Involvement of the RND efflux pump transporter SmeH in the acquisition of resistance to ceftazidime in *Stenotrophomonas maltophilia*

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Supplementary information.

Table S1. MICs of several antibiotics for *S. maltophilia* strains

Strain	MIC (µg/ml)											
	CAZ	CTX	FOX	CFZ	ATM	OFX	NOR	NAL	CHL	TET	TGC	PMB
D457	0.75	128	256	4,096	4	1	8	6	6	1.5	0.5	8
PBT101 (P326Q)	4	192	384	8,192	8	1	8	6	8	1.5	0.75	8
PBT102 (Q663R)	0.75	96	256	3,072	6	1	8	6	6	6	0.75	12
PBT103 (P326Q; Q663R)	8	256	384	8,192	24	1	24	6	4	2	0.5	8
PBT104 (*ΔsmeH*)	0.38	96	256	3,072	2	0.5	6	4	6	1	0.5	3

MIC, minimum inhibitory concentration; CAZ, ceftazidime; CTX, cefotaxime; FOX, cefoxitin; CFZ, cefazolin; ATM, aztreonam; OFX, ofloxacin; NOR, norfloxacin; NAL, nalidixic acid; CHL, chloramphenicol; TET, tetracycline; TGC, tigecycline; PMB, polymyxin B.
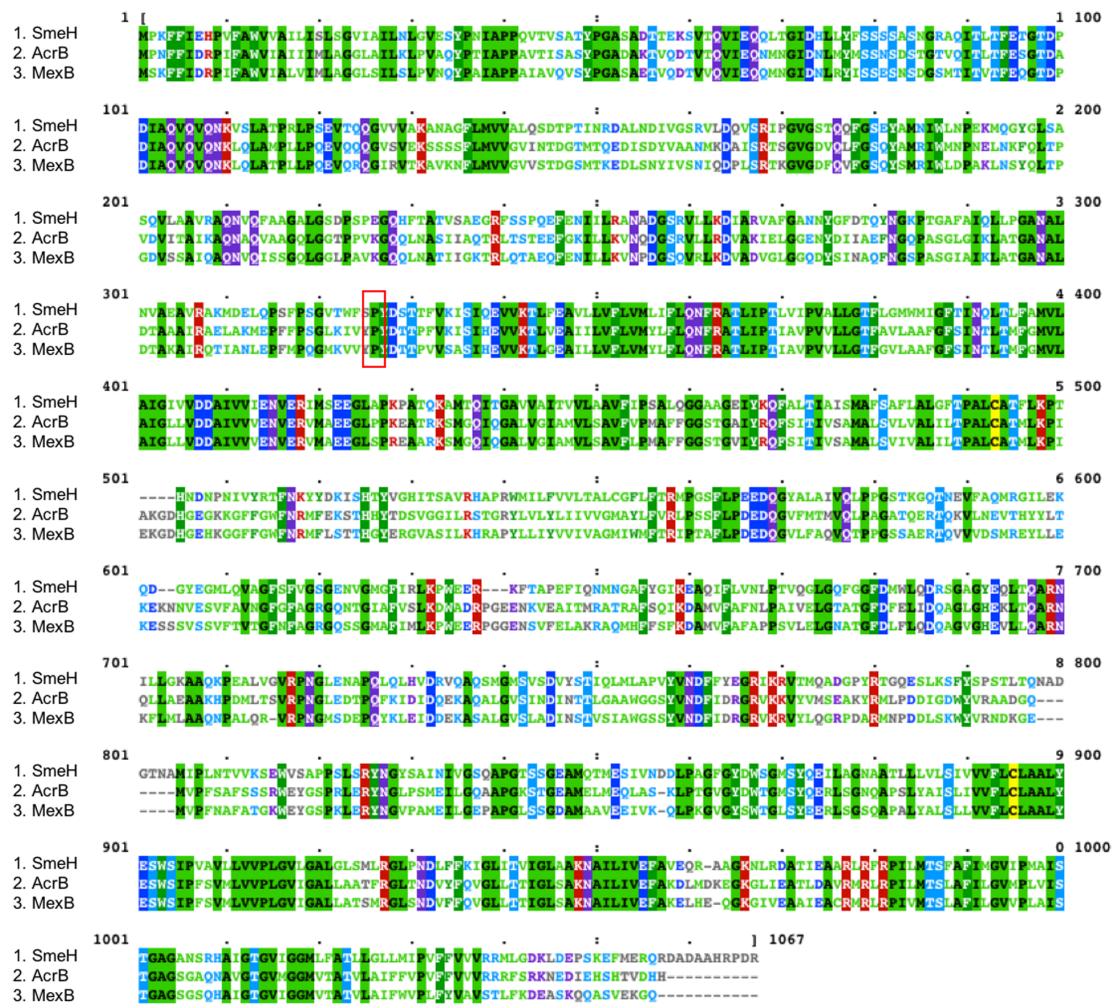
Table S2. Primers used in this study

Name	Sequence (5'-3')	Utilization
SmeH_snp1_F	GAATTCAGTACGCCATGAACATCTGG	Amplification of the 1000-bp fragment containing P326Q in *smeH*
SmeH_snp1_R	GAATTCACTTGTTGAAGGTGCGGTAG	
SmeH_snp2_F	GAATTCCCGGTGAGATCTACAAGCAG	Amplification of the 1000-bp fragment containing Q663R in *smeH*
SmeH_snp2_R	GAATTCGACTTGACCACCGTGTTGAG	
Comp_snp1_F	GTGACCTGGTTCTCGCA	Verification of Q326
Comp_snp1_R	GAACAGGGTCAGCTGGTT	
Comp_snp2_F	ACCTGCCCACCGTGCG	Verification of R663
Comp_snp2_R	CGGCCTTCGTAGAAGAAGTCGTT	
HAF	GAATTCCGAACATCCAGTCTTCGCCTGGGTGGTTGCGATCCTG	Amplification of the 489-bp fragment corresponding to the 5'-end of *smeH*
HAR	AGCTTTCATACAGGGCGGCCGGGGATACGCGAGACCTGGT	
HBF	ACCAGGTCTCGCGTATCCCCGGCCGCCCTGTATGAAAGCT	Amplification of the 489-bp fragment corresponding to the 3'-end of *smeH*
HBR	GAATTCTCAACGATCCGGGCGGTGTGCAGCATCCGC	
Ext_smeH_L	GATTCGAACAAGCAGTAAG	Amplification of the 3404-bp fragment including the complete *smeH* gene
Ext_smeH_R	ATTGGTAATCGTGGCAGTGT	
Int_smeH_L	ACAACTACGGCTTCGACAC	Amplification of a 211-bp fragment inside *smeH* gene
Int_smeH_R	GTCTTGACCACTTCCTGGAT	
acrD1_L	GTCGGCCAGCCAGGTACT	Verification of P326Q in *smeH*
acrD1_R	ATCTGGGTCATCGCCTTCT	

acrD2_L	ATGATCCTGTTCGTGGTGCT	Verification of Q663R in *smeH*
acrD2_R	GAAGCTCTTCAGCGACTCCT	
phoQ_cef_L	ACCCTGGCGATAACACGAT	Verification of I76N and P81L in *phoQ*
phoQ_cef_R	ACCTTGGTCAACTCGGTGAT	
phoQ_tig3_L	CGAATTCCCGTACACCATCT	Verification of S307L and P324L in *phoQ*
phoQ_tig3_R	CACTTGAAGGCGTTCTCCAG	
mrkC_L	GCTGGCACCTACCGTGTC	Verification of G187_F188del in *mrkC*
mrkC_R	AGATCAGCTGCTGGTTCTGG	
ftsI4_L	CAGATCATCGACGAGAACG	Verification of A592D in *ftsI*
ftsI4_R	AACATCGAAGGACTCATTGC	
yrbE_L	GTTCTCGCTGACCGTGCT	Verification of I49fs in *yrbE*
yrbE_R	GTGAACAACATTGCCGACAG	
yrbC_L	GTCGGCAAGTACATGTTCAG	Verification of Q126* in *yrbC*
yrbC_R	AAGTGCGTTACTTGCCATTG	
yciM_L	ATCGAAGATGGATTTCGTCA	Verification of A206fs in *yciM*
yciM_R	AGGTCAGCAACGCACTGA	
SMD_0534_L	TGCGGAATTTTTCGAGTATC	Verification of V398fs in *smd_0534*
SMD_0534_tig_R	AGGTTGGAGATGGACTGTGG	
SMD_1278_L	CCCAACCACTCTTCTGTGG	Verification of F91_G92insDF in *smd_1278*
SMD_1278_R	CGTTCCTGGTACTCCTTGAC	
SMD_0260_L	GATTGGAACCTGGTCGAG	Verification of K88R in *smd_0260*
SMD_0260_R	TCTTCGACCAGAAGGATACG	

| SMD_2719_L | GCAACGGGATCTGGGT | Verification of V232G in *smd_2719* |
| SMD_2719_R | ACCACGAACGGCAGCTTG | |

Figure S1. Alignment of the *S. maltophilia* SmeH amino acid sequence with its homologues AcrB from *E. coli*, and MexB from *P. aeruginosa*. The conserved P326 residue is marked with a red square in the amino acid sequences of the three species. Color scheme is based on amino acid identity.