The initial description of *Mycobacterium lentiflavum* was based on three isolates belonging to a single DNA homology group (1). Further phylogenetic analyses found >99.5% similarity in the 16S rRNA gene sequence with *Mycobacterium simiae* and *Mycobacterium genavense* (1). This observation qualified *M. lentiflavum* as a member of the *Mycobacterium simiae* complex. This environmental organism (2) has been isolated from human specimens, including an intervertebral disc (1), respiratory tract samples and gastric/gut aspirates (1, 3), lymph nodes (4), feaces (5), and bone marrow (5). *M. lentiflavum* emerges in cystic fibrosis patients (6) and was responsible for the death of one heart-transplanted immunocompromised patient (5). Routine identification of this fastidious mycobacterium can be achieved by partial *rpoB* gene sequencing (7).

We sequenced the whole genome of *M. lentiflavum* to exact the phylogenetic relationships within the *M. simiae* complex, design tools for its genotyping, and disclose any genotypic pattern possibly related to host-mycobacterium relationships.

Genomic DNA was extracted from *M. lentiflavum* strain CSUR P1491 (isolated from the sputum of a cystic fibrosis patient) grown on Middlebrook 7H10 solid medium at 37°C in a 5% CO₂ atmosphere for 3 weeks. Genomic DNA was sequenced on Illumina MiSeq throughout three runs, including one paired-end Nextera and two mate pair libraries, in a 2-by-2 using the BLAT algorithm (26, 27) against *M. simiae* and *M. genavense*. The DDH was estimated from a generalized linear model using a specific distance formula (28), resulting in following values: 27.5% (±2.43) with *M. simiae* and 34.6% (±2.47) with *M. genavense*. These data confirm *M. lentiflavum* as a unique species clearly distinct from *M. simiae* and *M. genavense*.

Nucleotide sequence accession numbers. The *M. lentiflavum* strain CSUR P1491 genome sequence has been deposited at EMBL under the accession numbers CTEE01000001 to CTEE01000005.

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