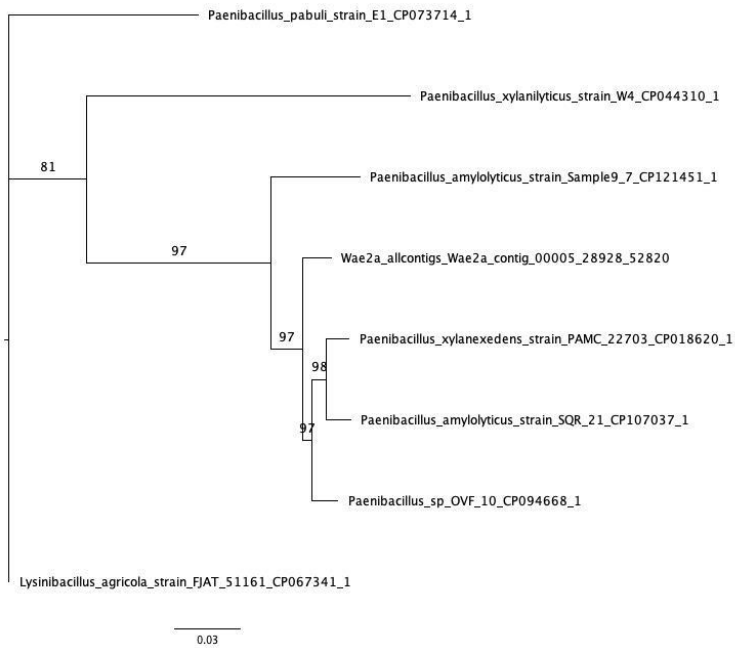
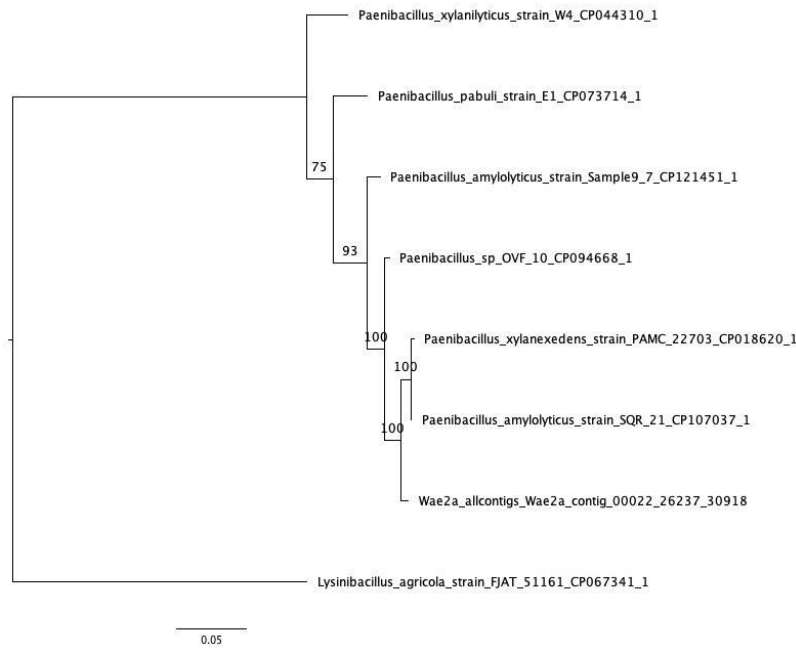
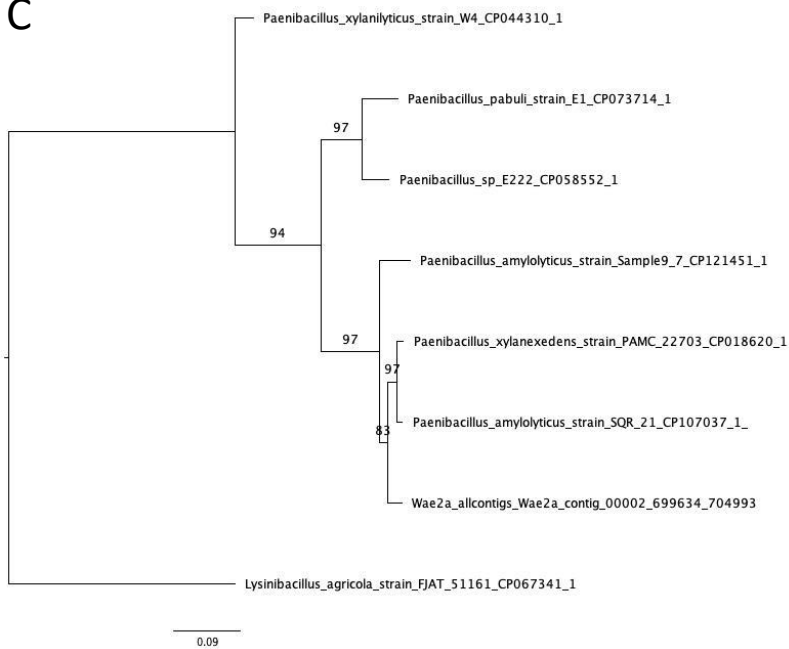
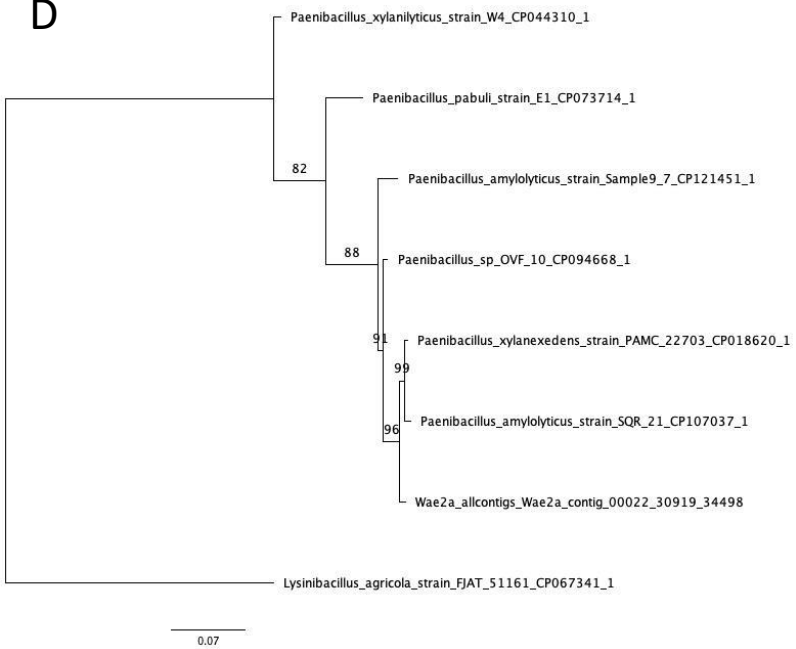


**A****B****C****D**

**Figure S2: Phylogenies inferred from genomic blocks.** Blocked alignments were completed for four conserved genomic blocks. (A-D). BLAST analysis was used to find seven closest relatives and an outgroup for the ClWae2A genome [1]. Taxon ID's indicate genus, species, isolate, and accession identification from NCBI. Genomic blocked alignments were created with Mugsy alignment tool [2]. RAxML was utilized to infer phylogenetic relationships with 100 bootstrap replicates [3]. Phylogenetic trees were inspected with TreeViewer [4] and figures were created and exported using FigTree [5]. Branch labels represent bootstrap support values. Scale bar represents inferred substitutions per site along branches.

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