Supplemental material

Table S1

Primers and PCR conditions used in this study.

Target	Primer	Sequence (5'-3')	Annealing temperature (°C)	Reference
bla$_{CTX}$	CTX-consensus primer F	GCA GYA CCA GTA ARG TKA TGG C	58	1
	CTX consensus primer R	ATC ACK CGG RTC GCC XGG RAT		
bla$_{OXA}$	blaOXA- F	ACC AGA TTC AAC TTT CAA	55	2
	blaOXA- R	TCT TGG CTT TTA TGC TTG		
bla$_{TEM}$	blaTEM- F	TCG GGG AAA TGT GCG	50	3
	blaTEM- R	GGA ATA AGG GCG ACA		
bla$_{SHV-1}$	blaSHV- F	TGA TTT ATC TGC GGG ATA CG	55	3
	blaSHV- R	TTA GCG TTG CCA GTG CTC G		
tet(A)	tetA-F	GCT ACA TCC TGC TTG CCT TC	55	4
	tetA-R	CAT AGA TCG CCG TGA AGA GG		
tet(B)	tetB-F	TTG GTT AGG GGC AAG TTT TG	55	4
	tetB-R	GTA ATG GGC CAA TAA CAC CG		
tet(O)	tetO-F	AAC TTA GGC ATT CTG GCT CAC	55	4
	tetO-R	TCC CAC TGT TCC ATA TCG TCA		
tet(Q)	tetQ-F	TTA TAC TTC CTC CGG CAT CG	55	4
	tetQ-R	ATC GGT TCG AGA ATG TCC AC		
catA1	catA1- F	CGC CTG ATG AAT GCT CAT CCG	58	2
	cat A1- R	CCT GCC ACT CAT CGC AGT AC		
catA2	catA2- F	ATG AAT TTT ACC AGA ATT GAT CTG AA	58	2
	catA2- R	ATT TCA GTA TGT TAT CAC ACA TCA TCT		
cat A3	catA3- F	AAA TTG GGT TCG CCG TGA	58	2
	catA3- R	ATT TAC TGT TAC ACA ACT CTT GTA GCC		
catB3	catB3- F	TCA AAG GCA AGC TGC TTT CTG AGC	58	2
	catB3- R	TAT TAG ACG AGC ACA GCA TGG GCA		
ermA	ermA1	TCT AAA AAG CAT GTA AAA GAA	52	5
	ermA2	CTT CGA TAG TTT ATT AAT ATT AGT		
ermB	ermB1	GAA AAG GTA CTC AAC CAA ATA	52	5
	ermB2	AGT AAC GGT ACT TAA ATT GTT TAC		
mefA	mefA- F	AGT ATC ATT AAT CAC TAG TGC	55	5
	mefA- R	TTC TTC TGG TAC TAA AAG TGG		
ereA	EreA- F	AACACCCTGAACCCAAGGGACG	55	5
	EreA- R	CTTCACATCCGGATTCGCTCGA		
ereB	EreB- F	CATATAATCATCACCAATGGCA	55	5
	EreB- R	AGAAATGGAGGTTCATACTTACCA		

msrA	msrA- F	GGCACAATAAGAGTGTTTAAAGG	50	6
	msrA- R	AAGTTATATCATGAATAGATTGTCCTGTT		
msrB	msrB- F	TATGATATCCATAATAATTATCCAATC	50	6
	msrB- R	AAGTTATATCATGAATAGATTGTCCTGTT		
aadE	aadE I	GCAGAACAGGATGAACGTATTCG	55	7
	aadE II	ATCAGTCGGAACTATGTCCC		
aphA3	aphA3- F	GGG ACC ACC TAT GAT GTG GAA CG	58	2
	aphA3- R	CAG GCT TGA TCC CCA GTA AGT C		
aac(6')-Ie-aph(2")-Ia	aac(6′)-Ie-aph(2")-Ia- F	CAGAGCCTTGGGAAGATGAAG	55	8
	aac(6′)-Ie-aph(2")-Ia- R	CCTCGTGTAATTCATGTTCTGGC		
aph(2")-Ib	aph(2")-Ib- F	CTTGGACGCTGAGATATATGAGCAC	55	8
	aph(2")-Ib- R	GTTTGTAGCAATTCAGAAACACCCTT		
aph(2")-Ic	aph(2")-Ic- F	CCACAATGATAATGACTCAGTTCCC	55	8
	aph(2")-Ic- R	CCACAGCTTCCGATAGCAAGAG		
aph(2")-Id	aph(2")-Id- F	GTGGTTTTTACAGGAATGCCATC	55	8
	aph(2")-Id- R	CCCTCTTCATACCAATCCATATAACC		
aph(3')-IIIa	aph(3′)-IIIa- F	GGCTAAAATGAGAATATCACCGG	55	8
	aph(3′)-IIIa- R	CTTTAAAAAATCATACAGCTCGCG		
ant(4')-Ia	ant(4′)-Ia- F	CAAACTGCTAAATCGGTAGAAGCC	55	8
	ant(4′)-Ia- R	GGAAAGTTGACCAGACATTACGAACT		
sul-I	sulI- F	CGCACCGGAAACATCGCTGCAC	56	9
	sulI- R	TGAAGTTCCGCCGCAAGGCTCG		
sulII	sulII- F	TCC GGT GGA GGC CGG TAT CTG G	61	9
	sulII- R	CGG GAA TGC CAT CTG CCT TGA G		
sulIII	sulIII- F	TCC GTT CAG CGA ATT GGT GCA G	60	9
	sulIII- R	TTC GTT CAC GCC TTA CAC CAG C		
vanA	vanA- F	GCT ATT CAG CTG TAC TC	52	2
	vanA- R	CAG CGG CCA TCA TAC GG		
vanB	vanB- F	CAT CGC CGT CCC CGA ATT TCA AA	58	2
	vanB- R	GAT GCG GAA GAT ACC GTG GCT		
dfrA	dfrA1	CTTTTCTACGCACTAAATGTAAG	50	10
	dfrA2	CATTATCAATAATTGTCGCTCAC		
dfrD	dfrD1	GGAAGGGCTTTACCTGACAGAAG	50	10
	dfrD2	CGACATAAGGCAAGAACATAACATA		
rpoB	rpoB- P5	TGATCAACGCCAAGCCGGT	55	11
	rpoB- P6	TTGCGCTCCATGCCGGTAC		
acrA	acrA- F	CTC TCA GGC AGC TTA GCC CTA A	60	12
	acrA- R	TGC AGA GGT TCA GTT TTG ACT GTT		
acrB	acrB- F	GGT CGA TTC CGT TCT CCG TTA	60	12
	acrB- R	CTA CCT GGA AGT AAA CGT CAT TGG T		
tolC	tolC- F	AAG CCG AAA AAC GCA ACC T	57	12
	tolC- R	CAG AGT CGG TAA GTG ACC ATC		

mexB	MxB- U	CAA GGG CGT CGG TGA CTT CCA G	62	13
	MxB- L	ACC TGG GAA CCG TCG GGA TTG A		
mexY	MxY- U	GGA CCA CGC CGA AAC CGA ACG	62	13
	MxY- L	CGC CGC AAC TGA CCC GCT ACA		
mexD	MxD- U	GGA GTT CGG CCA GGT AGT GCT G	62	13
	MxD- L	ACT GCA TGT CCT CGG GGA AGA A		
Int- 1,2,3	hep35	TGC GGG TYA ARG ATB TKG ATT T	55	14
	hep 36	CAR CAC ATG CGT RTA RAT		
Class 2 integron	intl2L	CAC GGA TAT GCG ACA AAA AGG T	63	15
	intl2R	GTA GCA AAC GAG TGA CGA AAT G		
Class 3 integron	intl3L	GCC TCC GGC AGC GAC TTT CAG	63	15
	intl3R	ACG GAT CTG CCA AAC CTG ACT		

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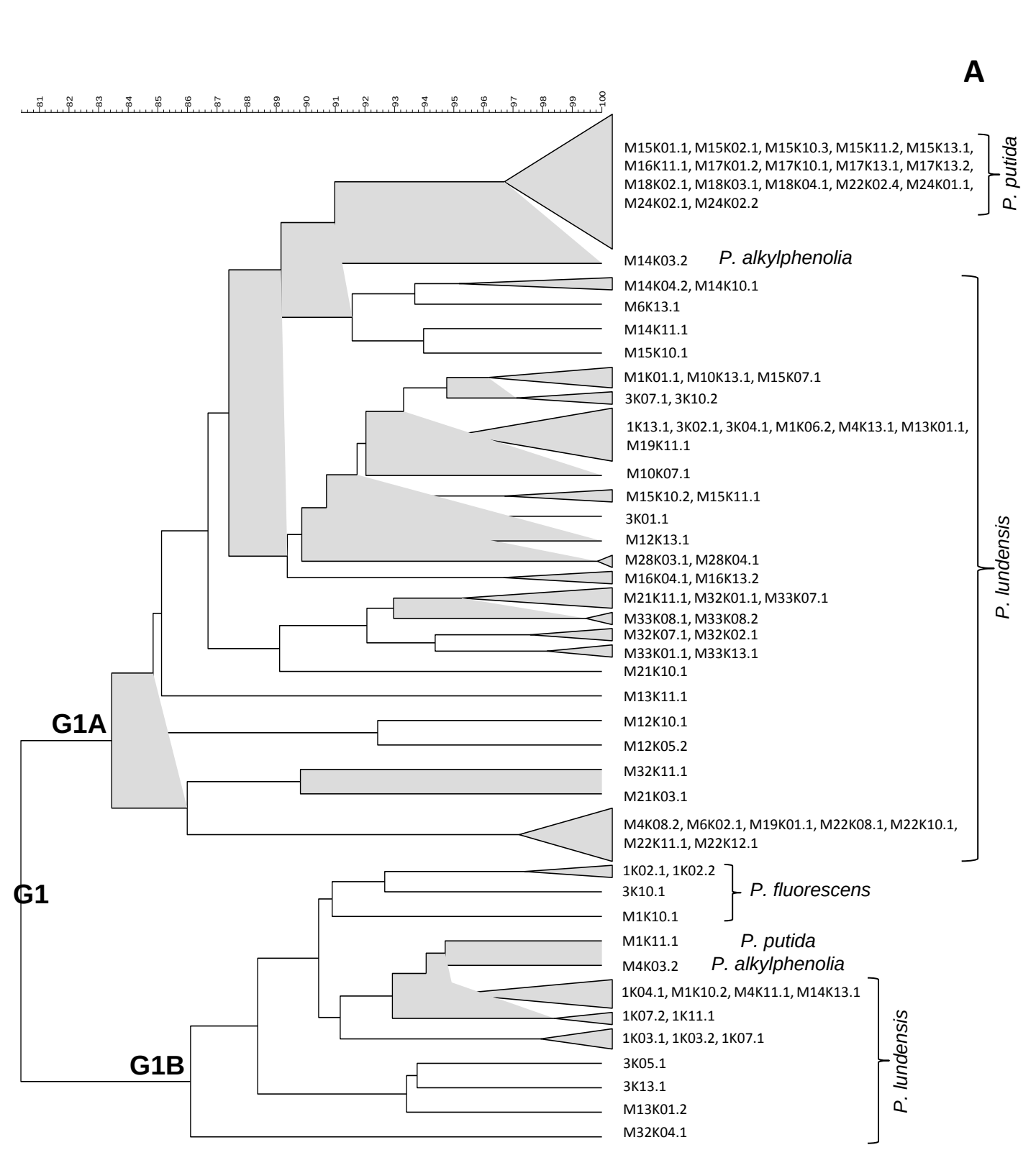
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P. putida
M14K03.2
P. alkylphenolia
M14K04.2, M14K10.1
M6K13.1
M14K11.1
M15K10.1
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3K10.1
M1K10.1
P. fluorescens
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P. putida
M4K03.2
P. alkylphenolia
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G1
G1B

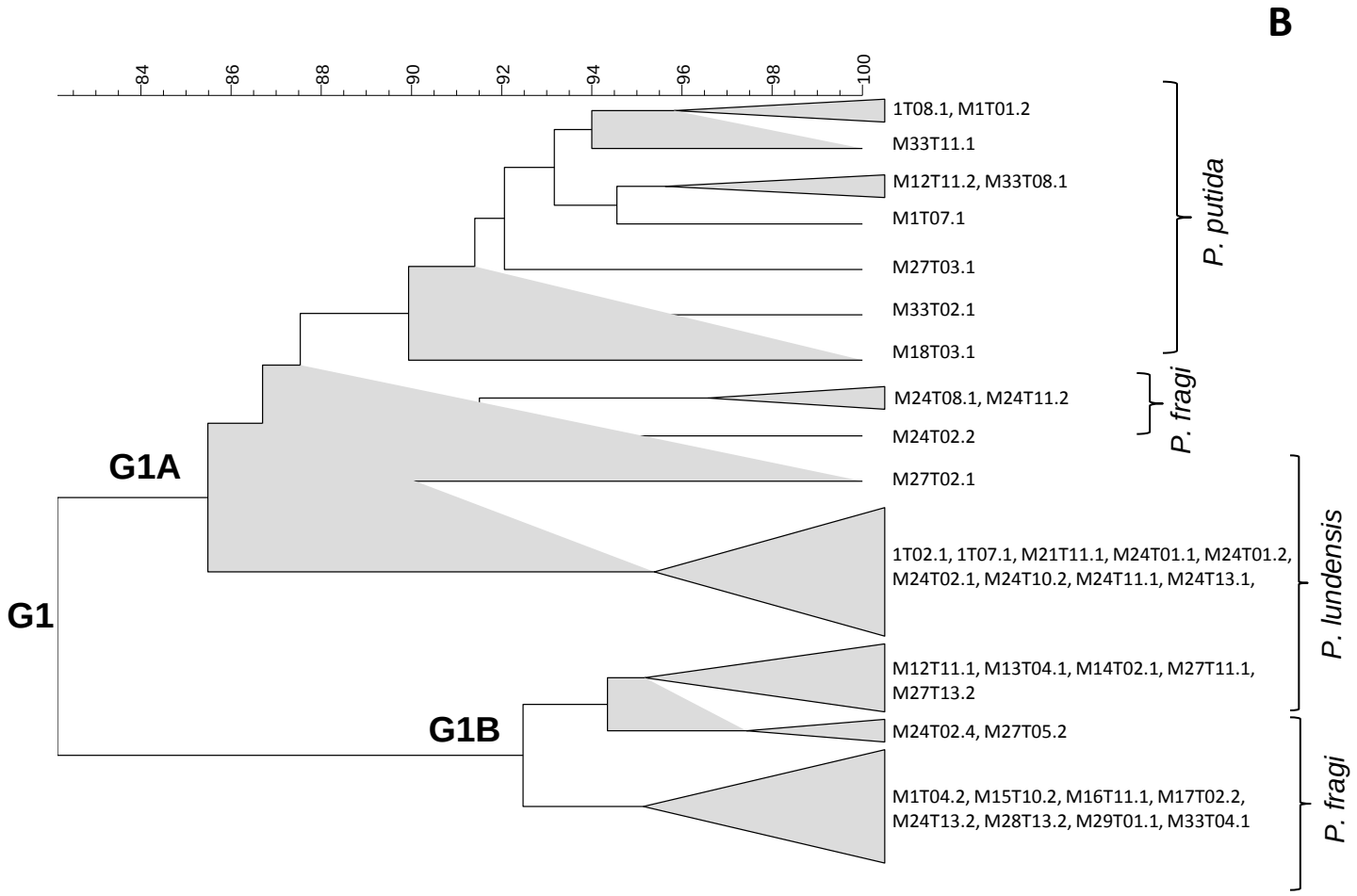

Fig. S1. Dendrograms obtained from ERIC-PCR fingerprints of mesophilic (A) and psychrotrophic (B) pseudomonads isolated from slaughterhouse surfaces throughout meat chain production and from the end products. Patterns were grouped with the unweighted pair group algorithm with arithmetic averages (UPGMA). Species identity is indicated on the right-hand side of the dendrogram.