

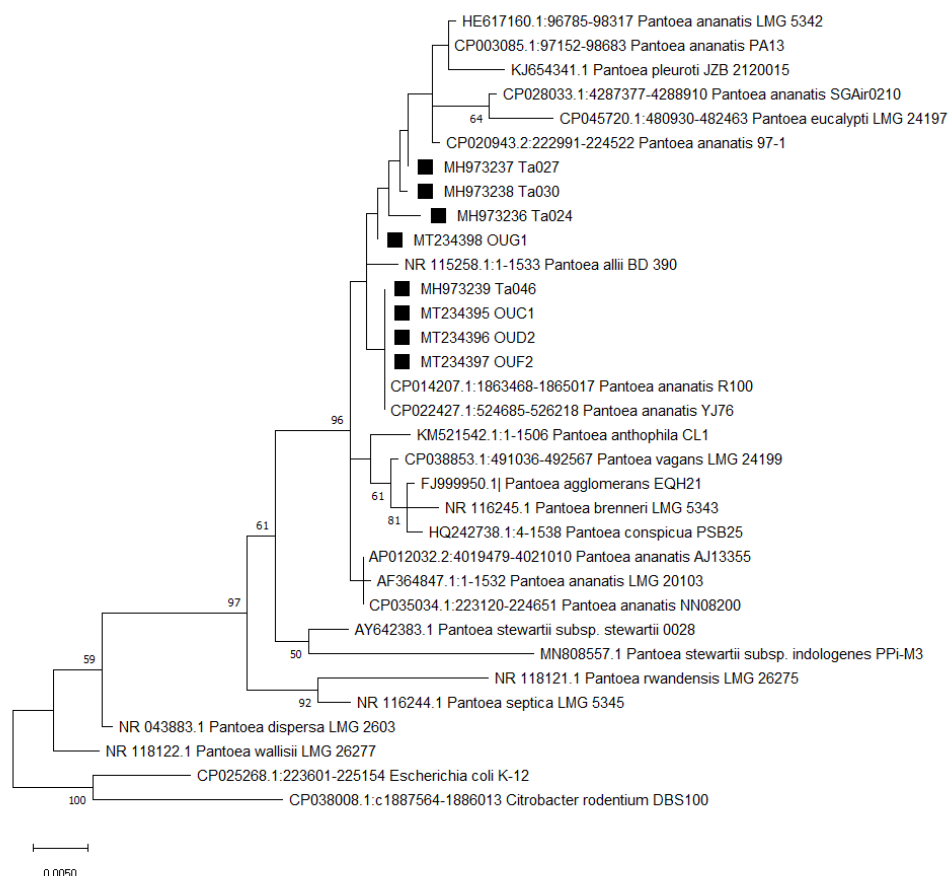
## Supplementary Materials

**Table S1.** BLAST sequence identity (%) of the *gyrB* sequences of the tested strains with other *Pantoea ananatis* sequences derived from the GenBank database.

Tested strain code /GenBank accession number	Gene tested	Amplicon size (bp)	Identity with the BLAST best hit result (%)	The most similar GenBank derived <i>Pantoea ananatis</i> sequence (accession no)
Ta024-MT091018	<i>gyrB</i>	864	100	CP022427
Ta027-MT091019	<i>gyrB</i>	864	100	CP022427
Ta030-MT091020	<i>gyrB</i>	864	100	MK928262
Ta046-MT091021	<i>gyrB</i>	864	99	MK928262
OUC1-MT091022	<i>gyrB</i>	864	99	MK928262
ODU2-MT091023	<i>gyrB</i>	864	99	MK928262
OUF2-MT091024	<i>gyrB</i>	864	99	MK928262
OUG1-MT091025	<i>gyrB</i>	864	99	MK928262

**Table S2.** BLAST sequence identity (%) of the 16S rRNA sequences of the identified strains with other *Pantoea ananatis* sequences derived from GenBank database.

Tested strain code /GenBank accession number	Gene tested	Amplicon size (bp)	Identity with the BLAST best hit result (%)	The most similar GenBank derived <i>Pantoea ananatis</i> sequence (accession no)
Ta024- MH973236	16S rRNA	1494	99	CP022427
Ta027- MH973237	16S rRNA	1532	99	DQ517335
Ta030- MH973238	16S rRNA	1527	99	DQ195525
Ta046- MH973239	16S rRNA	1488	100	KT957000
OUC1-MT234395	16S rRNA	1445	100	MK415050
ODU2-MT234396	16S rRNA	1477	100	MK415050
OUF2-MT234397	16S rRNA	1489	99	MK415050
OUG1-MT234398	16S rRNA	1443	99	MK415050



**Figure S1.** Maximum likelihood dendrogram of the partial, GenBank derived a nucleotide sequence of 16S rRNA gene of *Pantoea ananatis* and closely related species. Bootstrap values for phylogenetic comparisons were based on 1000 pseudoreplicates. The Polish strains are marked with black squares (■). *Escherichia coli* and *Citrobacter rodentium* strains were used as an outgroup. The bootstrap values lower than 50 were hidden. Scale bar represents the phylogenetic distance.