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GENOMIC PROFILING OF CERVICAL CANCER IN UKRAINIAN PATIENTS: HISTOLOGY-SPECIFIC FBXW7 AND STK11/TP53 MUTATION PATTERNS

Background. Despite advances in screening and prevention, cervical cancer still poses a major health concern globally and remains a leading cause of cancer deaths. In this study, we analyzed cervical tumor samples from Ukrainian patients using a next-generation sequencing panel covering 50 cancer-related genes, with emphasis on clinically relevant variants. These variants were further analyzed taking into account the stage of the disease and histological characteristics to assess their prognostic and therapeutic value. **Methods.** Tumor samples from 30 Ukrainian women with cervical cancer (ages 29–74) were collected during surgery in compliance with the Declaration of Helsinki and with informed consent. Sequencing was performed with the Ion AmpliSeq Cancer Hotspot Panel v2 on the Ion GeneStudio S5 Plus. The data were processed and filtered using standard pipelines. The associations were assessed with Fisher's exact test for categorical variables and the Mann-Whitney U test for age. **Results.** Two statistically significant clinicopathological associations were found ($p < 0.05$). First, FBXW7 mutations were present in 2 of 4 adenocarcinomas (50%) but in only 1 of 26 squamous cell carcinomas (3.8%; $p = 0.039$), consistent with TCGA data identifying FBXW7 as a preferential target in cervical adenocarcinoma; loss of this mechanism may contribute to glandular-specific oncogenesis. Given the small number of adenocarcinoma cases ($n = 4$), this finding is preliminary. Second, STK11 and TP53 mutations co-occurred in 2 of 30 tumors ($p = 0.039$), exceeding chance expectation. STK11 (LKB1)-deficient tumors have been reported to resist PD-1/PD-L1 blockade regardless of mutational burden, so concurrent TP53 loss may define a distinct, immunotherapy-resistant subgroup. As no correction for multiple comparisons was applied, both associations warrant validation in larger cohorts. **Conclusion.** The study identified two key associations: enrichment of FBXW7 alterations in adenocarcinoma and the co-occurrence of STK11 and TP53 mutations, suggesting a subgroup that may be resistant to immunotherapy. Due to the small sample size, these observations are preliminary and need validation in larger cohorts before clinical application.

Keywords: cervical cancer, FBXW7, STK11/TP53 co-mutation, targeted NGS.

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