CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS

Award ID:
RP130124

Project Title:
Deep sequencing oncoviral evolvomes as a personalized cancer diagnostic tool

Award Mechanism:
Individual Investigator

Principal Investigator:
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Entity:
The University of Texas at Austin

Lay Summary:

Infections of human papillomavirus (HPV) cause 100% of cervical cancers, but most HPV-infected individuals never develop cancer. Even if a high-risk HPV strain is detected in an individual, their cancer prognosis is uncertain: more than 91% of HPV infections are cleared naturally by the immune system. HPV vaccines exist that can prevent infection and thus cervical cancer, but they are currently ineffective against HPV strains which cause 30% of cervical cancer. So, there is a continued need to better understand why some HPV infections ultimately lead to cervical cancer and others do not. Our overall goal is to identify new HPV genetic variants associated with cancer. We will develop a personalized genomics approach to deeply profile HPV sequence diversity within an infected individual. With our targeted procedure it should be possible to detect subtle changes in HPV that increase cancer risk, even when they are exceptionally rare, as might be the case early in cancer development. We will test this method on DNA isolated from new cervical tumor samples and data from human genome sequencing projects. Our eventual goal is for the knowledge gained about HPV genetic variation to be applied in a clinical setting for earlier diagnosis of infections with an elevated risk of causing cervical cancer versus those that are likely to harmlessly clear on their own. It is estimated that between 25 and 90% of anal, vaginal, vulvar, penile, oral cavity, and oropharynx cancers are also caused by HPV, and six other viruses are currently known to cause a variety of other human cancers. With only slight modifications, the analysis strategy that we will develop could be used to profile viral variation associated with all of these cancers. Therefore, this project could ultimately improve our understanding of the causes of 15 to 20% of all human cancers and lead to more precise clinical tests for early detection in these cases.