

Supplementary Table S2. Direct sequencing of bacterial 16S rRNA gene sequences from cultured bacterial colonies on LB plates derived from crushed midgut M4 region of *M. gracilicorne*.

Sample ID and tissue-colony set ^{a,b}	Accession number of 16S rRNA gene	Sequence similarity to M4-derived 16S rRNA gene ^c	BLAST top hit ^d
CKSI20-01			
M4 tissue	LC594116	100% (1479/1479)	NR_104933; <i>Leclercia adecarboxylata</i> strain CIP 82.92 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-1	LC594117	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-2	LC594118	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-3	LC594119	99.8% (447/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-4	LC594120	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-5	LC594121	99.8% (447/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-6	LC594122	99.6% (446/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-7	LC594123	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-8	LC594124	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
CKSI20-02			
M4 tissue	LC594125	100% (1480/1480)	NR_104933; <i>Leclercia adecarboxylata</i> strain CIP 82.92 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-1	LC594126	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-2	LC594127	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-3	LC594128	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-4	LC594129	79.4% (350/441)	NR_136463; <i>Staphylococcus petrasii</i> subsp. <i>pragensis</i> strain CCM 8529 (Firmicutes) 16S ribosomal RNA, partial sequence
Colony-5	LC594130	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-6	LC594131	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-7	LC594132	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-8	LC594133	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
CKSI20-03			
M4 tissue	LC594134	100% (1480/1480)	NR_104933; <i>Leclercia adecarboxylata</i> strain CIP 82.92 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-1	LC594135	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-2	LC594136	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-3	LC594137	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-4	LC594138	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-5	LC594139	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-6	LC594140	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-7	LC594141	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-8	LC594142	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
CHBA20-01			
M4 tissue	LC594089	100% (1481/1481)	NR_116797; <i>Pantoea dispersa</i> strain DSM 30073 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence

			ribosomal RNA, partial sequence
Colony-6	LC594380	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-7	LC594381	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-8	LC594382	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
FKOK20-02			
M4 tissue	LC594383	100% (1480/1480)	NR_104933; <i>Leclercia adecarboxylata</i> strain CIP 82.92 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-1	LC594384	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-2	LC594385	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-3	LC594386	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-4	LC594387	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-5	LC594388	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-6	LC594389	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-7	LC594390	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-8	LC594391	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
FKOK20-03			
M4 tissue	LC594392	100% (1479/1479)	NR_104933; <i>Leclercia adecarboxylata</i> strain CIP 82.92 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-1	LC594393	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-2	LC594394	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-3	LC594395	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-4	LC594396	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-5	LC594397	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-6	LC594398	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-7	LC594399	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-8	LC594400	100% (448/448)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
TKSK20-01			
M4 tissue	LC594401	100% (1479/1479)	NR_104933; <i>Leclercia adecarboxylata</i> strain CIP 82.92 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-1	LC594402	90.4% (405/448)	NR_114154; <i>Leclercia adecarboxylata</i> strain NBRC 102595 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-2	LC594403	82% (360/439)	NR_114126; <i>Ralstonia pickettii</i> strain NBRC 102503 (β -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-3	LC594404	86.2% (376/436)	NR_114126; <i>Ralstonia pickettii</i> strain NBRC 102503 (β -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-4	LC594405	78.6% (341/434)	NR_104569; <i>Erwinia psidii</i> strain LMG 7039 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-5	LC594406	85.2% (381/447)	NR_116415; <i>Sphingomonas changbaiensis</i> NBRC 104936 strain V2M44 (α -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-6	LC594407	81.5% (358/439)	NR_149215; <i>Litorivivens aequoris</i> strain KMU-37 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-7	LC594408	81.7% (361/442)	NR_113806; <i>Sphingomonas echinoides</i> strain NBRC 15742 (α -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-8	LC594409	96.2% (431/448)	NR_114154; <i>Leclercia adecarboxylata</i> strain NBRC 102595 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
TKSK20-02			
M4 tissue	LC594410	100% (1480/1480)	NR_104933; <i>Leclercia adecarboxylata</i> strain CIP 82.92 (γ -

			Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-1	LC594411	86.2% (386/448)	NR_044454; <i>Acinetobacter soli</i> strain B1 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-2	LC594412	97.5% (437/448)	NR_025331; <i>Buttiauxella izardii</i> strain S3/2-161 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-3	LC594413	86.2% (386/448)	NR_044454; <i>Acinetobacter soli</i> strain B1 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-4	LC594414	73.2% (317/433)	NR_041912; <i>Chryseobacterium tenax</i> strain EP105 (Bacteroidetes) 16S ribosomal RNA, partial sequence
Colony-5	LC594415	78.6% (348/443)	NR_104776; <i>Nocardia coeliaca</i> strain DSM 44595 (Actinobacteria) 16S ribosomal RNA, partial sequence
Colony-6	LC594416	86.2% (386/448)	NR_044454; <i>Acinetobacter soli</i> strain B1 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-7	LC594417	97.5% (437/448)	NR_025331; <i>Buttiauxella izardii</i> strain S3/2-161 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-8	LC594418	97.5% (437/448)	NR_025331; <i>Buttiauxella izardii</i> strain S3/2-161 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
TKSK20-03			
M4 tissue	LC594419	100% (1479/1479)	NR_104933; <i>Leclercia adecarboxylata</i> strain CIP 82.92 (γ -Proteobacteria) 16S ribosomal RNA, partial sequence
Colony-1	LC594420	75.8% (332/438)	NR_117006; <i>Staphylococcus capitis</i> strain ATCC 27840 (Firmicutes) 16S ribosomal RNA, partial sequence
Colony-2	LC594421	77.9% (345/443)	NR_104776; <i>Nocardia coeliaca</i> strain DSM 44595 (Actinobacteria) 16S ribosomal RNA, partial sequence
Colony-3	LC594422	78.1% (346/443)	NR_104776; <i>Nocardia coeliaca</i> strain DSM 44595 (Actinobacteria) 16S ribosomal RNA, partial sequence
Colony-4	LC594423	78.1% (346/443)	NR_104776; <i>Nocardia coeliaca</i> strain DSM 44595 (Actinobacteria) 16S ribosomal RNA, partial sequence
Colony-5	LC594424	77.9% (345/443)	NR_104776; <i>Nocardia coeliaca</i> strain DSM 44595 (Actinobacteria) 16S ribosomal RNA, partial sequence
Colony-6	LC594425	77.9% (345/443)	NR_104776; <i>Nocardia coeliaca</i> strain DSM 44595 (Actinobacteria) 16S ribosomal RNA, partial sequence
Colony-7	LC594426	78.1% (346/443)	NR_104776; <i>Nocardia coeliaca</i> strain DSM 44595 (Actinobacteria) 16S ribosomal RNA, partial sequence
Colony-8	LC594427	78.1% (346/443)	NR_104776; <i>Nocardia coeliaca</i> strain DSM 44595 (Actinobacteria) 16S ribosomal RNA, partial sequence

^aFor sample ID, see Supplementary Table S1.

^bEach field-collected mother was subjected to dissection and isolation of midgut M4 region. The isolated symbiotic organ was homogenized. One half of the homogenate was subjected to DNA extraction, PCR amplification, cloning and sequencing of bacterial 16S rRNA gene. “M4 tissue” represents the sequence (also described in Supplementary Table S1). The remaining half of the homogenate was subjected to direct bacterial cell counting, and also serially diluted and spread onto LB agar plates, from which eight single colonies were picked and subjected to DNA extraction, PCR amplification and direct sequencing of bacterial 16S rRNA gene. “Colony-1” to “Colony-8” represent these sequences.

^cPercentage in terms of (number of matched nucleotide sites/number of aligned nucleotide sites), where gap-containing sites were omitted from the alignment.

^dAmong the BLAST top hit entries, a representative one with species identification is shown with sequence accession number and biological description.