Supplementary materials

The Mla pathway plays an essential role in the intrinsic resistance of *Burkholderia cepacia* complex species to antimicrobials and host innate components

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Running title:

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Supplementary Tables

		Antibiotic ^b					
Strain/mutant ID	Gene ^a	AZM 15	FEP 30	IPM 10	TOB 10		
WT K 56-2	-	6	27	9	6		
1566	BCAL0179	6	2.5	10	6		
36D7	BCAL0179	6	21	8	6		
37A8	BCAL0182	6	23	8	6		
25E5	BCAL0302	23	24	10	6		
30G10	BCAL0305	29	26	6	6		
2C5	BCAL0305	26	26	13	6		
12C7	BCAL0499	6	26	14	6		
14C3	BCAL1048	6	26	9	6		
37B7	BCAL1172	6	22	7	6		
28H12	BCAL1246	6	22	7	6		
37H7	BCAL3225	6	21	8	6		
2D10	BCAL3252	6	26	10	6		
35H10	BCAL3252	6	22	8	6		
4E2	BCAL3336	6	27	11	6		
8H11	BCAM0275a	6	24	11	6		
13F4	BCAM0324	6	26	8	6		
16H4	BCAM1948	6	24	8	6		
24C3	BCAM2426	6	26	11	6		
17F3	BCAM2618	6	26	11	6		
33C6	BCAM2620	6	22	7	6		

Table S1. Antibiotic resistance profile of B. cenocepacia K56-2 transposon mutants selected for their sensitivity to *P. aeruginosa* spent medium on agar surface

^a Gene affected by the transposon insertion as described in Table 1. ^b Zone of clearing in millimeters (mm) around the disk after 24 h. When no zone was present, the size of the disk (6 mm) was recorded. Abbreviations of the antibiotics tested with their concentration in µg on each disk in parentheses are as follow: azithromycin (AZM 15), cefepime (FEP 30), imipenem (IPM 10), and tobramycin (TOB 10).

Antibiotic class/Antibiotic	[ug]	WT	mlaE	mlaC	BCAL0499
Penicillins					
Ampicillin (AMP)	2	6	N.D.	6	N.D.
	10	6	N.D.	6	N.D.
	25	6	6	6	6
Amoxicillin-clavulanate (AMC) Penicillin (P)	30 10	6	0 N D	6	б N D
	10	0	N.D.	0	N.D.
Cephalosporins Cafenime (EEP)	30	28	20	28	28
Cefoxitin (FOX)	30	20 6	29 6	20 6	20
Ceftazidime (CAZ)	30	39	39	37	40
Ceftriaxone (CRO)	30	27	29	26	27
Carbapenems					
Imipenem (IPM)	10	12	13	13	13
Meropenem (MEM)	10	37	37	33	38
Monobactams					
Aztreonam (ATM)	30	25	24	23	25
Aminoglycosides					
Tobramycin (TOB)	10	6	6	6	6
Amikacin (AK)	30	6	6	6	N.D.
Tetracyclines					
Tetracycline (TE)	30	25	32	32	28
Doxycycline (DO)	30	34	50	51	37
Tigecycline (TGC)	15	20	34	34	17
Oxazolidonones					
Linezolid (LZD)	10	6	6	6	N.D.
	30	6	6	6	6
Chloramphenicol (C)	10	9	19	22	N.D.
	30	20	33	32	25
	50	28	35	39	N.D.
Macrolides					
Azythromycin (AZM)	15	6	26	26	6
Clarithromycin (CLR)	2	6	N.D.	7	N.D.
	5	6	N.D.	15	N.D.
Erythromycin (E)	15	6	25	22	6
	15	0	21	17	0
Lincosamides	2	6	6	6	6
	Z	0	0	0	0
Fluoroquinolones	_		25	20	
Ciprofloxacin (CIP)	5	24	3/	38	25 N D
	5	22	30	42	N.D.
Rifampicin (RD)	5	6	26	27	6
Others					
Piperacillin/tazobactam (TZP)	110	40	42	40	42
Fostomycin (FOS)	50	6	6	6	6

Table S2. Antibiotic resistance profiles of B. cenocepacia K56-2 mutants

Zone of clearing in millimeters (mm) around the disk after 24 h are reported. When no zone was present, the size of the disk (6 mm) was recorded. Gray zones represent antibiotics for which *mlaE* and *mlaC* insertional mutants are more sensitive than their WT parent.

	Zone of clearing (mm) ^a							
Antibiotic	[ug]	WT	$\Delta m la A$	∆mlaC	∆mlaD	∆mlaE	$\Delta yadG$	∆yadH
Azythromycin	15	17	17	16	16	15	16	16
Erythromycin	15	10	11	11	10	11	10	10
Clarithromycin	5	6	6	6	6	6	6	6
Rifampicin	5	13	13	14	13	13	12	15
Ciprofloxacin	5	37	37	36	38	35	37	37
Levofloxacin	5	35	34	34	38	35	35	35
Chloramphenicol	30	28	30	31	29	30	28	28
Tetracycline	30	32	32	31	31	31	33	32
Tigecycline	15	30	30	30	31	30	30	31
Doxycycline	30	29	30	30	30	30	30	31

Table S3. The Mla pathway and antibiotic resistance in *E. coli* K-12

^aZone of clearing in millimeters (mm) around the disk after 24 h are reported. When no zone was present, the size of the disk (6 mm) was recorded.

Deletion mutants of *E. coli* strain BW25113 (WT) are from the Keio collection (1) and described in Table S5.

		Zone of clearing (mm) ^a							
Antibiotic	[ug]	WT	vacJ	mlaC	mlaD	mlaE	mlaF	PA2811	PA2812
Azythromycin	15	6	6	6	6	6	6	6	6
Erythromycin	15	6	6	6	6	6	6	6	6
Clarithromycin	5	6	6	6	6	6	6	6	6
Rifampicin	5	6	6	6	6	6	6	6	6
Ciprofloxacin	5	43	44	44	44	44	44	42	41
Levofloxacin	5	38	40	40	40	40	40	37	37
Chloramphenicol	30	26	26	28	27	27	27	15	13
Tetracycline	30	34	37	35	35	36	34	31	32
Tigecycline	15	31	35	34	34	34	33	32	32
Doxycycline	30	32	36	35	35	35	36	31	32

Table S4. The Mla/VacJ pathway and antibiotic resistance in P. aeruginosa

^aZone of clearing in millimeters (mm) around the disk after 24 h. When no zone was present, the size of the disk (6 mm) was recorded.

Transposon mutants of *P. aeruginosa* strain PA14 (WT) are from (2) and described in Table S5.

64		D.C.
Strain or Plasmid	Relevant characteristics - genotype	Reference or Source
Strains		
E. coll		T
DH5a	F endAI glnV44 thi-I recAI relAI gyrA96 deoR nupG purB20	Invitrogen
	Φ 80d <i>lacZ</i> Δ M15 Δ (<i>lacZYA-argF</i>)U169, hsdR1/(r _K · m _K ·), λ -	
HB101	F mcrB mrr hsdS20(r_B m _B) recA13 leuB6 ara-14 proA2	Lab collection
	lacY1 galK2 xyl-5 mtl-1 rpsL20(Sm ^R) glnV44 λ^{-}	
BW25113	<i>E. coli</i> K-12 derivative	(1)
$\Delta m la F$	BW25113∆ <i>mlaF</i> ::KmFRT; Km ^R ; mutant ID (JW3162)	(1)
$\Delta m la E$	BW25113∆ <i>mlaE</i> ::KmFRT; Km ^R ; mutant ID (JW3161)	(1)
$\Delta m laD$	BW25113∆ <i>mlaD</i> ::KmFRT; Km ^R ; mutant ID (JW3160)	(1)
$\Delta m la C$	BW25113 <i>AmlaC</i> ::KmFRT; Km ^R ; mutant ID (JW3159)	(1)
$\Delta m la A$	BW25113 $\Delta mlaA$::KmFRT; Km ^R ; mutant ID (JW2343)	(1)
AvadG	BW25113AvadG··KmFRT·Km ^R · mutant ID (IW0123)	(1)
AvadH	BW25113AvadH:KmERT: Km^R : mutant ID (IW0124)	(1)
<u> </u>	$D \approx 25115 \Delta y a a 11.$ Kill K1, Kill , indiant $D (5 \approx 0.124)$	(1)
S. cerevisiae INVSc1	MATa his $3\Delta 1$ leu2 trp 1 -289 ura 3 -52	Invitrogen
P. aeruginosa		
PA14	Wild-type (WT); Burn patient isolate	(3)
$\Delta lasR$	PA14 $\Delta lasR$; In-frame deletion of <i>lasR</i>	(4)
rhlR	PA14 <i>rhlR</i> ::Tet; Disruption of <i>rhlR</i> ; Tet ^R	(4, 5)
$\Delta pqsR$	PA14 $\Delta pqsR$; In-frame deletion of $pqsR$	(6)
Δphz	PA14 $\Lambda phzA1$ -G1 $\Lambda phzA2$ -G2: In-frame deletion of the two	(7)
	<i>phzA-G</i> operons	
$\Lambda rhlA$	PA14 <i>rhlA</i> ::Gm: Internal deletion of <i>rhlA</i> : Gm ^R	(8-10)
Ahen ABC	$P \Delta 1 \Delta h cn A B C$	(11)
$m_{la}C \cdot (m_{la}C \cdot T_{n}M)$	PA 14 PA 14 57840 Tn M mutant ID (41806) PA 4453	(11)
mlaD: $(mlaD)$: TnM	PA14 PA14 57850. TnM, indunit ID (41000), PA4455	(2)
mlaE: (mlaE::TnM)	$D \land 14$ $D \land 14$ $57870Tn M$; mutant ID (41050), IA+454	(2)
mlaE, $(mlaE:TmM)mlaE$: $(mlaE:TnM)$	$D \land 14$ $D \land 14$ $57890Tn M$; mutant ID (70512); $D \land 4455$	(2)
mar, $(mar$, $1mm$)	$D \land 14 \ D \land 14 \ 27020 \cdots Tn M$; mutant ID (27037); $D \land 2800$	(2)
$DA 2811 \cdot DA 2811 \cdot T_n M$	DA14 DA14 27780TnM; mutant ID (32739); IA2000	(2)
FA2011, FA2011111//	$PA14_{PA14_{2770}, TnM}$, initialit ID (35140), $PA2011_{PA14_{2770}, TnM}$	(2)
FA2012, FA2012111/M	FA14_FA14_2///0111M, initialit 1D (34323), FA2612	(2)
B. cenocepacia		
K56-2	Wild-type; CF sputum isolate (Canada)	(12, 13)
<i>mlaE</i> ; (<i>mlaE</i> ::Tp)	K56-2 with pMQ87Tp inserted into <i>mlaE</i> (BCAL0302); Tp ^R	This study
<i>mlaC</i> ; (<i>mlaC</i> ::Tp)	K56-2 with pMQ87Tp inserted into <i>mlaC</i> (BCAL0305); Tp ^R	This study
BCAL0499; (BCAL0499::Tp)	K56-2 with pMQ87Tp inserted into BCAL0499; Tp ^R	This study
K56-2-15G6	BCAL0179::TnrhaBout derivative of K56-2; Tp ^R	This study
K56-2-36D7	BCAL0179::TnrhaBout derivative of K56-2; Tp ^R	This study
K56-2-37A8	BCAL0182::TnrhaBout derivative of K56-2; Tp ^R	This study
K56-2-25E5	BCAL0302::TnrhaBout derivative of K56-2; Tp ^R	This study
K56-2-30G10	BCAL0305::TnrhaBout derivative of K56-2; Tp ^R	This study
K56-2-2C5	BCAL0305::Tn <i>rhaB</i> out derivative of K56-2; Tp ^R	This study
K56-2-12C7	BCAL0499::Tn <i>rhaB</i> out derivative of K56-2; Tp ^R	This study
K56-2-14C3	BCAL1048::Tn <i>rhaB</i> out derivative of K56-2; Tp ^R	This study
K56-2-37B7	BCAL1172::Tn <i>rhaB</i> out derivative of K56-2; Tp ^R	This study
K56-2-28H12	BCAL1246::Tn <i>rhaB</i> out derivative of K56-2: Tp ^R	This study
К56-2-37Н7	(BCAL3225)::Tn <i>rhaB</i> out derivative of K56-2: Tp ^R	This study
K56-2-2D10	(BCAL3252)::Tn <i>rhaB</i> out derivative of K56-2: Tn ^R	This study
K56-2-35H10	(BCAL3252)::Tn <i>rhaB</i> out derivative of K56-2: Tp ^R	This study
K56-2-4E2	BCAL3336::Tn <i>rhaB</i> out derivative of K56-2: Tp ^R	This study

Table S5. Microbial strains and plasmids used in this study.

K56-2-8H11	(BCAM0275a)::TnrhaBout derivative of K56-2; Tp ^R	This study
K56-2-13F4	(BCAM0324)::Tn <i>rhaB</i> out derivative of K56-2; Tp ^R	This study
K56-2-16H4	BCAM1948::Tn <i>rhaB</i> out derivative of K56-2; Tp ^R	This study
K56-2-24C3	(BCAM2426)::Tn <i>rhaB</i> out derivative of K56-2; Tp ^R	This study
K56-2-17F3	BCAM2618::Tn <i>rhaB</i> out derivative of K56-2; Tp ^R	This study
K56-2-33C6	BCAM2620::Tn <i>rhaB</i> out derivative of K56-2; Tp ^R	This study
<i>vacJ2</i> ; 36D10	vacJ2::TnrhaBout derivative of K56-2; BCAM2829; Tp ^R	This study
B. dolosa		
PC543	CF sputum isolate (USA)	(14, 15)
<i>mlaC</i> ; (<i>mlaC</i> ::Tp)	PC543 with pMQ87Tp inserted into <i>mlaC</i> (BDSB_RS14790); Tp ^R	This study
<i>vacJ</i> ; 2A6	<i>vacJ</i> (BDSB RS14795)::Tn <i>rhaB</i> out derivative of PC543; Tp ^R	(16)
<i>bamC</i> ; 1A2	$bam\overline{C}_{(BDSB_RS14795)::TnrhaBout derivative of PC543; Tp^R$	(16)
Plasmids		
pSC <i>rhaB</i> out	pTn <i>Mod</i> -OTp', <i>rhaR rhaS P_{rhaB}</i> ; Tp ^R	(17)
pRK2013	Mobilizing vector, ColE1 Tra (RK2); Km ^R	(18)
pMQ87Tp	Suicide vector, URA3 CEN6/ARSH4 lacZa; Gm ^R , Tp ^R	(16)
pMQ87Tp- <i>mlaE</i>	mlaE (BCAL0302) insertional mutant construct in pMQ87Tp	This study
pMQ87Tp-mlaC	mlaC (BCAL0305) insertional mutant construct in pMQ87Tp	This study
pMQ87Tp-BCAL0499	BCAL0499 insertional mutant construct in pMQ87Tp	This study
pCR [®] 2.1	Cloning vector; Km ^R , Amp ^R	Invitrogen
pCR [®] 2.1- <i>mlaCB</i>	pCR [®] 2.1 with 1367-bp PCR fragment containing <i>mlaCB</i> and native promoter region; Km ^R , Amp ^R	This study
pHERD26T	Broad-host-range shuttle vector; Tet ^R	(19)
pHERD26T-mlaCB	pHERD26T with 1321-bp KpnI-EcoRI fragment from	This study
-	pCR [®] 2.1- <i>mlaCB</i> ; Tet ^R	•

•

^a Tn mutants with genes in parentheses indicate that the insertion was in an intergenic region and that the gene is likely the one affected by the Tn insertion. Tp, trimethoprim; Tet, tetracycline; Gm, gentamicin; Km, kanamycin; Amp, ampicillin.

Table S6. Primers used in this study.

Primer	Sequence (5'- 3')	Reference
M13F	GTAAAACGACGGCCAGT	Lab
		collection
M13R	CAGGAAACAGCTATGAC	Lab
		collection
824	GCCCATTTTCCTGTCAGTAACGAGA	(17)
BCAL0302-5L	CCAAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCGAATTCTTCCCGCTGCTGCG	This study
BCAL0302-3L	AACAGCTATGACCATGATTACGAATTCGAGCTCGGTACCCCAGCGCAATGAAGGTCACGG	This study
BCAL0305-5L	CCAAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCAGTCGAACCCGCAGGCGCTG	This study
BCAL0305-3L	AACAGCTATGACCATGATTACGAATTCGAGCTCGGTACCCCAAGTTGCTGGTTGCGCTGC	This study
BCAL0499-5L	CCAAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCCCTGGTGATCGACGACAACG	This study
BCAL0499-3L	AACAGCTATGACCATGATTACGAATTCGAGCTCGGTACCCTGCGGCGGTGCATGTTCAGC	This study
mlaCB-For	GTACGACCTGCCGGAAGACG	This study
mlaCB-Rev	TTGGCTGCCCGCAAAACGC	This study

Supplementary Figures



FIG S1. Selection of hypersensitive transposon mutants. (A) The selected transposon mutants of *B. cenocepacia* K56-2 (B) were grown for 24 h at 37°C and 72 h at room temperature with the addition of 25% spent medium (+s.m.) extracted from planktonic cultures of *P. aeruginosa* PA14 and compared to growth in absence of spent medium (- s.m.).



FIG S2. Susceptibility to Gram-positive antibiotics. Resistance profile of transposon mutants (*vacJ2* and *bamC*) selected for their susceptibility to azithromycin (AZM) and rifampicin (RD) in comparison to WT and *mlaC* mutants in *B. cenocepacia* K56-2 and *B. dolosa* PC543.



FIG S3. Susceptibility to the SDS detergent. The sensitivity of WT and *mlaC* mutants of *B. cenocepacia* K56-2 and *B. dolosa* PC543 was assessed on agar using 10 μ l of a 10% SDS solution on a sterile disk. Zones of inhibition are greater in *mlaC* mutants compared to WT, but WT PC543 is more resistant than WT K56-2.

REFERENCES

- 1. Baba T, Ara T, Hasegawa M, Takai Y, Okumura Y, Baba M, Datsenko KA, Tomita M, Wanner BL, Mori H. 2006. Construction of *Escherichia coli* K-12 in-frame, single-gene knockout mutants: the Keio collection. Mol Syst Biol 2:2006 0008.
- 2. Liberati NT, Urbach JM, Miyata S, Lee DG, Drenkard E, Wu G, Villanueva J, Wei T, Ausubel FM. 2006. An ordered, nonredundant library of *Pseudomonas aeruginosa* strain PA14 transposon insertion mutants. Proc Natl Acad Sci U S A 103:2833-8.
- 3. Rahme LG, Stevens EJ, Wolfort SF, Shao J, Tompkins RG, Ausubel FM. 1995. Common virulence factors for bacterial pathogenicity in plants and animals. Science 268:1899-902.
- 4. Hogan DA, Vik A, Kolter R. 2004. A *Pseudomonas aeruginosa* quorum-sensing molecule influences *Candida albicans* morphology. Mol Microbiol 54:1212-23.
- 5. Hogan DA, Kolter R. 2002. *Pseudomonas-Candida* interactions: an ecological role for virulence factors. Science 296:2229-32.
- 6. Cugini C, Morales DK, Hogan DA. 2010. *Candida albicans*-produced farnesol stimulates *Pseudomonas* quinolone signal production in LasR-defective *Pseudomonas aeruginosa* strains. Microbiology 156:3096-107.
- 7. Gibson J, Sood A, Hogan DA. 2009. *Pseudomonas aeruginosa-Candida albicans* interactions: localization and fungal toxicity of a phenazine derivative. Appl Environ Microbiol 75:504-13.
- 8. Caiazza NC, Shanks RM, O'Toole GA. 2005. Rhamnolipids modulate swarming motility patterns of *Pseudomonas aeruginosa*. J Bacteriol 187:7351-61.
- 9. Pukatzki S, Kessin RH, Mekalanos JJ. 2002. The human pathogen *Pseudomonas aeruginosa* utilizes conserved virulence pathways to infect the social amoeba *Dictyostelium discoideum*. Proc Natl Acad Sci U S A 99:3159-64.
- 10. Rahim R, Ochsner UA, Olvera C, Graninger M, Messner P, Lam JS, Soberon-Chavez G. 2001. Cloning and functional characterization of the *Pseudomonas aeruginosa rhlC* gene that encodes rhamnosyltransferase 2, an enzyme responsible for di-rhamnolipid biosynthesis. Mol Microbiol 40:708-18.
- 11. Bernier SP, Workentine ML, Li X, Magarvey NA, O'Toole GA, Surette MG. 2016. Cyanide Toxicity to *Burkholderia cenocepacia* Is Modulated by Polymicrobial Communities and Environmental Factors. Front Microbiol 7:725.
- 12. Mahenthiralingam E, Coenye T, Chung JW, Speert DP, Govan JR, Taylor P, Vandamme P. 2000. Diagnostically and experimentally useful panel of strains from the *Burkholderia cepacia* complex. J Clin Microbiol 38:910-3.
- Varga JJ, Losada L, Zelazny AM, Kim M, McCorrison J, Brinkac L, Sampaio EP, Greenberg DE, Singh I, Heiner C, Ashby M, Nierman WC, Holland SM, Goldberg JB. 2013. Draft Genome Sequences of *Burkholderia cenocepacia* ET12 Lineage Strains K56-2 and BC7. Genome Announc 1.
- 14. Coenye T, LiPuma JJ, Henry D, Hoste B, Vandemeulebroecke K, Gillis M, Speert DP, Vandamme P. 2001. *Burkholderia cepacia* genomovar VI, a new member of the *Burkholderia cepacia* complex isolated from cystic fibrosis patients. Int J Syst Evol Microbiol 51:271-9.
- 15. Workentine ML, Surette MG, Bernier SP. 2014. Draft Genome Sequence of *Burkholderia dolosa* PC543 Isolated from Cystic Fibrosis Airways. Genome Announc 2.

- 16. Bernier SP, Hum C, Li X, O'Toole GA, Magarvey NA, Surette MG. 2017. *Pseudomonas aeruginosa*-Derived Rhamnolipids and Other Detergents Modulate Colony Morphotype and Motility in the *Burkholderia cepacia* Complex. J Bacteriol 199.
- 17. Cardona ST, Mueller CL, Valvano MA. 2006. Identification of essential operons with a rhamnose-inducible promoter in *Burkholderia cenocepacia*. Appl Environ Microbiol 72:2547-55.
- 18. Figurski DH, Helinski DR. 1979. Replication of an origin-containing derivative of plasmid RK2 dependent on a plasmid function provided in trans. Proc Natl Acad Sci U S A 76:1648-52.
- 19. Qiu D, Damron FH, Mima T, Schweizer HP, Yu HD. P_{BAD}-Based Shuttle Vectors for Functional Analysis of Toxic and Highly Regulated Genes in *Pseudomonas* and *Burkholderia* spp. and Other Bacteria. Applied and Environmental Microbiology. 2008;74(23):7422-7426.