Supplementary Table S1. Primers used in this study

k/o 6246 F-SmaI	5'-ACCCGGGCTAGACGGGCAGCACG-3'
k/o 6246 R-BamHI	5'-ATGGATCCTCAGTCCAGACCCAGGC-3'
k/o 6247 F-KpnI	5'-AAGGTACCGAACCCCAAGGCGATAGT-3'
k/o 6247 R-BamHI	5'-ATGGATCCTCAGTCCAGACCCAGGC-3'
k/o 6248 F-SacI	5'-ATGAGCTCTCTCCATCATGATCGGCACT-3'
k/o 6248 R-PstI	5'-AACTGCAGATCGACGCTCTGCTCGCA-3'
k/o 6249 F-SacI	5'-TAGAGCTCGGTGGCCTGGATAGACTGCCT-3'
k/o 6249 R-BamHI	5'-TAGGATCCAGGAACAGGGACGCGCCGATCA-3'
k/o 6250 F-BamHI	5'-ACGGATCCATGAAAAAGATCCTGATC-3'
k/o 6250 R-HindIII	5'-TTAAGCTTTCAGTCCACCGCTAGGAG-3'
k/o 6251 F-MfeI	5'-AACAATTGGAACGCCGCACCGAACAT-3'
k/o 6251 R-XbaI	5'-TTTCTAGACTACGCCGCCGAGCCCA-3'
PsPA7_6248 F-SmaI	5'-TACCTGCCCGGGATGGAAGTCTTCGGCT-3'
PsPA7_6248 R-PstI	5'-CGATCTGCAGTCAGTCCAGACCCAGGC-3'
PA1416 F-Stul	5'-ATCAGGCCTGACCCGGAGCCC-3'
PA1416 R-PstI	5'-AACTGCAGTCAGGGTATGACCTTG-3'
MSMEG_6382 F-NcoI	5'-TACCATGGATGGGCGCGGGTAC-3'
MSMEG_6382 R-HindIII	5'-TTAAGCTTTCAGAGCAGTTGCAGGC-3'
Rv3790 F-NcoI	5'-TACCATGGATGTTGAGCGTGGGA-3'
Rv3790 R-HindIII	5'-ACAAGCTTCTACAGCAGCTCCAAG-3'
6245-6251 F-SmaI	5'-ACCCGGGCTAGACGGGCAGCACG-3'
6245-6251 R-XbaI	5'-TTTCTAGACTACGCCGCCGAGCCCA-3'
6247-6251 F-SmaI	5'-ACCCGGGAAGAGTTGGTGATGAAGCTGGC-3'
6247-6251 R-XbaI	5'-TTTCTAGACTACGCCGCCGAGCCCA-3'
6245-6249 F-SmaI	5'-ACCCGGGCTAGACGGGCAGCACG-3'

6245-6249 R-XbaI	5'-AATCTAGATCAGAGGCTGAGCTTCTTGAAAAG-3'
6246-6249 F-SmaI	5'-AACCCGGGTCAGTGCGGCCAGAGCG-3'
6246-6249 R-XbaI	5'-AATCTAGATCAGAGGCTGAGCTTCTTGAAAAG-3'

<u>Supplementary Fig. S1.</u> Genomic context of the genes involved in D-Araf biosynthesis in *P. aeruginosa. A.* In PA7, the DPA biosynthetic genes are adjacent to the A-band LPS biosynthetic genes (light green). Specific gene numbers for PA7 (PsPA7_xxxx) and PAO1 (PAxxxx) are shown below the gene map, while the conventional names are shown above (20). In PAO1, the same position is occupied by another putative polysaccharide biosynthetic cluster (PA5455-5459). Homologues of a subset of those ORFs can be identified downstream of the D-Araf biosynthetic cluster by homology searches of the PA7 genome, although they are oriented on the opposite strand. Genes encoding similar products are similarly coloured in blue and orange; genes in white have no homologues. *B.* Alignment of Rmd proteins from PAO1 and PA7. Rmd is highly conserved among *P. aeruginosa* strains with the exception of PA7. The N-terminus of PA7 Rmd is less conserved than the C-terminus, suggesting that the D-Araf biosynthetic genes may have been acquired through horizontal gene transfer and homologous recombination within the *rmd* locus.

<u>Supplementary Fig. S2</u>. Alignment of polyprenyl-P-D-ribose-5-P synthases (PPPRS). PPPRS proteins from *Azorhizobium caulinodans* (NoeC), *P. syringae* pv syringae (Psyr), *M. tuberculosis* H37Rv (Mtb) and *P. aeruginosa* PA7 were aligned in Geneious (Drummond AJ, Ashton B, Cheung M, Heled J, Kearse M, Moir R, Stones-Havas S, Thierer T, Wilson A (2010) Geneious v5.0, <u>http://www.geneious.com</u>) using the MUSCLE algorithm. Identical residues are shown in reverse text, while highly conserved residues are highlighted in grey. The putative active site motif NDxxD found in other polyprenyl transferases such as UbiA (33,34) is boxed in red. Residues marked with red asterisks were previously shown by site-directed mutagenesis to be important for activity of the *M. tuberculosis* enzyme (33), while the residue marked with a blue asterisk was not required, consistent with its lack of conservation in PA7.

<u>Supplementary Fig. S3</u>. Alignment of DprE1 proteins. DprE1 proteins from *P. aeruginosa* PA7, *M. tuberculosis* and *M. smegmatis* were aligned in Geneious (Drummond AJ, Ashton B, Cheung M, Heled J, Kearse M, Moir R, Stones-Havas S, Thierer T, Wilson A (2010) Geneious v5.0, <u>http://www.geneious.com</u>) using the MUSCLE algorithm. The key Cys residue that is required for sensitivity of the enzyme to benzothiazinones and dinitrobenzamides (13-15,28) is boxed in red and highlighted with an asterisk. The PA7 enzyme has an Ala at the corresponding position, suggesting it would be resistant to inactivation.





Identities = 251/304 (82%), Positives = 272/304 (89%), Gaps = 1/304 (0%)

Β.

PA01:	1	MTQRLFVTGLSGFVGKHLQAYLAAAHTPWALLPVPHRYDLLEPDSLGDLWPELPDAVIHL 6 M + L VTGL+GFVG+HL+ + + PW+LLP P +DL P+SL E+PDAVIHL	0
PA7:	1	MKKSLLVTGLNGFVGRHLRQRIESHDLPWSLLPHPA-FDLAVPESLESWRCEMPDAVIHL 5	9
PA01:	61	AGQTYVPEAFRDPARTLQINLLGTLNLLQALKARGFSGTFLYISSGDVYGQVAEAALPIH 1	.20
PA7:	60	AGQITVPTTF DP RI TTN LGILTLLQALK GFTGIFLIISSGDVIGQV EAALPIN AGQTFVPDSFLDPRRTFEVNFLGTLSLLQALKRNGFAGTFLYISSGDVYGQVPEAALPIN 1	19
PA01:	121	EELIPHPRNPYAVSKLAAESLCLQWGITEGWRVLVARPFNHIGPGQKDSFVIASAARQIA 1	. 8 0
PA7:	120	EE +P PRNPIAVSKLAAESLCLQWGI+EGWRVLVARPFNHIGPGQKDSFVIASAARQIA EEFLPRPRNPYAVSKLAAESLCLQWGISEGWRVLVARPFNHIGPGQKDSFVIASAARQIA 1	.79
PA01:	181	RMKQGLQANRLEVGDIDVSRDFLDVQDVLSAYLRLLSHGEAGAVYNVCSGQEQKIRELIE 2 RMKQGLQA+RLEVGDIDVSRDFLDVQDVLSAYLRLLSHGE GAVYNVCSGQEQKIR+LIE	40
PA7:	180	RMKQGLQAHRLEVGDIDVSRDFLDVQDVLSAYLRLLSHGEPGAVYNVCSGQEQKIRDLIE 2	39
PA01:	241	LLADIAQVELEIVQDPARMRRAEQRRVRGSHARLHDTTGWKPEITIKQSLRAILSDWESR 3 LLADIAOVELEIVODPARMRRAEORRV GSHARL D TGWKPEITIKOSLRAILSDWESR	00
PA7:	240	LLADIAQVELEIVQDPARMRRAEQRRVCGSHARLRDATGWKPEITIKQSLRAILSDWESR 2	99
PA01:	301	VREE 304 VREE	
PA7:	300	VREE 303	

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1 No. C from Acceleration	1	10 20 I	30	40	50	60	70
2. PPPRS from Psyr 3. DPPRS from Mtb 4. PPPRS from PA7	MPGTQGRAL	EVDTPLVVDLDG	TLLRSDLLFET	AVA FIRGR PLQV	FRLFTWLLQGKA	A P L K Q G L A L G	TDIDVAL
	80	90	100	110	120	130	140
 NoeC from Azorhizobium PPPRS from Psyr DPPRS from Mtb PPPRS from PA7 	LPYDAAVIA	YIQTSRQHGRRV	V LA TA S HE T LA I	N QIAAHL QMFDQ MLRSPP	MWNKEWAAKIP- VWASDGKTNLSA MSEDVVTQPP- ITCRSGPASSP-	AHRKRDLLVS	F HYGEGGF A
	150	160	170	180	190 20	20 * * 2	10
1. NoeC from Azorhizobium 2. PPPRS from Psyr 3. DPPRS from Mtb 4. PPPRS from PA7	M T Y	LCIWKVSRKAIV	A S P L A G V E R A A I A G V L A Q L K G L	RAQGNVEQVIKS	CEA TSSRRSAWYKAI VKAI LALN	CRPHHWLKNG LRLHOWLKNT LRPROWVKNV IRPROWVKNA 280	LLF-VPV LIF-VPL LVLAAPL FVV-APL
1. NoeC from Azorhizobium 2. PPPRS from Psyr 3. DPPRS from Mtb 4. PPPRS from PA7	LICGRAE LAAHQVQST AALGGGVRY LFSGEFLQV	DLLQAPLWLA QLLLDGL-LA DYVEVLSKVSMA DAVLHAL-AA	FMTECSVASGI FLCEGLCASSV FVVESLAASAV VLLECLASSAT	YVINDLMDRAHD YLINDLLDLAD YLVNDVRDVEAD YLVNDLHDIERD	RRHPSKRH-RPI RHHRSKRE-RPI REHPTKRF-RPI RLHPKKALTRPI	FASRKLSGLT FASGQL IASGVV LASGLV	GVWMCLV SIESGLL PEWLAYT SPLQAKY
1. NoeC from Azorhizobium 2. PPPRS from Psyr 3. DPPRS from Mtb 4. PPPRS from PA7	LIALGGVCA VIPLLAAA VAVVLGVTS LLALLYLAL	INC GERL $FAGAAIMLPWQF$ $LAG - AWMLTPNL$ $LGG LLISPO$	¹⁰ ³²⁰ FALTASYVALS AAVLAAYYLLT ALVMVVYLAMO INVIGIYLLN	³³⁰ 7 I YVGKVRGEYV VYSLYLKRHMA AYCFGLKHQAV AYTFFLKHQPV	JDLFVLSALYT VDVIVLAMLYT VEICVVSSAYLJ LDIFTIALGFVJ	³⁵⁰ FRILAGATAA FRILAGAAAF IRAIAGGVAT LRVYAGAVAL	NIPVPAS QLPLTFW KIPLSKW AVPVSSW
1. NoeC from Azorhizobium 2. PPPRS from Psyr 3. DPPRS from Mtb 4. PPPRS from PA7	F L AF S AMAF I L AF S MFLF F L LIMAFGS MFVT T LCLA 440	VSLASIKRINEL LSLALVKRYAEL LFMVAGKRYAEL LYLAAVKRRQEL 450	T Q L R R D G A P - D $R D A R L C D V T V K$ $H L A E R T G A I R$ $A R N G S Q S R$ 460	LYGRGYELSDHS IRGRGYYPGDLD KSLESYTSTYLR EVLQHYSLALVD 470	I VALICVSAGYA MIASIGASSGNI FVWTISAT2 RYAEMSAT0 480	AAVVFLELFV LAVMVLALYI AVVLCYGLWA GALLFYSLFV 490	QMSS HEGATVA FERD ITSR 500
1. NoeC from Azorhizobium 2. PPPRS from Psyr 3. DPPRS from Mtb 4. PPPRS from PA7	VAQGPAPIF LYQHPHVIW GYSGSW EELV ⁵⁰⁶	VSNAMCVVVAYW LACPILLFW FAVSMIPFT VTIPLVLFG	ISRAV-VQAHR ITRIW-MLTHR IAILRYAVDVD IFRYWYVEAK	G DMRSDTLCYAV G QMNEDPVVFA G LAGEPEDIAL EG – GESPTDAL	TDGSSLVCILG RDRIS RDRVL SDWQL1	LA LG LV ELM Y QG I G F LE LL V QL LA LA WI A T LA TVVLWGLA	C – R S QS I F – – – – W I VGA A VA F CA Y A LW P
1. NoeC from Azorhizobium 2. PPPRS from Psyr 3. DPPRS from Mtb 4. PPPRS from PA7	G A <mark>A</mark> G H						

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	1	10	20	30	40		50	60	70
1. DprE1 PA7			MEVFGW	IGR YPRINA	TLVSPRSV	DELRRRI	QL SS	GITLRC	HGKSYGDSAL
DprE1 smegmatis	MGAVPSL	TMSTTEFPT	TKRLMGW	<u>GR</u> TAPTVA	SVLSTSDP	EVIVRAV	TRAAEE-	GGRGVIARC	GLGRSYGDNAQNO
3. DprE1 tuberculosis	M	SVGATT	TATRLTGW	GRTAPSVA	NVLRTPDA	EMIVKAV	ARVAESG	GGRGAIARC	LGRSYGDNAQNO
	80	90		100	110	120		130	140 15
1. DprE1 PA7	GESIADS	R N L D H L Q S F	'GEP T G VL R	CEAGTTLA	D L A A T F L P	RGWFLPV	T <mark>PGT</mark> AHI	SVGGAIASI	DVHGKNHHLH <mark>G</mark> CI
DprE1 smegmatis	GGLVIDM	PALNRIHSI	DSGTRLVD	V DAG VS LD	DQLMKAALP	HGLWVPV	L PG TR QV	TVGGAIGCI	DIHGKNHHSA <mark>G</mark> SI
DprE1 tuberculosis	GGLVIDM	TP LNTIHSI	DADTKLVD	DAGVNLD	DQLMKAALP	FGLWVPV	LPGTRQV	TVGGAIACI	DIHGKNHHSA <mark>G</mark> SI
		160	170	180	190		200	210	220
1. DprE1 PA7	SEFVDSF	R L L M A D G D L	LH-CSRNE	HPELFHAT	CGGMGLTG	ALVDVTL	RLRRVPS	AWIDQVTCF	KAN <mark>NLEE</mark> AFE L FI
DprE1 smegmatis	GNHVRSM	ELLTANGEV	RHLTPAGE	DSDLFWAT	VGGNGLTG	IILRATI	EMTPTE	AYFIADGDV	7 TG <mark>SLDE</mark> TIAFHS
DprE1 tuberculosis	GNHVRSM	DLLTADGEI	RHLTPTGE	DAELFWAT	VGGNGLTG	IIMRATI	EMTPTSI	AYFIADGDV	TA <mark>SLDE</mark> TIALHS
	230	240		250	260	270	:	280	290 30
1. DprE1 PA7	QQAAA	TYSVAWIDC	LANGASLC	RSLLMFGE	E H S S	– – – – HGG	LALPPRR	ALAVPLEMI	SALLNHYSVRVI
2. DprE1 smegmatis	DGSEANY	TYSSAWFDA	ISKPPKLC	RAAISRGS	LAKLDQLP	SKLQKDP	LKFDAPO	LLTLPDIFI	PNGLANKFTFM PI
3. DprE1 tuberculosis	DGSEARY	TYSSAWFDA	ISAPPKLC	RAAVSRGR	LATVEQLP.	AKLRSEP	LKFDAPO	LLTLPDVFI	PNGLANKYTFG PI
		310	320	330	340		350	360	370
1. DprE1 PA7	NSLYFQR	IRQPRVEQR	VDYRSFFY	PLDGIĠDW	NRMYG RNĠ	FLQYQFV	IPASAGI	PGMRRILEF	RIAASGRGSFLAV
2. DprE1 smegmatis	GELWYRK	SGTYRNKVQ	– N L T Q F Y H	IPLD <mark>MF</mark> GEW	NRAYGSAG	FLQYQFV	VPTEA-V	EEFKSIIVI	DIQRSGHYSFLNV
3. DprE1 tuberculosis	GELWYRK	SGTYRGKVQ	– N L T Q F Y H	IPLD <mark>MF</mark> GEW	NRAYG PAG	FLQYQFV	IPTEA-V	DEFKKIIG	I QASGHYSFLNV
	380	390	*	400	410	420		430	440 45
1. DprE1 PA7	LKAFGEG	NENPLSFPO	KGYTLALI	FKMDASLI	PLLDELDR	MVLDHGGI	RLYLAKD	ARMSEATFF	KOSYPRWENFQE!
2. DprE1 smegmatis	FKLFGPG	NOAPLSFPI	PGWNVCVD	FPIKAGLH	EFVTELDR	RVLEFGGI	RLYTAKD	SRTTAETFI	IAMYPRIDEWIRI
3. DprE1 tuberculosis	FKLFGPR	NQAPLSFPI	PGWNICVE	FPIKDGLG	KFVSELDR	RVLEFGGI	RLYTAKD	SRTTAETFH	IAMYPRVDEWISV
		460	471						
1. DprE1 PA7	RERYGAL	GKFTSLOAR	RLGLD						
2. DprE1 smegmatis	RRSVDPD	GVFASDMAR	RLQLL						
3. DprE1 tuberculosis	RRKVDPL	RVFASDMAR	RLELL						