Comparison of PFGE and core genome MLST for Detection of Local Salmonella and STEC clusters, Tennessee

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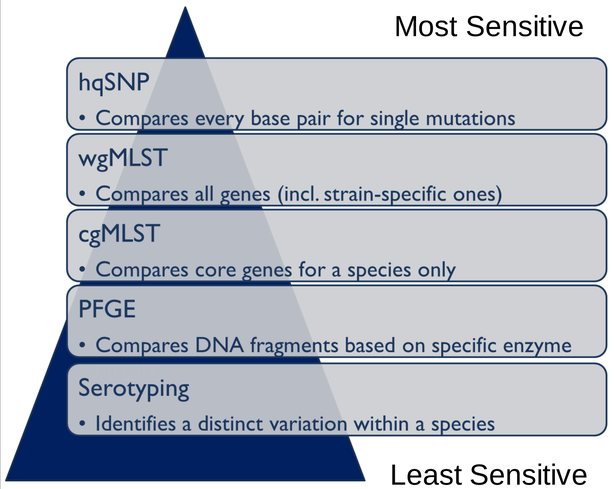
BACKGROUND

- Historically, pulsed-field gel electrophoresis (PFGE) has been the primary method of molecular subtyping by which clusters of bacterial foodborne diseases have been identified
- PFGE-based cluster detection in Tennessee (TN) focused on *Salmonella* and Shiga toxin-producing *Escherichia coli* (STEC)
- In 2019, the Tennessee Department of Health (TDH) State Public Health Laboratory (SPHL) transitioned from PFGE to whole genome sequencing (WGS) for molecular subtyping of bacterial foodborne pathogens
- In order to compare protocol and thresholds for local cluster detection between the two methods, the TN SPHL performed PFGE and WGS on all specimens during the transition period and compared PFGE cluster detection to core genome multilocus sequence testing (cgMLST) cluster detection

OBJECTIVE

Compare characteristics of clusters previously identified by PFGE using cgMLST and analyze concordance based on established cluster definitions.

CHARACTERIZATION METHODS



METHODS

- *Salmonella* and STEC isolates for which both PFGE and WGS was conducted were identified in local BioNumerics 7.6 databases
- Fast matching cgMLST analysis was used to create dendrograms representing core genome allelic differences among isolates by pathogen
- Allele differences were compared among isolates previously identified as part of a PFGE cluster of two or more non-household cases with the same PFGE pattern within 60 days of one another
- The dendrogram was examined to determine if additional local isolates, not previously identified as part of a cluster by PFGE, clustered by cgMLST

RESULTS

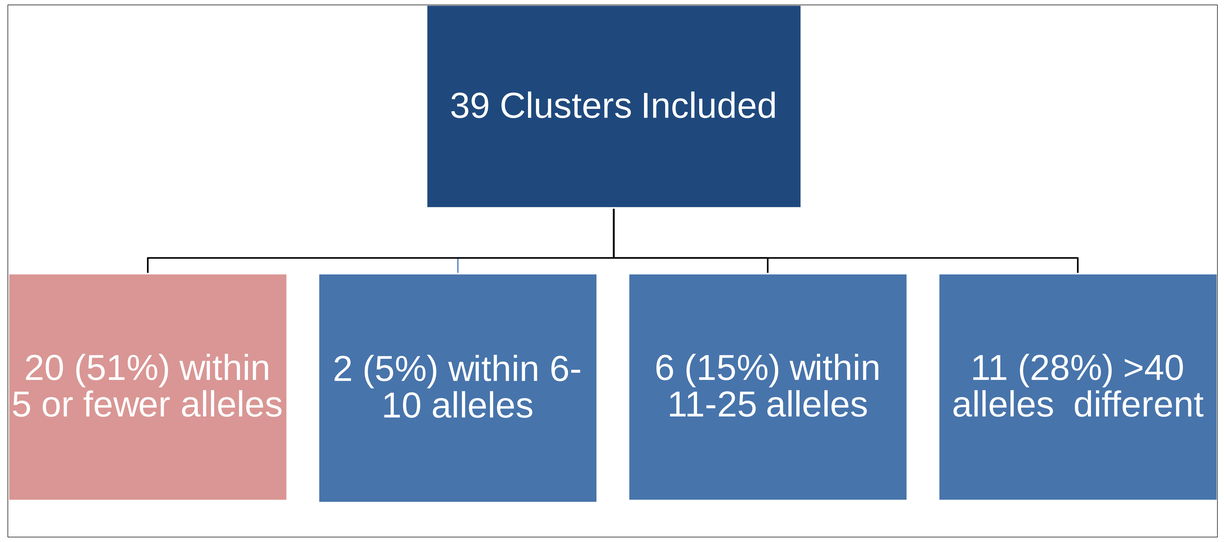


Figure 1. WGS analysis comparison of clusters initially identified by PFGE, TN, November 2018 – July 2019

- From November 2018- July 2019, 39 PFGE clusters (35 Salmonella, 4 STEC) were identified with parallel sequencing information available
- The average number of isolates per cluster when first identified was two
- Isolates in twenty (51%) PFGE clusters fell within 5 or fewer alleles of one another, including all isolates associated with all 4 clusters that were confirmed as outbreaks in this time frame
- Two (5%) clusters were a maximum of 6-10 alleles different, 6 (15%) clusters were a maximum of 11-25 alleles different, and 11 (28%) were greater than 40 alleles maximum difference
- Among PFGE clusters differing by 6 or more alleles, cgMLST identified four WGS sub-clusters within 0-5 alleles.
- Over 40% of clusters previously identified by PFGE may not have been considered clusters based on current proposed cluster cutoff thresholds from PulseNet CDC.

CONCLUSIONS

- The majority of PFGE clusters, including all confirmed outbreaks within this period, fell within a maximum cgMLST difference of 0-5 alleles. This suggests a potential threshold for initial cluster identification for *Salmonella* and STEC
- cgMLST provided critical additional granularity to PFGE in identifying more closely related isolates within clusters (e.g. sub-clusters) for additional epidemiological assessment, especially among common PFGE patterns
- Continued work is needed to assess allele thresholds for different enteric pathogens.

LIMITATIONS & CHALLENGES

- A limited time window was available to do this analysis as PFGE was not concurrently maintained after July 2019 due to limited funding. As enteric disease cases peak during the summer months, additional time for analysis may have provided further important insights
- Comparison data was only available to hqSNP analysis from the NCBI pipeline. As such, allele threshold cutoffs for classification were difficult to categorize
- PFGE was not routinely conducted for pathogens other than *Salmonella* and STEC, limiting the scope of this analysis

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