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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. This work has revealed that HPV integration occurs much less frequently in this cancer than in cervical cancer. Furthermore, we have found that the common fragile sites and the extremely large genes contained within these unstable regions are hot-spots for HPV integration in this cancer. We further present evidence that whole genome sequencing technologies provide valuable clinical information about the cancers being sequenced and thus could be used as a clinical tool to characterize each individual cancer to guide clinical treatment strategies.**

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