Methods We retrospectively identified patients with FIGO stage IB cervical cancer who underwent either primary open RH or laparoscopic RH at three tertiary institutional hospitals between 2000 and 2018. Patients’ clinicopathologic, image, and survival data were collected. The whole dataset was separated into training and test sets with a 4:1 ratio. Combining both statistical and deep neural network models, we constructed hybrid ensemble predictive models for 5-year PFS and OS rates. Only the variables that could be obtained before surgery were used. Model development was conducted in the training set with ten-fold cross-validation, and the developed models were validated in the test set.

Results In total, 1,141 patients were included; 578 and 563 received open RH and laparoscopic RH, respectively. The median length of observation was 57.6 months during which 157 patients (13.8%) experienced disease recurrence and 86 patients (7.5%) died. In terms of preoperative prediction, while the logistic regression model showed AUCs of 0.68 and 0.71 for 5-year PFS and OS rates, respectively, the ensemble model showed better performance: AUCs, 0.71 and 0.78. These models commonly included the surgical approach as the main prognostic factor.

Conclusion We developed preoperative models predicting survival outcomes according to the surgical approach in early-stage cervical cancer. These models will be useful for making decisions in choosing open RH or laparoscopic RH in individualized counseling practices.

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DETERMINING THE HAEMATOLOGICAL MORBIDITY ASSOCIATED WITH CYTOREDUCTIVE SURGERY

Abstracts

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DISTANT METASTATIC SPREAD AND CLONAL EVOLUTION OF HIGH-GRADE ENDOMETRIAL CANCERS

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Introduction The incidence and mortality of endometrial cancer (EC) is rising worldwide. The biological underpinnings of EC progression are poorly understood. We sought to characterize the genetic alterations and clonal evolution of two primary high-grade ECs and their matched multiple distant metastases.

Methods Research autopsies were performed on two women: one with treatment-naïve, widely metastatic undifferentiated carcinoma at diagnosis (case 1); and one with serous EC and heavily treated metachronous disease (case 2). Whole-exome sequencing of primary tumors, metastases (n=8 and n=7), and normal tissues was performed and analyzed using validated bioinformatics methods.

Results In case 1, a truncal hotspot PIK3CA p.H1047L hotspot mutation was present in the primary tumor and all metastases, with a primary subclonal TP53 frameshift mutation becoming clonal in a subset of metastases (n=3). Evidence of clonal progression between metastatic sites was observed as well as a combination of aging and homologous recombination-deficiency mutational signatures.

Conclusion Genetic alterations identified in case 1 were likely early events in the clonal expansion of the primary tumor, reflective of aggressive disease and absence of treatment. In case 2, evidence of clonal diversity and progression was observed, potentially representing clonal selection due to therapeutic effect.