Figure S1. Methodology chart

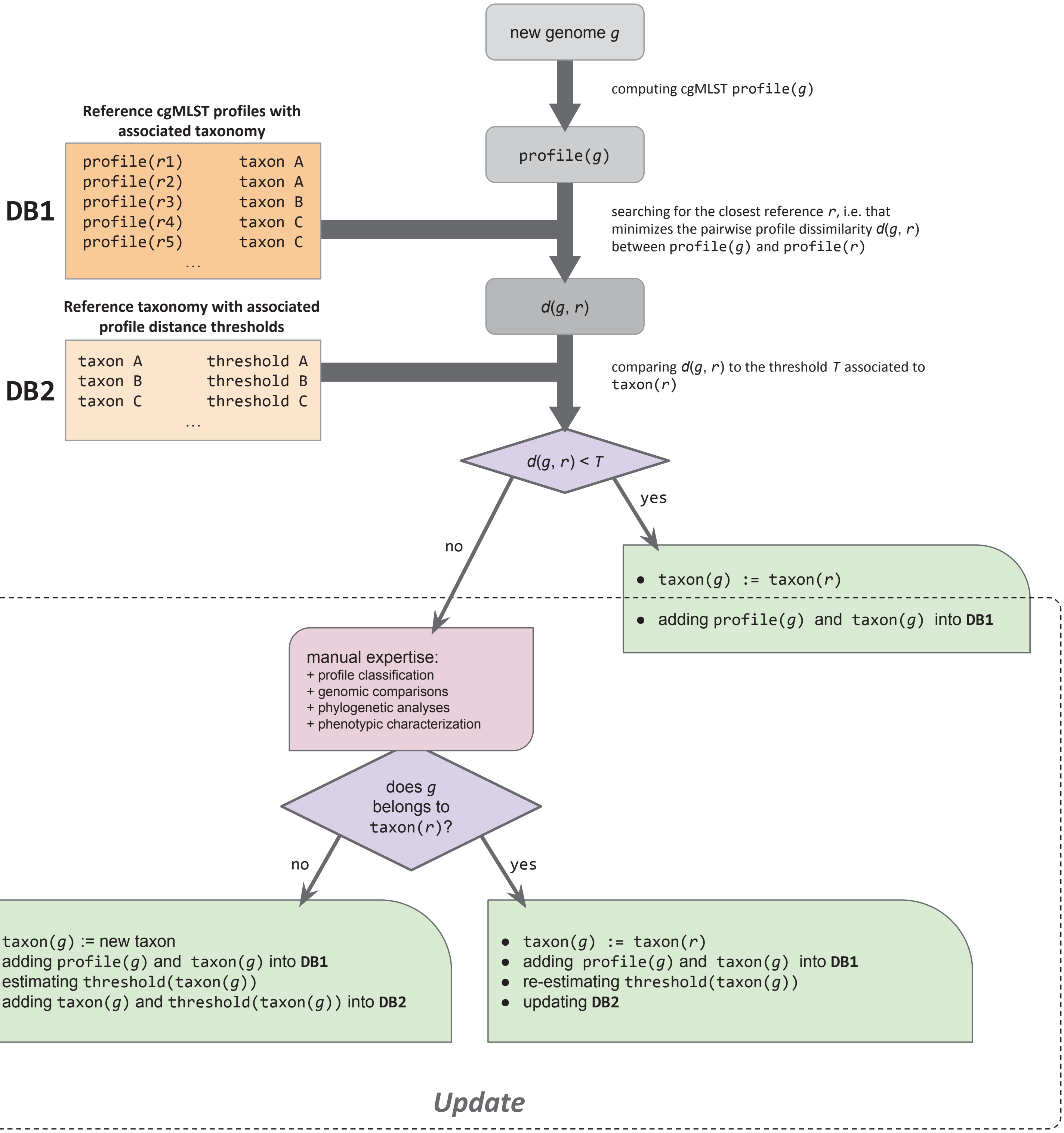


Figure S2. Maximum-likelihood phylogenetic tree of the *Yersinia* genus based on concatenated multiple sequence alignments of 7-gene MLST genes. Only bootstrap-based branch support values >70% are shown. Scale bar refers to 0.05 nucleotide substitutions per character.

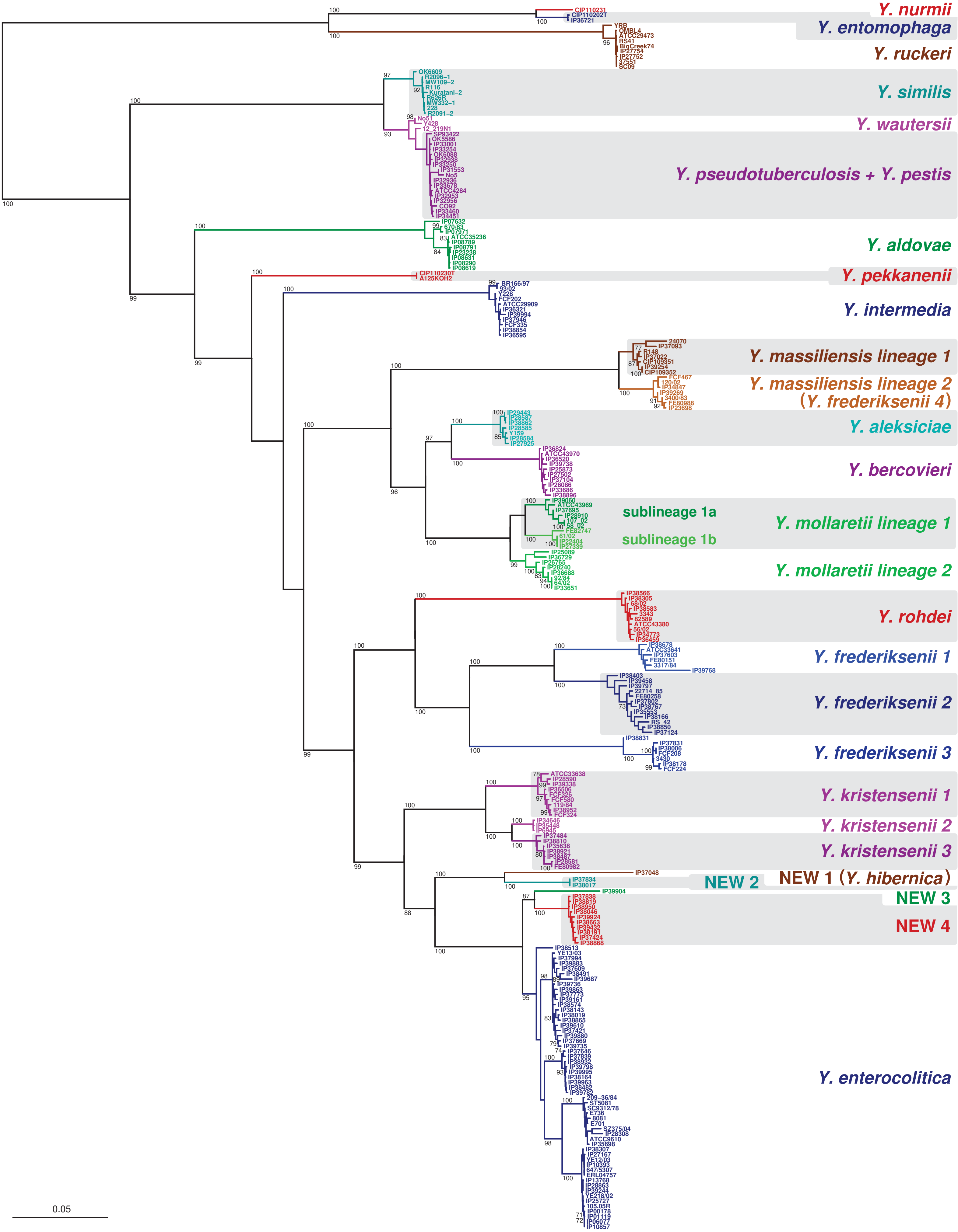


Figure S3. Identification procedure of *Yersinia* isolates on the public “Sequences and profiles database”: https://bigsdb.pasteur.fr/yersinia/

Procedure for identification of *Yersinia* isolates

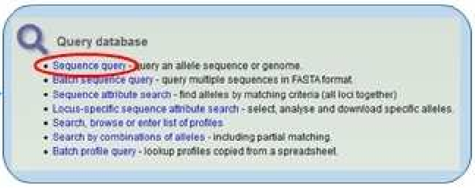
1
- ✓ Connexion to https://bigsdb.pasteur.fr/yersinia
- ✓ Access to the public « Sequences and profile database »


Yersinia Sequence Typing

Sequences and profiles database
[Public]

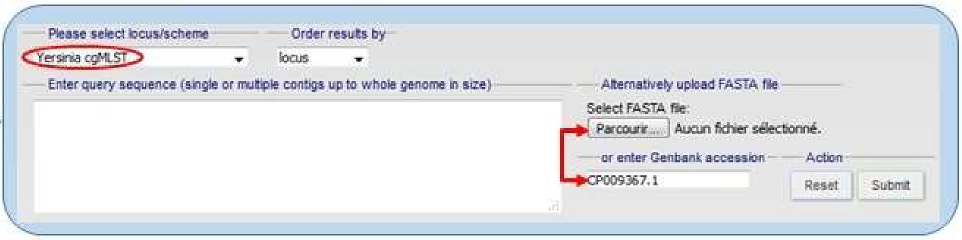
Isolates database
[Public] [Private]

2
- ✓ Click on « Sequence query »


Query database

- Sequence query - query an allele sequence or genome.
- Batch sequence query - query multiple sequences in FASTA format.
- Sequence attribute search - find alleles by matching criteria (all loci together)
- Locus-specific sequence attribute search - select, analyse and download specific alleles.
- Search, browse or enter list of profiles.
- Search by combinations of alleles - including partial matching.
- Batch profile query - lookup profiles copied from a spreadsheet.

3
- ✓ Select the « Yersinia cgMLST » scheme
- ✓ copy/paste or upload the genome (fasta file) or enter a GenBank accession number
- ✓ Click on submit to scan the genome


Please select locus/scheme: Yersinia cgMLST

Order results by: locus

Enter query sequence (single or multiple contigs up to whole genome in size)

Alternatively upload FASTA file

Select FASTA file: Parcourir... Aucun fichier sélectionné.

or enter Genbank accession: CP009367.1

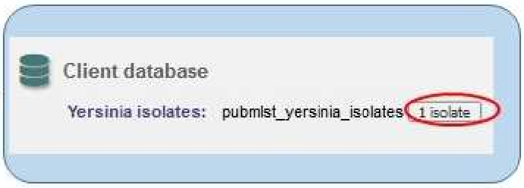
4
- ✓ Click on the Y_cgST type to get the closest allelic profile


Yersinia cgMLST

Matching profile

Y cgST: 221

5
- ✓ Click on the link close to « pubmlst_yersinia isolates » to get the taxonomic assignment


Client database

Yersinia isolates: pubmlst_yersinia_isolates 1 isolate

6
- ✓ Note the classification results of the matching isolates (‘species_genotypic’ method and ‘genotype’)


Isolate fields							Yersinia cgMLST
id	isolate	species phenotypic	biotype	serotype	species genotypic	genotype	Y cgST
233	WA	enterocolitica	1B	O:8	enterocolitica	1B	221