In March 2009, an inmate with pulmonary tuberculosis (TB) was reported to the Florida Department of Health, which triggered an outbreak investigation. Twenty-seven more cases, all U.S.-born, were identified among the prison population between March 2009 and October 2013. Genotyping by Spoligotyping and 24-locus MIRU-VNTR on culture confirmed cases showed they all shared identical genotype profile. A review of the Florida TB genotyping management system identified 44 more cases with the same genotype profile in the community; the majority Haitian-born. Contact tracing could not identify a source for the outbreak. We used whole genome sequencing (WGS); phylogenetic analyses and the available contact investigation data to delineate the outbreak. We tested the hypothesis that the outbreak bacterial population is more diverse than observed using traditional genotyping methods compared to WGS.

**METHODS**

We sequenced 21 of the 74 cases involved in the outbreak, which constituted a representative spatial and temporal sample of the cases. Short read-end reads were trimmed and independently de novo assembled into contigs, then the contigs were ordered, aligned and variable sites (SNPs) called using the reference strain CDC1551. We evaluated the evolutionary history between the sequences by comparing the SNP difference within and between prison and community cases, foreign-born and U.S.-born cases. We investigated the phylogenetic relationship between the strains using distance-based and maximum likelihood methods. We calculated the time to most recent common ancestor (TMRCA) in years and estimated the time of the outbreak starting with Bayesian coalescence theory implemented in BEAST v2.4.1.

**FIGURE 1**

Characteristics of the Cases Involved in the Outbreak by Whole Genome Sequencing Status. **Includes** 1 case born in the Dominican Republic; 1 case born in Vietnam and 1 case born in Grenada; **Includes** injection and non injection drug use. Cases reported as part of the Putative FL0117 outbreak.

**FIGURE 2**

Epidemic Curve of the Spoligotyping and 24-locus MIRU-VNTR Defined M. tuberculosis Outbreak. Red bars indicate sequenced isolates as a proportion of all outbreak isolates reported in that quarter.

**FIGURE 3**

Minimum Spanning Tree (MST) of FL0117 Cases. Nodes represent each of the sequenced cases (n=21). Cyan identifies cases diagnosed in the community and Yellow identifies the three cases diagnosed while incarcerated. Yellow outline identifies central nodes. The numbers on the branches represent single-nucleotide variant (SNV) between each pair of isolates.

**FIGURE 4**

Midpoint rooted Maximum Likelihood Phylogeny of the 21 FL0117 isolates and ONE (1) Reference Isolate. Tip labels colors indicate patient birth origin. Blue indicates U.S.-born cases, Red indicates Foreign-born cases and the reference strain is in Black. **Indicates** patients diagnosed while incarcerated; all others were diagnosed in the community. Numbers indicate bootstrap support for clusters. The analysis assumes the sequences are evolving according to the Kimura 3-parameter model.

**FIGURE 5**

Maximum Clade Credibility Phylogeny of the FL0117 Cluster illustrating the relationship between U.S.-born (Blue) and Foreign-born cases (Red) cases. Results assume a strict molecular clock with a strong prior of $3.03 \times 10^{-10}$. **Indicates** cases diagnosed while incarcerated; all others were diagnosed in the community; @ indicates pediatric case born to Haitian parents. Blue horizontal bars indicate the level of uncertainty in the node age estimates. Branches colors represent the posterior distribution of trees. The analysis assumes the sequences are evolving according to the General Time Reversible (GTR) model.

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