

Supplementary Data

Article

Bacteria from the Midgut of Common Cockchafer (*Melolontha melolontha* L.) Larvae Exhibiting Antagonistic Activity Against Bacterial Symbionts of Entomopathogenic Nematodes: Isolation and Molecular Identification

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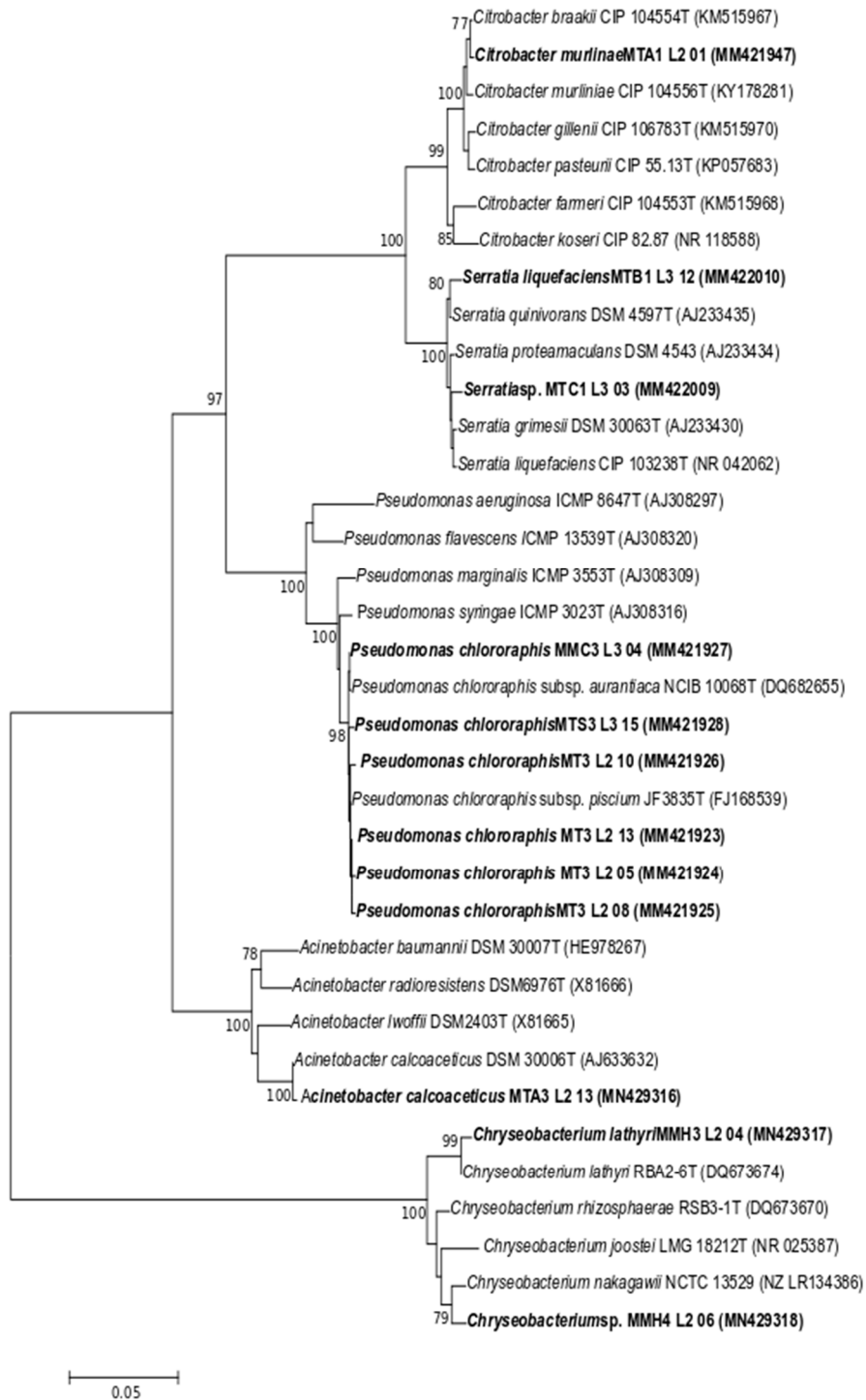


Figure S1. Neighbor joining tree based on 16S rRNA gene sequences showing the phylogenetic relationships of the studied *M. melolontha* midgut isolates (bolded) exhibiting antagonistic activity against bacterial symbionts of entomopathogenic nematodes. The GeneBank accession numbers are given in parentheses. The numbers at the branching points are bootstrap values >50%. The bar indicates 0.05 substitution per nucleotide positions.

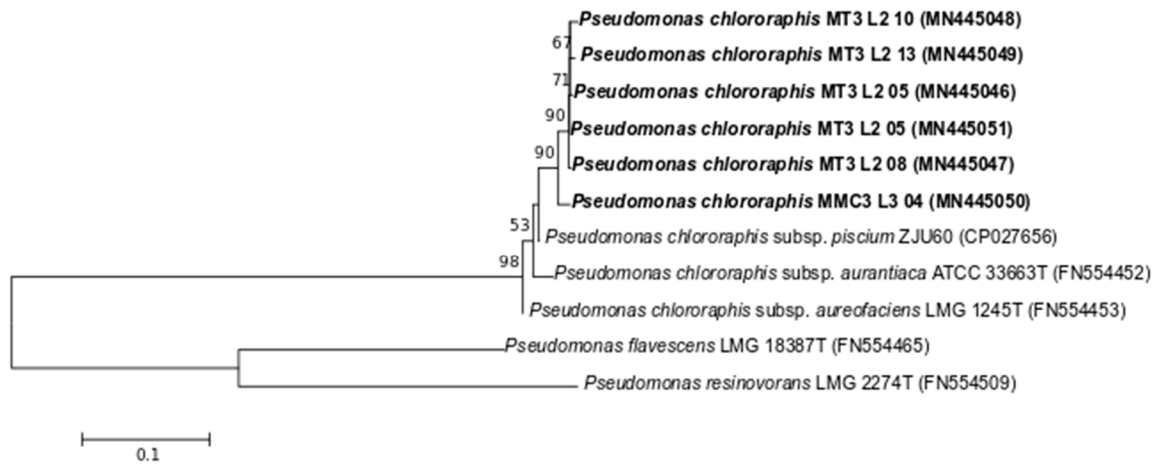


Figure S2. Neighbor joining tree based on *rpoD* gene sequences showing the phylogenetic relationships of the studied *M. melolontha* midgut *Pseudomonas* isolates (bolded) exhibiting antagonistic activity against bacterial symbionts of entomopathogenic nematodes. The GeneBank accession numbers are given in parentheses. The numbers at the branching points are bootstrap values >50%. The bar indicates 0.01 substitution per nucleotide positions.

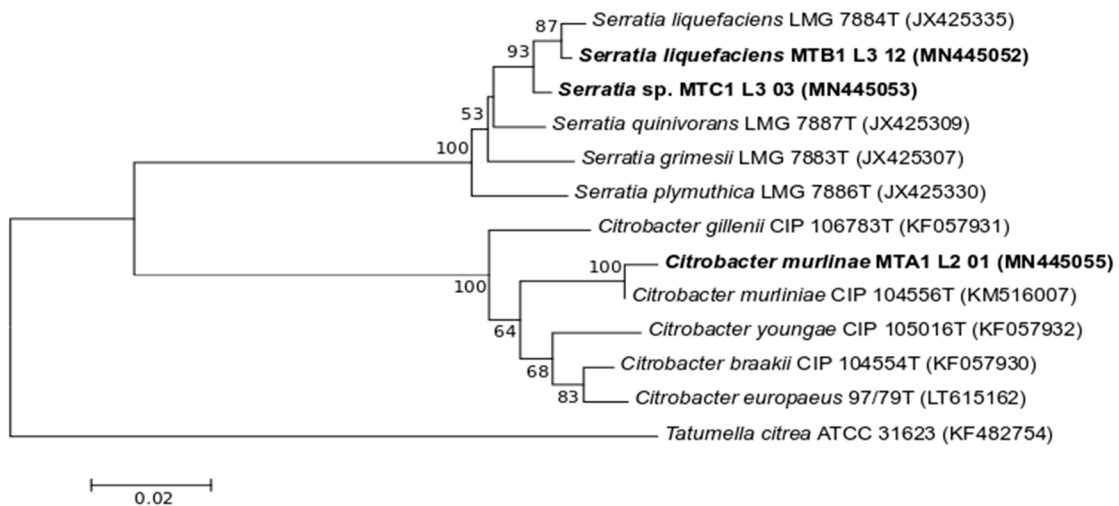


Figure S3. Neighbor joining tree based on *rpoB* gene sequences showing the phylogenetic relationships of the studied *M. melolontha* midgut *Serratia* and *Citrobacter* isolates (bolded) exhibiting antagonistic activity against bacterial symbionts of entomopathogenic nematodes. The GeneBank accession numbers are given in parentheses. The numbers at the branching points are bootstrap values >50%. The bar indicates 0.02 substitution per nucleotide positions. The sequence of *Tatumella citrea* was used as an outgroup.

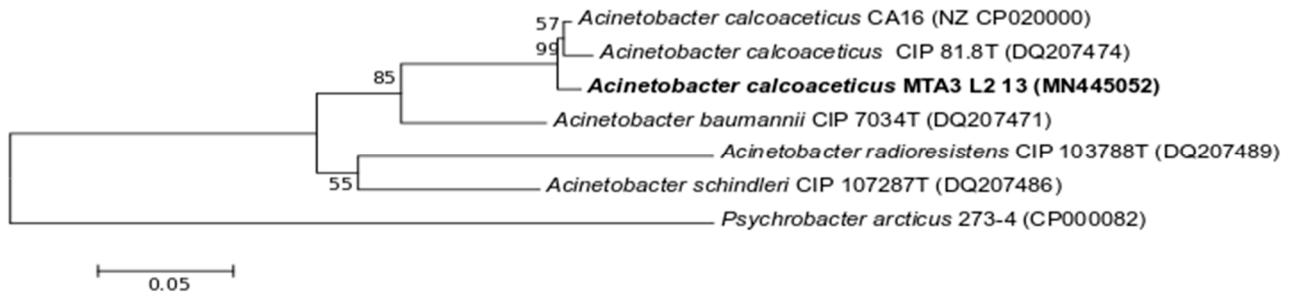


Figure S4. Neighbor joining tree based on *rpoB* gene sequences showing the phylogenetic relationships of the studied *M. melolontha* midgut *Acinetobacter* isolate (bolded) exhibiting antagonistic activity against bacterial symbionts of entomopathogenic nematodes. The GeneBank accession numbers are given in parentheses. The numbers at the branching points are bootstrap values >50%. The bar indicates 0.05 substitution per nucleotide positions. The sequence of *Psychrobacter arcticus* was used as an outgroup.

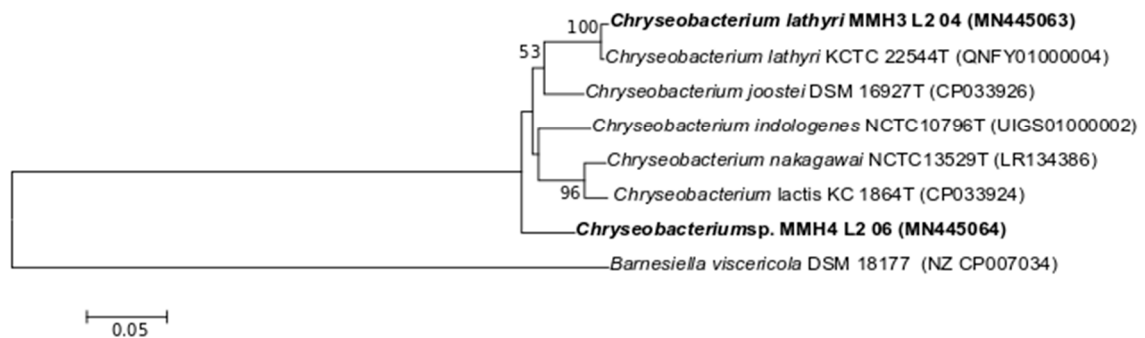


Figure S5. Neighbor joining tree based on *rpoB* gene sequences showing the phylogenetic relationships of the studied *M. melolontha* midgut *Chryseobacterium* isolates (bolded) exhibiting antagonistic activity against bacterial symbionts of entomopathogenic nematodes. The GeneBank accession numbers are given in parentheses. The numbers at the branching points are bootstrap values >50%. The bar indicates 0.05 substitution per nucleotide positions. The sequence of *Bamesiella viscericola* was used as an outgroup.

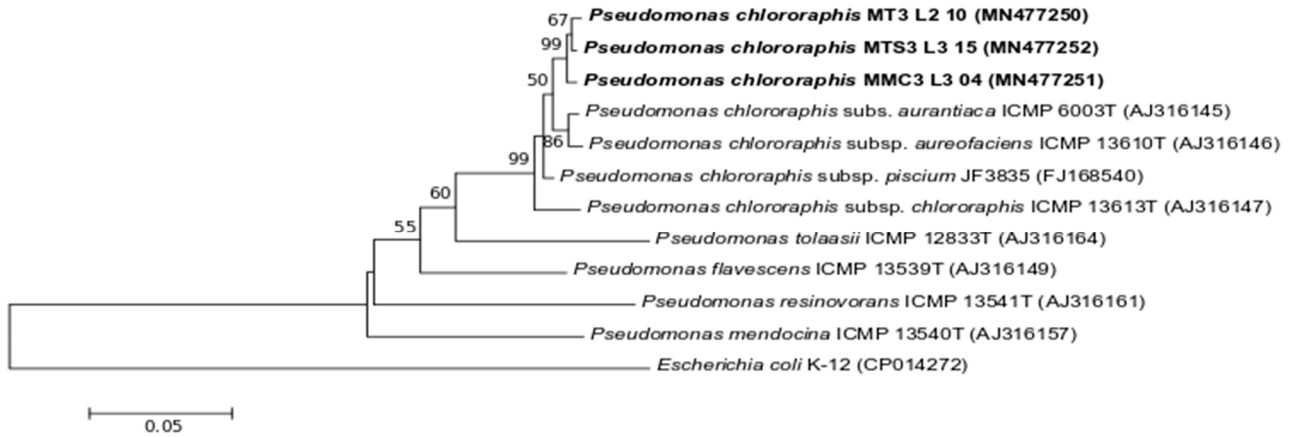


Figure S6. Neighbor joining tree based on *recA* gene sequences showing the phylogenetic relationships of the studied *M. melolontha* midgut *Pseudomonas* isolates (bolded) exhibiting antagonistic activity against bacterial symbionts of entomopathogenic nematodes. The GeneBank accession numbers are given in parentheses. The numbers at the branching points are bootstrap values >50%. The bar indicates 0.05 substitution per nucleotide positions. The sequence of *Escherichia coli* was used as an outgroup.