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SSI surveillance

Plus barriers and challenges

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PH WGS workshop, Copenhagen 2014

Who are we all?

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- Character traits in typing method development
  - Technocratic utopian
  - The evangelist/the champion
  - The Luddite (will not embrace)

- Need for ‘skeptical enthusiasts’ or the ‘Open minded pragmatist’

SSI surveillance

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- *Listeria*
  - WGS as primary method in real time surveillance since Sep 2013
  - Overall focus on optimal cluster detection
- *E. coli*
  - The runner up for this years WGS real time implementation
  - Much focus on gene variant detection
- *Salmonella*
  - Currently WGS on clusters/outbreaks
  - WGS real time pushed forward to 2015-16
    - Due to the sheer volume
    - Economy – need to stop other methods

Listeria workflow

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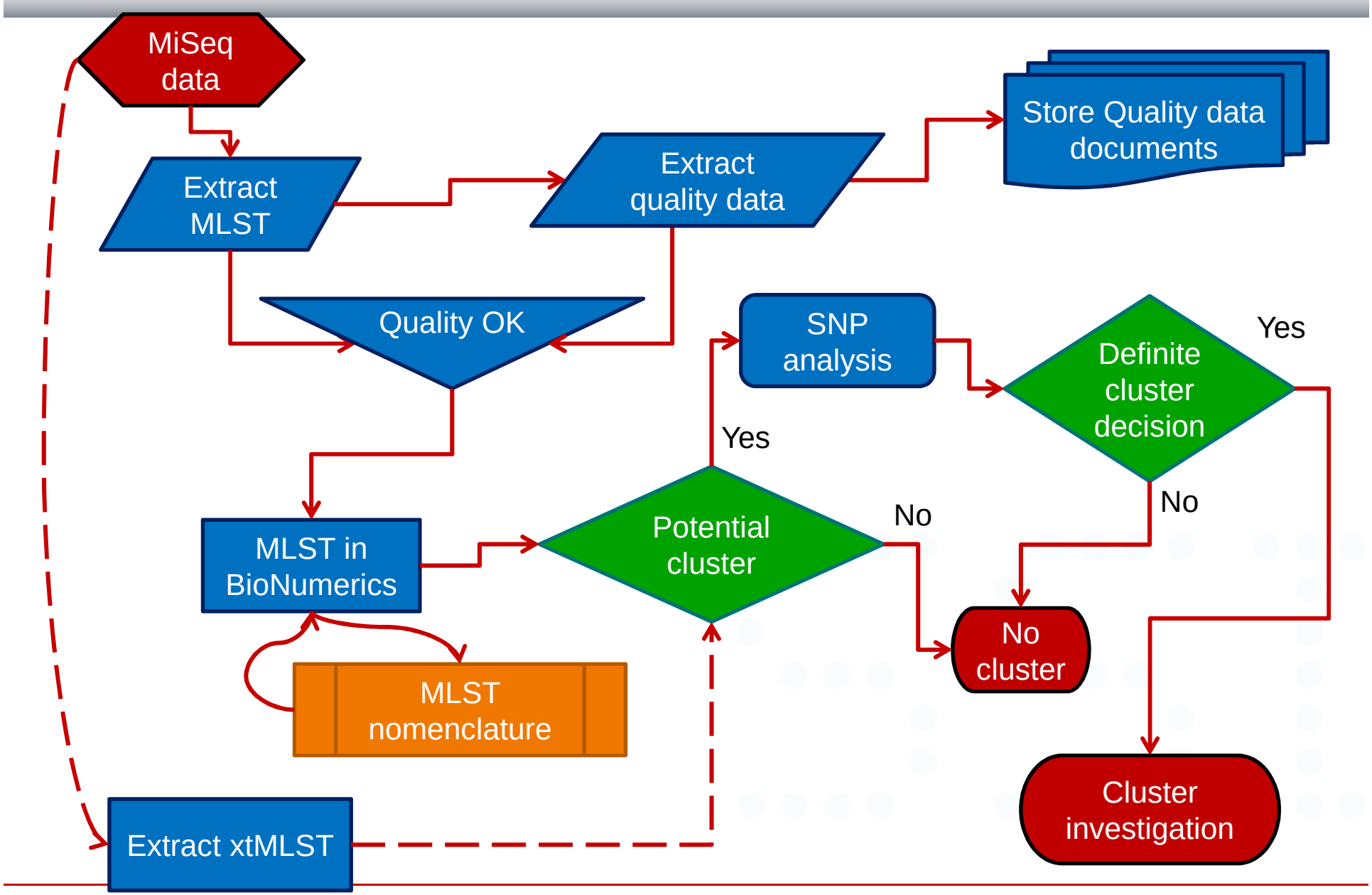

Listeria

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- Extraction of MLST sequences via mapping
  - Keeps the quality calls
  - No need for assembly
  - Has potential problems if MLST loci contains indels
- MLST sequences imported into BioNumerics

- SNP analysis within ST
  - .fasta file with string of SNPs imported to BN

- Script to extract Molecular Serotype from assembled data

Fast enough?

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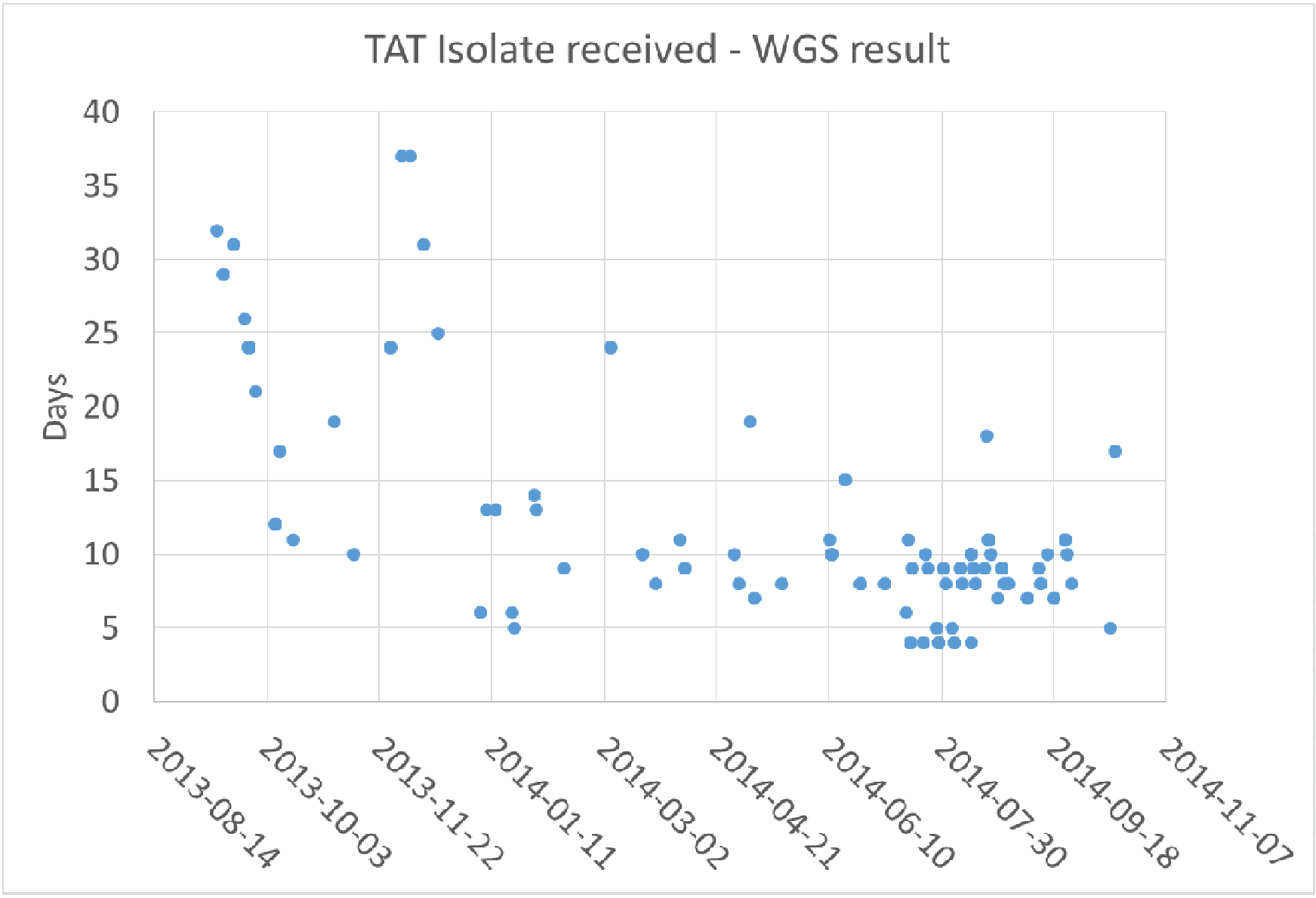
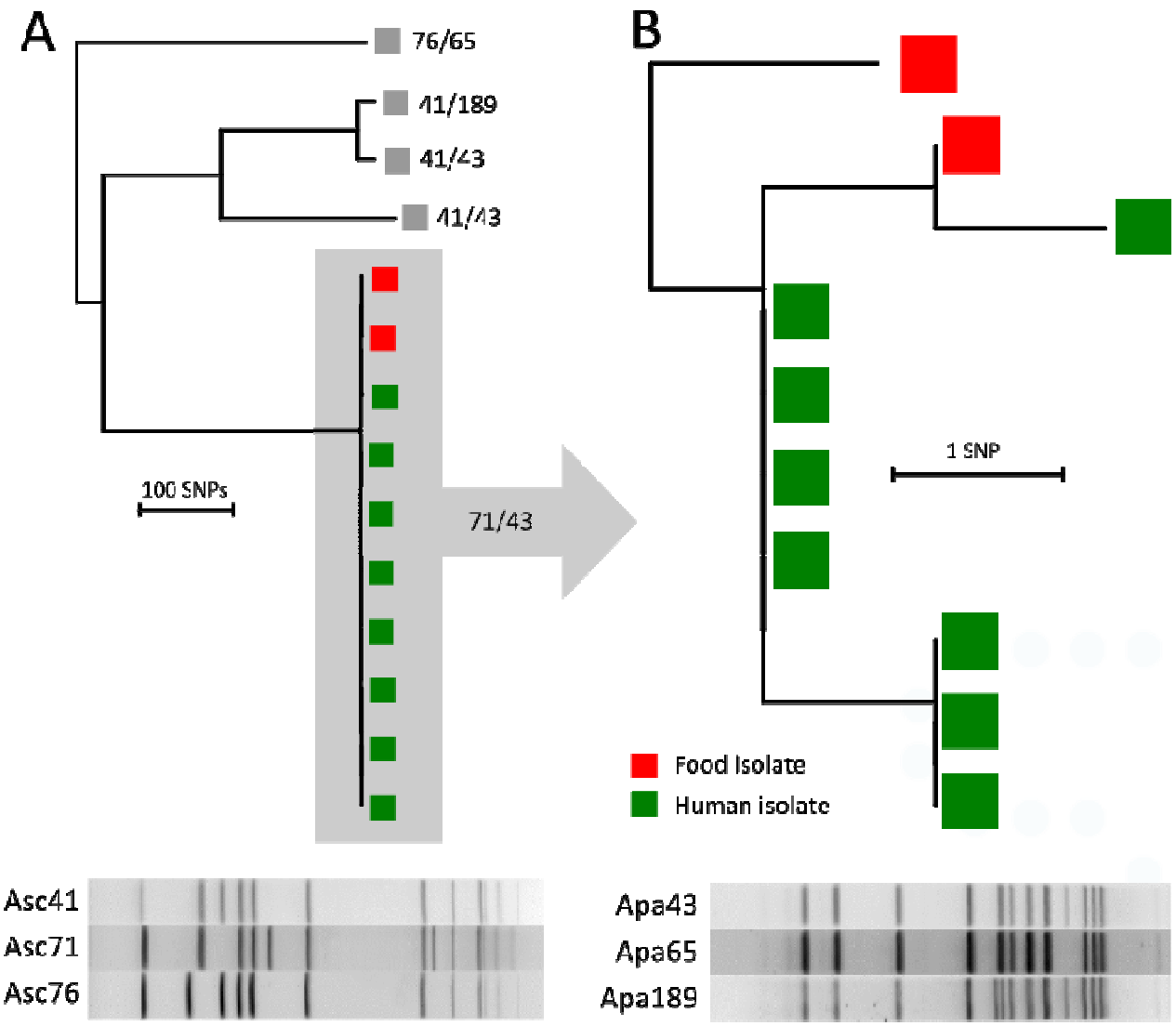


How many SNPs and still considered a cluster?



Confirmed outbreak: meals-on-wheels catering

- 8 patients with listeriosis within 1 week
- One isolate from each patient
- Two isolates from a later batch of food sampled at same company
- PFGE pattern not seen in DK before 2009
- MLST: ST-9

How many SNPs and still considered a cluster?

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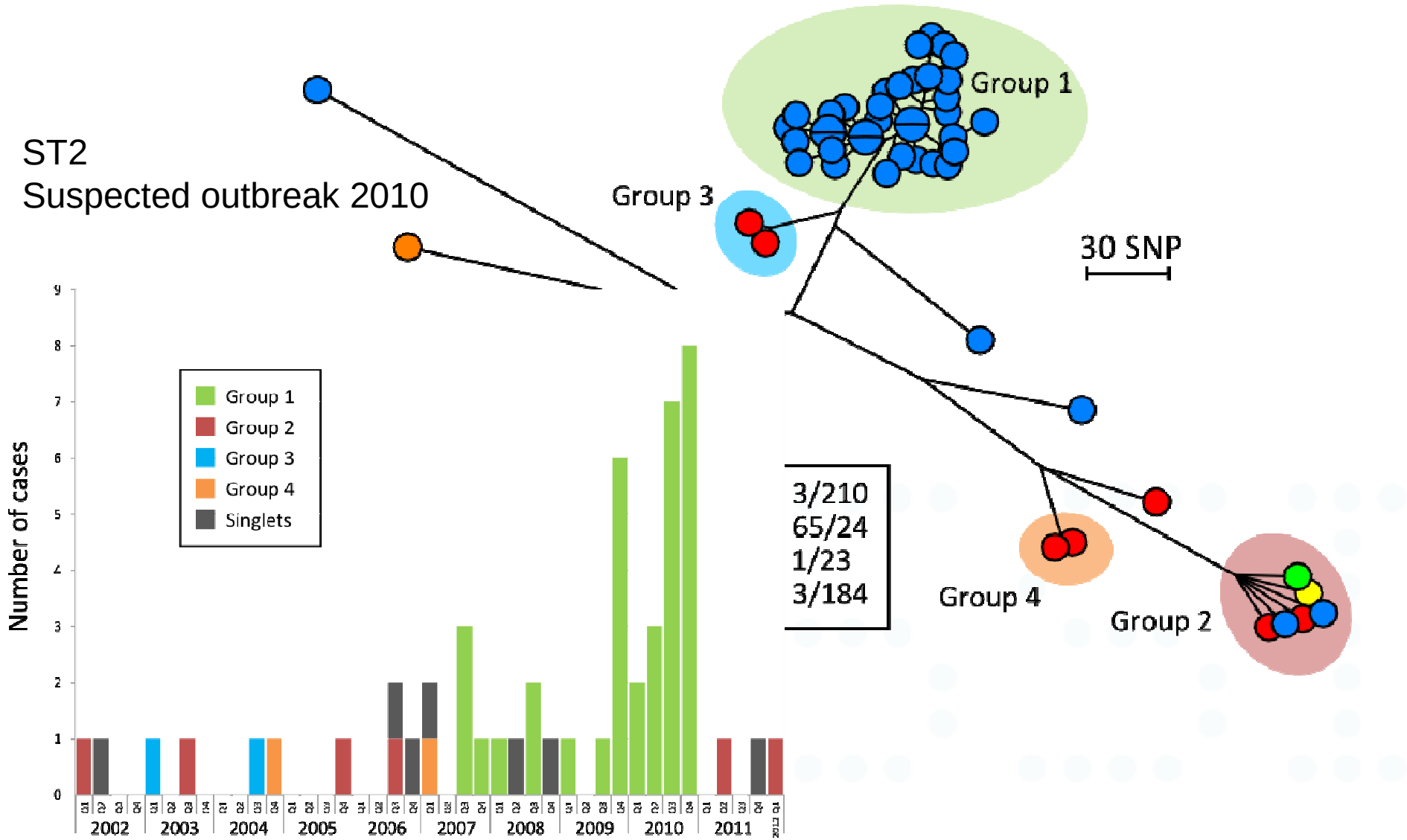

How many SNPs and still considered a cluster?

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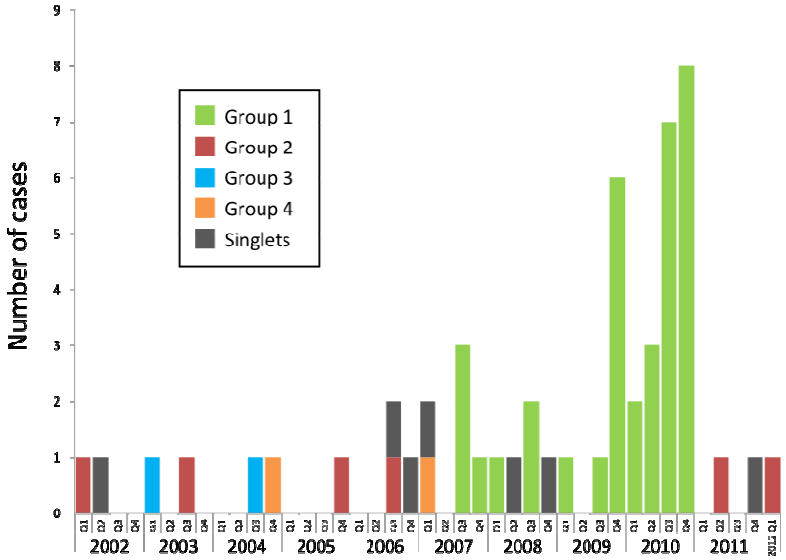
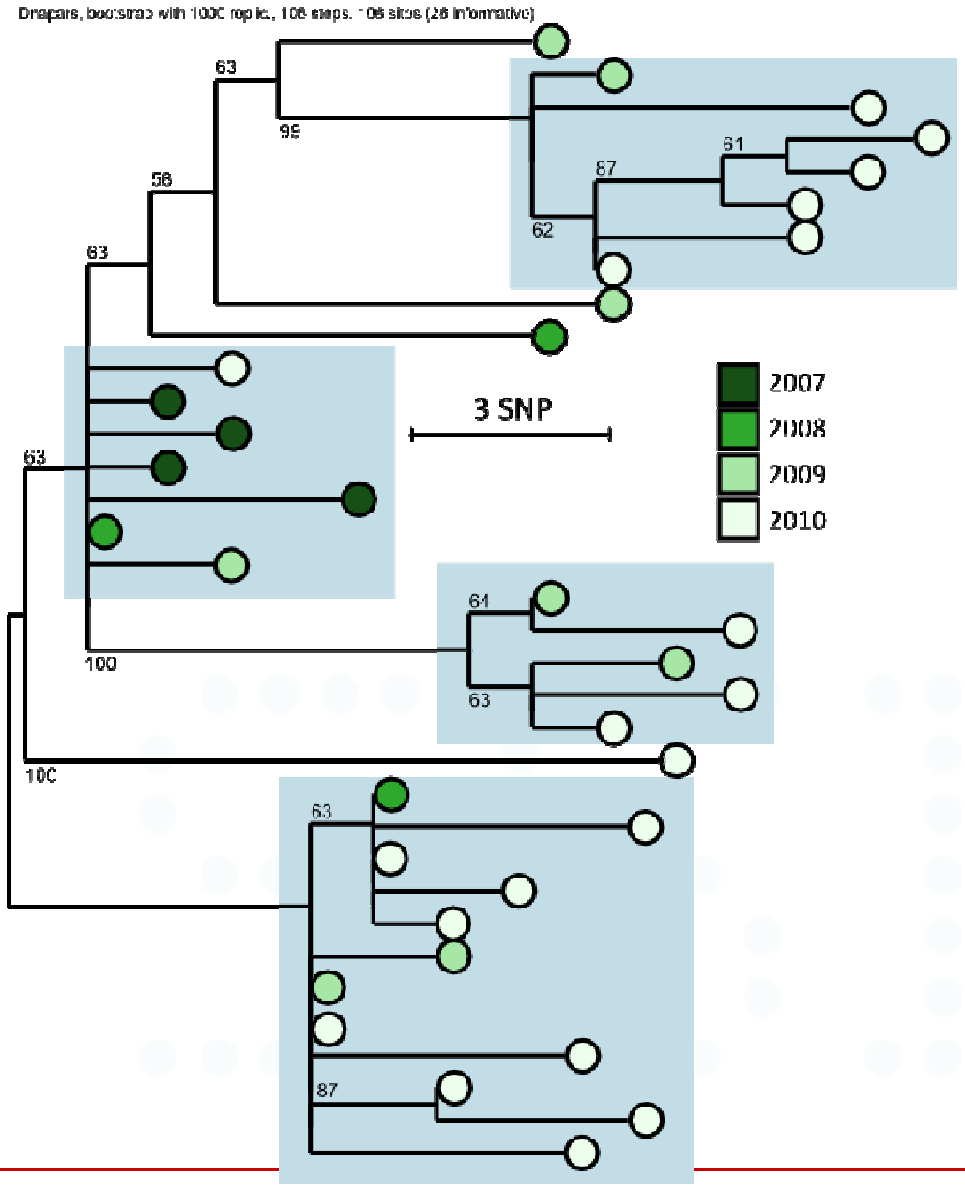
Group 1





Choose your reference for mapping

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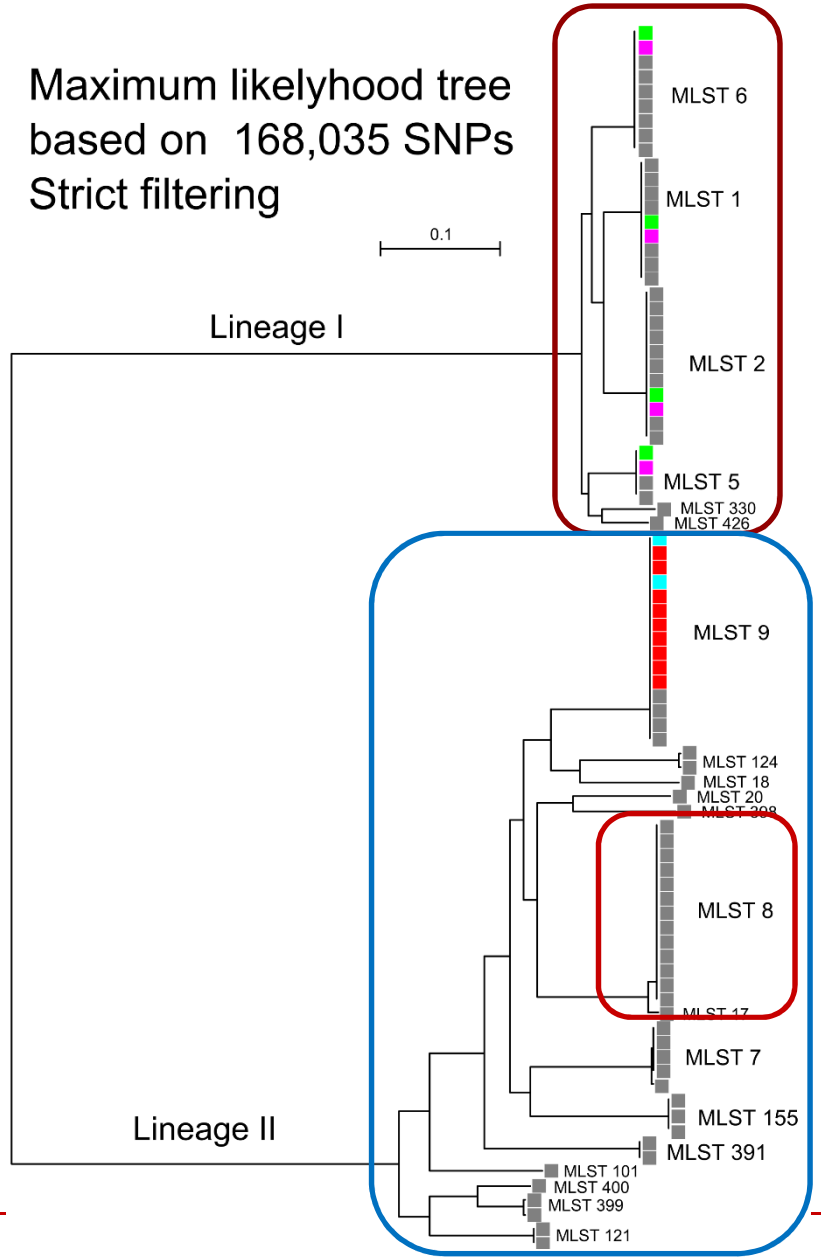
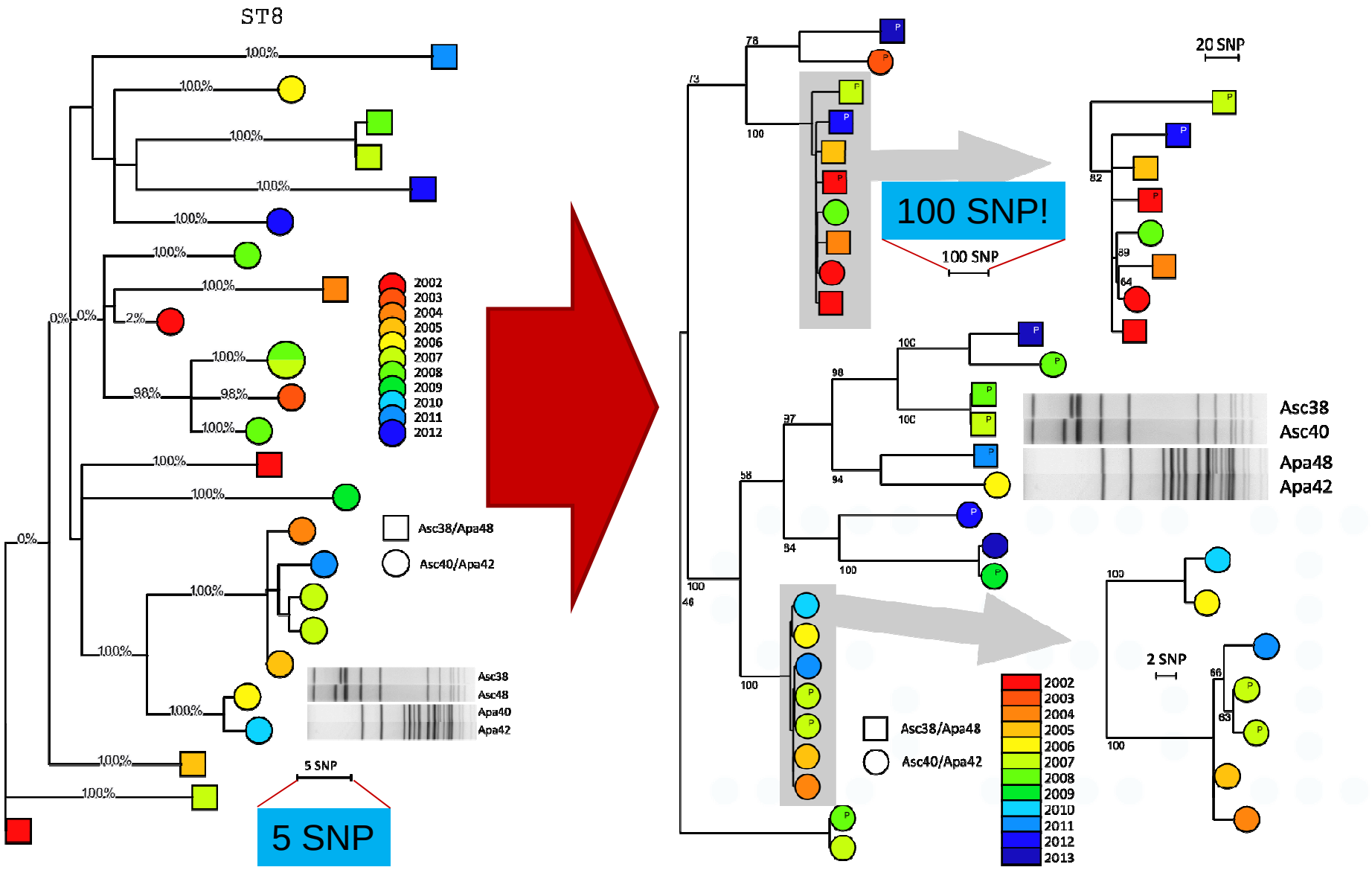
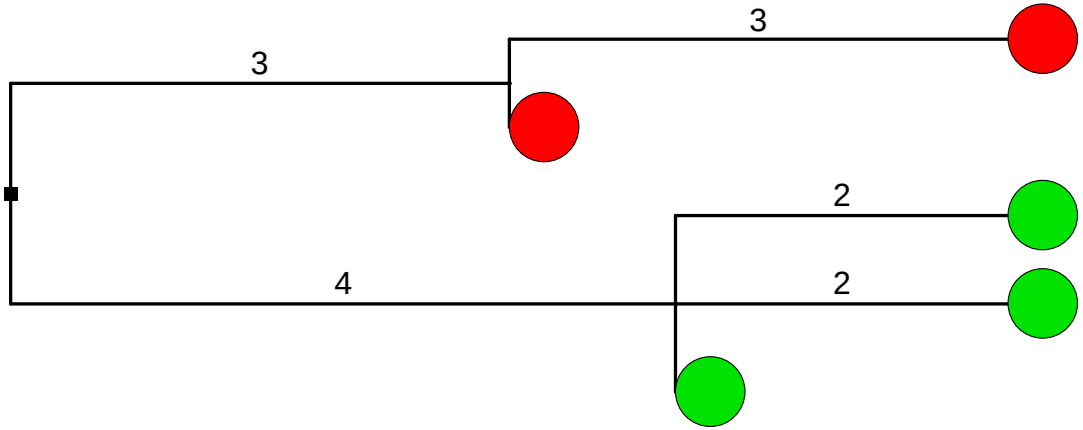


- Starting point
  - Lineage specific references
  - Works fine most of the time for cluster detection
- Closer study of ST8

From general to ST-specific reference ST8

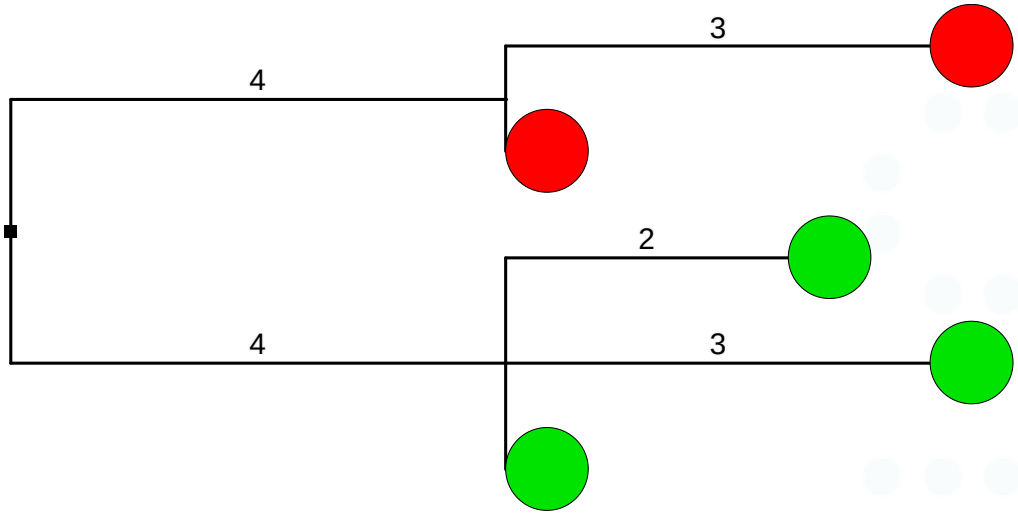


Not always a big difference - ST14



Mapping against lineage specific reference

n(SNP) = 14



Mapping against **cluster** specific reference

n(SNP) = 16

Clusters over time

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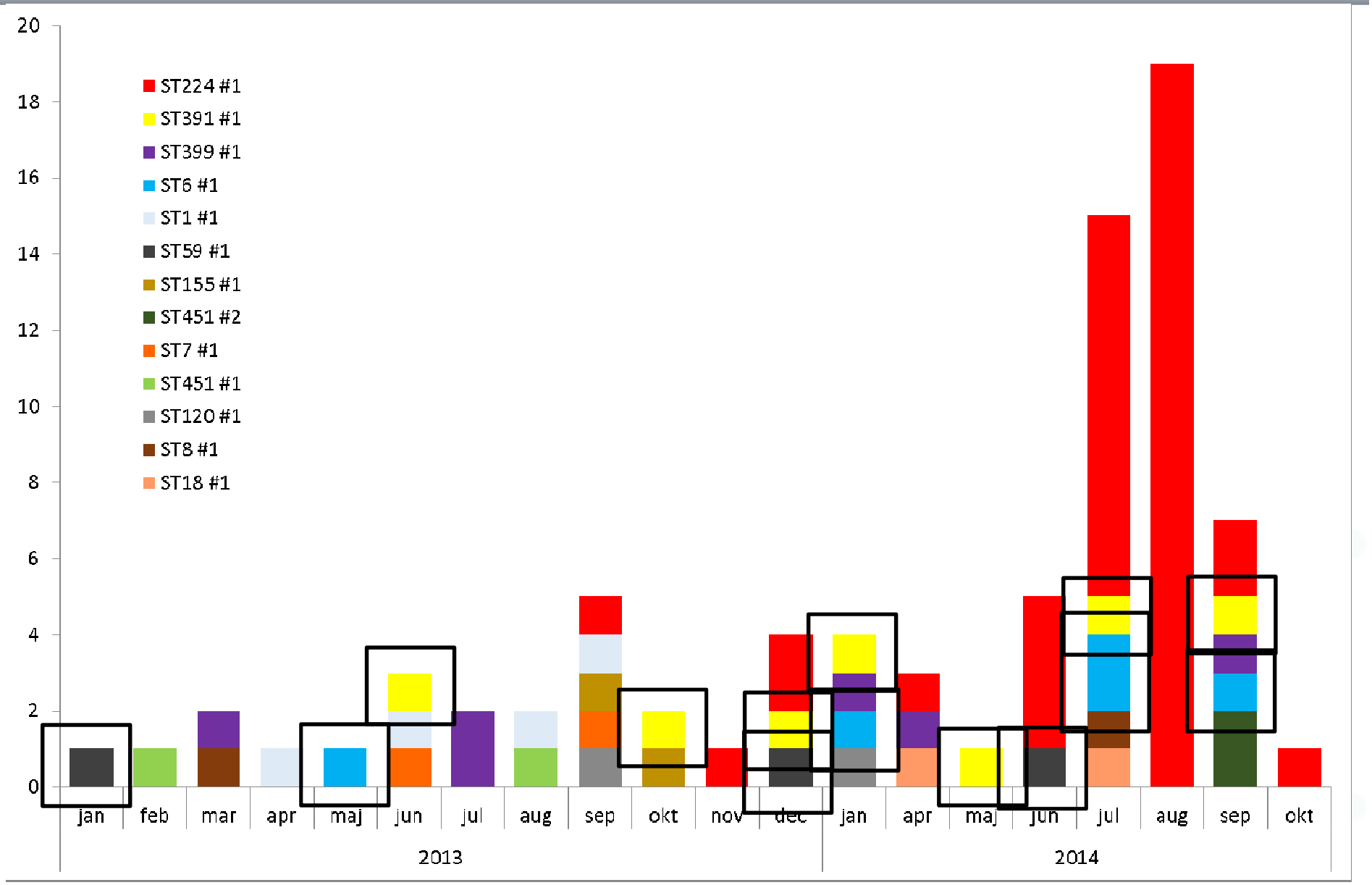

Cluster definition

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- Do we need several definitions? E.g.
  - Point source human cluster
  - Food isolates from a farm with a steady population
- Or, should we always define clusters ad hoc?

- Support with Epi-data

Salmonella Typhimurium typing: MLVA and WGS

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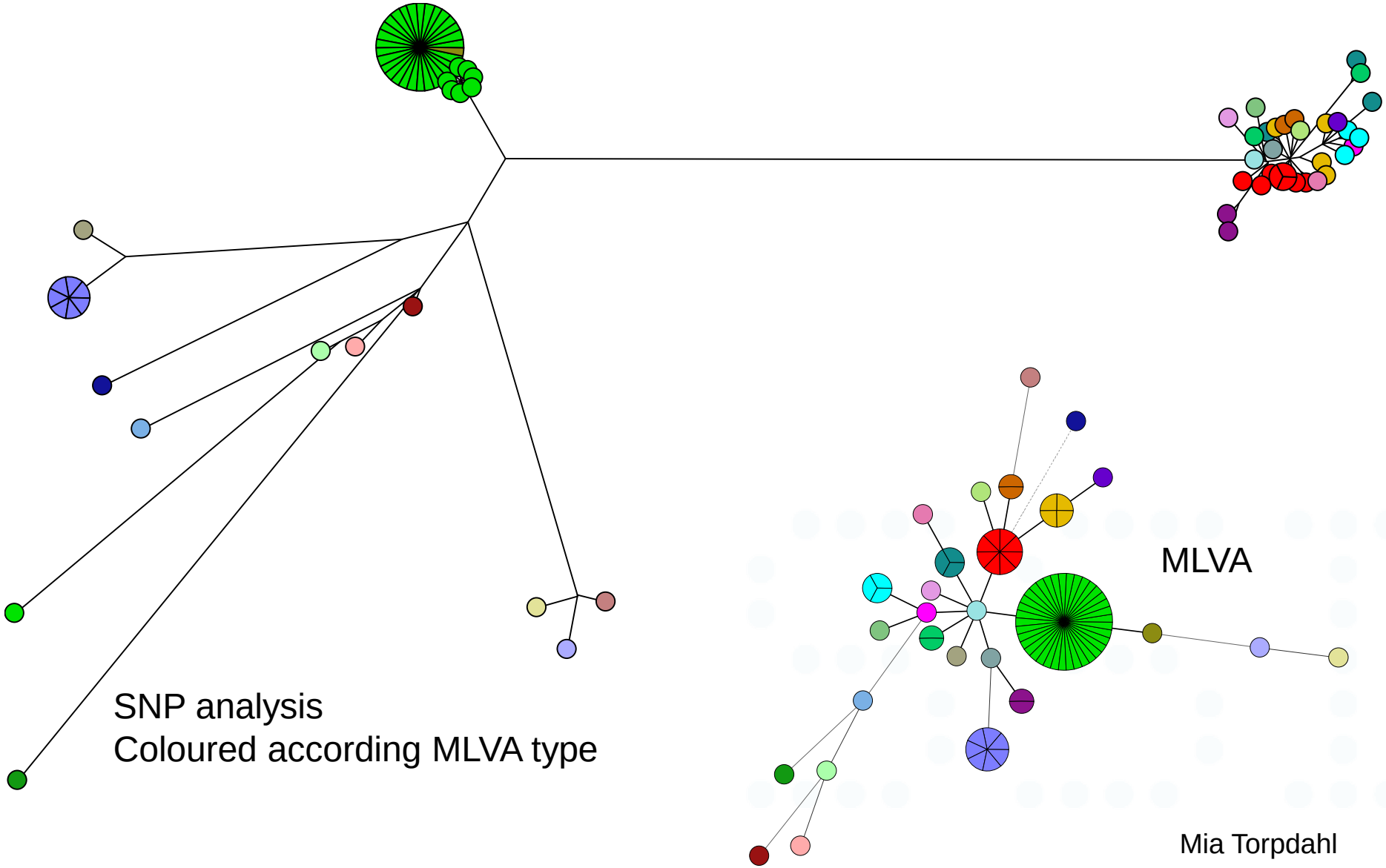

Mia Torpdahl

Clusters of MLVA- and SNP-types

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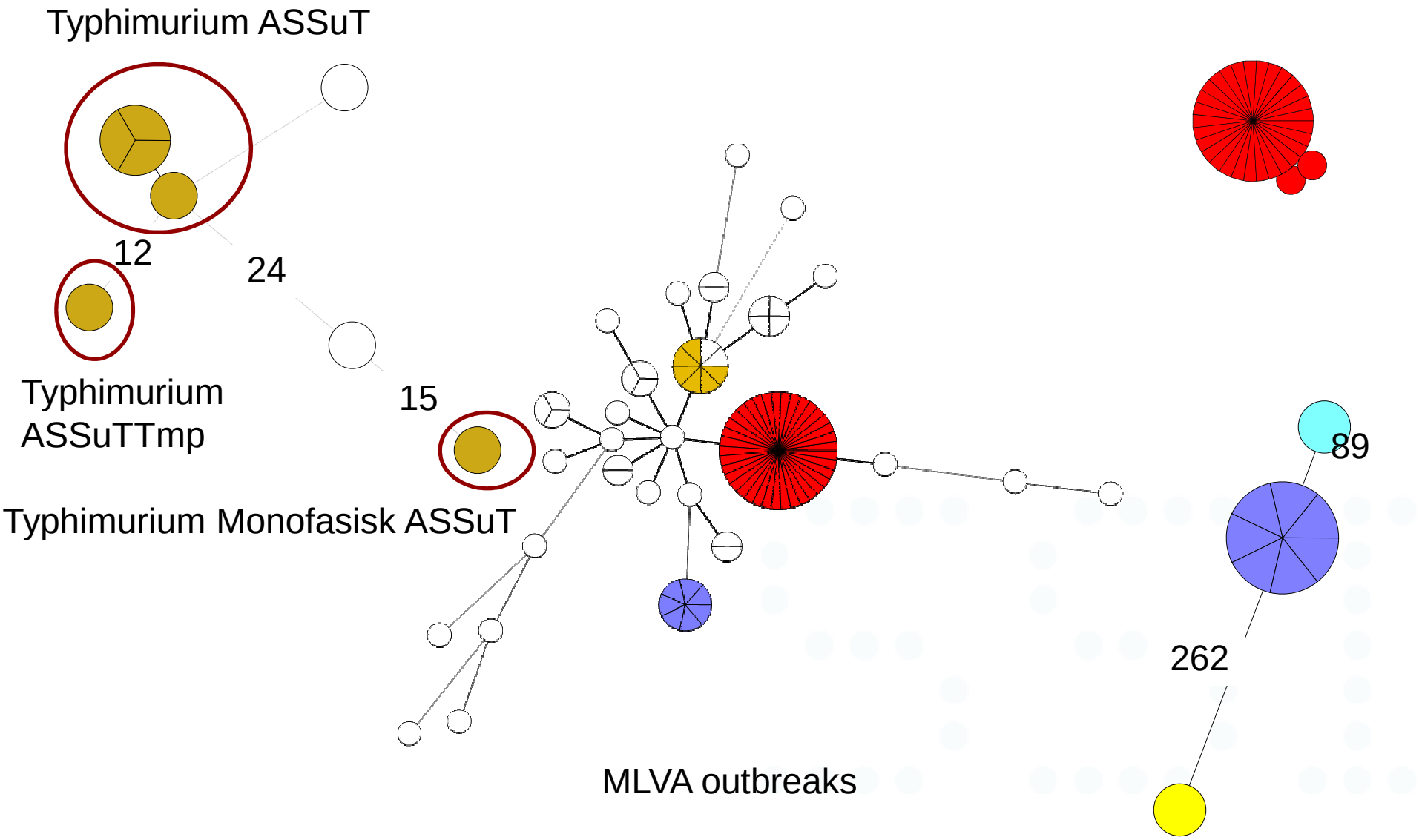

Pathogenic E. coli (verotoxin-producing E.coli)

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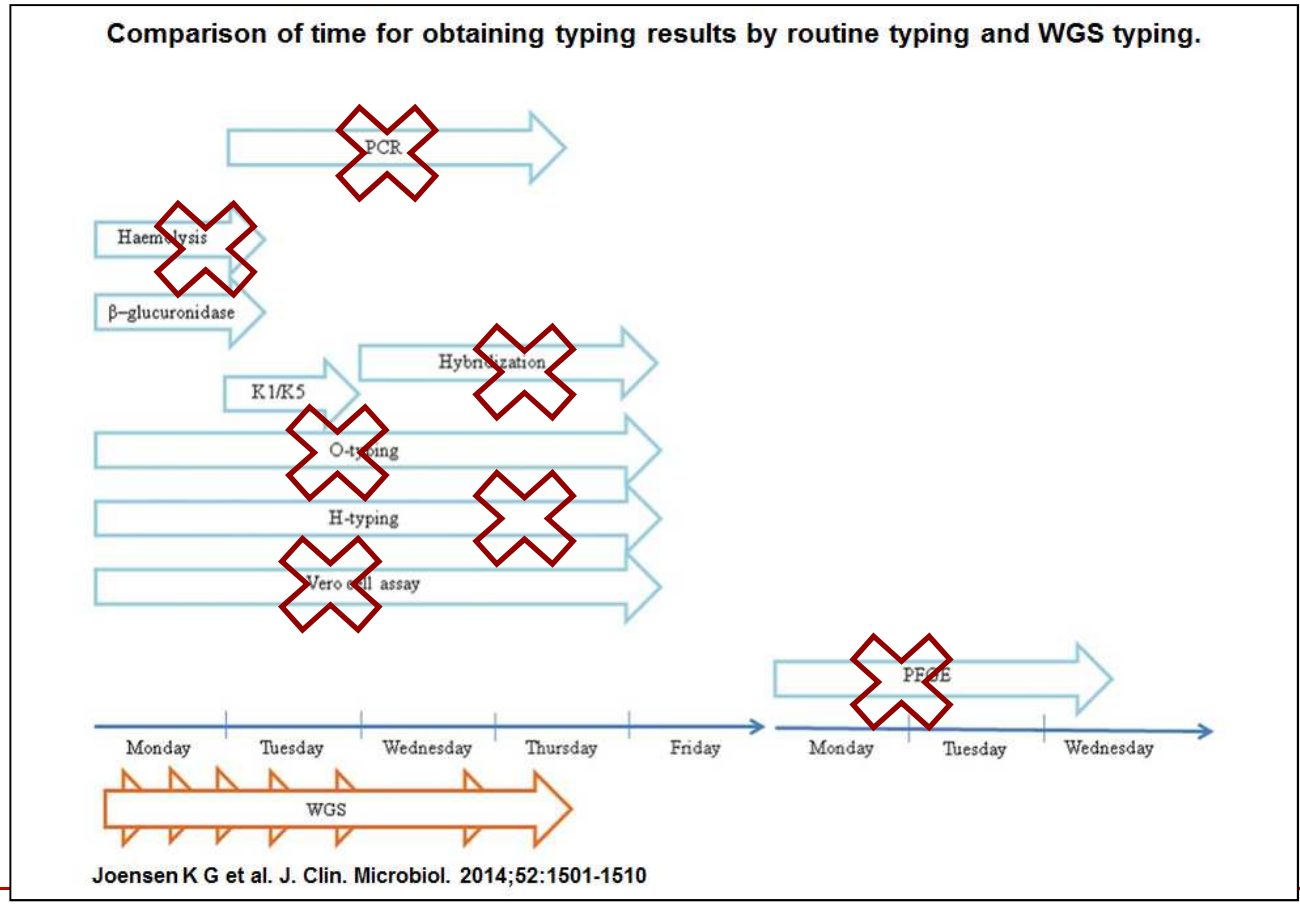
- Expensive and time consuming characterisation:
  - Virulence profile → pathogroup, virulence potential, HUS-associated types
  - O:H-serotype is useful, e.g. related to expected epidemiology, sources/reservoirs
  - High-discriminatory typing needed for outbreaks
- Cost-effective to replace this by WGS - if sufficient validation results are obtained



BARRIERS AND CHALLENGES

Barriers and challenges

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- Sharing of data
  - Cloud storage?
  - Do we need to share raw data?
- Communicate results to
  - Epidemiologists
  - Hospitals
  - Media
- Nomenclature
  - Gene by gene
  - SNP
  - Curation of nomenclature
- Interpretation of result
  - 0-10 genes/SNP difference in Listeria?
- Turn around time
  - Fast enough?
- Harmonization - Do we need to standardise?
  - Equipment?
  - DNA/Library prep?
  - Analysis tools?
- Analysis
  - Web tools/pipelines
  - Is a bioinformatician essential?
  - BioNumerics
- Drop old methods
  - Serotyping
  - AB resistanace
    - Resfinder-like tools
    - Fewer genes/antibiotics detected
    - Trust a single point mutation?

SNP cluster colour

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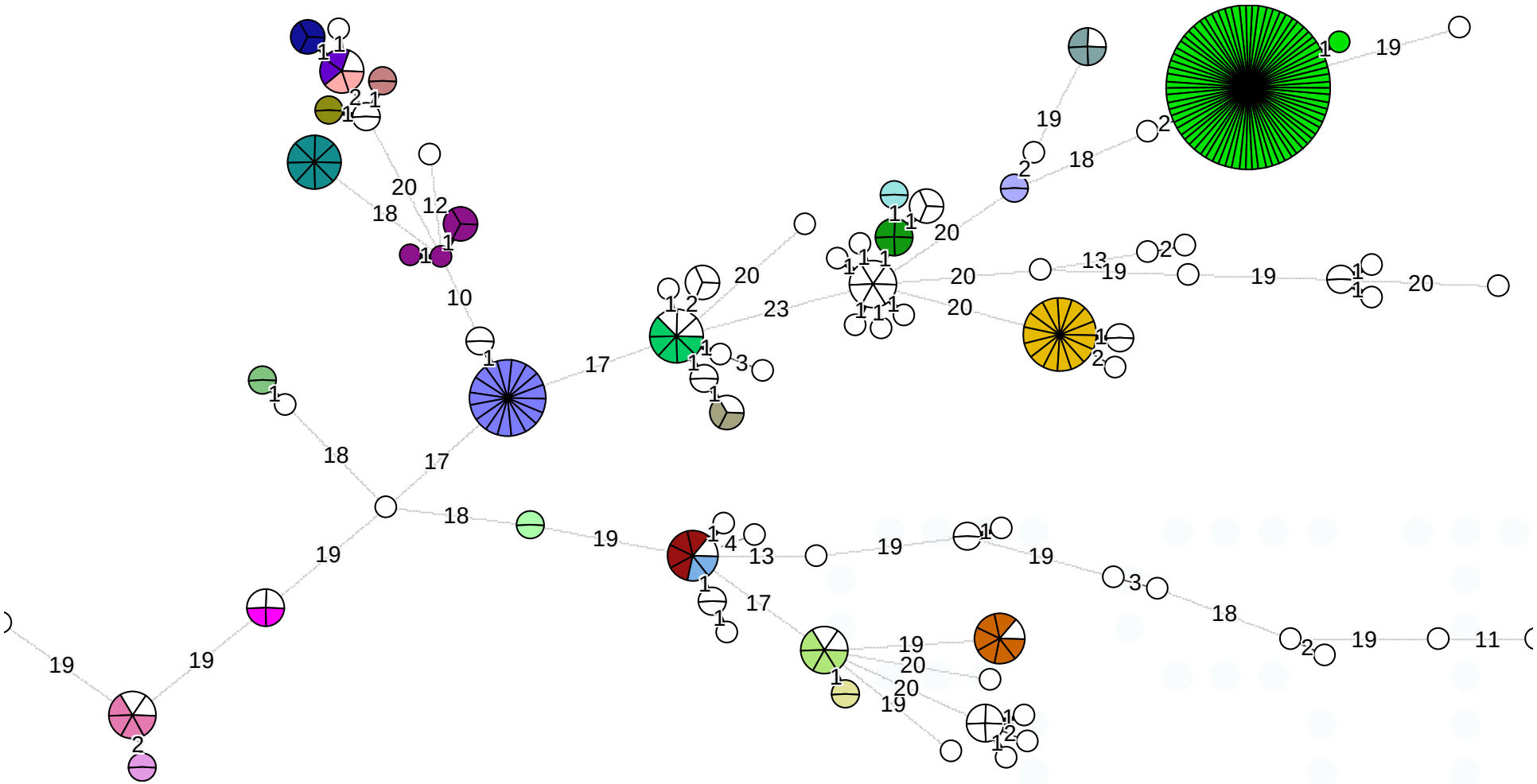

SNP cluster colour MLST ST labels

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