

Analysis of the diversity of *Xylophilus ampelinus* strains held in CIRM-CFBP reveals a strongly homogenous species.

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Table S1: information on strains used in this study

Table S2: *gyrB-rpoD* sequence alignment for all strains listed in table S1. The *gyrB* sequence span from nucleotides 1 to 723 and *rpoD* sequence from nucleotide 724 to 1383.

Table S3: Results of CheckM [1] Analysis run on the 13 genomes of *Xylophilus* downloaded from Genbank along with the genome of CFBP 1192^T.

[1]: Parks, D.H.; Imelfort, M.; Skennerton, C.T.; Hugenholtz, P.; Tyson, G.W. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *Genome Res.* **2015** 25(7):1043-55

Figure S1: Phylogenetic tree reconstructed from concatenated partial sequences of *gyrB* and *rpoD* housekeeping genes for 93 strains of *Xylophilus ampelinus* and the type strain of *Acidovorax anthurii* as outgroup. The phylogenetic tree was reconstructed with concatenated alignments of all genes with MEGA 7.0.26 using the neighbour-joining method with 1000 bootstrap replicates, and the evolutionary distances were computed by using the Kimura two-parameter method.

>CFBP1193 *Xylophilus ampelinus*

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GAC

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GAC