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Application of two novel NGS-based detection methods in HPV genomic studies

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Human papillomavirus (HPV) is deemed as the leading cause of cervical cancer which is the fourth most common cancer in women. Here we will show two novel detection assays applied in genomic studies of HPV based on NGS. Probe seq could be used in the scenario of acquiring the full virus genome and integration sites at the same time from HPV positive swabs which are collected in HPV routine surveillance. Single tube long fragment read (stLFR) technology could be performed on large molecular HPV genomes which are amplified through rolling cycle amplification (RCA). stLFR shed light on revealing differences among HPV viruses in the same host and may help in illuminating important virus mutations

that contribute to the progress after virus infection. The two novel HPV detection methods are developed and tested and showed potential in HPV genomic studies, as well as in finding new targets for HPV infection prognosis.

Speaker Biography

Zhu Houshun has completed his PhD study in 2017 at The University of Hong Kong. He became the researcher of BGI, China from the year 2018 and employed as a visiting professor by Anhui Medical University at 2019. He has 14 publications that have been cited over 200 times. The main study filed of Houshun is focused on pathogenesis of infectious pathogens such as influenza virus as well as HPVs

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