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M. Montesion
Foundation Medicine, Inc.

C. H. Chung
Lee Moffitt Cancer Center andResearch Institute

E. S. Sokol
Foundation Medicine, Inc.

S. A. Khan
University ofTexas Southwestern Medical Center

H. Kang
Johns Hopkins University School of Medicine

Authors

M. Montesion, C. H. Chung, E. S. Sokol, S. A. Khan, H. Kang, L. A. Albacker, J. M. Johnson, G. M. Frampton, V. A. Miller, J. S. Ross, and S. M. Ali

68P Pan-squamous genomic profiling stratified by anatomic tumor site and viral association

M. Montesion[1], C.H. Chung[2], E.S. Sokol[1], S.A. Khan[3], H. Kang[4], L.A. Albacker[1], J.M. Johnson[5], G.M. Frampton[1], V.A. Miller[6], J.S. Ross[7], S.M. Ali[6]

[1]Cancer Genomics Research, Foundation Medicine, Inc., Cambridge, MA, USA, [2]Department of Head and Neck-Endocrine Oncology, H. Lee Moffitt Cancer Center and Research Institute, Tampa, FL, USA, [3]Department of Internal Medicine, University of Texas Southwestern Medical Center, Dallas, TX, USA, [4]Department of Oncology, Johns Hopkins University School of Medicine, Baltimore, MD, USA, [5]Department of Medical Oncology, Thomas Jefferson University, Philadelphia, PA, USA, [6]Clinical Development, Foundation Medicine, Inc., Cambridge, MA, USA, [7]Pathology, Foundation Medicine Inc., Cambridge, MA, USA

Background: Squamous cell carcinomas (SCC) have diverse anatomic etiologies but may share common genomic biomarkers. We profiled 7,871 unique SCCs across nine anatomic sites to investigate commonality in genomic alterations (GA), tumor mutational burden (TMB), human papillomavirus (HPV) association, and mutational signatures.

Methods: Tissue from over 8,100 unique SCC samples originating from nine anatomic sites (anogenital (anus, cervix, penis, vagina, vulva), esophagus, head and neck, lung, and skin) were sequenced by hybrid capture-based comprehensive genomic profiling to evaluate GA and TMB. About 3% of non-cutaneous SCC samples had UV signatures, indicative of potential primary site misdiagnoses, and were filtered from the analysis. Detection of HPV, including high-risk strains 16, 18, 31, 33, and 45, was implemented through de novo assembly of non-human sequencing reads and BLASTn comparison against all viral nucleotide sequences in the NCBI database.

Results: The proportion of HPV+ patients by anatomic site varied, with the highest being anal (91%) and cervical (83%). The mutational landscape of each cohort was similar, regardless of anatomic origin, but clustered based on HPV status. The largest differences in GA frequency as stratified by HPV- vs. HPV+ were TP53 (87% vs. 12%), CDKN2A (45% vs. 6%), and PIK3CA (22% vs. 33%). The median TMB in cases originating from HPV-associated sites was similar, regardless of HPV status. Higher median TMB was observed in lung and skin cases, which exhibited significant enrichment of mutational signatures indicative of tobacco- and UV-induced DNA damage, respectively.

Conclusions: HPV+ and HPV- SCC populations have distinct genomic profiles and, for the latter, anatomic site is correlated with TMB distribution, secondary to associated carcinogen exposure. As such, biomarkers such as TMB and UV signature can provide unexpected insight into site of origin misdiagnoses and may correlate with benefit from immune checkpoint inhibitors.

Table: 68P

Tumor Site	% HPV+	Median TMB (Interquartile Range)	% TMB >= 10	% TMB >= 20
Anogenital (n = 1213)	76	5 (6)	17	5
Head and Neck (n = 1843)	36	4 (5)	15	5
Esophageal (n = 416)	6	5 (4)	13	2
Lung (n = 3977)	5	9 (8)	43	9
Skin (n = 422)	8	40 (69)	68	62

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