Supplemental material

TABLE S1. Primers used to sequence the *arc* operon of *Lactobacillus sakei* CTC 494, designed based on the genome sequence of *Lactobacillus sakei* 23K.

PCR target[a]	**Forward primer (5’ → 3’)**	**Reverse primer (5’ → 3’)**	**Amplicon length (bp)**
372,772-373,556	AATTAAGGATGATACGATTGTTG	GCAGCGAGGTTTTCTAAGTA	785
373,430-374,238	ACATTATGTATCGTTTATTGTTTG	TAAGATAAGTGTCAACCATGC	809
374,082-374,883	TAACCACAGTGGCTTTGAA	GCTGTATCTTCAACTGATTCTT	802
374,762-375,552	AAAAATTCAACCAGAACG	ATTCTGTTTTCAGCTTCTTC	791
375,430-376,238	TGATATTGAAACTGAATATGGTAAG	GGTGCTTCTTGAATACCAAT	809
376,106-376,900	GACCTTTCTATAGCGAAGCA	ACCGTTTGATACAATTCACTAAC	795
376,758-377,564	ATGACCATGTCAGAATTGATG	ATCAACGAGTGGTTCTTGTG	807
377,434-378,242	GTGTTTTCAGTGATCAGTTAGC	ATATGTTAAGCTCCACGATAAAA	809
378,098-378,895	TTATTGGTTGTCAGCATGG	AAGTTATAAGCTTTCGTTGTGAA	798
378,767-379,573	AAATTTATTGCCAGCTTACTTC	AGCTAAGTTTGCTTGATATACG	807
379,434-380,240	TTCATAAGGGCCAGGAAT	ACTGTCAGTATGAAGAGGATCAC	807

[a] Position in the genome of *Lactobacillus sakei* 23K

TABLE S2. Primers used for RT-qPCR analysis of target (*arc* operon) and reference genes of *Lactobacillus sakei* CTC 494.

Gene	**Forward primer (5’ → 3’)**	**Reverse primer (5’ → 3’)**	**Amplicon length (bp)**
Target genes			
arcA	TCTATATGGATCCAATGCCTAACCT	GTTAAGCCATCCCCCATTGA	70
arcB	AACAGGTTCAATGTTAGGCGTAAAT	TCAGCTAAATCACGGACTTCTTGT	84
arcC	AGCTTTCCAAAACCCAACGA	TGGGTTGATACTTTGTTGTTTCTTAGC	79
arcD	GAAGGGATTTTCTCTTACGCTGAA	AACCATGCTGACAACCAATAACC	86
arcT	CAAGCAGGTTTTAGCCCGTAA	GCAACCCACGCTTTAAAAATCT	69
arcR	GGTGAAGGAATTAGCGACAATGA	TTTTGGGCAACCAACTGTTTAA	73
Reference genes			
secY	GTTAGGGAATGGTGTTTCAATGATT	GATGATTTGATGAAGGCCACTTG	54
rpoB	AACCAATTCCGTATIGGTTT	CCGTCCCAAGTCATGAAAC	65
recA	CGAAGCGTCGGAGTAGGT	AGCATGTAACGCAACGGTTGT	74
pfk	GCAACCCCGCCTTTGC	AGCTAGCCGCTTAGGCTCAA	60
fusA	AACCCAAACGTCACCATATTGAC	GCATCTGCACAAGGTAAATTCG	66
ileS	CAGCCCGCCACCCATTA	ATGTCACGTGGTTCCCTAAGATC	60
pcrA	CCCCGTTTAGGGCTGTTGA	TGGTTAATGCGGCCGATT	58

TABLE S3. Primers used for RT-qPCR analysis of target (*arc* operon and putative second *arc* operon) and reference genes of *Lactobacillus sakei* 23K.

Gene	**Forward primer (5’ → 3’)**	**Reverse primer (5’ → 3’)**	**Amplicon length (bp)**
Target genes			
arc *operon*			
arcA	TCTATATGGATCCAATGCCTAACCT	GTTAAGCCATCCCCCATTGA	70
arcB	AACAGGTTCAATGTTAGGCGTAAAT	TCAGCTAAATCACGGACTTCTTGT	84
arcC	AGCTTTCCAAAACCCAACGA	TGGGTTGATACTTTGTTGTTTCTTAGC	79
arcD	GAAGGGATTTTCTCTTACGCTGAA	AACCATGCTGACAACCAATAACC	86
arcT	CAAGCAGGTTTTAGCCCGTAA	GCAACCCACGCTTTAAAAATCT	69
arcR	GGTGAAGGAATTAGCGACAATGA	TTTTGGGCAACCAACTGTTTAA	78
Putative second* arc *operon			
LSA0067	AGATGGGCATGCAATTCGTT	ATTCTTTTGACCGATTGCTAATGTT	80
LSA0068	GCAAATTCCCCAAGCCATTA	CATCCCGAAAGCTGCGAATA	73
LSA0069	TTAAACGACATTATCGCAACGATT	AGAAGAATGCCCAGAAAATATTGG	79
LSA0070	CTAAACCAGCGCAAGCAACTT	GCCAACGGTCACACTTTCAA	71
LSA0071	GTGACGCAAACCATTGTAGCA	TCTTCATAAAAAGGACCGATTGG	77
LSA0072	CCAATGTTTGCGACTCAAGAAG	CCTGGATAGCGAGGCAAGAG	71
Reference genes			
fusA	AACCCAAACGTCACCATATTGAC	GCATCTGCACAAGGTAAATTCG	66
ileS	CAGCCCGCCACCCATTA	ATGTCACGTGGTTCCCTAAGATC	60
pcrA	CCCCGTTTAGGGCTGTTGA	TGGTTAATGCGGCCGATT	58

TABLE S4. Optimized concentrations and amplification efficiencies (calculated with the DART-PCR applet) of the primers used to calculate the relative expression of the target (*arc* operon) and reference genes for *Lactobacillus sakei* CTC 494. Amplification efficiencies, with the corresponding standard deviations, are mean efficiencies for the late-exponential, end-exponential, early-stationary, and late-stationary growth phase time points of all fermentations performed in quadruplicate.

Gene	**Concentration (nM)**		**Amplification efficiency**
	Forward primer	**Reverse primer**	
Target genes			
arcA	300	300	1.98 ± 0.02
arcB	300	300	1.91 ± 0.01
arcC	300	300	1.95 ± 0.02
arcD	300	300	1.90 ± 0.01
arcT	300	300	1.93 ± 0.02
arcR	300	300	1.92 ± 0.08
Reference genes			
fusA	500	500	1.88 ± 0.03
ileS	500	500	1.92 ± 0.02
pcrA	500	500	1.89 ± 0.03

TABLE S5. Optimized concentrations and amplification efficiencies (calculated with the DART-PCR applet) of the primers used to calculate the relative expression of the target genes (*arc* operon and a putative second *arc* operon) and reference genes for *Lactobacillus sakei* 23K. Amplification efficiencies, with the corresponding standard deviations, are mean efficiencies for the late-exponential, end-exponential, early-stationary, and late-stationary growth phase time points of all fermentations performed in quadruplicate.

Gene	**Concentration (nM)**		**Amplification efficiency**
	Forward primer	**Reverse primer**	
Target genes			
arc *operon*			
arcA	300	300	2.00 ± 0.01
arcB	300	300	1.97 ± 0.01
arcC	300	300	1.98 ± 0.00
arcD	300	300	1.94 ± 0.01
arcT	300	300	1.94 ± 0.01
arcR	300	300	1.94 ± 0.07
Putative second* arc *operon			
LSA0067	300	300	1.95± 0.01
LSA0068	300	300	1.93 ± 0.01
LSA0069	300	300	1.98 ± 0.02
LSA0070	300	300	1.97 ± 0.01
LSA0071	300	300	1.97 ± 0.01
LSA0072	300	300	1.90 ± 0.03
Reference genes			
fusA	500	500	1.87 ± 0.07
ileS	500	500	1.95 ± 0.02

TABLE S6. Primers used to screen for a putative second *arc* operon in *Lactobacillus sakei*, which were designed based on the genome sequence of *Lactobacillus sakei* 23K.

PCR target[a]	**Forward primer (5’ → 3’)**	**Reverse primer (5’ → 3’)**	**Amplicon length (bp)**
63,638-64,312	TTTTGTGTATTACTAAAATGGTG	ACATTAATGAAACACAGACTTG	675
64,202-64,910	AAATCGGCGATATCATCA	GACATTAATACGGCATCAAATA	709
64,776-65,483	AGATCCAGCATTAAAAGACTTA	ACCACTTCAAAACCTAAGAAG	708
65,349-66,045	ACTTGGTATTTACCATGCTG	GGATAACCACTGCATTACC	697
65,957-66,663	GTTGATGTTCCCATCATTT	TTCACAAACCTTTTGAGC	707
66,544-67,253	GTTAATGATAAAGGCGACAG	CGATCTGGATATAATTTTTGA	710
67,124-67,818	TAGCAGGAGATCGATTAGC	GGCATCTTCCATCATTTG	695
67,718-68,425	CATTTCACCAACCCACTA	CTGGTAAATAGTATTGGTCCTC	708
68,292-69,001	GTTTTCAAAGAAGCGACTA	AATAACCTAGTTTTAACCAAATC	710
68,886-69,571	CGAGGAATCTATTCTTTCTG	CATCCATATTTTTAATGACGTA	686

[a] Position in the genome of *Lactobacillus sakei* 23K

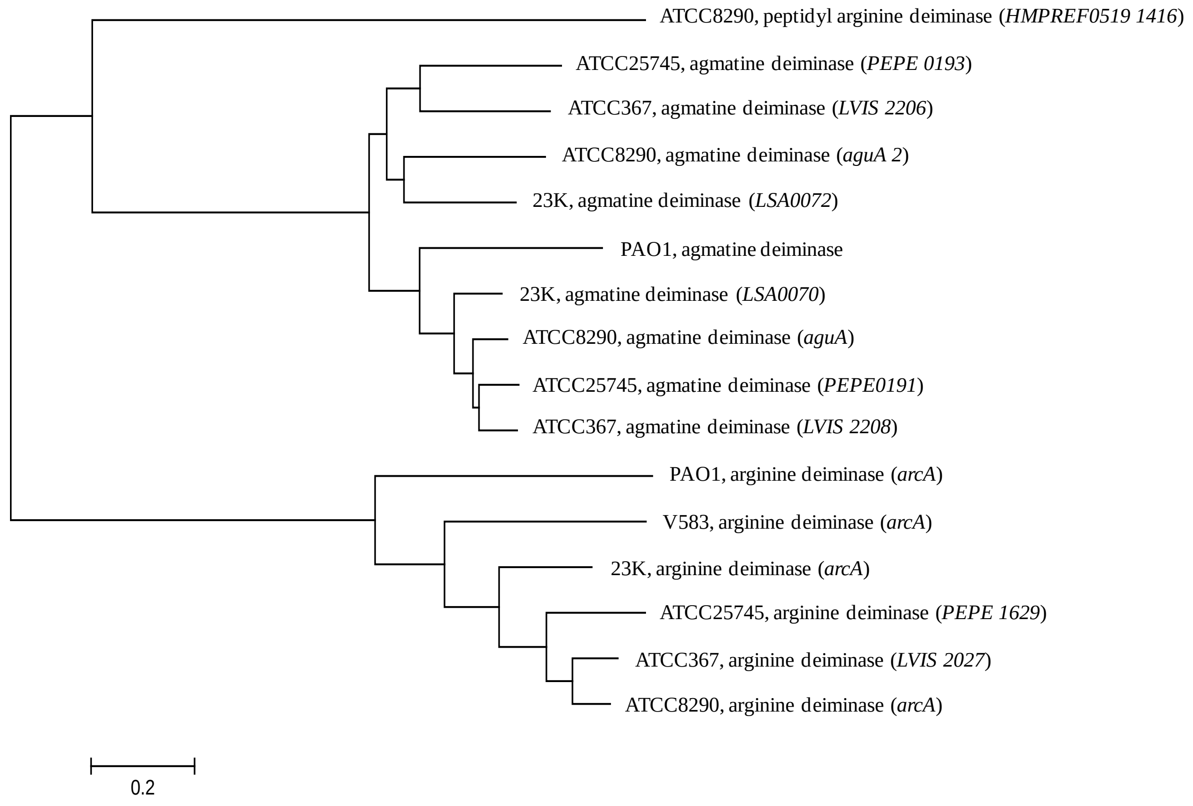

FIG. S1. Clustering trees of arginine and agmatine deiminases based on their amino acid sequences, for *Pseudomonas aeruginosa* PAO1, LASB58, UCBPP-PA14, and PA7; *Enterococcus faecalis* 62, V583, and ATCC 4200; *L. sakei* 23K; *Lactobacillus hilgardii* ATCC 8290; *Lactobacillus brevis* ATCC 367; and *Pediococcus pentosaceus* ATCC 25745, applying MEGA 4.0 and using the neighbor-joining clustering method.

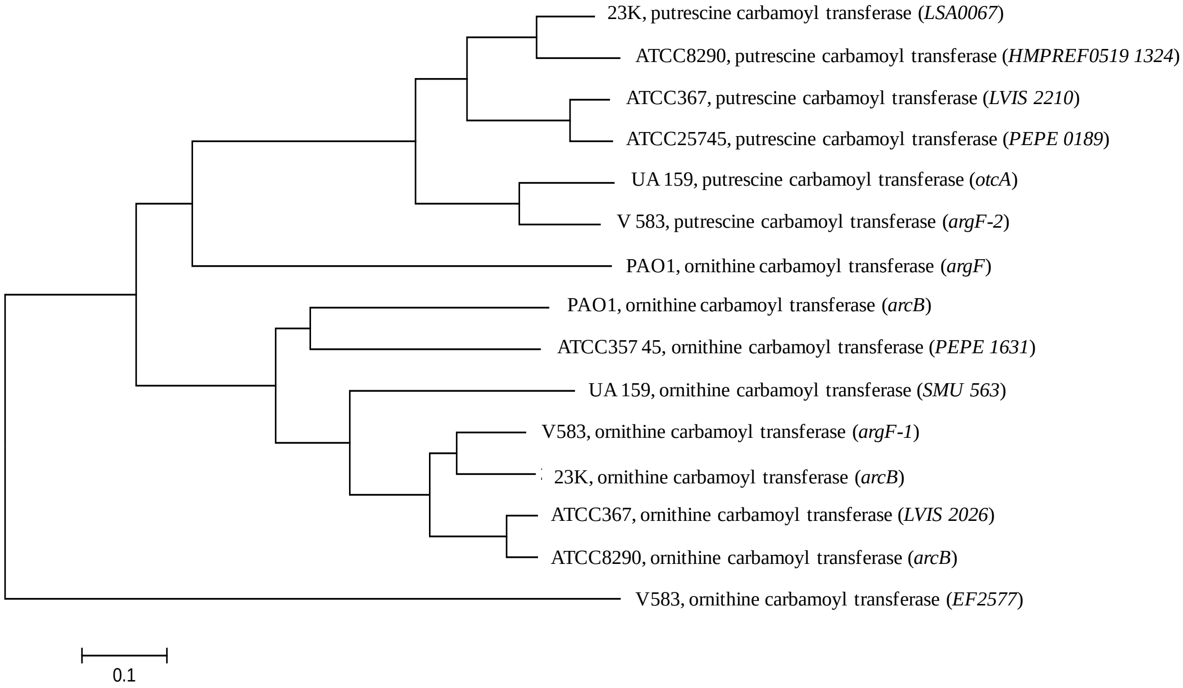

FIG. S2. Clustering trees of ornithine and putrescine carbamoyl transferases based on their amino acid sequences, for *Pseudomonas aeruginosa* PAO1, LASB58, UCBPP-PA14, and PA7; *Enterococcus faecalis* 62, V583, and ATCC 4200; *L. sakei* 23K; *Lactobacillus hilgardii* ATCC 8290; *Lactobacillus brevis* ATCC 367; and *Pediococcus pentosaceus* ATCC 25745, applying MEGA 4.0 and using the neighbor-joining clustering method.