

Genomic surveillance for canine rabies

Roman Biek

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University
of Glasgow

Genetic sequencing in pathogen epidemiology



Sample



Sequencing



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ATTCTCTG
ATTTCCTTA
ATGTCCTTA
ATGTCCTTA
ATGTCCTCA
```

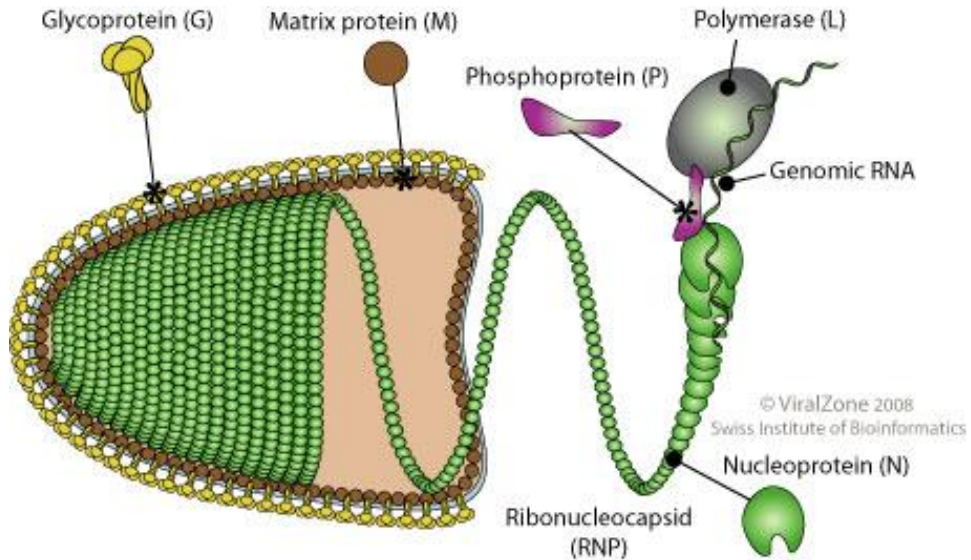
Interpretation

Which pathogen?

What strain type?

‘Who infected whom’?

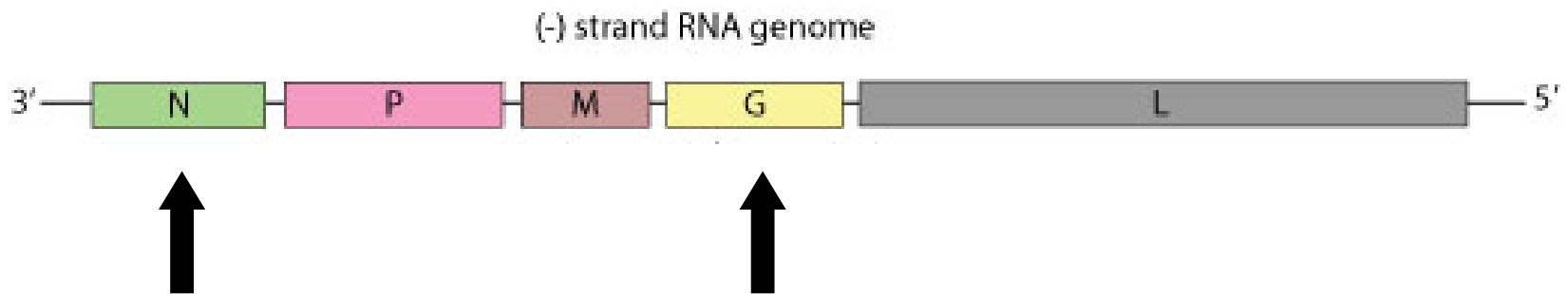
Rabies virus



Enveloped, negative strand RNA virus

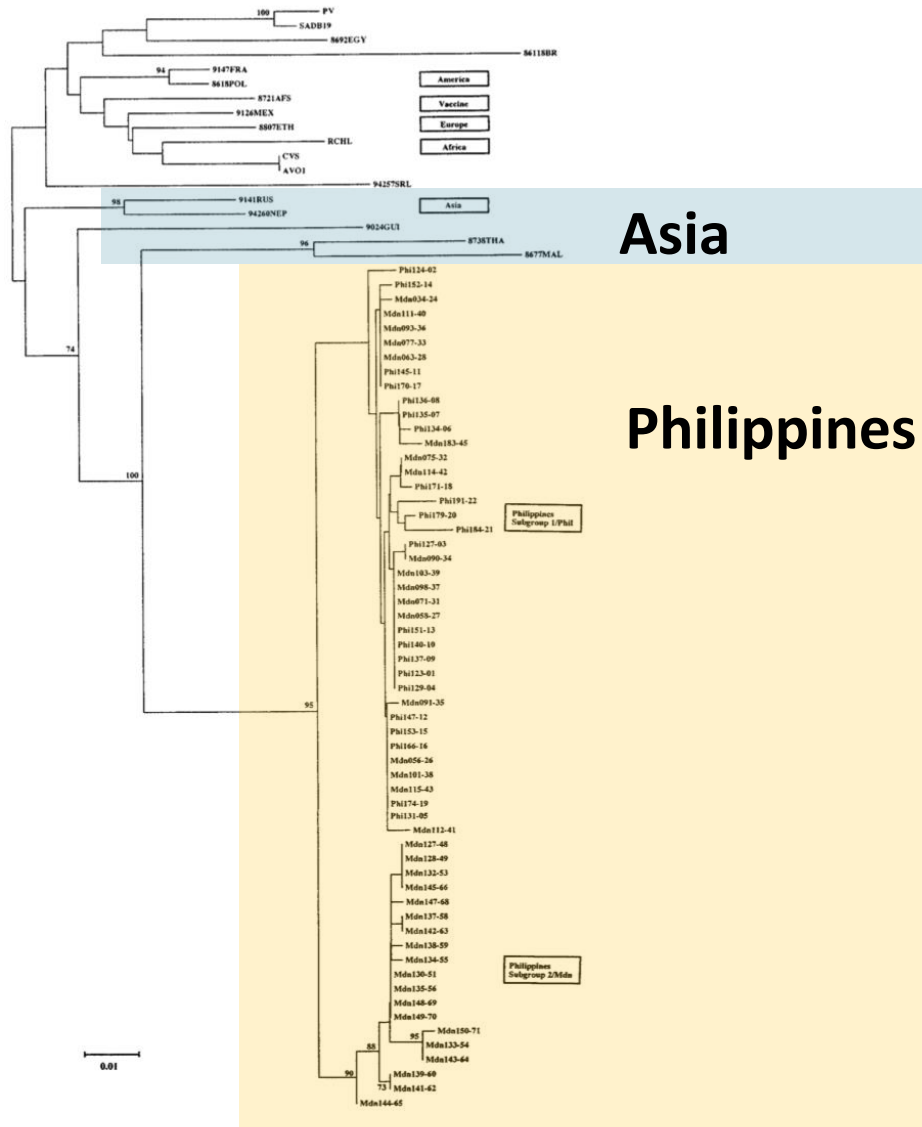
Small genome:

- ~12,000 base pairs (bp)
- 5 genes



Traditional targets of rabies virus sequencing

Partial N gene data from Philippines



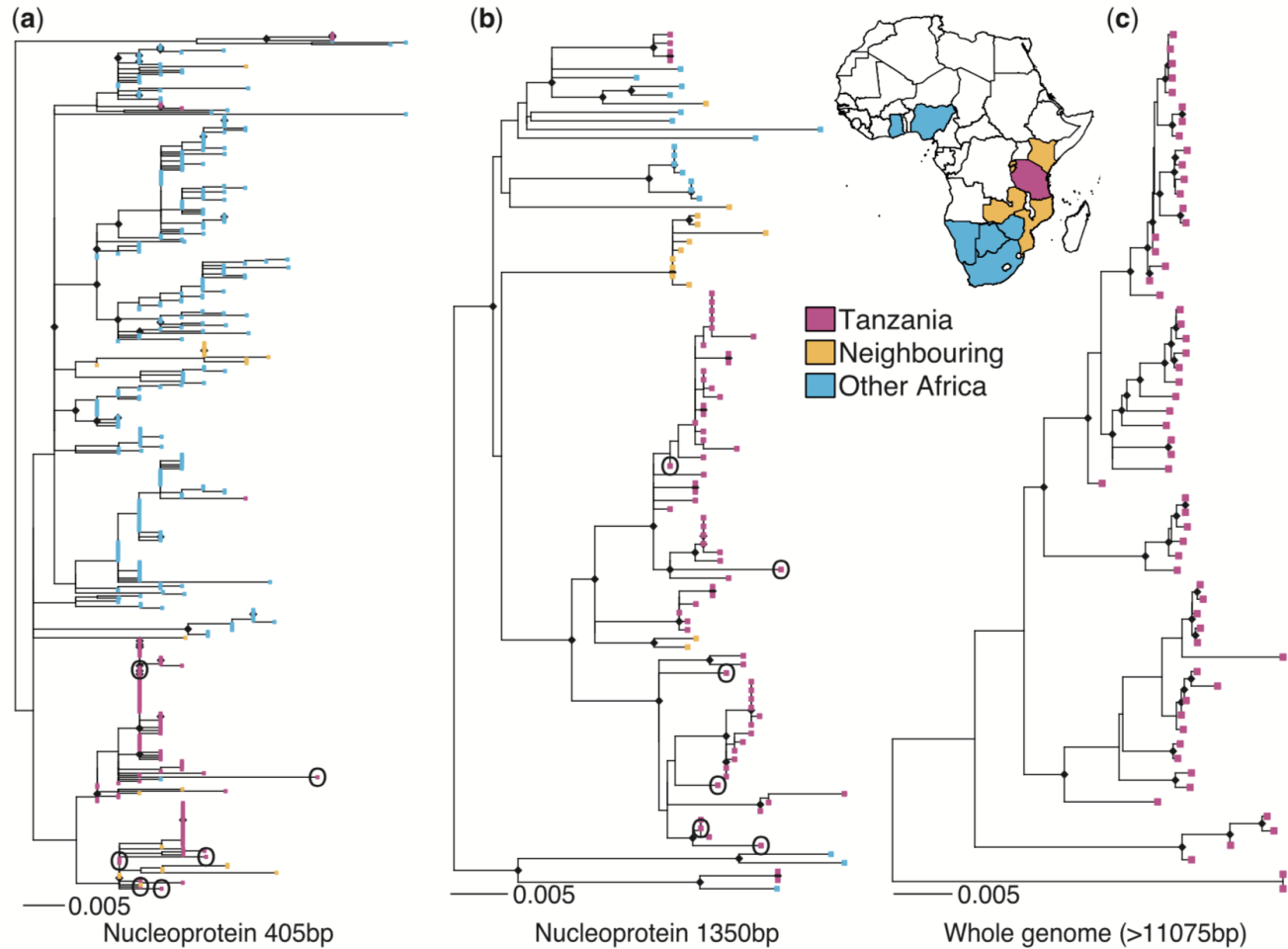
Short sequences (362 bp)

Allows basic strain typing

Limited resolution: many sequences identical

Nishizono et al. 2002

Higher resolution from whole genomes



Brunker et al.
2015

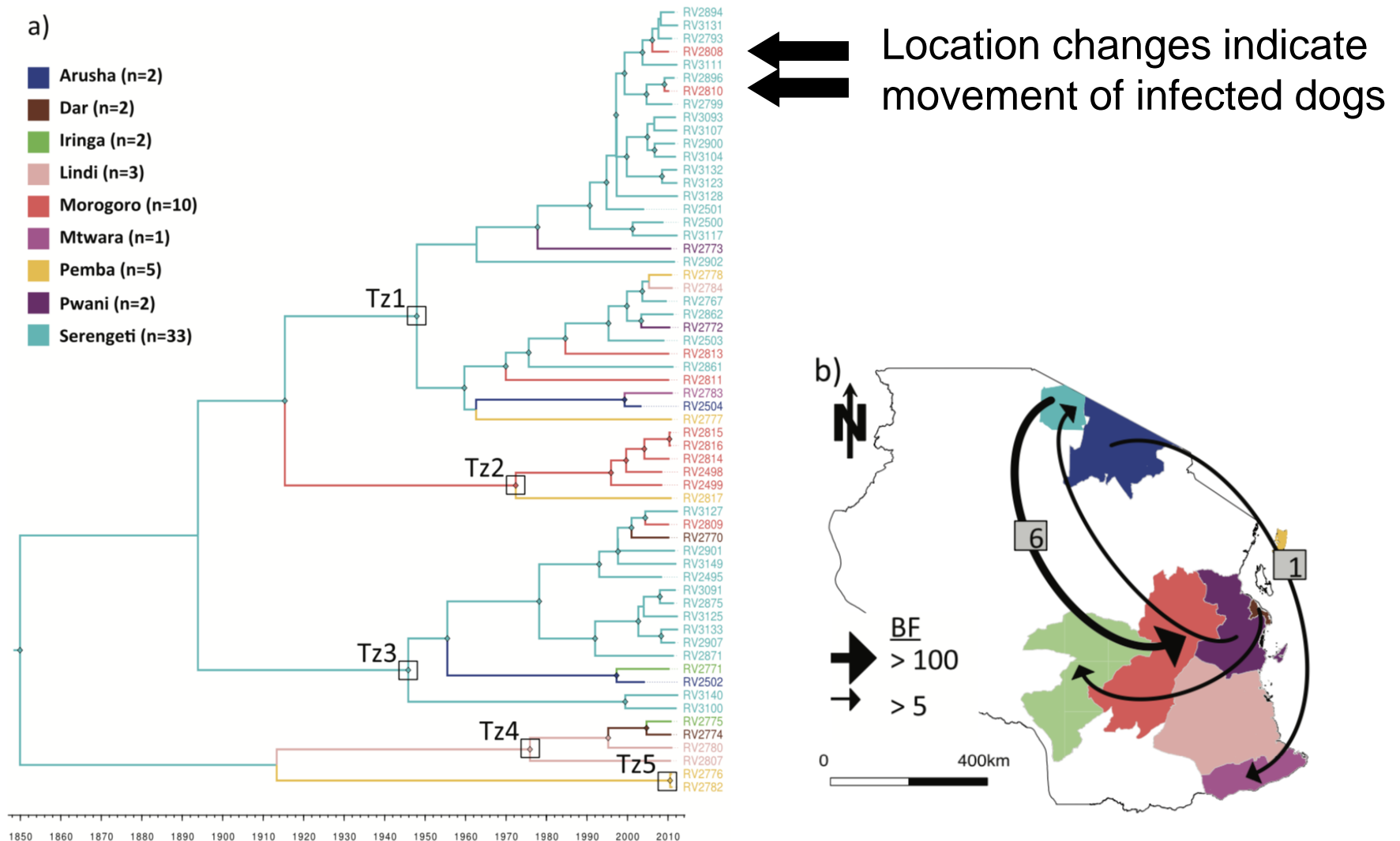
Identical
Sequences

very common

common

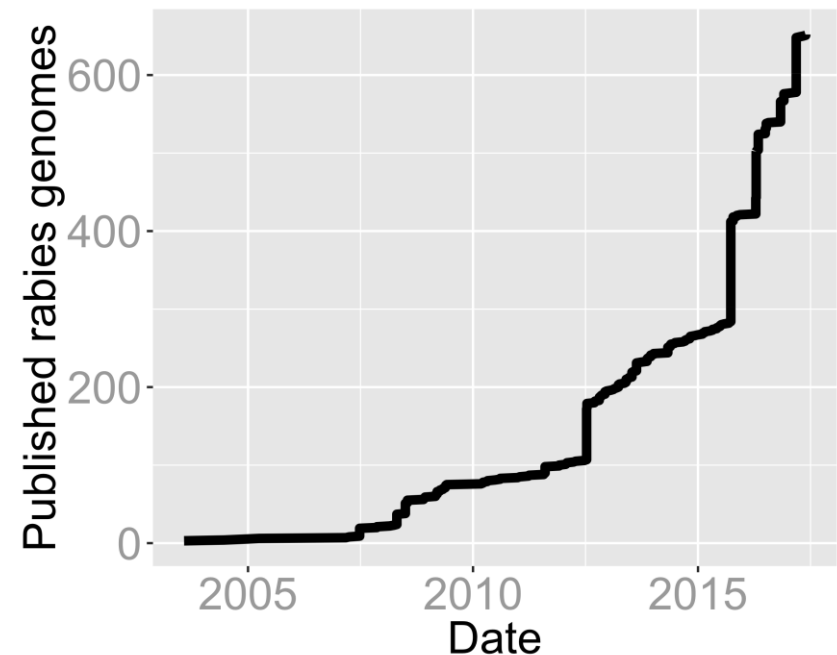
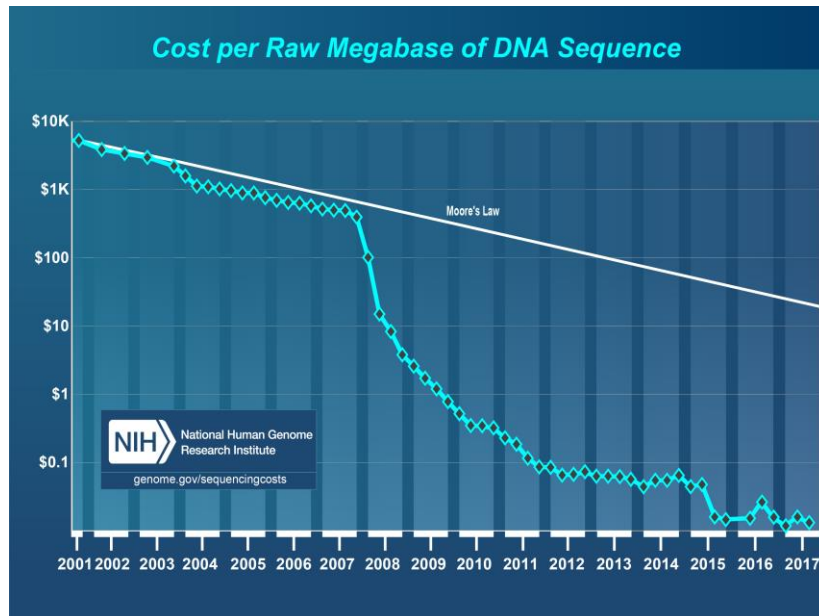
rare

Insights from genomic data



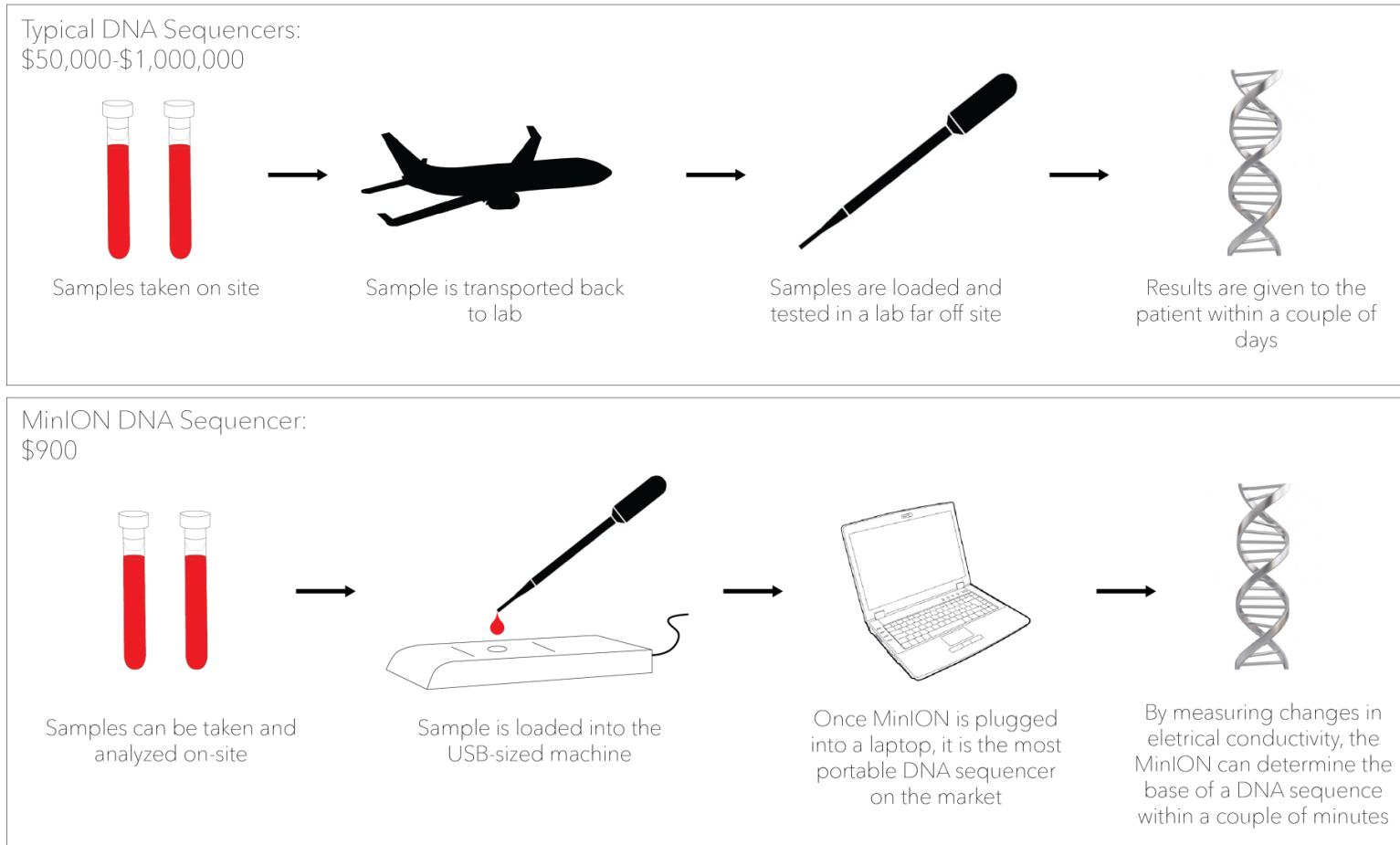
Adopting a genomic surveillance approach

Generating whole genome data made possible by massive parallel sequencing technologies that have brought down costs



But often long time lags until data are available

Portable DNA sequencers: genomes in real-time



Genomic surveillance: closing the loop

