

Cg-MLST reveals a more differentiated transmission than MLST in a rise of VRE in a University Hospital

S.K. Hansen, L. Andersen, M. Detlefsen, A. Holm, M.N. Skov, P. Antoniadis and M. Kemp
Department of Clinical Microbiology, Odense University Hospital, Denmark

P37

**HIS 2018
Liverpool, GB**



1. Background

Vancomycin resistant *Enterococcus faecium* (VREfm) was only detected sporadically in the Region of Southern Denmark until 2016, when a rise in number of cases appeared in the University Hospital.

Multi Locus Sequence Typing (MLST) and core genome MLST (cg-MLST) based on Whole Genome Sequencing (WGS) were carried out in order to:

- trace transmission routes
- assess the two methods as epidemiological tools using sequence types (STs) and complex types (CTs)

2. Materials/methods

- One VREfm isolate from each of all 38 patients
 - Period: January 2014 - June 2017
 - WGS
 - MLST and cg-MLST
 - Cluster arrangement and phylogeny
 - Epi-curves of ST and CT
- MiSeq Instrument
SeqSphere software, Ridom

3. Results

MLST:

- 6 different STs
- ST-80: 26 isolates

Cg-MLST:

- 19 different CTs
- ST-80: subdivided into 7 different CTs and 5 isolates with no assigned CT
- CT-993: dominated and consisted of 12 of the ST-80 isolates

Epi-curves:

- CT-993 was transmitted between 7 patients

4. Conclusion

□ Cg-MLST

- allowed a more detailed distinction between types than MLST
- gave evidence of transmission of specific CTs
- may prove to be a valuable tool in infection control

□ Both MLST and cg-MLST should be supplemented with admission history in outbreak investigation

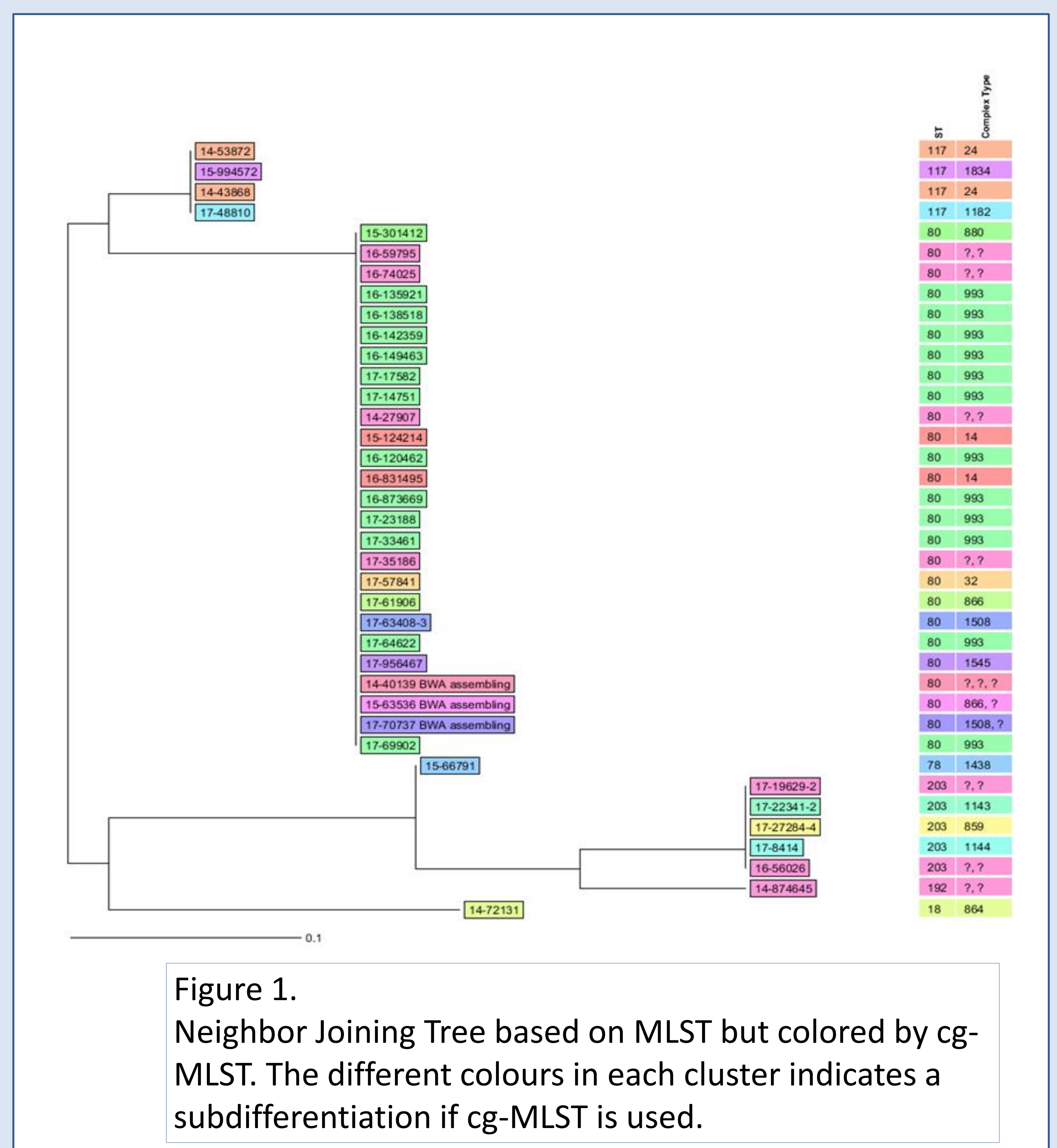


Figure 1. Neighbor Joining Tree based on MLST but colored by cg-MLST. The different colours in each cluster indicates a subdifferentiation if cg-MLST is used.

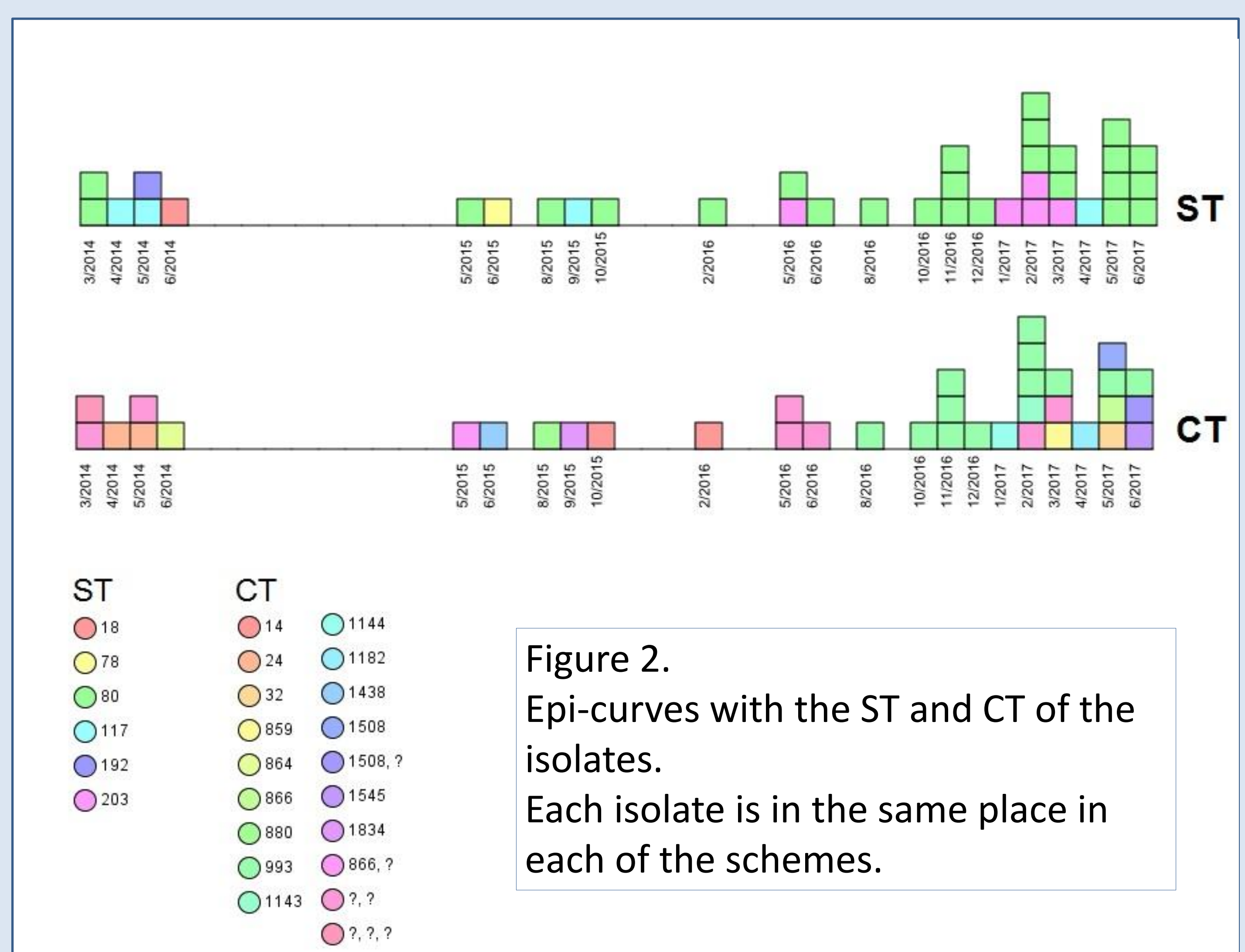


Figure 2. Epi-curves with the ST and CT of the isolates. Each isolate is in the same place in each of the schemes.