EPV101/#203

THE INCREASING INCIDENCE OF OBESITY AND UTERINE CANCER IN PATIENTS UNDER 55 IN ASIA AND THE UNITED STATES – WHO IS MOST AT RISK?

¹C-I Liao, ²M Richardson*, ³K Darcy, ³C Tian, ⁴D Kapp, ⁵J Chan. ¹Kaohsiung Veterans General Hospital, Obstetrics and Gynecology, Kaohsiung City, Taiwan; ²University of California Los Angeles, Obstetrics and Gynecology, Los Angeles, USA; ³Gynecologic Cancer Center of Excellence, Obstetrics and Gynecology, Washington, USA; ⁴Stanford University School of Medicine, Department of Radiation Oncology, Stanford, USA; ⁵California Pacific Medical Center, Obstetrics and Gynecology, San Francisco, USA

10.1136/ijgc-2021-IGCS.171

Objectives To evaluate the association between age, race, country of residence, and obesity with the rising incidence of uterine cancer in the United States (US) and Taiwan.

Methods Data were obtained from the United States Cancer Statistics (USCS) program, Behavioral Risk Factor Surveillance System (BRFSS), and Taiwan Cancer Registry from 2001 to 2017. SEER*Stat and Joinpoint regression program were used for statistical analyses.

Results 560,131 White and 22,963 Asian women were identified in USCS and 13,950 women in the Taiwan Cancer Registry with uterine cancer, with an incidence rate per 100,000 of 21.9 White and 17.3 Asian women in the US and 15.0 women in Taiwan. The proportion diagnosed <55 years of age with uterine cancer varied by race and country of residence with 22% of Whites in the US, 40% Asians in the US and 52% of women in Taiwan ($P < 0.0001$). Evaluation of annual percent changes (APC) in incidence of uterine cancer between 2001–2017 within different age groups indicated that the largest APC was observed in the women diagnosed between 35–39 years old with APC increases of 2.4% in Whites and 3.5% in Asians in the US and 7.2% in Taiwan ($P < 0.001$). Evaluation of obesity trends in women between 2001–2017 using US BRFSS data indicated an APC of 2.4% in Whites (range: 19–28%) and 2.1% in Asians (range: 9–13%).

Conclusions Compared to US Whites and US Asians, Native Asians were diagnosed with uterine cancer at a younger age and rates are increasing annually. This finding may be attributed to the rise in obesity rates.

EPV102/#216

IMPLEMENTATION OF MOLECULAR STRATIFICATION IN ENDOMETRIAL CANCER THROUGH MIRNAS CHARACTERIZATION

¹AM Perrone, ²G Ravegnini, ³A de Leo, ²D de Biase, ²F Gorini, ¹E de Crescenzo, ¹G Dondi, ¹M Tesi, ¹M di Stanislao, ¹P de Iaco. ¹IRCCS Azienda Ospedaliero-Universitaria di Bologna, Division of Oncologic Gynecology, Bologna, Italy; ²University of Bologna, Pharmacy and Biotechnology, Bologna, Italy; ³University of Bologna, Dept of Experimental, Diagnostic and Specialty Medicine, Bologna, Italy

10.1136/ijgc-2021-IGCS.172

Objectives Introduction. The TCGA project identified four distinct prognostic groups of endometrial carcinoma (EC) based on molecular alterations among which two are correlated with an intermediate prognosis: the Mismatch Repair deficient (MMRd) and the No Specific Molecular Profile (NSMP) groups. NSMP represents a heterogeneous subset of patients frequently harboring CTNNB1 alterations and presenting

distinctive clinicopathologic features comparing with the CTNNB1 non mutant ones. miRNAs are oncological key players that have not been integrated with the TCGA EC classification. The study aimed to evaluate the miRNA expression profile in EC to identify potential novel biomarkers of diagnosis and prognosis.

Methods We analyzed miRNA expression in 72 ECs specimens previously classified as MMRd (31) and NSMP (41), including 15 with CTNNB1 mutations. In the discovery step, miRNA expression profile was evaluated in 30 cases through TaqMan Advanced miRNA arrays. Subsequently, in the validation step, four miRNAs were analyzed in the total cohort of ECs by specific miRNA Assays.

Results Comparison of CTNNB1 mutant versus non-mutant ECs (irrespective of MMRd/NSMP status) in the discovery cohort showed 39 differentially expressed miRNAs. The top deregulated 4 miRNAs (miR-187, miR-325, miR-499a-3p and 5p) were further validated in 72 ECs. miR-499a-3p and miR-499a-5p maintained the statistical significance showing higher expression in CTNNB1 mutant ECs ($p < 0.0001$, for both). Furthermore, miR-499a expression was able to identify EC subgroups with longer recurrence free survival.

Conclusions Conclusion. miR-499a may be a useful biomarker and could be integrated in the current TCGA classification scheme to better stratify EC patients

EPV103/#218

NUCLEAR FEATURES ALLOW FOR HIGHLY SENSITIVE SELECTION OF ENDOMETRIAL CARCINOMAS FOR P53 TESTING

¹E-Y Kang*, ¹N Wiebe, ²C Aubrey, ^{3,4}C-H Lee, ⁵M Anglesio, ⁶D Tilley, ²P Ghatage, ²G Nelson, ¹S Lee, ¹M Köbel. ¹University of Calgary, Department of Pathology and Laboratory Medicine, Calgary, Canada; ²University of Calgary, Department of Oncology, Division of Gynecologic Oncology, Calgary, Canada; ³BC Cancer, Department of Pathology and Laboratory Medicine, Vancouver, Canada; ⁴University of British Columbia, Department of Pathology and Laboratory Medicine, Vancouver, Canada; ⁵University of British Columbia, Department of Obstetrics and Gynecology, Vancouver, Canada; ⁶Alberta Health Services, Cancer Control, Calgary, Canada

10.1136/ijgc-2021-IGCS.173

Objectives The World Health Organization endorses molecular subclassification of endometrial endometrioid carcinomas. Our objectives were to test the sensitivity of tumor morphology in capturing p53-abnormal (p53abn) cases and to model the impact of p53abn on changes to ESGO/ESTRO/ESP risk stratification.

Methods 292 consecutive endometrial carcinoma resections received at Foothills Medical Centre, Calgary, Canada (2019–2021) were retrieved and assigned to ESGO risk groups without and with p53 status. Three pathologists reviewed representative H&Es, predicted the p53 status, and indicated whether p53 immunohistochemistry would be ordered. Population-based survival for endometrial carcinomas diagnosed 2008–2016 in Alberta was obtained from the Alberta Cancer Registry.

Results The cohort consisted mostly of grade 1/2 endometrioid carcinomas (EEC12; N=218, 74.6%). 152 EEC12 (52.1% overall) were stage IA and 147 (50.3%) were low-risk by ESGO. The overall prevalence of p53abn and subclonal p53 was 14.5% and 8.3%. The average sensitivity of predicting p53abn among observers was 83.6% and observers requested