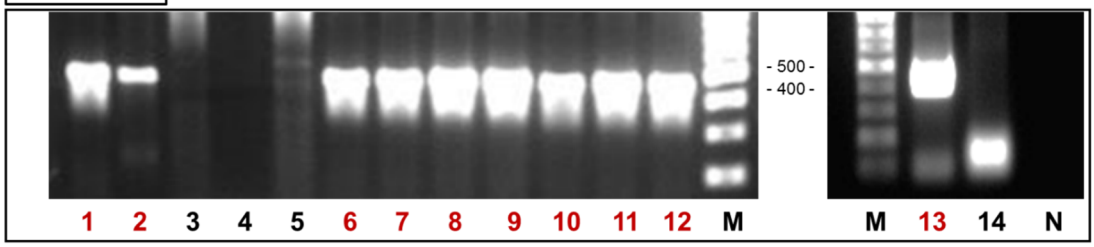
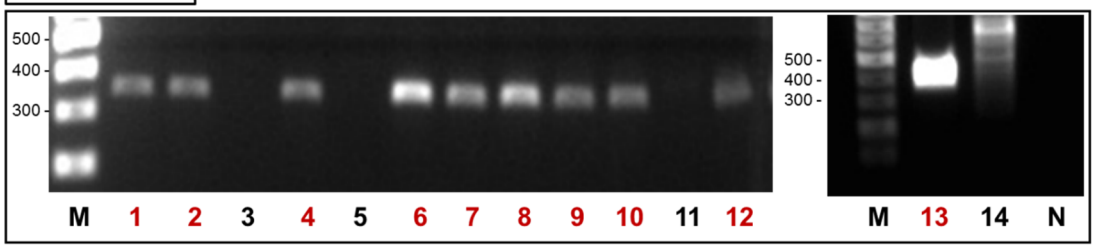
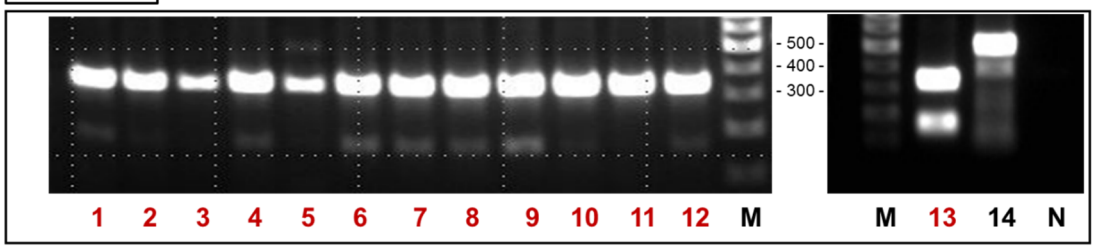
act **(431bp)**



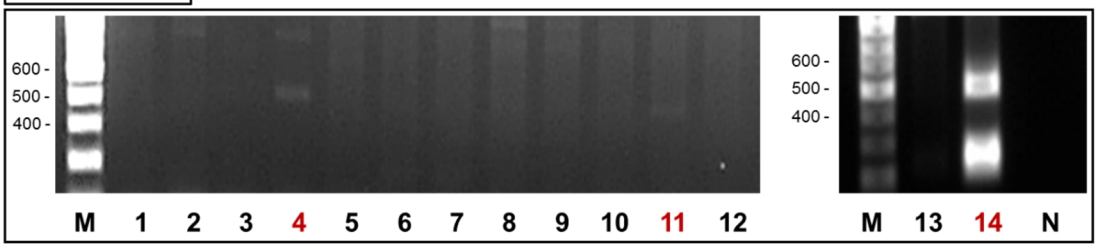
aspA **(350bp)**



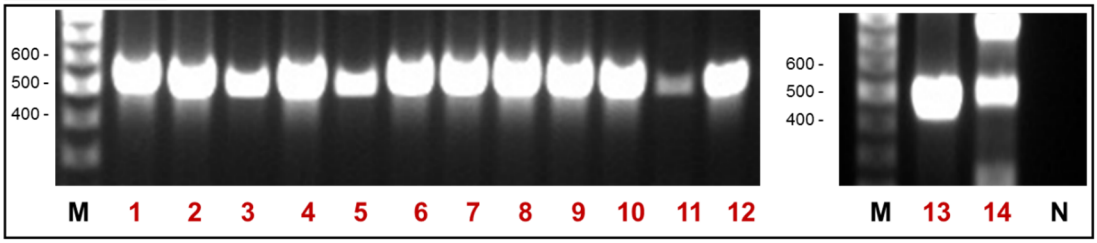
alt **(320bp)**



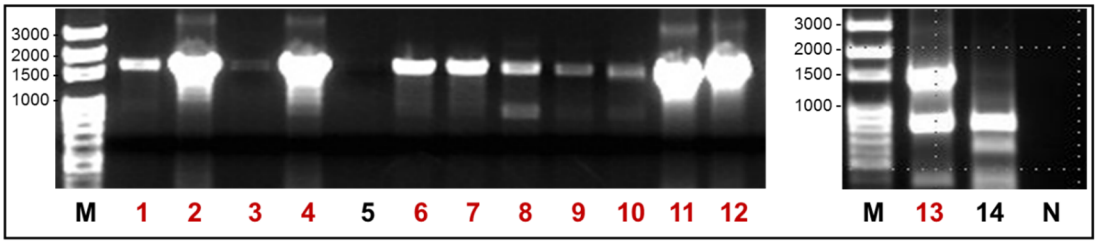
aexT **(535bp)**

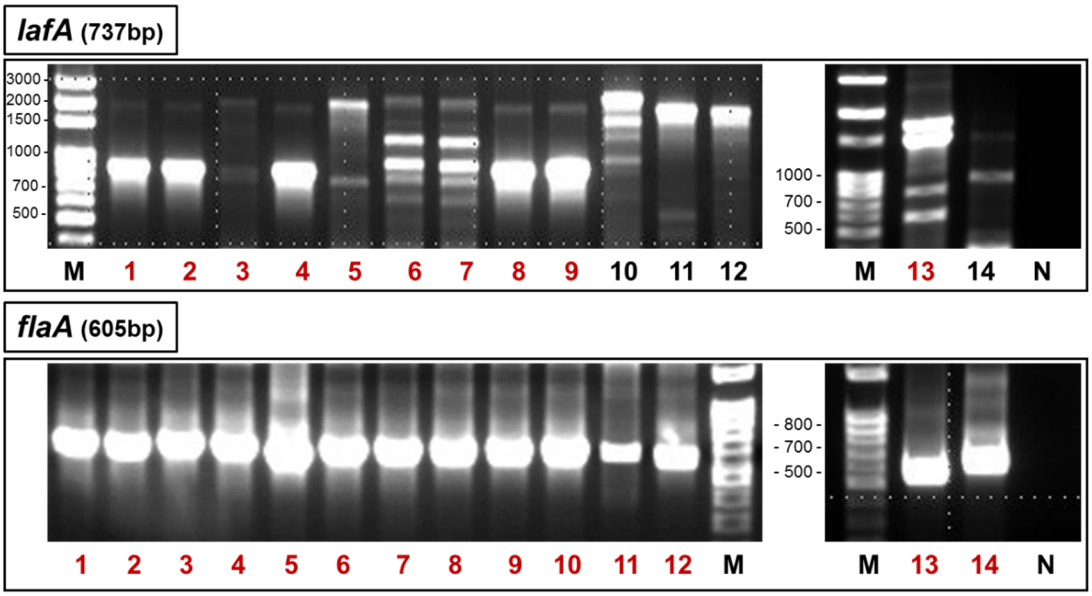


ast **(504bp)**



vasH **(1652bp)**





Supplementary Figure S1. Gel electropherogram of virulence-related gene amplicons from the 14 *Aeromonas* isolates used in this study. Virulence genes showing positive amplicons are only shown and red numbers indicate positive amplicons, respectively. *Aeromonas* strains were arranged in the following order: 1, *A. hydrophila* KN-Mc-1R1; 2, *A. hydrophila* KN-Mc-1R2; 3, *A. cavieae* KN-Mc-1R3; 4, *A. hydrophila* KN-Mc-2R1; 5, *A. cavieae* KN-Mc-3R1; 6, *A. hydrophila* KN-Mc-4N1; 7, *A. hydrophila* KN-Mc-4N3; 8, *A. hydrophila* KN-Mc-5R1; 9, *A. hydrophila* KN-Mc-5R2; 10, *A. hydrophila* KN-Mc-6U21; 11, *A. dhakensis* KN-Mc-6U2; 12, *A. hydrophila* KN-Mc-6U22; 13, *A. hydrophila* KN-Mc-10N1; 14, *A. rivipollensis* KN-Mc-11N1; N, negative control; M, SiZer™-100 plus DNA marker (Intron Biotech, Seongnam, Republic of Korea).

Supplementary Table S1. List of PCR primers used in this study.

Gene	Primer sequence (5′ to 3′)	Ref
Bacterial identification (Product size (bp))		
16S rRNA (1466)	F(27F): AGAGTTTGATCMTGGCTCAG R(1492R): TACGGYTACCTTGTTACGACTT	Universal primer
gyrB (≈1100)	F(gyrB3F): TCCGGCGGTCTGCACGGCGT R(gyrB14R): TTGTCCGGGTTGTACTCGTC	[1]
rpoB (560)	F(Pasrpob-L): GCAGTGAAAGARTTCTTTGGTTC R(Rpob-R): GTTGCATGTTNGNACCCAT	[2]
Virulence-associated genes (Product size (bp))		
Act (431)	F: CCTATGGCCTGAGCGAGAAG R: CCAGTTCCAGTCCCACCACT	[3]
aexT (535)	F: GGCGCTTGGGCTCTACAC R: GAGCCCGCGCATCTTCAG	[4]
Alt (320)	F: AAAGCGTCTGACAGCGAAGT R: AGCGCATAGGCGTTCTCTT	[5]
ascV (710)	F: ATGGACGGCGCCATGAAGTT R: TATTCGCCTTCACCCATCCC	[6]
aspA (350)	F: CACCGAAGTATTGGGTCAGG R: GGCTCATGCGTAACTCTGGT	[3]
Ast (504)	F: ATCGTCAGCGACAGCTTCTT R: CTCATCCCTTGGCTTGTTGT	[5]
BfpA (251)	F: CCGCAGGTGTGATGTTTTAC R: TGCGGTGTTATTGTTTGCT	[7]
BfpG (233)	F: ATGCCAAAGCTGACTGGTCT R: GACATGATTCCCGTTATAAA	[7]
flaA (608)	F: TCCAACCGTYTGACCTC R: GMYTGGTTGCGRATGGT	[8]
lafA (737)	F: CCAACTTYGCYTCYMTGACC R: TCTTGGTCATRTTGGTGCTY	[5]
stx-1 (180)	F: ATAAATTGCCATTCGTTGACTAC R: AGAACGCCCACTGAGATCATC	[9]

	stx-2 (255)	F: GGCACTGCTTGAAACTGCTCC R: TCGCCAGTTATCTGACATTCTG	[9]
	vasH (1,652)	F: GCTCTAGACCGGTGAACCCATCAAGCGCGTCCACT R: TCCCCCCGGGCTGGTGGCCAGCAGCAGAGGCAATA	[10]
Antimicrobial-resistance genes (Product size (bp))			
T*	*tetA* (211)	F(*tet*AF): GCTACATCCTGCTTGCCTTC R(*tet*AR): GCATAGATCGCCGTGAAGAG	[11]
	tetB (391)	F(ClassB *tet*AF): TCATTGCCGATACCACCTCAG R(ClassB *tet*AR): CCAACCATCATGCTATTCCATCC	
	tetC (897)	F(ClassC *tet*AF): CTGCTCGCTTCGCTACTTG R(ClassC *tet*AR): GCCTACAATCCATGCCAACC	
	tetD (844)	F(ClassD *tet*AF): TGTGCTGTGGATGTTGTATCTC R(ClassD *tet*AR): CAGTGCCGTGCCAATCAG	
	tetE (744)	F(ClassE *tet*AF): ATGAACCGCACTGTGATGATG R(ClassE *tet*AR): ACCGACCATTACGCCATCC	
Q*	*gyrA* (663)	F(ASGYRA1): CCATGAGCGTGATCGTAGGA R(ASGYRA2): CTTTGGCACGCACATAGACG	[12]
	parC (418)	F(ASPARC3): CAGCGGCGCATCATCTAC R(ASPARC4): GGATATCGGTGGCCATGC	
	qnrA1 to *qnrA6* (580)	F(qnrAm-F): AGAGGATTTCTCACGCCAGG R(qnrAm-R): TGCCAGGCACAGATCTTGAC	[13]
	qnrB1 to *qnrB6* (264)	F(qnrBm-F): GGMATHGAAATTCGCCACTG R(qnrBm-R): TTTGCYGYYCGCCAGTCGAA	
	qnrS1 to *qnrS2* (428)	F(qnrSm-F): GCAAGTTCATTGAACAGGGT R(qnrSm-R): TCTAAACCGTCGAGTTCGGCG	
I*	Class 1 integron (0.7~3.0 k)	F(5'-CS): GGCATCCAAGCAGCAAG R(3'-CS): AAGCAGACTTGACCTGA	[14]
B*	CTX-M-1 group (688)	F(CTXGp1-F): TTAGGAARTGTGCCGCTGYA R(CTXGp1-R): CGATATCGTTGGTGGTRCCAT	[15]
	CTX-M-2 group (404)	F(CTXGp2-F): CGTTAACGGCACGATGAC R(CTXGp2-R): CGATATCGTTGGTGGTRCCAT	
	CTX-M-9 group (561)	F(CTXGp9-F): TCAAGCCTGCCGATCTGGT R(CTXGp9-R): TGATTCTCGCCGCTGAAG	
	TEM (800)	F(TEM-F): CATTTCCGTGTCGCCCTTATTC R(TEM-R): CGTTCATCCATAGTTGCCTGAC	
	SHV (713)	F(SHV-F): AGCCGCTTGAGCAAATTAAAC R(SHV-R): ATCCCGCAGATAAATCACCAC	
	OXA-A variants (564)	F(OXAA-F): GGCACCAGATTCAACTTTCAAG R(OXAA-R): GACCCCAAGTTTCCTGTAAGTG	[16]
	MOX-1, MOX-2, CMY-1, CMY-8 to -11 (520)	F(MOXMF): GCTGCTCAAGGAGCACAGGAT R(MOXMR): CACATTGACATAGGTGTGGTGC	
	LAT-1 to -4, CMY-2 to -7, BIL-1 (462)	F(CITMF): TGGCCAGAACTGACAGGCAAA R(CITMR): TTTCTCCTGAACGTGGCTGGC	
	DHA-1 to -2 (405)	F(DHAMF): AACTTTCACAGGTGTGCTGGGT R(DHAMR): CCGTACGCATACTGGCTTTGC	
	ACC (346)	F(ACCMF): AACAGCCTCAGCAGCCGGTTA R(ACCMR): TTCGCCGCAATCATCCCTAGC	
	MIR-1, ACT-1 (302)	F(EBCMF): TCGGTAAAGCCGATGTTGCGG R(EBCMR): CTTCCACTGCGGCTGCCAGTT	
	FOX-1 to -5b (190)	F(FOXMF): AACATGGGGTATCAGGGAGATG R(FOXMR): CAAAGCGCGTAACCGGATTGG	
C*	*cphA* (≈720)	F(ANY-SSD/F):GCTTAGAGCTCCTAAGGAGCAAGATGAAAGGTTGG R(ANI-SSD/R):GCATAGGTACCTTATGACTGGGGTGCGGCCTTG	[17]

* T, tetracycline; Q, quinolones; I, integrons; B, β-lactams; C, carbapenems.

Supplementary Table S2. Biochemical characterization of *Aeromonas* spp. used in this study.

	Strains													
	KN-Mc-1R1	KN-Mc-1R2	KN-Mc-1R3	KN-Mc-2R1	KN-Mc-3R1	KN-Mc-4N1	KN-Mc-4N3	KN-Mc-5R1	KN-Mc-5R2	KN-Mc-6U2	KN-Mc-6U21	KN-Mc-6U22	KN-Mc-10N1	KN-Mc-11N1
ONPG	+	+	+	+	+	+	+	-	-	+	+	+	+	+
ADH	+	+	+	+	+	+	+	+	+	+	+	+	+	+
LDC	+	+	-	+	-	+	+	+	+	+	+	+	+	-
ODC	-	-	-	-	-	-	-	-	-	-	-	-	-	-
CIT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
H_2S	-	-	-	-	-	-	-	-	-	-	-	-	-	-
URE	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TDA	+	+	+	+	+	+	+	+	+	+	+	+	+	+
IND	+	+	+	+	+	+	+	+	+	+	+	+	+	+
VP	+	+	-	+	-	+	+	+	+	+	+	+	+	-
GEL	+	+	+	+	+	+	+	+	+	+	+	+	+	-
GLU	+	+	+	+	+	+	+	+	+	+	+	+	+	-
MAN	+	+	+	+	+	+	+	+	+	+	+	+	+	+
INO	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SOR	-	-	-	-	-	-	-	-	-	-	-	-	-	-
RHA	-	-	-	-	-	-	-	-	-	+	-	-	-	-
SAC	+	+	+	+	+	+	+	+	+	+	+	-	+	+
MEL	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AMY	-	-	+	-	+	+	+	-	-	-	-	-	-	-
ARA	+	+	+	+	+	+	+	+	+	+	-	+	+	+

ONPG; β-galactosidase, ADH; arginine dihydrolase, LDC; lysine decarboxylase, ODC; ornithine decarboxylase, CIT; citrate utilization, H_2S; H_2S production, URE; urease, TDA; tryptophane deaminase, IND; indole production, VP; Voges–Proskauer, GEL; gelatinase, GLU; glucose, MAN; mannitol, INO; inositol, SOR; sorbitol, RHA; rhamnose, SAC; saccharose, MEL; melibiose, AMY; amygdalin, ARA; arabinose.

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