

Description of Additional supplementary files

Supplementary Data 1. Genomes of 263 Ye biotype 4 used for core-genome single-nucleotide polymorphism analysis.

*NK: not known

Supplementary Data 2. SNP specific.

Supplementary Data 3. Synapomorphic genes.

Supplementary Data 4. Small insertions/deletions and list of CDS absent in Ye.3 and Ye.4 strains' genome, along log₂(foldchange) of protein abundance in all pairwise comparisons. Loci are expressed on Y11 reference genome. P-value and adjusted p-value can be found in Supplementary Data 6. 0 corresponds to proteins not detected in any conditions of the comparison. 15 corresponds to proteins detected only in the first condition of the comparison. Core-genome corresponds to genes identified in more than 95% of strains, while shell-genome corresponds to genes identified in less than 95% and more than 15% of strains, and cloud-genome corresponds to genes identified in less than 15%.

Supplementary Data 5. Pan-genome fraction definition. Repartition of genes from Ye.1 to Ye.4 (differentiating mutated genes between isolates, as used for proteome identification) and repartition of identified proteins in the clinical isolate proteomes in the pan-genome fractions.

Supplementary Data 6. Ye.1 to Ye.4 proteome pairwise comparisons. Proteins were mapped on the Y11 reference genome. 0 corresponds to proteins not detected in any conditions of the comparison. +15 and -15 corresponds to proteins detected only in the first or second condition of the comparison, respectively.

Supplementary Data 7. Protein abundance foldchanges mapped on the Y11 KEGG pathways.

Supplementary Data 8. Published Ye transcriptomes comparisons to which the proteomes comparisons were correlated

Supplementary Data 9. Statistics of genome assemblies

Supplementary Data 10. Sequences of primers used for mutagenesis and PCR programs.