CLADE X
A PANDEMIC EXERCISE

SEQUENCING OF PARAINFLUENZA—BACKGROUND

Prepared by: Christopher Hurtado

The International Gene Synthesis Consortium (IGSC) is composed of 11 companies, which together represent approximately 80% of commercial gene synthesis capacity worldwide.[1] The companies are:

- GINKGO BIOWORKS
- BGI
- BLUE HERON
- ATUM
- IDT
- THERMO FISHER SCIENTIFIC
- SGI-DNA
- GENSCRIPT
- TWIST BIOSCIENCE
- BIONEER CORP.
- EDINBURGH GENOME FOUNDRY

HUMAN PARAINFLUENZA

Genome size: Negative sense RNA (~15,000 nucleotides) [15kb][2]

- Estimated sequencing time: 1-2 days
- Estimated viral bioinformatics time for novel virus: ~1 week[3]
  - Read quality control
  - Reference strain determination
  - Read mapping to the reference strain
  - Single-nucleotide polymorphism (SNP) and small insertion or deletion (indel) detection
  - De novo genome assembly
  - Genome annotation
  - Phylogenetic tree construction
  - Phylogenetic analysis
    - Several software solutions are available for each step.

REFERENCES

1. International Gene Synthesis Consortium. https://genesynthesisconsortium.org/. Accessed May 7, 2018.
2. Henrickson KJ. Parainfluenza viruses. *Clin Microbiol Rev* 2003;16(2):242-264.
3. Oakeson KF, Wagner JM, Mendenhall M, Rohrwasser A, Atkinson-Dunn R. Bioinformatic analyses of whole-genome sequence data in a public health laboratory. *Emerg Infect Dis* 2017;23(9):1441-1445.

Date: May 3, 2018

Prepared as background material by the Johns Hopkins Center for Health Security
for the Clade X tabletop exercise