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USING DIFFERENT NEXT GENERATION SEQUENCING TECHNOLOGIES TO STUDY THE ROLE OF HUMAN PAPILLOMAVIRUS INTEGRATION IN THE DEVELOPMENT OF CANCER

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Human papillomavirus (HPV) is involved in the development of cervical cancer and a number of other anogenital cancers. It is also increasingly involved in the development of one type of head and neck cancer, namely oropharyngeal squamous cell carcinoma (OPSCC). One key step in the development of many of these cancers is integration of the HPV viral genome somewhere within the human genome, but it is unclear precisely when this occurs, and the precise role that the integration event plays in cancer development. In order to study the different ways that HPV is involved in the development of OPSCC we have been using different genome sequencing technologies to study the physical status of HPV in this cancer. We have used mate-pair next generation sequencing on the Illumina platform and also whole genome sequencing on the BGI Seq500 sequencing platform. This has enabled us to compare these two platforms for their ability to characterize important physical attributes of this cancer including the site of HPV integration, and the resulting dramatic genomic changes of the HPV integration event. We have also been able to determine genome-wide changes in OPSCC separate from the HPV integration event.

Recent Publications

1. **Gao G and Smith D I (2015) Mate-pair sequencing as a powerful clinical tool for the characterization of cancers with a DNA viral etiology. Viruses 7(8):4507-4528.**
2. **Gao G and Smith D I (2016) Role of the common fragile sites in cancers with a human papillomavirus etiology. Cytogenetic and Genome Research 150(3-4):217-226.**
3. **Gao G and Smith D I (2016) Human papillomavirus and the development of different cancers. Cytogenetic and Genome Research 150(3-4):185-193.**
4. **Gao G and Smith D I (2015) WWOX, large common fragile site genes, and cancer. Experimental Biology and Medicine (Maywood) 240(3):285-295.**

Biography

David I Smith received his PhD in Biochemistry from the University of Wisconsin in Madison in 1978. His first academic position was at Wayne State University School of Medicine and in 1996 he moved to the Mayo Clinic as a Professor in the Department of Laboratory Medicine and Pathology. He is also the Chairman of the Technology Assessment Group for the Mayo Clinic Center for Individualized Medicine. His laboratory utilizes next generation sequencing to study the different ways that human papillomavirus can cancer in different tissues. His group also studies the common fragile sites which are regions of profound instability found in all individuals.

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