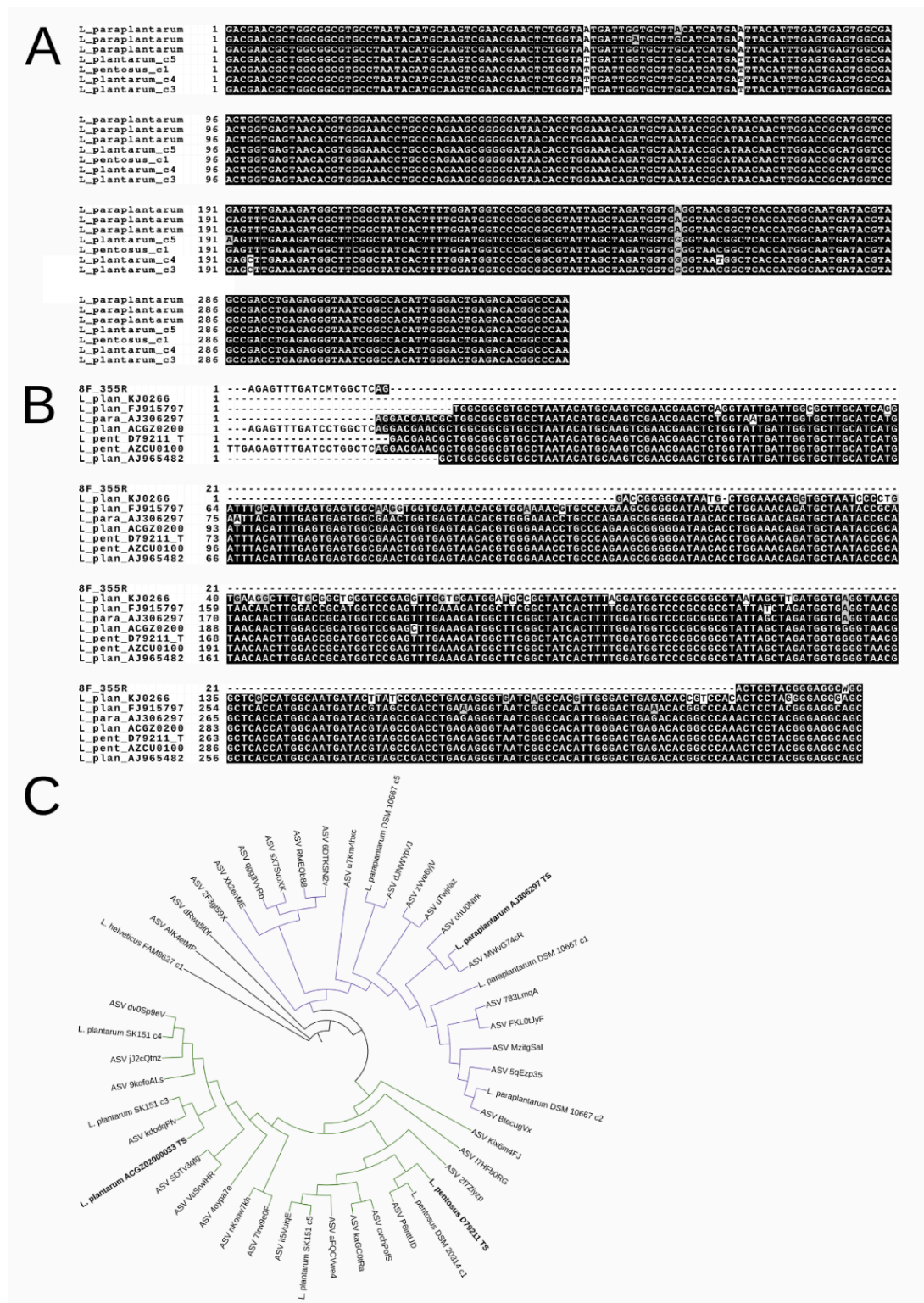


Supplementary figures



Supplementary Figure S1: Analysis of the potential to differentiate *Lactiplantibacillus plantarum* group species based on V1–V2 variable regions of the 16S rRNA gene

A) Alignment of the V1–V2 16S rRNA gene region of the representative genomes of *Lactiplantibacillus plantarum*, *L. paraplantarum* and *L. pentosus*. B) Alignment of the DAIRYdb 16S rRNA gene reference sequences. C) The best-scoring maximum likelihood tree from alignments of the V1–V2 16S rRNA gene sequences including the representative genomes, the DAIRYdb reference sequences, and the ASVs for *L. plantarum*, *L. paraplantarum* and *L. pentosus*.

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L_pentosus_c1      1  ACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGACGAAAGTCTGATGGAGCAACGCCGCGTGAGTGAAGAAGGGTTTCGGCTCGTAAA
L_paraplantarum    1  ACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGACGAAAGTCTGATGGAGCAACGCCGCGTGAGTGAAGAAGGGTTTCGGCTCGTAAA
L_plantarum_c1     1  ACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGACGAAAGTCTGATGGAGCAACGCCGCGTGAGTGAAGAAGGGTTTCGGCTCGTAAA
L_plantarum_c5     1  ACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGACGAAAGTCTGATGGAGCAACGCCGCGTGAGTGAAGAAGGGTTTCGGCTCGTAAA

L_pentosus_c1      96  ACTCTGTTGTTAAAGAAGAACATATCTGAGAGTAAGTCTTTCAGTATTGACGGTATTTAAACAGAAAGCCACGGCTAACTACGTGCCAGCAGCCG
L_paraplantarum    96  ACTCTGTTGTTAAAGAAGAACATATCTGAGAGTAAGTCTTTCAGTATTGACGGTATTTAAACAGAAAGCCACGGCTAACTACGTGCCAGCAGCCG
L_plantarum_c1     96  ACTCTGTTGTTAAAGAAGAACATATCTGAGAGTAAGTCTTTCAGTATTGACGGTATTTAAACAGAAAGCCACGGCTAACTACGTGCCAGCAGCCG
L_plantarum_c5     96  ACTCTGTTGTTAAAGAAGAACATATCTGAGAGTAAGTCTTTCAGTATTGACGGTATTTAAACAGAAAGCCACGGCTAACTACGTGCCAGCAGCCG

L_pentosus_c1      191  CGGTAATACGTAGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTTTTAAGTCTGATGTGAAAGCCTTCGGCTCAA
L_paraplantarum    191  CGGTAATACGTAGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTTTTAAGTCTGATGTGAAAGCCTTCGGCTCAA
L_plantarum_c1     191  CGGTAATACGTAGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTTTTAAGTCTGATGTGAAAGCCTTCGGCTCAA
L_plantarum_c5     191  CGGTAATACGTAGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTTTTAAGTCTGATGTGAAAGCCTTCGGCTCAA

L_pentosus_c1      286  CCGAAGAAGTGCAATCGGAAACTGGGAAACTTGAGTGCAGAAAGAGGACAGTGGAACTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAAGAAC
L_paraplantarum    286  CCGAAGAAGTGCAATCGGAAACTGGGAAACTTGAGTGCAGAAAGAGGACAGTGGAACTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAAGAAC
L_plantarum_c1     286  CCGAAGAAGTGCAATCGGAAACTGGGAAACTTGAGTGCAGAAAGAGGACAGTGGAACTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAAGAAC
L_plantarum_c5     286  CCGAAGAAGTGCAATCGGAAACTGGGAAACTTGAGTGCAGAAAGAGGACAGTGGAACTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAAGAAC

L_pentosus_c1      381  ACCAGTGGCGAAGCGGCTGTCTGGTCTGTAAGTACGCTGAGGCTCGAAAGTATGCGTAGCAAAACAGG
L_paraplantarum    381  ACCAGTGGCGAAGCGGCTGTCTGGTCTGTAAGTACGCTGAGGCTCGAAAGTATGCGTAGCAAAACAGG
L_plantarum_c1     381  ACCAGTGGCGAAGCGGCTGTCTGGTCTGTAAGTACGCTGAGGCTCGAAAGTATGCGTAGCAAAACAGG
L_plantarum_c5     381  ACCAGTGGCGAAGCGGCTGTCTGGTCTGTAAGTACGCTGAGGCTCGAAAGTATGCGTAGCAAAACAGG

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Supplementary Figure S2: *Lactiplantibacillus plantarum* group discrimination of 16S rRNA gene amplicon sequencing targeting the V3–V4 region

	16S rRNA gene primer (forward)	16S rRNA gene variable region	16S rRNA gene primer (reverse)
27F_355R	1 AGAGTTTIGATCTTGGCTCAGG	... 21	ACTCCTACGGGAGGC
L_lacti_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 308	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
S_therm_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 308	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
E_faeca_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 320	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_pento_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 326	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_plant_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 326	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_parap_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 326	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_parab_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 335	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
P_pento_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 336	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_brevi_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 326	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_coryn_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 327	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_curva_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 330	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_sakei_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 332	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_parac_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 327	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_rhamn_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 327	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_delbr_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 322	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_helve_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 324	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC
L_mesen_c1	1 AGAGTTTIGATCTTGGCTCAGG	... 309	GGCCACATGGGACTGAGACACGGCCCAACTCCTACGGGAGGC

Supplementary Figure S3: Alignment of the 16S rRNA gene primer binding regions