

5th International Conference on Oncology & Virology

July 25-26, 2019 Rome, Italy

Risk Stratification of Cervical Lesions Using Capture Sequencing and Machine Learning Method Based on HPV and Human Integrated Genomic Profiles

Zifeng Cui^{1*}, Rui Tian¹, Weiwen Fan¹, Zhuang Jin¹, Dan He² and Zheng Hu¹

¹Department of Obstetrics and Gynecology, The First Affiliated Hospital of Sun Yat-Sen University, China

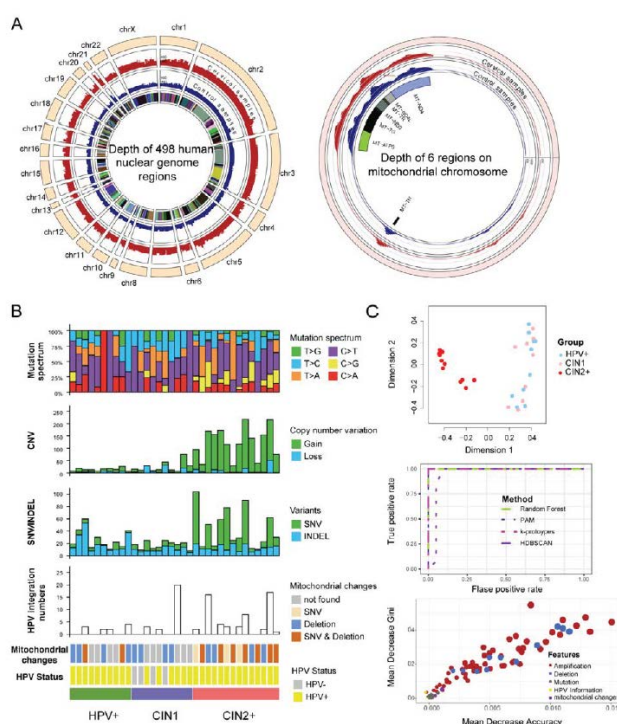
²Department of Neurology, The First Affiliated Hospital of Sun Yat-Sen University, China

Background: From initial HPV infection and precursor stages, the development of cervical cancer takes decades. High-sensitivity HPV DNA testing is currently recommended as primary screening method for cervical cancer, while better triage methodologies are encouraged to provide accurate risk management for HPV positive women.

Methods: Given that virus-driven genomic variation accumulates during cervical carcinogenesis, we designed a 39 Mb custom capture panel targeting 17 HPV types and 522 mutant genes related to cervical cancer. Using capture-based next-generation sequencing, HPV integration status, somatic mutation and copy number variation were analyzed on 34 paired samples, including 10 cases of HPV infection (HPV+), 10 cases of CIN1 and 14 cases of CIN2+ (CIN2: n=1; CIN2-3: n=3; CIN3: n=9; SCC: n=1). Finally, the Machine Learning Algorithm-Random Forest was applied to build the risk stratification model for cervical precursor lesions based on CIN2+ enriched biomarkers.

Results: Generally, HPV integration events (11 in HPV+, 25 in CIN1 and 56 in CIN2+), non-synonymous mutations (2 in CIN1, 12 in CIN2+) and copy number variations (19.1 in HPV+, 29.4 in CIN1 and 127 in CIN2+) increased from HPV+ to CIN2+. Interestingly, “common” deletion of mitochondrial chromosome was significantly observed in CIN2+ (P value=0.009). Together, CIN2+ enriched biomarkers, classified as HPV information, Mutation, Amplification, Deletion and mitochondrial change, successfully predicted CIN2+ with average accuracy probability score of 0.814, and Amplification and Deletion ranked as the most important features.

Conclusion: Our custom capture sequencing combined with machine learning method effectively stratified the risk of cervical lesions and provided valuable integrated triage strategies.



Biography

Zifeng Cui is a PhD student. Presently working under Professor Zheng Hu (Doctoral Supervisor, Chief Special Scientist of the Ministry of Science and Technology, Young Top Talents in Ten-thousand Talents Program).