**Estimates of early hMPXV1 outbreak epidemiological parameters from genomic data**

Community transmission of hMPXV1 was first detected on May 14th, 2022. As of this writing, over 85,000 confirmed cases have been reported from 110 countries and resulted in at least 112 deaths. Due to infrequent case reporting during earlier periods of the outbreak, as well as a lengthy viral incubation period between [5] and [21] days, the extent of the outbreak remains unclear. Due to abundant APOBEC editing of the hMPXV1 genome, the heightened viral evolutionary rate permits phylodynamic estimates of outbreak spread. We used publicly available viral genome sequence data (N=223) from the 2022 global mpox epidemic to analyze viral evolutionary dynamics and epidemic growth rate through time. Using BEAST v. 1.10.4, we implemented a coalescent logistic growth model with HKY+Γ substitution under a strict molecular clock. We use doubling time in days to quantify the exponential growth rate r, from which we estimate 0.039 new infections per day (95% CI: 0.023, 0.056) compared to 0.049 reported cases per day. Temporal dynamics of effective population size Ne indicate steady increases in viral population size a few months prior to initial community detection. We estimate the TMRCA of the 2022 outbreak viruses to be between October 22, 2021 and Feb 5, 2022 (95% credible interval), arriving at a median estimate of December 20, 2021. Thus, a phylodynamic analysis suggests that the 2022 monkeypox outbreak had been building for approximately 5 months before it was detected as an outbreak. We plan to re-estimate epidemiological parameters after upscaling our data to at least 600 sequences. Finally, to characterize regional features of epidemic spread, we will implement a discrete trait model to perform phylogeographic analysis of hMPXV1 evolutionary dynamics across five regions (North America, Western Europe, Southern Europe, Central/Eastern Europe, South America).