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Hybridization capture optimization for monkeypox virus genomics

Inhalt

Mpox is a zoonotic disease endemic in West and Central Africa. It is caused by spillovers of monkeypox virus (MPXV) from its rodent reservoir(s) into humans and animals, where it often generates self-limiting outbreaks. MPXV spillovers became more common over the last decades, increasing the risk of longer human to human (h-t-h) transmission chains, such as those recently caused by MPXV clades 1b and 2b. MPXV genomes from such long h-t-h transmission chains exhibit distinct APOBEC3G mutational profiles that can readily be identified through sequencing. So, genomic surveillance can directly aid MPXV control by rationalizing resource distribution via the prioritization of events involving sustained h-to-h transmission. MPXV genome is sequenced using hybridization capture (HC) coupled to high-throughput sequencing, that is very effective but also very expensive, which hinders its routine use in developing countries. Here, we aimed to reduce HC cost through the very simple means of bait dilution. We compared the effects of diluting baits (down to a dilution 1/64) on capture efficiency performed on libraries derived from clinical samples with different virus concentrations. Our results suggest that high-quality, assignable genomes can still be recovered from majority of the samples using baits diluted to 1/32. We conclude that combined with half-reactions during library preparation and pooled library HC, bait dilution can significantly lower the costs of MPXV genomic surveillance.

Keywords

diluted baits; cost optimization; virus concentrations

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No, I am not a Junior Scientist.

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