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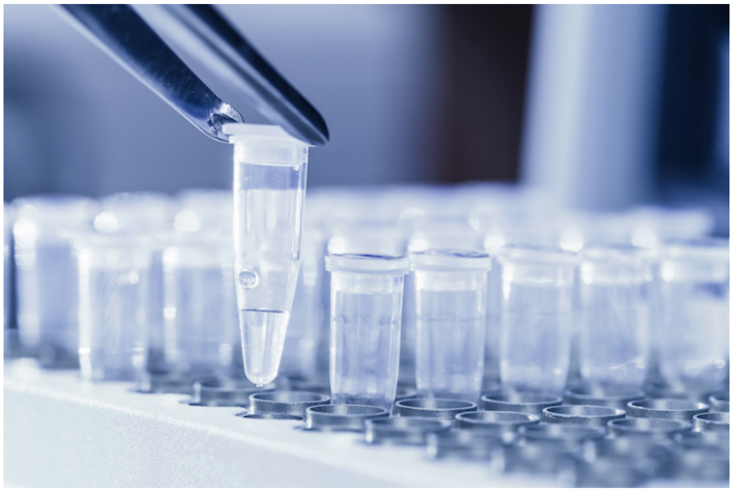
Korea using new rapid test for early outbreak control of Hantavirus

01 March 2024 | News

Cost-efficient Flongle sequencing's potential for rapid hantavirus genome-based diagnostics andphylogeographical surveillance



Orthohantaviruses, highly transmissible zoonotic pathogens, are notorious for causing haemorrhagic fever with renal syndrome (HFRS) in Eurasia and hantavirus cardiopulmonary syndrome in the Americas. With a significant impact on public health, they have been extensively researched for effective outbreak control and intervention strategies. Gyeonggi Province in South Korea has reported a significant number of HFRS cases, making it a critical area for epidemiological surveillance and understanding the genomic diversity of orthohantaviruses.

To gain insights into the prevalence, viral loads, and genetic variations of *Hantaan orthohantavirus* (HTNV), a team of researchers at the Department of Microbiology, Korea University College of Medicine, conducted a study in Gyeonggi Province. Notably, the study showcased the application of Flongle sequencing, an innovative, cost-efficient, and rapid method, for detecting HTNV genomes.

The study's approach is rooted in the adoption of next-generation sequencing technologies, with a spotlight on the Oxford MinION nanopore sequencer. The comprehensive sampling strategy involved the capture of rodents and shrews from diverse regions in the Republic of Korea (ROK) using live traps. Subsequently, the team employed a multifaceted approach, incorporating mitochondrial DNA analysis, indirect immunofluorescence antibody tests, and various molecular methods for species identification and virus detection. This comprehensive methodology facilitated a thorough understanding of viral prevalence and genetic diversity.

The findings emphasise the pivotal role of genomics in disease surveillance and offer hope for more effective responses to emerging infectious agents in the future.