

Integrated sequencing analysis for virus detection in Human disease

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Abstract: Virus infection and its interaction with the host genome in human disease remains challenges in term of structural variation in the human genome. The limitation is that the major tool for interrogating genome organization – Next Generation Sequencing (NGS) is inadequate for resolving large structural change in the genome or the genome assembly. Here, we adopted a novel technique, the optical genomic mapping (OGM) in conjunction with NGS to detect virus and to check the molecular structure of virus associated with human genome. Additionally, we investigate the instability correlated with integrated and episomal virus genomes in cancer cell. Our objective is to analyze the state of the viral genome in the cancer cell, analyze the effect of viral genome integration on adjacent host genomic structure and correlate findings to patient clinical outcomes.

Our results show that established OGM and NGS can identify the nature of viral association with the genome in cancer cells and in the case of integration, determine the structure of viral integration sites. Our preliminary data from human sample suggests viral integration may be associated with greater levels of genomic instability in comparison to episomal viral structures.