

Subspecies-specific sequence detection for differentiation of *Mycobacterium abscessus* complex

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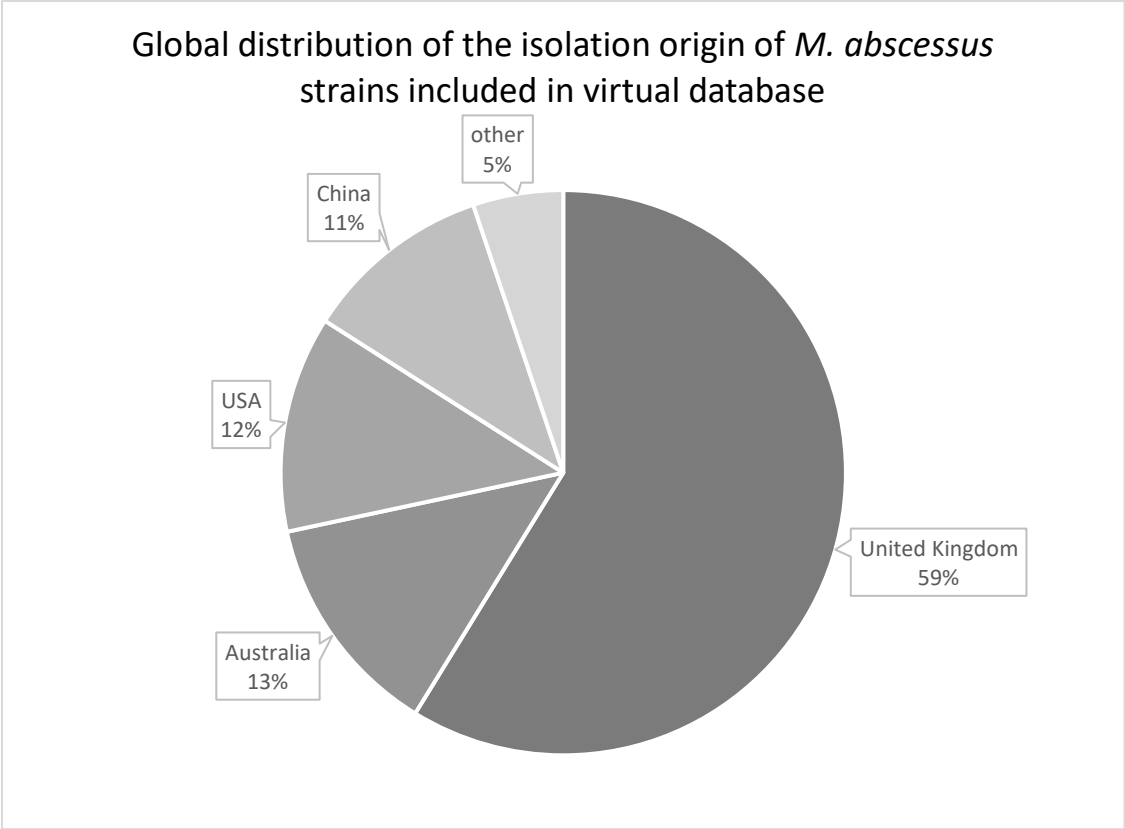


Fig. S1. The geographic origin of the *M. abscessus* strains included in virtual database. The majority of strains included in the database were isolated in United Kingdom. Four continents- Europe, Australia, North America and Asia were represented in the database by at least ten percent of the strains each.

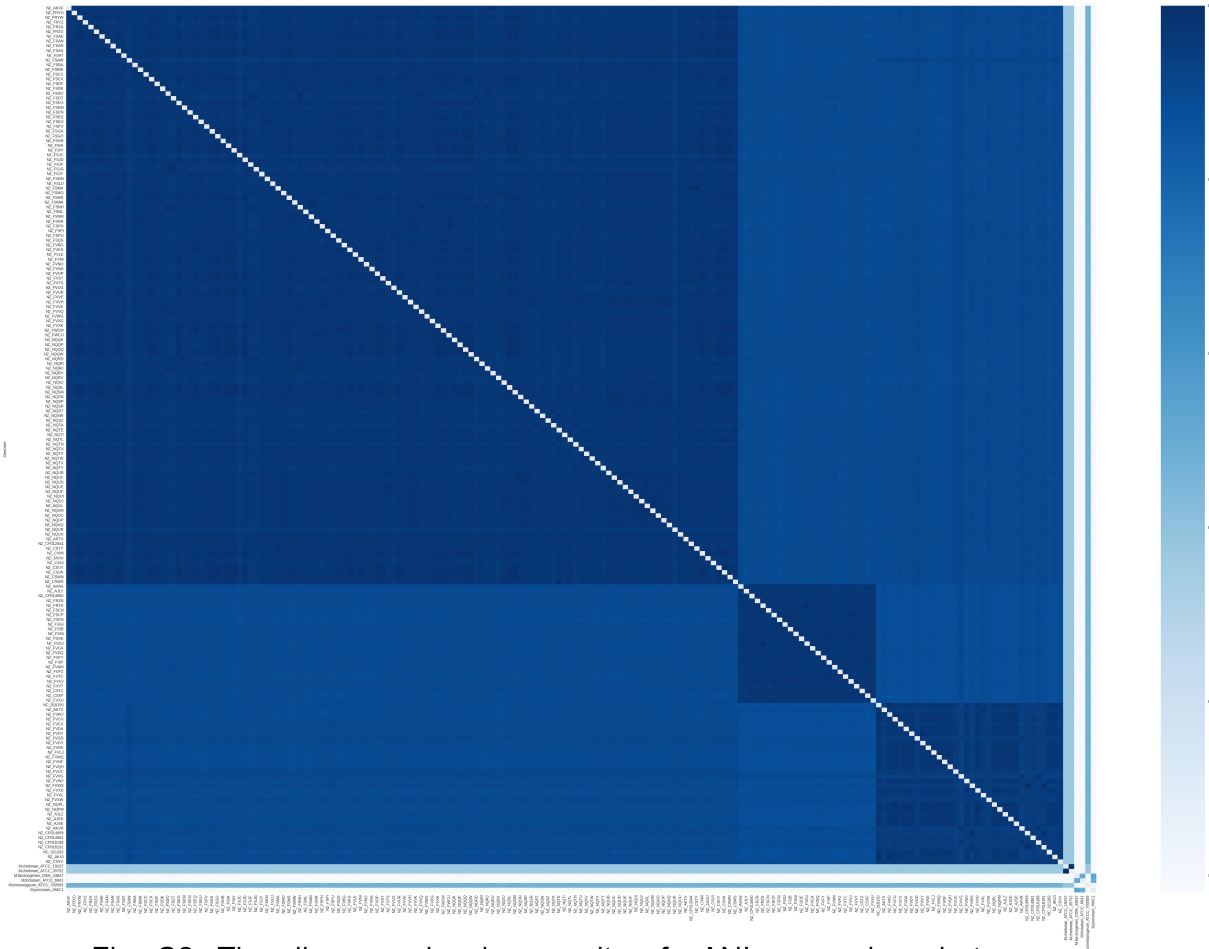


Fig. S2. The diagram showing results of gANI comparison between individual strains of *M. abscessus* complex strains for which the results of differentiation by different methods were inconsistent. The dataset included reference strains for each subspecies- *NC_018150* representing *M. abscessus* subsp. *massiliense*, *NZ_CP014950* representing *M. abscessus* subsp. *bolletii* and *NC_010397* representing *M. abscessus* subsp. *abscessus*. The blue band on the right of the chart shows the level of similarity between the strains, where dark color represents high similarity of the genomes and light color represents less similar genome sequences.

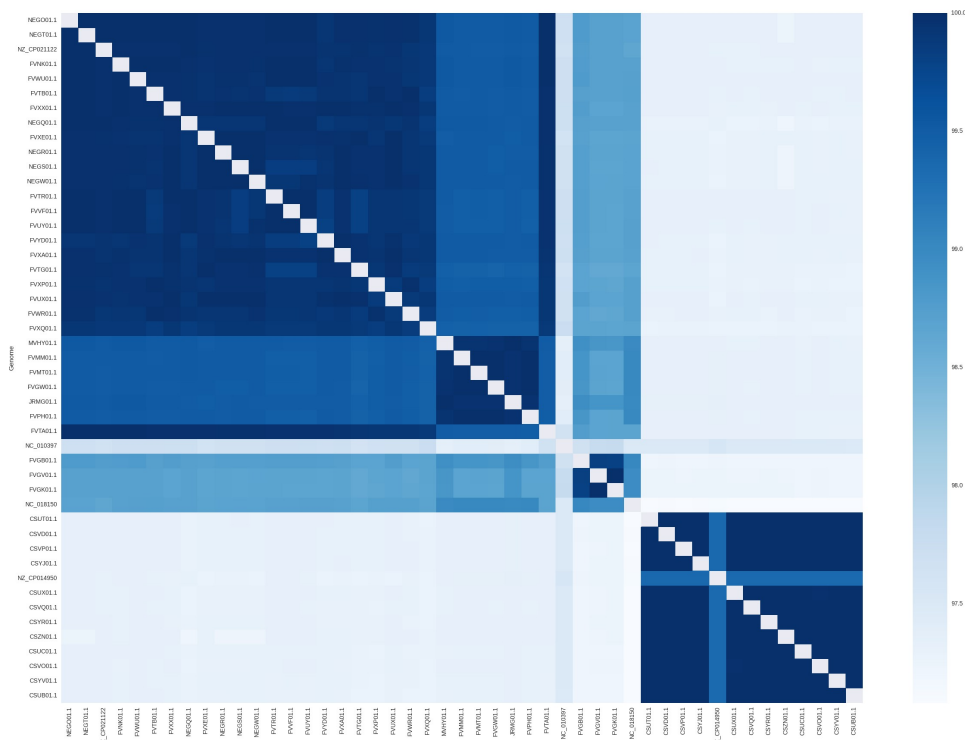


Fig. S3. The diagram showing results of gANI comparison between individual strains of *M. abscessus* complex strains for which the results of differentiation by different methods were inconsistent. The dataset included reference strains for each subspecies- *NC_018150* representing *M. abscessus* subsp. *massiliense*, *NZ_CP014950* representing *M. abscessus* subsp. *bolletii* and *NC_010397* representing *M. abscessus* subsp. *abscessus*. The blue band on the right of the chart shows the level of similarity between the strains, where dark color represents high similarity of the genomes and light color represents less similar genome sequences.

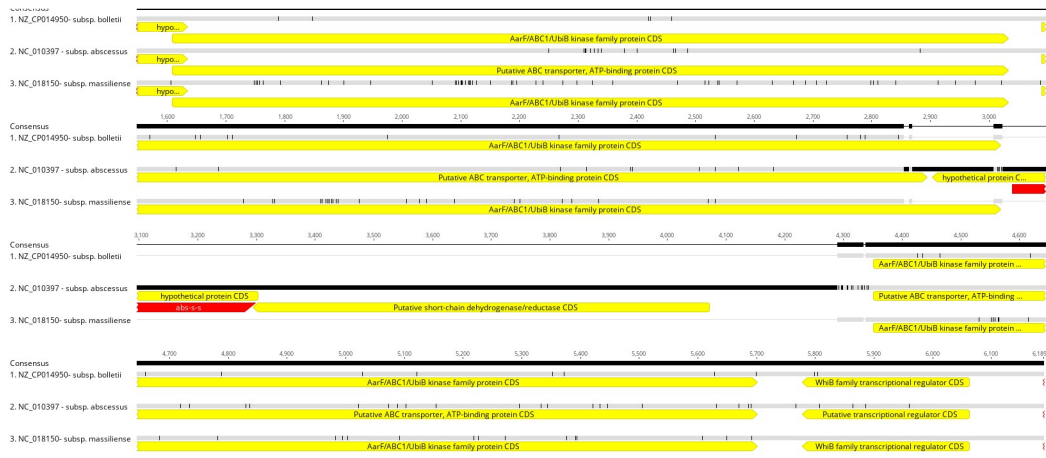


Fig. S4. The alignment between genomic regions surrounding (*abs-s-s*) sequence in three reference genomes: NC_018150 representing *M. abscessus* subsp. *massiliense*, NZ_CP014950 representing *M. abscessus* subsp. *bolletii* and NC_010397 representing *M. abscessus* subsp. *abscessus*. Disagreements in the aligned sequences are marked with colored lines. The extent of the genes is marked in yellow. The probe used to detect the sequence in clinical validation of SSSD is marked in red.



Fig. S5. The alignment between genomic regions surrounding (*bol-s-s*) sequence in three reference genomes: NC_018150 representing *M. abscessus* subsp. *massiliense*, NZ_CP014950 representing *M. abscessus* subsp. *bolletii* and NC_010397 representing *M. abscessus* subsp. *abscessus*. Disagreements in the aligned sequences are marked with colored lines. The extent of the genes is marked in yellow. The probe used to detect the sequence in clinical validation of SSSD is marked in red.



Fig. S6. The alignment between genomic regions surrounding (*mas1-s-s*) sequence in three reference genomes: NC_018150 representing *M. abscessus* subsp. *massiliense*, NZ_CP014950 representing *M. abscessus* subsp. *bolletii* and NC_010397 representing *M. abscessus* subsp. *abscessus*. Disagreements in the aligned sequences are marked with colored lines. The extent of the genes is marked in yellow. The probe used to detect the sequence in clinical validation of SSSD is marked in red.

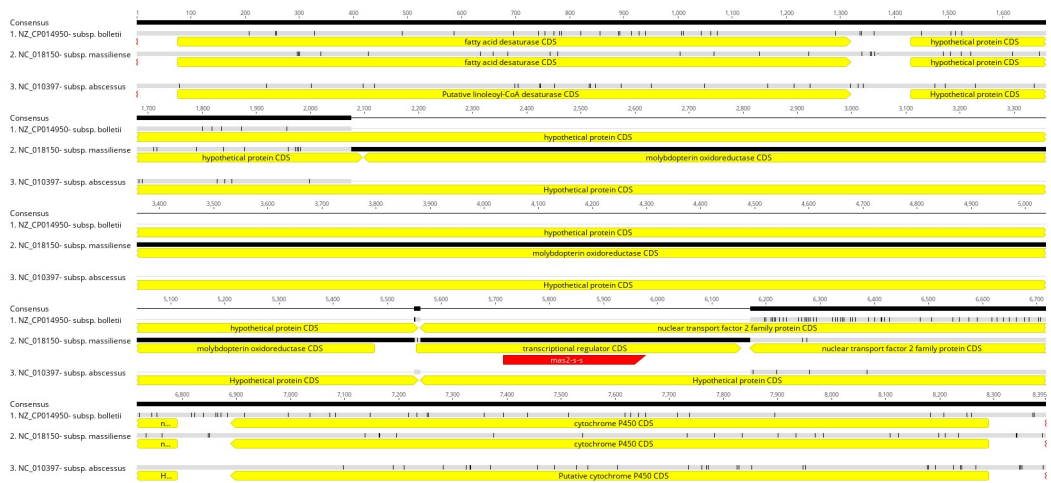


Fig. S7. The alignment between genomic regions surrounding (*mas2-s-s*) sequence in three reference genomes: NC_018150 representing *M. abscessus* subsp. *massiliense*, NZ_CP014950 representing *M. abscessus* subsp. *bolletii* and NC_010397 representing *M. abscessus* subsp. *abscessus*. Disagreements in the aligned sequences are marked with colored lines. The extent of the genes is marked in yellow. The probe used to detect the sequence in clinical validation of SSSD is marked in red.