomogram of vaginal invasion

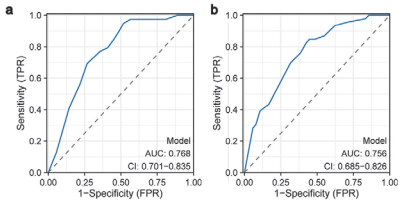

Figure 3. AUC in the training set(A); AUC in the validating set(B)

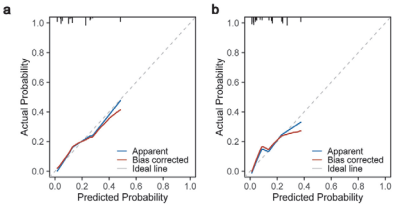

Figure 4. Calibration curves in the training set(A) and validating set(B)

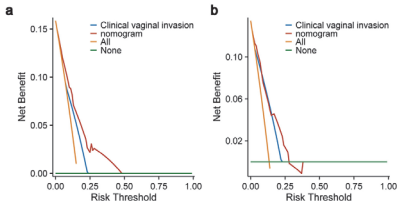

Figure 5. DCA in the training set(A); DCA in the validating set(B).

Abstract #864 Figures 1–5

postoperative VI by univariate and multivariate logistic regression showed. The nomogram predicts the occurrence of VI had a robust predict performance, which was demonstrated by the AUC (AUCtraining=0.775 and AUCvalidating=0.769) and the calibration curves and DCA.

Conclusion Our study is the first to develop a multifactorial diagnostic model integrated preoperative parameters of MRI, serum SIRI, and PAR level to predict VI in CC patients with early stage. Our nomogram may assist surgeons in determining the length of vaginal resection when performing a procedure.

Disclosures The authors have no financial conflicts of interest.

#901 UNRAVELING THE TRANSCRIPTOMIC LANDSCAPE OF SMALL CELL CARCINOMA OF THE UTERINE CERVIX: INSIGHTS INTO SUBTYPES AND DIAGNOSTIC CHALLENGES

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Introduction/Background Small cell carcinoma of the uterine cervix (SCCC) is a rare neuroendocrine tumour associated with HPV infection. Transcriptomic subtypes have been described in small cell carcinomas of the lung, including NEUROD1 and ASCL1-driven tumours with a neuroendocrine phenotype, as well as a distinct POU2F3 subtype lacking neuroendocrine features. This study aimed to investigate the existence and characteristics of these subtypes in HPV-related SCCC using RNA sequencing.

Methodology We conducted whole exome RNA sequencing on 14 histopathologically reviewed SCCC cases. Pathological review included expert assessment and immunohistochemical analysis notably using neuroendocrine and SWI/SNF complex markers, p16, RB1, TTF1 and POU2F3. Various bioinformatics tools were employed for fusion transcript detection, mutational analyses, gene expression profiling, and clustering analyses. Differential diagnoses, such as undifferentiated carcinoma and squamous cell carcinoma specimens, were also analysed.

Results The mutational profile of SCCC was heterogeneous, with notable findings including RB1 mutations in 2 cases, TP53 mutations in 2 cases, RAS/RAF mutations in 2 cases, PIK3CA mutations in 2 cases, and HRD-related gene alterations in 3 cases. Gene expression profiling identified 7 tumors overexpressing NEUROD1, 2 tumors overexpressing ASCL1, and 2 tumors overexpressing POU2F3. Additionally, 3 tumors lacked a specific transcriptional profile. Notably, the two POU2F3-expressing tumors did not exhibit neuroendocrine features, presenting a diagnostic challenge. Immunohistochemistry for POU2F3 proved valuable in this context. Clustering analyses correlated each of the subtypes identified in these cervical tumours with their well-described lung counterparts.

Conclusion This study presents the first comprehensive transcriptomic analysis of a series of SCCC confirming the existence in the uterine cervix of small cell carcinoma subtypes described in other organs and highlighting the diagnostic challenge of the POU2F3-overexpressing subtype lacking neuroendocrine immunohistochemical features. These findings have potential implications for reclassifying a subset of undifferentiated carcinomas of the cervix and may inform therapeutic adaptations in the management of SCCC.