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Impact of Library Miniaturization on Influenza Whole-Genome Assembly Quality

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Influenza viruses remain a major public health concern due to their rapid evolution, zoonotic potential, and capacity to cause seasonal epidemics. Several past influenza pandemics originated from animal-to-human transmission events, and recent outbreaks of avian influenza A(H5N1) in mammals have raised concerns about the emergence of novel strains with pandemic potential. Continuous genomic surveillance is therefore essential for monitoring viral evolution and supporting public health decision-making.
As Germany's national public health institute, the Robert Koch Institute routinely performs whole-genome sequencing, genome reconstruction, and downstream analyses of seasonal influenza A and B viruses and makes the resulting data publicly available for surveillance and research purposes. Sustained genomic surveillance is critical for tracking viral evolution, informing vaccine strain selection, and supporting outbreak preparedness. However, despite declining costs of next-generation sequencing, library preparation remains a major cost driver, limiting sequencing throughput and scalability.
We developed a miniaturized library preparation protocol that reduces reagent consumption ninefold compared with our standard workflow using the Mosquito HV Genomics liquid handling system. We evaluated its performance using 181 seasonal influenza samples by comparing sequencing run metrics, consensus genome sequences, and quality indicators generated during genome reconstruction.

Keywords

`Public health, Genomic surveillance, Next-generation sequencing`

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`Yes, I am a Junior Scientist.`

Authors: MATAR, Katia; TERNOVOJ, Dimitri; Dr WEDDE, Marianne; Dr FUCHS, Stephan; Dr LATARETU, Marie; Dr SEDAGHATJOO, Somayyeh

Presenter: MATAR, Katia

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