

Predominance of *Acinetobacter baumannii* Sequence Type 2 (ST2) among Clinical isolates from two Detroit Hospitals using Whole Genome Sequencing (WGS)

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Introduction

- Healthcare-associated infections (HAIs) caused by *Acinetobacter baumannii*, an opportunistic gram-negative pathogen, often contribute to morbidity and mortality among hospitalized patients.
- Recently, carbapenem resistance in *A. baumannii* (CRAB) isolates is increasing due to intra-hospital spread.
- To determine molecular epidemiology of circulating hospital *Acinetobacter* strains in the Detroit area in a non-outbreak situation, we performed **whole genome sequencing (WGS) and whole genome multilocus sequence typing (wgMLST) analysis** to characterize genomic diversity.



Adapted from the CDC.gov website

Methods

- We performed WGS on patient isolates from two disparate, geographically distinct tertiary care Detroit hospitals admitted to 16 intensive care units (ICU) and non-ICU wards between 2017-2019.
- The samples were obtained 48 hours following admission of a patient in the hospital and genomic DNA was extracted using the QIAamp DNA Micro Kit (Qiagen, Hilden, Germany). Subsequently, libraries were prepared using the Nextera® DNA Flex Library Prep Kit (Illumina, San Diego, CA). Paired-end reads (2 × 151 bp) were generated using the Illumina NextSeq reagent kit and run on NextSeq instrument (Illumina, San Diego, CA).
- The contigs were *de novo* assembled using SPAdes assembler version 3.7.1 and WgMLST analysis was performed using BioNumerics software v7.6. (Applied Maths NV, Sint-Martens-Latem, Belgium). Minimum spanning tree (MST) was constructed to demonstrate the clusters in each hospital and their wards.

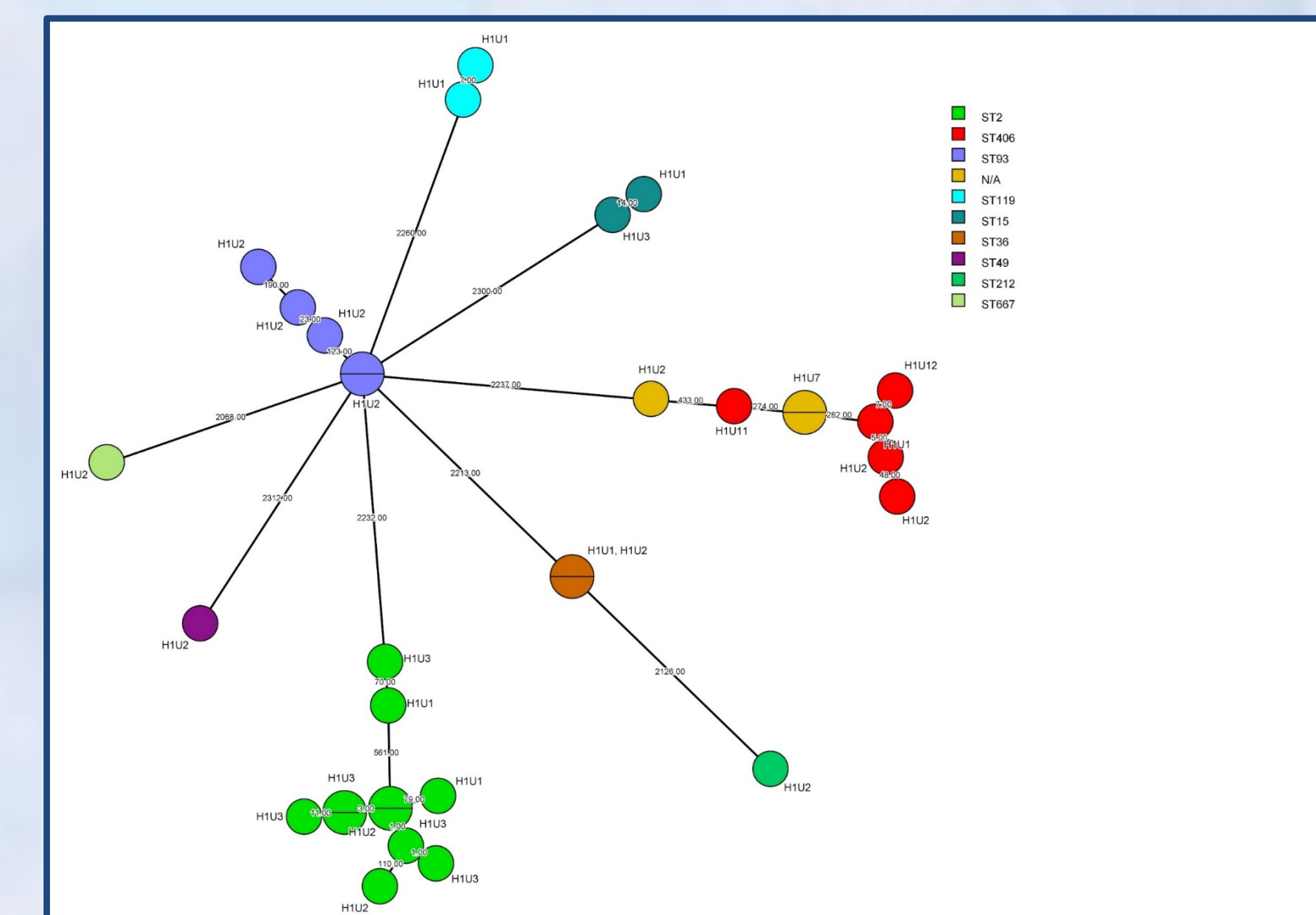


Figure 1a: Minimum spanning tree (MST) was constructed for H1 to demonstrate the clusters in H1 and their wards.

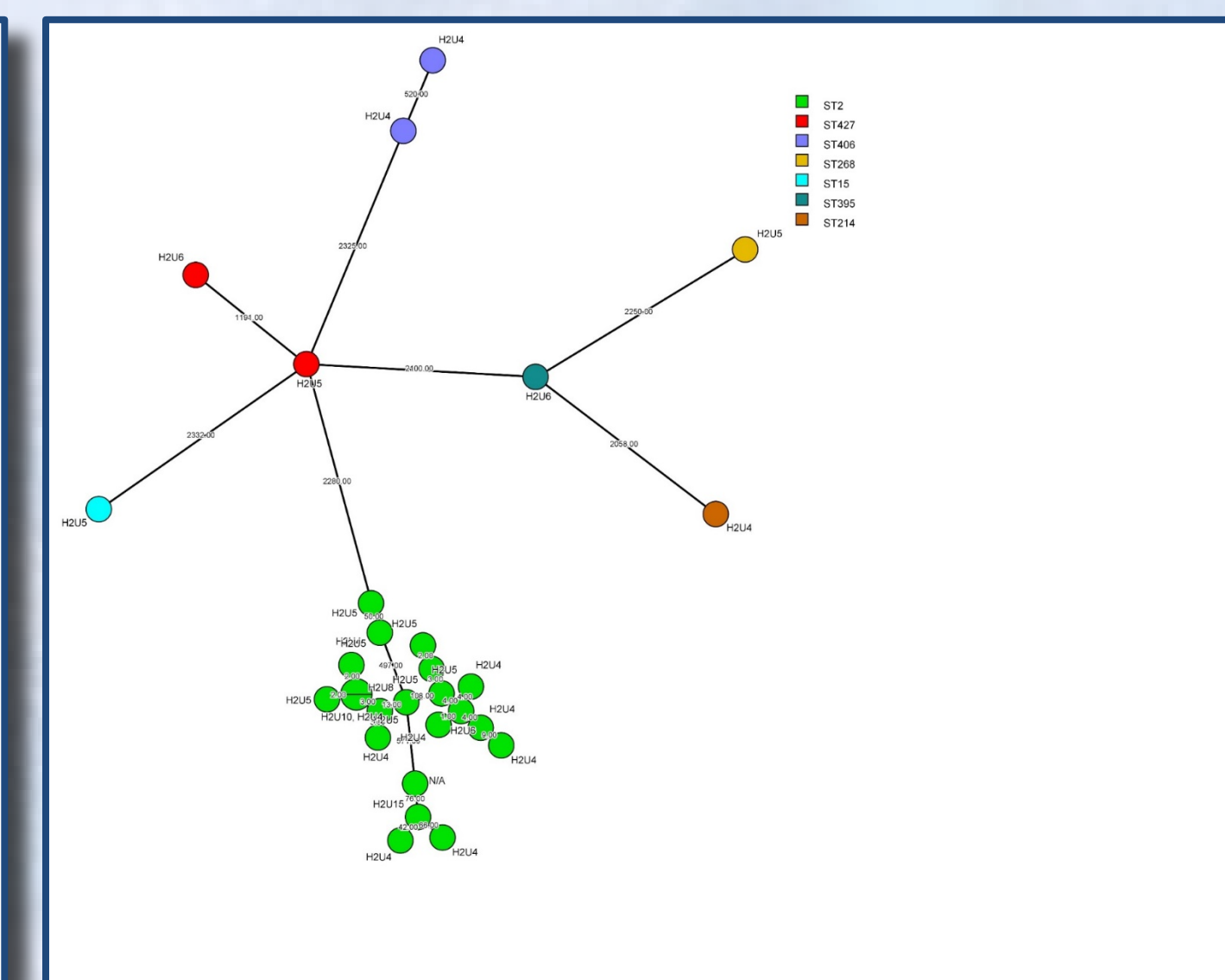


Figure 1b: Minimum spanning tree (MST) was constructed for H2 to demonstrate the clusters in H2 and their wards.

Sequence Type (ST)	H1	H2
ST2	11	20
ST406	7	2
ST93	5	0
ST15	2	1
ST427	0	2
ST36	2	0
ST119	2	0
ST49	1	0
ST212	1	0
ST268	0	1
ST395	0	1
ST214	0	1
ST667	1	0

Table 1: Total number of each sequence type (ST) in H1 and H2

Results

- WgMLST analysis was performed on a total of 62 *Acinetobacter baumannii* patient isolates, 33 of which were from hospital # 1 (H1) Fig.1a and 29 were from hospital # 2 (H2), Fig1b.
- Sequence type ST2 (52%) was the predominant sequence type for both hospitals (Table1, Fig 2a). In addition to ST2, ST93 (8%) and ST406 (8%) clusters were also found in H1 (Table1, Fig 2a).
- Most of the isolates were predominantly clustered in the intensive care unit (ICU) setting.
- Several identical sequence types of ST93 (2 identical in H1), ST36 (2 identical in H1) and ST2 (5 identical for H1 and 2 identical for H2) were also observed from different patients in both hospitals (Fig 2a). Unlike H1, H2 only has ST2 as a predominant cluster (Fig 1a,b,2a).
- Other sporadic sequence types such as ST119, ST36, ST49, ST212, ST667 for H1 and ST395, ST214, ST427 and ST268 for H2 were also observed (Table1, Fig 2a).

Conclusions

Our data suggests that-

- ST2 is the predominant sequence type circulating in both the geographically distinct hospitals and is endemic to the ICU.
- There was in hospital spread of this distinct *Acinetobacter* sequence type from one patient to the other raising concerns about infection control practices and the role of environment in the spread of these infections.
- ST2 has been previously reported to be the cause of outbreaks and is associated with antimicrobial resistance and virulence factors in other hospitals.
- Other common circulating sequence types in both the hospitals include ST406 and ST15. Early detection of these endemic strains within the hospital may be critical in preventing healthcare-associated infections in the future.

Acknowledgements

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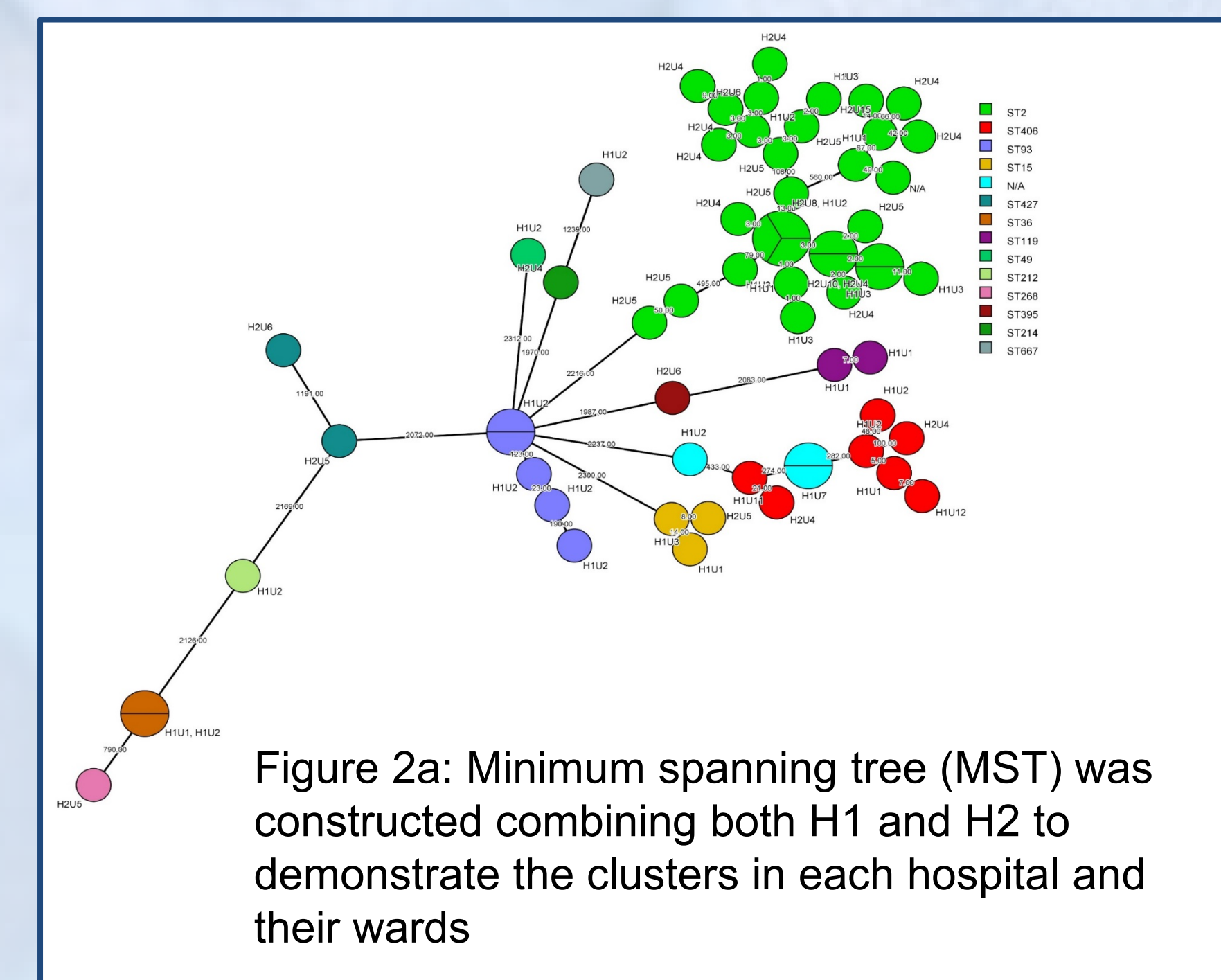


Figure 2a: Minimum spanning tree (MST) was constructed combining both H1 and H2 to demonstrate the clusters in each hospital and their wards.

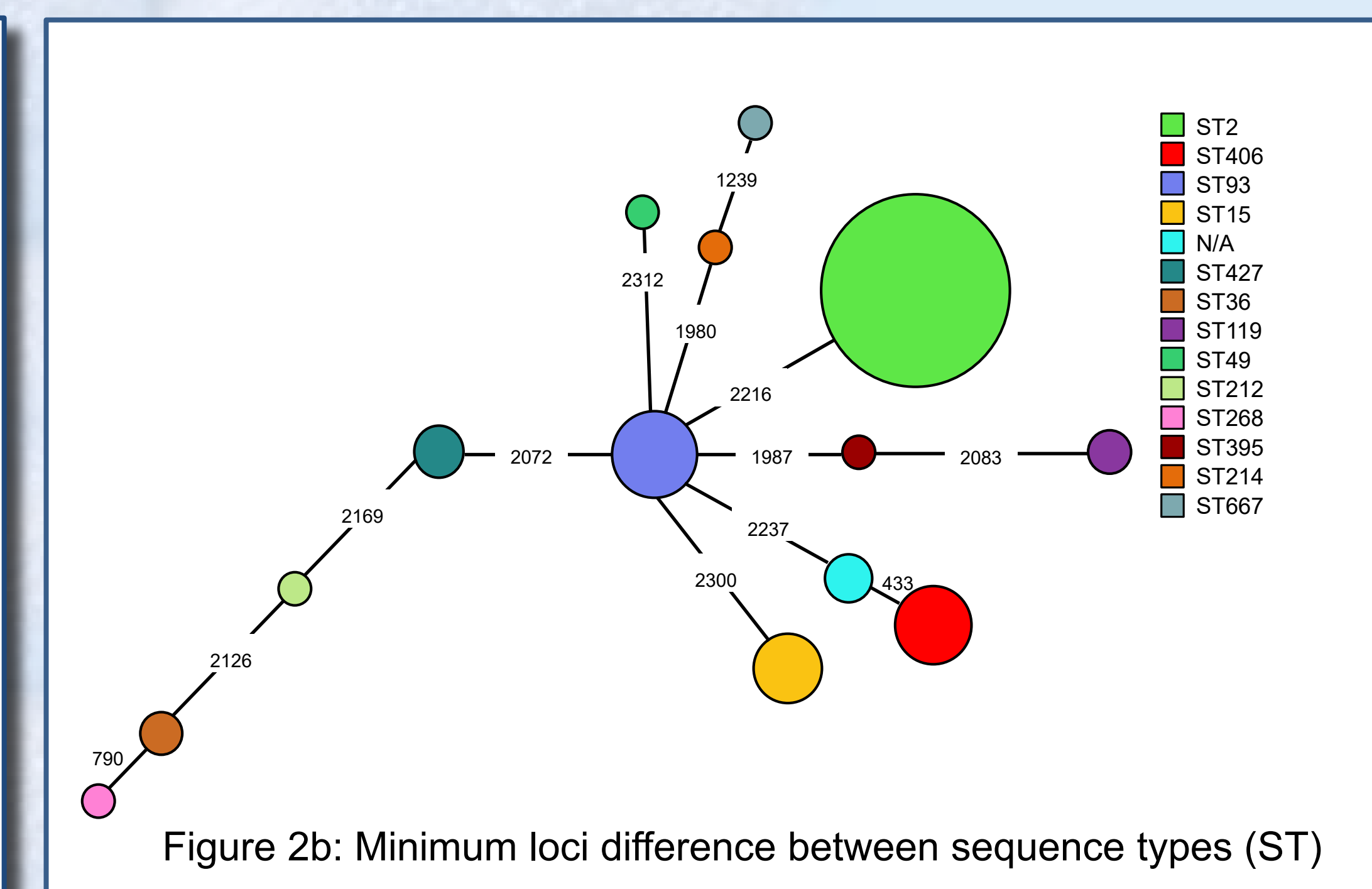


Figure 2b: Minimum loci difference between sequence types (ST)