Supplementary Table 1: Disk diffusion test results, results determined by reference to the EUCAST Clinical Breakpoint tables for Enterobacterales

Antibiotic	**AB1157, Zone diameter (mm)**	**Result**	**AB1157: pMERPH, Zone diameter (mm)**	**Result**
Penicillin's				
Amoxycillin/clavulanic acid (20/10 μg)	20	Susceptible	19	Susceptible
Ampicillin (10 μg)	20	Susceptible	19	Susceptible
Piperacillin (36 μg)	38	Susceptible	29	Susceptible
Piperacillin/tazobactam 30/6 μg)	19	Intermediate	19	Intermediate
Ticarcillin/clavulanic acid, 75/10 μg)	29	Susceptible	25	Susceptible
Cephalosporins				
Cefoxitin (30 μg)	30	Susceptible	20	Susceptible
Cefpodoxime (10 μg)	32	Susceptible	29	Susceptible
Ceftazidime (10 μg)	24	Susceptible	24	Susceptible
Ceftiofur (30 μg)	20	Susceptible	16	Intermediate
Cephalothin (30 μg)	20	Susceptible	17	Intermediate
Carbapenems				
Meropenem (10 μg)	35	Susceptible	39	Susceptible
Monobactams				
Aztreonam (30 μg)	33	Susceptible	30	Susceptible
Fluoroquinolones				
Ciprofloxacin (5 μg)	29	Susceptible	30	Susceptible
Nalidixic acid (30 μg)	25	Susceptible	25	Susceptible
Norfloxacin (10 μg)	15	Susceptible	26	Susceptible
Ofloxacin (5 μg)	32	Susceptible	29	Susceptible
Aminoglycosides				
Amikacin (30 μg)	23	Susceptible	22	Susceptible
Gentamin (10 μg)	21	Susceptible	20	Susceptible
Erythromycin (15 μg)	0	Resistant	0	Resistant
Kanamycin (30 μg)	23	Susceptible	19	Susceptible
Neomycin (30 μg)	21	Susceptible	19	Susceptible
Tetracyclines				
Tetracycline (30 μg)	30	Susceptible	29	Susceptible
Minocycline (30 μg)	24	Susceptible	24	Susceptible
Miscellaneous agents				
Nitrofurantoin (100 μg)	22	Susceptible	23	Susceptible
SXT (1.25/23.75 μg)	31	Susceptible	28	Susceptible
Trimethoprim (5 μg)	22	Susceptible	28	Susceptible

Supplementary Table 2: Identified ICE$_{SXT/R391}$ family members with complete genome sequence available incorporated into Figure 2

Element	**Strain**	**Accessory Genes/Reported Functions**	**Acc. No.**	**Size (kb)**	**Ref**
ICE R391	*Providencia rettgeri*	Km^r, Hg^r, DNA repair genes, sulphate transporter, toxin-antitoxin system, ATP-dependent Lon protease	AY090559	89	1
ICE pMERPH	*Shewanella putrefaciens*	Hg^r , As^r	MH974755	110	This paper
ICE SXT (MO10)	*Vibrio cholerae* O139 MO10	Cm^r, Su^r, Tm^r, Spt^r, DNA repair genes, toxin-antitoxin system, ATP-dependent Lon protease, histidine kinase, diguanylate cyclase, deoxycytidine triphosphate deaminase	AY055428	99	2
ICE R997	*Proteus mirabilis*	B-lactamase gene, DNA repair genes, RM system, toxin-antitoxin system	KY433363	85	3
ICE*Ama*AS1	*Alteromonas macleodii* 'Aegean Sea MED64'	type I RMS	NC_023045	80	4
ICE*Ama*IS1	*Alteromonas macleodii* Ionian Sea UM7	Heavy metal resistance, type I RMS	NC_021713	99	4
ICE*Mfu*Ind1a	*Marinomonas fungiae* JCM 18476	RMS	LIQF00000000	66	4
ICE*Mfu*Ind1b	*Marinomonas fungiae* JCM 18476	RMS	LIQF00000000	75	4
ICE*Mpr*Chn1	*Marinomonas profundimaris* D104	RMS	AYOZ01000000	86	4
ICE*Pal*Ban1	*Providencia alcalifaciens*	Cm^r, Spt^r, Su^r, Tm^r, toxin-antitoxin system, phenazine biosynthesis protein, lysine exporter, glyoxalase resistance, RMS	GQ463139	97	5
ICE*Pda*Spa1	*Photobacterium damselae* subsp. *piscicida* PC554.2	Tet^r, heat-shock protein (dnaK), AAA ATPase, toxin-antitoxin system, ATP-dependent Lon protease ICE*Pmi*USA1	AJ870986	103	6
ICE*Pmi*Jpn1	*Proteus mirabilis*	Amx^r, Amc^r, Fox^r, Ctx^r	KT894734	93	7
ICE*Pmi*USA1	*Proteus mirabilis strain* HI4320	ATP-dependent helicase, DNA repair proteins, toxin-antitoxin system	AM942759	81	5

Element	**Strain**	**Accessory Genes/Reported Functions**	**Acc. No.**	**Size (kb)**	**Ref**
ICE*Spu*PO1	*Shewanella putrefaciens* W3-18-1	Cu^r, Zn/Co/Cd RND efflux pump, DNA repair genes, restriction modification system	CP000503	111	8
ICE*Va*lA056-1	*Vibrio alginolyticus* A056	Spt^r, Su^r, Az^r, type III RM system	KR231688	89	9
ICE*Val*A056-2	*Vibrio alginolyticus* A056	type I RM system	KR231689	104	9
ICE*Val*ASI1	*Vibrio alginolyticus* ANC4-19	L-lactate degradation system	NZ_LTYK00000000	N/A	10
ICEValInd1	*Vibrio alginolyticus,* ANC4-1	Error-prone repair protein	AB115497.1	67	N/A
ICE*Val*E0601	*Vibrio alginolyticus* E0601	type III RM system	KT072768	106	10
ICE*Val*HN396	*Vibrio alginolyticus* HN396	type II RMS	KT072770	87	10
ICE*Val*HN437	*Vibrio alginolyticus* HN437	type I RM system	KT072771	94	10
ICE*Val*HN492	*Vibrio alginolyticus* HN492	type III RM system	KT072769	106	9
ICE*Vch*Ban11	*Vibrio cholerae* 4672	Type II restriction system	ERS016137	96	11
ICE*Vch*Ban5	*Vibrio cholerae* O1	Cm^r, Spt^r, Su^r, Tm^r, toxin-antitoxin system	GQ463140	102	5
ICE*Vch*Ban8	*Vibrio cholerae* O37 strain MZ03	Ac^r, Toxin-antitoxin system	JQ345361	103	5
ICE*Vch*Ban9	*Vibrio cholerae* MJ-1236	Cm^r, Spt^r, Su^r, Tm^r, Tet^r	CP001485	108	5

Element	**Strain**	**Accessory Genes/Reported Functions**	**Acc. No.**	**Size (kb)**	**Ref**
ICE*Vch*Chn0143	*Vibrio cholerae* ICDC-VC0143	Spt^r, Su^r, Tm^r, Tet^r, toxin-antitoxin system	KT151654	87	13
ICE*Vch*Chn0956	*Vibrio cholerae* ICDC-VC956	Spt^r, Su^r, Tm^r, toxin-antitoxin system	KT151655	94	13
ICE*Vch*Chn1605	*Vibrio cholerae* ICDC-VC1605	Spt^r, Su^r, Tm^r, toxin-antitoxin system	KT151656	98	13
ICE*Vch*Chn1627	*Vibrio cholerae* ICDC-VC1627	Spt^r, Su^r, Tm^r, Tet^r, toxin-antitoxin system	KT151657	102	13
ICE*Vch*Chn1909	*Vibrio cholerae* ICDC-VC1909	Spt^r, Su^r, Tm^r, toxin-antitoxin system	KT151658	109	13
ICE*Vch*Chn1944	*Vibrio cholerae* ICDC-VC1944	Spt^r, Su^r, Tm^r, toxin-antitoxin system	KT151659	101	13
ICE*Vch*Chn2255	*Vibrio cholerae* ICDC-VC2255	Spt^r, Su^r, Tm^r, Tet^r ,type I RM system, toxin-antitoxin system	KT151660	95	13
ICE*Vch*Chn2605	*Vibrio cholerae* ICDC-VC2605	Spt^r, Su^r, Tm^r, toxin-antitoxin system	KT151661	87	13
ICE*Vch*Chn*306*	*Vibrio cholerae* E306	toxin-antitoxin system, ATP-dependent Lon protease	NZ_AWWA01000000	N/A	14
ICE*Vch*Chn4210	*Vibrio cholerae* ICDC-VC4210	Spt^r, Su^r, Tm^r, Tet^r, toxin-antitoxin system	KT151662	110	13
ICE*Vch*Chn57	*Vibrio cholerae* ICDC-VC57	Spt^r, Su^r, Tm^r, Tet^r, toxin-antitoxin system	KT151664	93	13
ICEVchChn1307	*Vibrio cholerae* ICDC-1307	Cm^r, Tm^{r,} DNA repair genes	KJ817376.1	104	N/A
ICE*Vch*ChnAHV1003	*Vibrio cholerae* AHV1003	Ery^r, Spt^r, Su^r, Tm^r, type I RM system, toxin-antitoxin system	KT151663	102	13
ICE*Vch*Hai1	*Vibrio cholerae* VC1786	Tm^r, Su^r, Spt^r, toxin-antitoxin system	JN648379	98	15
ICE*Vch*Hai2	*Vibrio cholerae* HC-1A2	RM system	AJRO01000008	84	16
ICE*Vch*Ind4	*Vibrio cholerae* 0139	Cm^r, Sptr, Su^r, Toxin-antitoxin system	GQ463141	95	5
ICE*Vch*Ind5	*Vibrio cholerae* O1	Cm^r, Spt^r, Su^r, Tm^r, glyoxalase resistance, toxin-antitoxin system	GQ463142	98	5

Element	**Strain**	**Accessory Genes/Reported Functions**	**Acc. No.**	**Size (kb)**	**Ref**
ICE*Vch*Ind6	*Vibrio cholerae* 4605	Tm^r	ERS013257	90	11
ICE*Vch*Mex1	*Vibrio cholerae* non O1-0139	RMS, toxin-antitoxin system	GQ463143	83	17
ICE*Vch*Moz10	*Vibrio cholerae* B33	Spt^r, Su^r, Tet^r, toxin-antitoxin system	ACHZ00000000	104	5
ICE*Vfl*Bra1	*Vibrio fluvialis* 560	RMS	JQHX00000000	N/A	18
ICE*Vfl*Bra2	*Vibrio fluvialis* 539	RMS	JQHW00000000	N/A	18
ICE*Vfl*Ind1	*Vibrio fluvialis*	Cm^r, Spt^r, Su^r, Tm^r, toxin-antitoxin system, RMS	GQ463144	114	5
ICE*Apl*2	*Actinobacillus pleuropneumoniae MIDG3553*	Spt^r, Su^r, Tm^r, DNA repair genes, RMS	MF187965.1	94	21
ICE*Vch*Thd1	*Vibrio Cholerae TSY216*	Cm^r, Su^r, Tet^r, Tm^r, Ma^r and RMS	CP007653.1	100	22
ICE*VFlH*-08942	*Vibrio fluvialis* H08942	Spt^r, Cm^r, Tm^r, DNA repair genes, RMS	KM213605.1	103	23
ICE*Id*BUSA1	*Idiomarinaceae bacterium,* HL-53	RMS	LN899469.1	69	N/A
ICE*Alt*Mex1	*Alteromonas sp.* Mex14	RMS, Heavy metal resistance protein	CP018023	83	N/A
ICEPrSt33672	*Providencia stuartii* ATCC 33672	RMS, Hg^r	CP008920.1	76	24
ICE*Val*Chn1	*Vibrio alginolyticus* ZJ-T	Fq^r, Tm^r, Su^r, Ag^r, RMS	CP016224.1	86	25
ICE*Vch*Rua1	*Vibrio Cholerae* RND68789	Bm^r, Spt^r, Su^r, DNA repair genes, abortive phage resistance protein	KY382507.1	98	N/A
ICE*Vch*Rua2	*Vibrio cholerae O1 biovar El Tor* Inaba RND18826	Bm^r, Spt^r, Su , DNA repair genes, abortive phage resistance protein	KY382506.1	98	N/A
ICE*Vch*Nig1	*Vibrio Cholerae* VC833	Spt^r, Tm^r Bm^r Su^r, Flo^r , DNA repair genes	KC886258.1	98	26
ICE*Vch*Nep1	*Vibrio Cholerae* VC504	Spt^r, Tm^r Bm^r Su^r , DNA repair genes	KC886257.1	98	26

Element	**Strain**	**Accessory Genes/Reported Functions**	**Acc. No.**	**Size (kb)**	**Ref**
ICE*Prvu*Chn1	*Proteus vulgaria* 08MA2213	Bm ^{r}DNA repair genes, RMS	KX243403.1	94	27
ICE*Pmi*Chn1	*Proteus mirabilis* PM13C04	DNA repair genes, Flo^r, Tet^r, Spt^r, Su^r	KT962845.1	94	28
ICE*Pmi*Chn2	*Proteus mirabilis* JN7	Su^r, Bm^r ultraviolet light resistance protein B, DNA repair genes	KY437726.1	106	29
ICE*Pmi*Chn3	*Proteus mirabilis* JN28	Hm^r, Tm^r, Ery^r, Spt^r, DNA repair genes	KY437727.1	57	29
ICE*Pmi*Chn4	*Proteus mirabilis* JN14	β-lactamase, DNA repair genes, Sum^r, Spt^r, Flo^r	KY437728.1	91	29
ICE*Pmi*CHN1586	*Proteus mirabilis* 08MAS1586	Tm^r, Flo$_r$, Bm^r, Spt^r, Su^r, DNA repair genes	KX243404.1	99	27
ICE*Pmi*CHN2407	*Proteus mirabilis* 09MAS2407	Tet^r, RMS, Co-Zn-Cd resistance, DNA repair genes, Hg^r	KX243405.1	97	27
ICE*Pmi*CHN2410	*Proteus mirabilis* 09MAS2410	DNA repair polymerases, RMS, Co-Zn-Cd resistance, Hg^r, Am^{r,} Azm^r, Cm^r, Kn^r, Sptr, SXT^r, Su^r, Tet^r, CFZ^r, Cip^r	KX243406.1	93	27
ICE*Pmi*CHN2416	*Proteus mirabilis* 09MAS2416	RMS, Co-Zn-Cd resistance, DNA repair genes, Hg^r	KX243407.1	92	27
ICE*Pmi*CHN901	*Proteus mirabilis* MD20140901	Tm^r, Bm^r, Flo^r, Spt^r, RMS, DNA repair genes	KX243208.1	89	27
ICE*Pmi*CHN902	*Proteus mirabilis* MD20140902	Bm^r, Spt^r, Su^r, Am^r Azm^r, Az^r, Amk^r, Cm^r, Cip^r, Kn^r ,SXT^r, Tet^t , DNA repair genes, RMS	KX243409.1	89	27
ICE*Pmi*CHN903	*Proteus mirabilis MD20140903*	Bm^r, Tm^r, Sptr, Spt^r, RMS, DNA repair genes	KX243410.1	89	27
ICE*Pmi*CHN904	*Proteus mirabilis* MD20140904	Bm^r, RMS, Co-Zn-Cd resistance, DNA repair genes, Spt^r, Su^r, Tet^r	KX243411.1	95	27
ICE*Pmi*CHN905	*Proteus mirabilis* MD20140905	Bm^r, RMS, Tet^r, Spt^r, Su^r, Co-Zn-Cd resistance protein	KX243412.1	95	27
ICE*Pmi*CHN809	*Proteus mirabilis* TJ1809	Am^r, Kn^r, SXT^r, Azm^r, Cm^r, Su^r, Tet^r, Cf^r	KX243413.1	76	27
ICE*Pmi*CHN3237	*Proteus mirabilis* TJ3237	DNA repair genes, RMS, CFZ^r ,Am^r, Azm^r, SXT^r, Tet^r, Su^r	KX243414.1	87	27

Element	Strain	Accessory Genes/Reported Functions	Acc. No.	Size (kb)	Ref
ICE*Pmi*CHN3300	*Proteus mirabilis* TJ3300	Tm^r, Azm^r, Cm^r, SXT^r, Su^r, Spt^r, DNA repair genes	KX243415.1	108	27
ICE*Pmi*CHN3335	*Proteus mirabilis TJ3335*	Azm^r , Bm^r, RMS, Tet^r, Spt^r, DNA repair polymerases	KX243416.1	90	27
ICE*Pmi*Chn18	*Proteus mirabilis Pm15C1*	DNA repair genes, Tm^r, RMS	KX268685.1	65	N/A
ICE*Pmi*Chn19	*Proteus mirabilis PM14C28*	quaternary ammonium-compound resistance	KT894734.1	93	28
ICE*Vfl*Chn1*	*Vibrio fluvialis* 12605	Bile resistance genes (toxR, ompU, ompT, tolC), Heat stock proteins (GroES, GroEL, HspA), virulence factors & prophage regions	CP019118.1	N/A	N/A
ICE*Vflu*Chn2*	*Vibrio fluvialis* 12605	Bile resistance genes (toxR, ompU, ompT, tolC), Heat stock proteins (GroES, GroEL, HspA), virulence factors & prophage regions	CP019119.1	N/A	N/A
ICE*Pmi*AR_0159	*Proteus mirabilis* AR_0159	Cm^r, Flo^r, Tm^r, Heavy metal resistance protein.	CP021550.1	99	N/A
ICE*Sup*CHN110003	*Shewanella upenei* 110003	DNA repair genes, Bm^r, Cm^r, Spt^r, Su^r, RMS.	MG014393.1	92	N/A
ICE*Pmi*Fra1	*Proteus mirabilis* PmPHI	Flo^r, Cm^r Spt^r, Su^r, Tetr, Kn^{r,} Tm^r, Ery^r, Nm^r, RMS, merR family gene & DNA repair genes	MF490434.1	107	30
ICE*Sha*Jpn1*	*Shewanella Halifaxiensis* 6JANF4-E-4	Ma^r, Flo^r, Su^r, β-lactamase	BFBQ01000001.1	N/A	N/A
ICE*Sha*Jpn2*	*Shewanella Halifaxiensis* 6JANF4-E-4	Ma^r, Flo^r, Su^r, β-lactamase	BFBQ01000005.1	44.6	N/A
ICE*Apl*Chn1	*Actinobacillus pleuropneumoniae* App6	Flo^{r,} Cm^r, Tetr, Amk^r, Km^r, Spt^r, Til^r, Ery^r, Clr^r, Lm^r, Su^r	KX196444	100	31
ICE*Pmi*ChnBCP11	*Proteus mirabilis* BCP11	Tetr, Km^r, Nm^r, Blm^r, Rif^r, Hym^r, Am^r, Spt^r, Ctx^r, Az^r, Spm^r, Ap^r, To^r, Tm^r, SXT, Cf^r, Nf^r, Fm^r, Cm^r, Flo^r, RMS, Nal^r	MG773277.1	141	32

AAA: ATPases Associated with diverse cellular activities **,** **Ac^r** : Acriflavin resistance , **Af^r**: Actiflavine resistance**,** **Ag^r**: Aminoglycoside resistance, **Am^r**: Ampicillin resistance, **Amk^r** :Amikacin resistance**,** **Ap^r**: Apramycin resistance, **As^r:** Arsenic resistance, **Azm^r:** Azithromycin resistance, **Az^r**: Aztreonam resistance, **Bm^r**- Bicyclomycin resistance, **Blm^r**: Bleomycin resistance, **Co**: Cobalt**,** **Cd**: Cadmium **, CFZ^r:** Cefazolin resistance **Ctx^r**: Cefotaxime resistance**,** **Cip^r**: Ciprofloxacin resistance**,** **Cli^r**: Clindamycin resistance**,** **Cm^r**: Chloramphenicol resistance, **Cu^R**: Copper resistance, **Ery^r**: Erythromycin resistance, **Flo^r**: Florfenicol

resistance, **Fm**^{r}: Fosfomycin resistance, **Fq**^{r}: Fluoroquinolone resistance, **Hg**^{r}: Mercury resistance, **Hm**^{r}: Hygromycin resistance, **Km**^{r}: Kanamycin resistance, **Lm**^{r}: lincomycin resistance, **Ma**^{r}: Macrolide resistance, **Nal**^{r}: Nalidixic acid resistance, **Nm**^{r}: Neomycin resistance, **Nf**^{r}: Norfloxacin resistance, **Rif**^{r}: Rifampin resistance**, RND**: Resistance Nodulation Cell Division, **RMS**: Restriction modification system, **Spt**^{r}: Spectinomycin resistance, **Sp**^{r}: Streptomycin resistance, **Sum**^{r}**:** Sulphonamide resistance, **Su**^{r}: Sulfamethoxazole resistance, **SXT**: Trimethoprim-Sulfamethoxazole resistance, **Til**^{r}: Tilmicosin resistance**, Tet**^{r}: Tetracycline resistance, **Tm**^{r}: Trimethoprim resistance, **To**^{r}: Tobramycin resistance, **Zn**: Zinc.
N/A: Not Available

In some of these cases no name was given to the ICE that was sequenced. In these cases, names were assigned based on the nomenclature system used in Burrus *et al*. (20).

*Unpublished Sequence data

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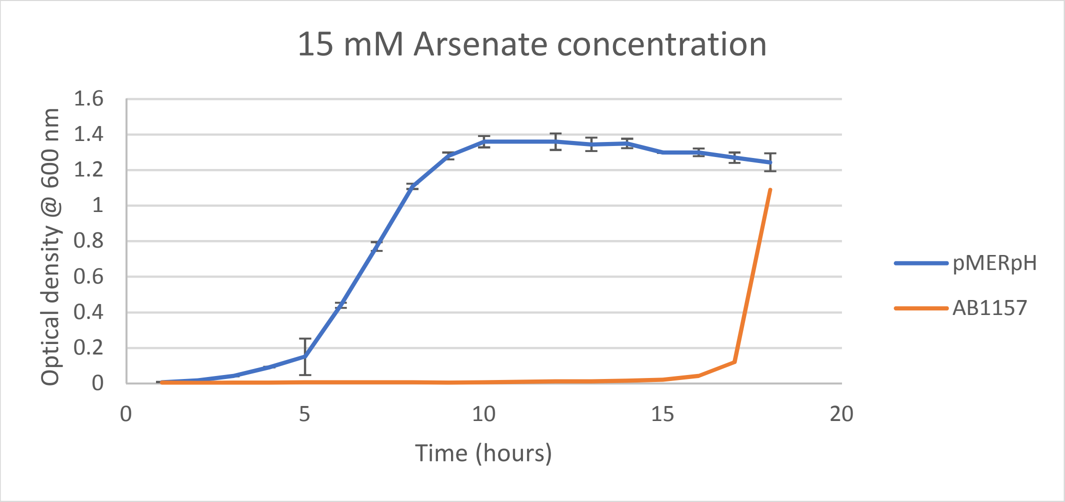
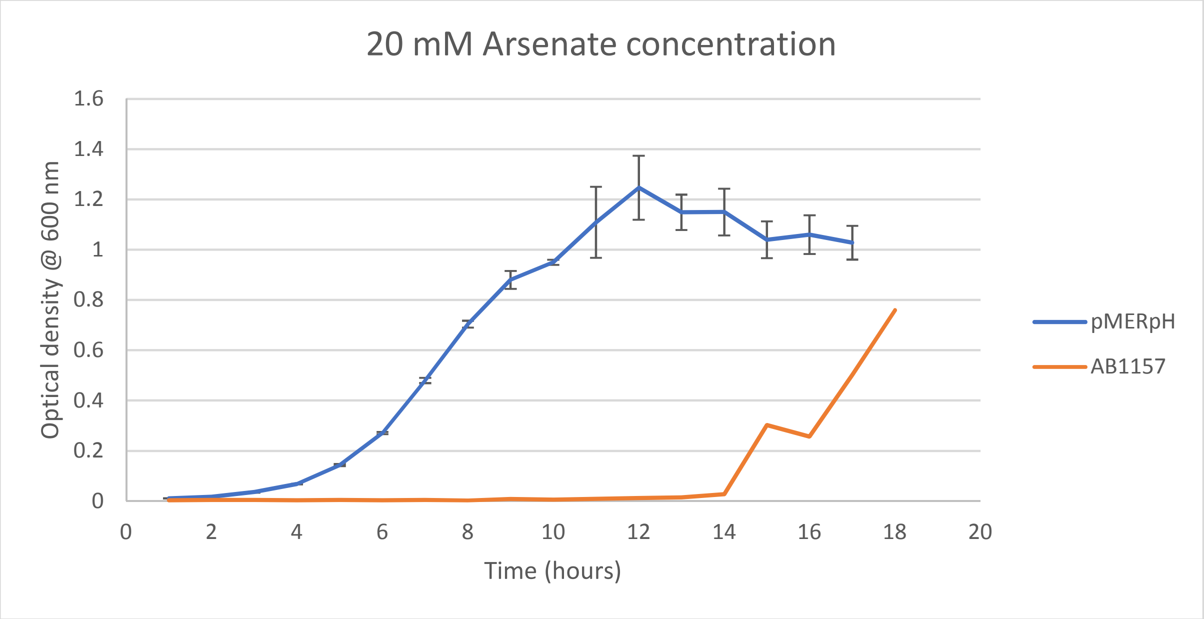
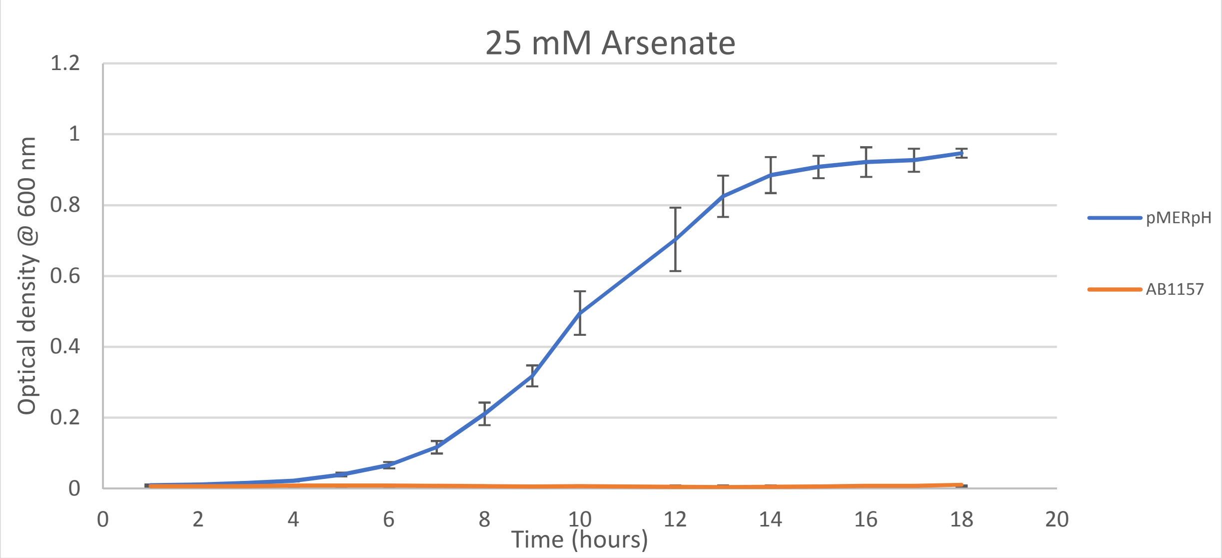
Growth curves of AB1157pMERpH and AB1157 with varying concentrations of Arsenate



Supplementary Figure 1: Growth curve of AB1157pMERpH (blue line) and AB1157 (orange line) over an 18-hour growth period with 15 mM Arsenate supplemented into the LB Broth culture. Optical density readings are measured at 600 nm. AB1157pMERpH shows resistance to Arsenate as it grows at a steady rate whereas AB1157 shows almost no growth until after 16 hours of growth. AB1157 is an E.coli strain and is known to have minimal arsenic resistance. AB1157pMERpH has a more adaptive system of resisting arsenate than AB1157 which is clearly displayed in the graph.



Supplementary Figure 2: Growth curve of AB1157pMERpH (blue line) and AB1157 (orange line) over an 18-hour growth period with 20 mM Arsenate supplemented into the LB Broth culture. Optical density readings are measured at 600 nm. AB1157pMERpH shows resistance to Arsenate as it grows at a steady rate whereas AB1157 shows almost no growth until after 15 hours of growth. Arsenate at a 20 mM concentration shows similar results to the 15 mM concentration (Figure 1).



Supplementary Figure 3: Growth curve of AB1157pMERpH (blue line) and AB1157 (orange line) over an 18-hour growth period with 25 mM Arsenate supplemented into the LB Broth culture. Optical density readings are measured at 600 nm. AB1157pMERpH shows resistance to Arsenate as it grows at a steady rate whereas AB1157 shows almost no growth during this period.

Summary of Results:

From observing the data, in an arsenate environment AB1157pMERpH will be able to adapt and continue to grow whereas AB1157 is susceptible to arsenate over a longer period. To AB1157, the arsenate acts as a bacteriostatic agent or bacteriostat, by way that it arrests the growth, but it doesn't kill the bacteria. This makes AB1157pMERpH the more dominant strain for survival in an arsenic environment. This resistance to arsenate is linked to a two gene system present in Hotspot 4 of the element. ORF 68, an organoarsenical efflux MFS transporter ArsJ and ORF 69, an NAD-dependent glyceraldehyde-3-phosphate dehydrogenase. A similar system is found in *Pseudomonas aeruginosa* DK2, it is new pathway of arsenate resistance involving biosynthesis and extrusion of an unusual pentavalent organoarsenical. [1]

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