Benchmark. Slides were scanned and counted for the number of tumor and immune cells expressing PD-L1 in 3 parts in each slide by one pathologist. Tumor cell proportion score (TC) and immune cell proportion score (IC) were calculated.

Results: Median of TC in 22C3, SP263, and SP142 was 35.0%, 50.7%, and 9.1%, respectively. Median of IC in 22C3, SP263, and SP142 was 1.7%, 1.8%, and 1.8%, respectively. Those 3 antibodies showed a high correlation in TC of PD-L1 staining. The percentage agreement was 85.7% between 22C and SP263 ($\kappa=0.440$, $p=0.047$). The percentage agreement was 92.9% and 85.7% between 22C3 and SP142 using 1% ($\kappa=0.811$, $p=0.002$) of TC, respectively. Using clinically relevant cut-off, the percentage agreement between SP263 and 22C3, and 22C3 and SP142 was 71.4% ($\kappa=0.152$, $p=0.571$) and 92.9% ($\kappa=0.811$, $p=0.002$), respectively. Intratumoral agreement of positivity of PD-L1 expression among different 3 parts in the same slide was 100% in 22C3 and SP263.

Conclusion: Those 3 antibodies showed a good correlation in TC of PD-L1 expression. 22C3 and SP142 may be interchangeable to determine PD-L1 due to its high agreement to evaluate the positivity for PD-L1 in PSTT/ETT. SP263 showed a higher positivity rate than others, and the agreement was acceptable with 22C3.

Oral (OMi3)

Endometrial Hyperplasia, Endometrial Intra-epithelial Neoplasia, and Endometrial Cancer

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Feasibility of identifying circulating tumor DNA based on cervical smear samples in endometrial cancer patients

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Objective: Cervical smear samples are easy to obtain and may effectively reflect the tumor environment in the pelvis due to anatomic proximity. Thus, we have investigated the feasibility of using cervical smear samples for tumor DNA analysis in endometrial cancer patients.

Methods: Patients undergoing endometrial cancer staging were prospectively enrolled since January 2021. Cervical smear samples were obtained preoperatively via vaginal sampling. Cell-free DNA was extracted and analyzed with a custom panel which covers 101 endometrial cancer-related genes. Prepared

libraries were sequenced using NovaSeq 6000 System (Illumina) and analyzed using Piseq analysis (Dxome).

Results: Cervical smear samples were obtained from 13 patients, and among them whole blood was available for ctDNA analysis in 12 patients. This predominantly early-stage cohort consisted of stage IA (n=7), stage IB (n=3), and stage II, III, and IV patients (n=1 for each). Overall, the detection rate for cervical cytology-based tumor DNA was 8 out of 13 patients (62%), whereas only 2 out of 13 patients (15%) had detectable ctDNA based on blood. Specifically, for stage IA patients, ctDNA was detected in 3 out of 7 patients, despite that all 7 patients had normal PAP smear result. Based on cytology-based tumor DNA analysis of cervical smear samples, the most frequently identified gene mutations were PTEN (n=6), PIK3CA (n=4), ARID1A (n=3), KRAS (n=3), TP53 (n=2), MSH6 (n=2), and ATM (n=2).

Conclusion: In this pilot study with predominantly early-stage endometrial cancer patients, cervical smear was more sensitive than whole blood or conventional PAP smear in terms of detecting tumor DNA.

Oral (OMi4)

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Pilot study on biomarkers for screening endometrial hyperplasia and early-stage endometrioid cancer

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Objective: Endometrial cancer is the most common malignancy of the female reproductive system in developed countries including Taiwan. Ways to screen precancerous endometrial lesion and early-stage endometrial cancer are mandatory. We performed proteomics study on endometrioid endometrial cancer and proteinase-3 (PRTN-3) showed significant expression in cancerous tissue compared with normal endometrial tissue. High expression of vascular endothelial growth factor (VEGF) and interleukin-6 (IL-6) was noted through literature review. We then conducted a pilot study to check if these are effective markers in vaginal discharge for the detection of early-stage endometrial cancer and its precancerous lesion.

Methods: After granted by Institutional Review Board, vaginal discharge samples of 133 patients between 2015 and 2017 at