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-StuI	5'-ATCAGGCCTGACCCGGAGCCC-3'
PA1416 R-PstI	5'-AACTGCAGTCAGGGTATGACCTTG-3'
MSMEG_6382 F-NcoI	5'-TACCATGGATGGGCGCGGTAC-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’

Supplementary Fig. S1. Genomic context of the genes involved in D-Ara*f* 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-Ara*f* 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-Ara*f* biosynthetic genes may have been acquired through horizontal gene transfer and homologous recombination within the *rmd* locus.

Supplementary Fig. S2. 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, http://www.geneious.com) 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.

Supplementary Fig. S3. 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, http://www.geneious.com) 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.

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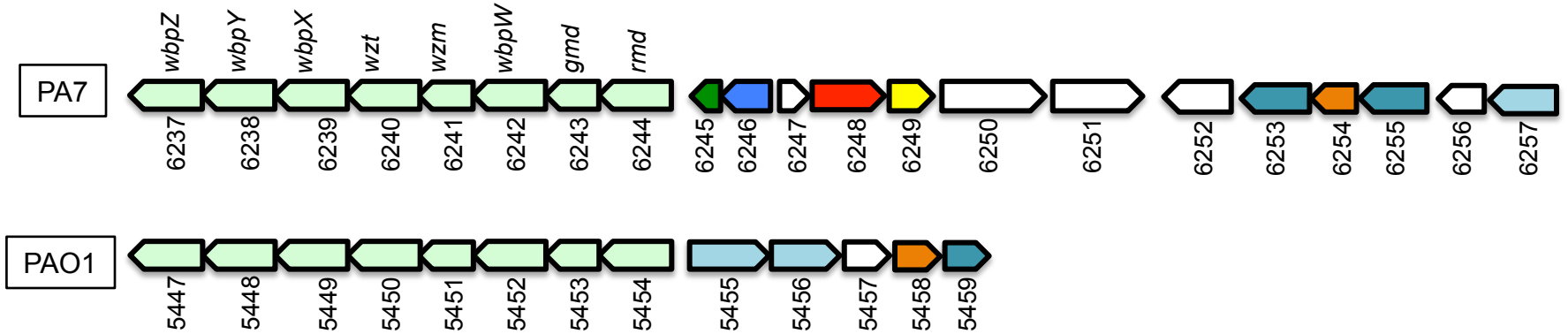
A.



B.

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

PAO1:  1   MTQRLFVTGLSGFVGKHLQAYLAAAHTPWALLPVPHRYDLLEPDSLGDLWPELPDAVIHL 60
          M + L VTGL+GFVG+HL+  + +   PW+LLP P  +DL  P+SL     E+PDAVIHL
PA7:   1   MKKSLLVTGLNGFVGRHLRQRIESHDLPWSLLPHPA-FDLAVPESLESWRCEMPDAVIHL 59

PAO1:  61  AGQTYVPEAFRDPARTLQINLLGTLNLLQALKARGFSGTFLYISSGDVYGQVAEAALPIH 120
          AGQT+VP++F DP RT ++N LGTL+LLQALK  GF+GTFLYISSGDVYGQV EAALPIH
PA7:   60  AGQTFVPDSFLDPRRTFEVNFLGTLSLLQALKRNGFAGTFLYISSGDVYGQVPEAALPIH 119

PAO1:  121 EELIPHPRNPYAVSKLAAESLCLQWGITEGWRVLVARPFNHIGPGQKDSFVIASAARQIA 180
          EE +P PRNPYAVSKLAAESLCLQWGI+EGWRVLVARPFNHIGPGQKDSFVIASAARQIA
PA7:   120 EEFLPRPRNPYAVSKLAAESLCLQWGISEGWRVLVARPFNHIGPGQKDSFVIASAARQIA 179

PAO1:  181 RMKQGLQANRLEVGDIDVSRDFLDVQDVLSAYLRLLSHGEAGAVYNVCSGQEQKIRELIE 240
          RMKQGLQA+RLEVGDIDVSRDFLDVQDVLSAYLRLLSHGE GAVYNVCSGQEQKIR+LIE
PA7:   180 RMKQGLQAHRLEVGDIDVSRDFLDVQDVLSAYLRLLSHGEPGAVYNVCSGQEQKIRDLIE 239

PAO1:  241 LLADIAQVELEIVQDPARMRRAEQRRVRGSHARLHDTTGWKPEITIKQSLRAILSDWESR 300
          LLADIAQVELEIVQDPARMRRAEQRRV GSHARL D TGWKPEITIKQSLRAILSDWESR
PA7:   240 LLADIAQVELEIVQDPARMRRAEQRRVCGSHARLRDATGWKPEITIKQSLRAILSDWESR 299

PAO1:  301 VREE 304
          VREE
PA7:   300 VREE 303
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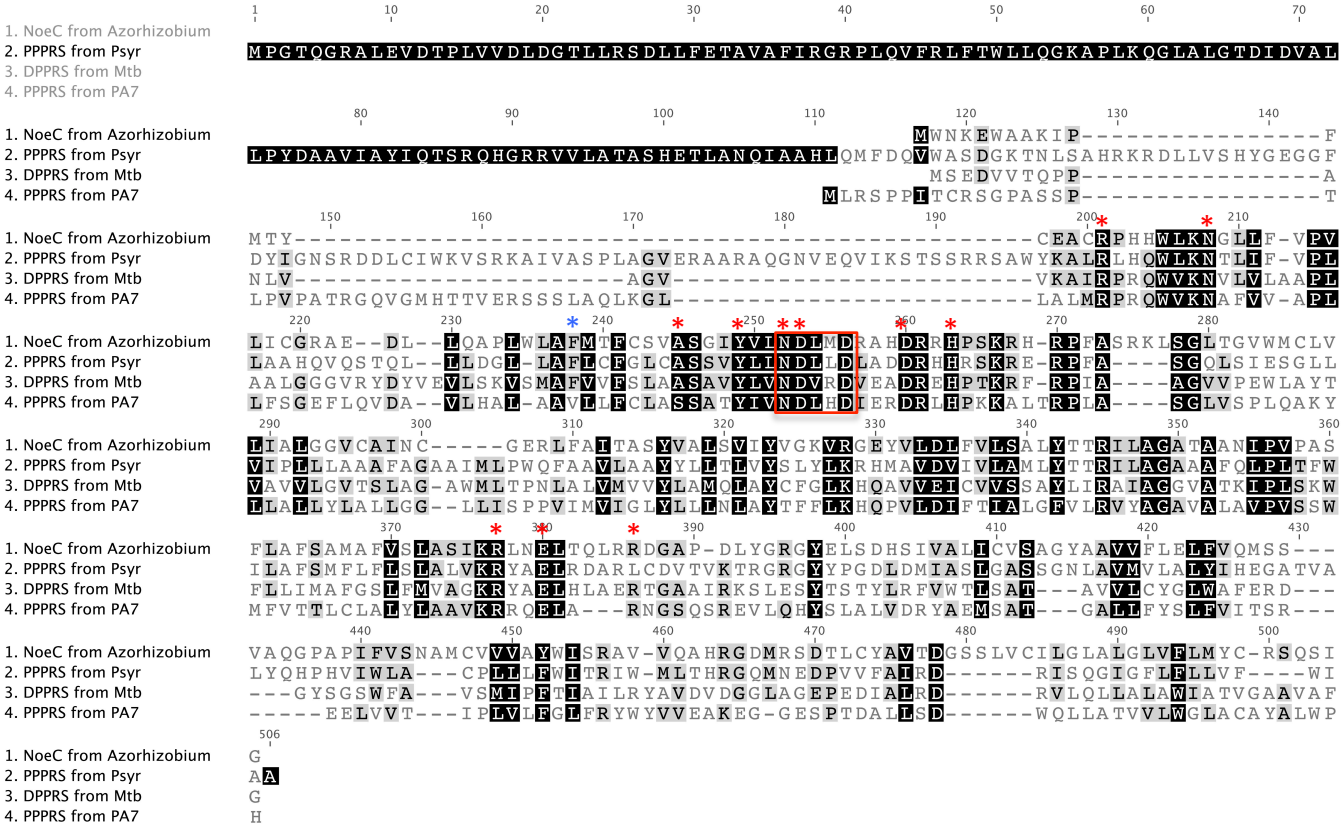

Harvey et al., Supplementary Figure S3