Table 5 Percentage of *Salmonella* isolates conferred resistance to antimicrobial agents by disc diffusion method.

Antimicrobial agent	% of *Salmonella* isolates[a]											Total
	Fecal sample								Environmental sample			
	Sire	Dam	Suckling	Nursing	Fattening	Rearing	Pregnant sow	Replacement gilt	Feeds	Water	Lizard	
	(n = 4)[b]	(n = 48)[b]	(n = 25)[b]	(n = 73)[b]	(n = 39)[b]	(n = 12)[b]	(n = 12)[b]	(n = 3)[b]	(n = 2)[b]	(n = 4)[b]	(n = 8)[b]	(n = 230)[b]
Ampicillin	100	96	100	96	85	58	58	100	100	100	100	91
Amikacin	0	4	0	0	10	0	0	0	0	0	0	3
Amoxicillin / clavulanic acid	0	4	0	0	0	0	8	0	0	50	0	2
Apramycin	0	0	16	22	21	8	8	0	100	100	0	16
Ceftriaxone	0	0	0	0	0	0	0	0	0	0	0	0
Ceftriofur	0	0	0	0	0	0	0	0	0	0	0	0
Cephalothin	0	2	0	0	5	0	0	0	0	0	0	1
Chloramphenicol	25	15	48	66	64	67	58	100	100	100	0	51
Ciprofloxacin	0	0	0	0	0	0	0	0	0	0	0	0
Gentamicin	25	48	68	23	33	8	0	0	100	100	50	36
Kanamycin	0	8	12	53	25	33	25	0	0	0	0	27
Nalidixic acid	0	0	36	63	46	33	17	67	100	100	0	38
Streptomycin	75	69	88	75	80	83	67	100	100	100	63	78
Sulfamethoxazole	100	100	100	100	100	100	100	100	100	100	100	100
Trimethoprime / sulfamethoxazole	50	19	48	29	67	58	67	100	100	100	0	41
Tetracycline	100	94	100	92	97	100	83	100	100	100	100	95

Note: [a] % of *Salmonella* isolates from pigs which collected from five farms (A, B, C, D and E) in Thailand.
[b] n = total number of *Salmonella* isolates from each original sources.

Table 6 Antimicrobial resistance patterns of MDR *Salmonella* isolated from five pig farms (A, B, C, D and E) in Thailand.

Resistance pattern^a	Number of *Salmonella* isolates																						Total	
	Fecal sample																Environmental sample							
	Sire		Dam		Pregnant sow		Rearing		Replacement gilt		Suckling period		Nursing		Fattening		Feed		Water		Lizard			
Serogroup	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C
ASuT	1		9									1	14	2	4						3		31	3
NSuT							1	1															1	1
SSuT				2	1	1	1	1															2	4
ASSuT				8								2	1		1						1		3	10
AGSSuT		1		17								9										4	0	31
AApCSSuT															2								2	0
ASSuSxtT	1														1	1							2	1
ACSuSxtT			1			1																	1	1
ACGSuSxtT			1																				1	0
AGSSuSxtT				2																			0	2
ACSSuSxtT	1				2		2		1		2	1			1	3							9	4
ACGSSuSxtT												1											0	1
ACCtGSSuSxtT				1											1								1	1
ACCtNSSuSxtT															1								1	0
ACKSuT				1																			0	1
ACKSSuSxtT				1	1			2						8		3							1	14
ACGKSSuSxtT								1															0	1
ACKNSSuT													22		2								24	0

Note: ^{a} A = ampicillin, Ak = amikacin, Am = amoxicillin/clavulanic acid, Ap = apramycin, C = chloramphenicol, Ct = cephalothin, G = gentamicin, K = kanamycin, N = nalidixic acid, S = streptomycin, T = tetracycline, Su = sulfamethoxazole and Sxt = sulfamethoxazole/trimethoprim.

Table 6 (continued)

Resistance pattern[a]	Number of *Salmonella* isolates																						Total	
	Fecal sample																Environmental sample							
	Sire		Dam		Pregnant sow		Rearing		Replacement gilt		Suckling period		Nursing		Fattening		Feed		Water		Lizard			
Serogroup	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C
ACKNSuSxtT												2											0	2
ANSSuSxtT													1	1		1							1	2
ACNSSuSxtT							1			2			2										3	2
AGKNSSuT												1											0	1
AGNSSuSxtT															1								1	0
ACGNSSuSxtT												2	1		2								3	2
ACKNSSuSxtT					1										1								2	0
AAkGKNSSuT															1								1	0
AAkCGKNSSuSxtT															3								3	0
AAkAmCGKSSuSxtT				2																			0	2
AApCGKNSSuT													9										9	0
AApCGNSSuSxtT											4		4	2	5		4		2				19	2
AApCKSSuSxtT								1															0	1
AAmApCSSuSxtT						1																	0	1
Total	4	0	11	34	5	3	5	6	1	2	6	19	54	13	26	8	4	0	2	0	4	4	211	

Note: [a] A = ampicillin, Ak = amikacin, Am = amoxicillin/clavulanic acid, Ap = apramycin, C = chloramphenicol, Ct = cephalothin, G = gentamicin, K = kanamycin, N = nalidixic acid, S = streptomycin, T = tetracycline, Su = sulfamethoxazole and Sxt = sulfamethoxazole/trimethoprim.

Table 7 Antimicrobial resistance patterns of MDR *Salmonella* isolates from pigs of Farm A.

Resistance pattern[a]	Number of *Salmonella* isolates																	
	Fecal sample										Environmental sample						Total	
	Sire		Dam		Suckling period		Nursing		Fattening		Feed		Water		Lizard			
Serogroup	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C
ASuT	1		9			1	14	2	4						3		31	3
SSuT				2													0	2
ASSuT				8		2	1								1		2	10
AGSSuT		**1**		**17(5)**		**9(3)**										**4(2)**	**0**	**31(10)**
AApCSSuT									2								2	0
ASSuSxtT	1																1	0
ACSuSxtT			1														1	0
ACGSuSxtT			1														1	0
AGSSuSxtT				2													0	2
ACSSuSxtT										2							0	2
ACCtGSSuSxtT				1					1								1	1
ACCtNSSuSxtT									1								1	0
ACKSuT				1													0	1
ACKSSuSxtT				**1(1)**				**8(3)**		**3(3)**							**0**	**12(10)**
ANSSuSxtT										1							0	1
ACNSSuSxtT							2										2	0
AGKNSSuT						1											0	1
AGNSSuSxtT									1								1	0
ACGNSSuSxtT						2	1		2								3	2
ACKNSSuSxtT									1								1	0
AAkGKNSSuT									1								1	0
AAkCGKNSSuSxtT									3								3	0
AAkAmCGKSSuSxtT				2													0	2
AApCGNSSuSxtT					**4(2)**		**4(2)**	**2**	**5(3)**		**4(2)**		**2(1)**				**19(10)**	**2**
Total	2	1	11	34	4	15	22	12	21	6	4	0	2	0	4	4	142	

Note: [a] A = ampicillin, Ak = amikacin, Am = amoxicillin/clavulanic acid, Ap = apramycin, C = chloramphenicol, Ct = cephalothin, G = gentamicin, K = kanamycin, N = nalidixic acid, S = streptomycin, T = tetracycline, Su = sulfamethoxazole and Sxt = sulfamethoxazole/trimethoprim.

Bold letters were the high prevalent resistance patterns of *Salmonella* strains and numbers in blanket were the amount of isolates using in conjugation, plasmid profiles and RFLP analysis.

Table 8 Resistance patterns, resistance gene cassettes and sequence identity of *Salmonella* strains containing class 1 integron.

Salmonella strain[a]	Farm	Resistance pattern[b]	Gene[c]	Length of CDS (bp)	Length of *attC* site (bp)	Gene cassette length (bp)	% Identity to reference gene[d]	Accession no. of reference gene
S. Stanley CC1	C	ACGSSuSxtT	*aadA1*	792	60	859	99	AY887066
							99	DQ388123
							99	DQ141317
							99	AY126947
S. Panama CB2	C	ACSSuSxtT	*aadA4*	789	57	896	98	Z50802
							98	AY138986
							98	AF364344
							94	AY214164
S. Panama CB3	C	ACSSuSxtT	*aadA4*	789	57	896	98	Z50802
							97	AY138986
							97	AF364344
							94	AY214164
S. Anatum EC3	E	AAmApCSSuSxtT	*aadA2*	792	60	859	97	DQ219465
							97	PAU12338
							97	L06822
							97	AY125352

Note: [a] Isolates name: 1st letter C or E = *Salmonella* isolated from pigs of Farm C or E, 2nd letter B or C = *Salmonella* serogroup B or C, number = Lab number of the isolates.

[b] A = ampicillin, Am = amoxicillin/clavulanic acid, Ap = apramycin, C = chloramphenicol, G = gentamicin, S = streptomycin, Su = sulfamethoxazole, Sxt = sulfamethoxazole/trimethoprim and T = tetracycline.

[c] All *aadA1*, *aadA4* and *aadA2* genes encoded for aminoglycoside adenyltransferase that conferred resistance to spectinomycin and streptomycin.

[d] Comparison of nucleotide sequences alignment was shown in Figure 10-13.

Table 9 Antimicrobial resistance phenotype of *Salmonella* donor isolates of Farm A, *E. coli* transconjugants and the size of conjugative plasmid.

Salmonella donor strain[a]	Resistance pattern[b] Donor	Transconjugant	Plasmid profiles and size of donor (kbp)[c]	Conjugative plasmid size (kbp)[d]
S. Corvallis AC11	AGSSuT	AG	54, 10	54
S. Corvallis AC23	AGSSuT	AG	54, 10, 4.3	54
S. Corvallis AC26	AGSSuT	AG	54, 10	54
S. Corvallis AC30	AGSSuT	AG	54, 10	54
S. Corvallis AC74	AGSSuT	AG	54, 10, 4.3	54
S. Corvallis AC119	AGSSuT	AG	54, 10	54
S. Corvallis AC125	AGSSuT	AG	54, 10	54
S. Corvallis AC138	AGSSuT	AG	54, 10	54
S. Corvallis AC149	AGSSuT	AG	54, 10	54
S. Corvallis AC151	AGSSuT	AG	54, 10	54
S. Rissen AC40	ACKSSuSxtT	ACKSuSxt	> 54, 10, 9, 5.6	> 54
S. Rissen AC41	ACKSSuSxtT	ACKSuSxt	> 54, 10, 9, 5.6	> 54
S. Rissen AC46	ACKSSuSxtT	ACKSuSxt	> 54, 10, 9, 5.6	> 54
S. Rissen AC49	ACKSSuSxtT	ACKSuSxt	> 54, 10, 9, 8, 5.1, 4	> 54
S. Rissen AC50	ACKSSuSxtT	ACKSuSxt	> 54, 10, 9, 8, 5.1, 4	> 54
S. Rissen AC69	ACKSSuSxtT	ACKSuSxt	> 54, 10, 9, 8, 5.1, 4	> 54
S. Rissen AC80	ACKSSuSxtT	ACKSuSxt	> 54, 10, 9, 5.6	> 54
S. Rissen AC105	ACKSSuSxtT	ACKSuSxt	> 54, 10, 9, 5.6	> 54
S. Rissen AC106	ACKSSuSxtT	ACKSuSxt	> 54, 10, 9, 5.6	> 54
S. Rissen AC108	ACKSSuSxtT	ACKSuSxt	> 54, 10, 9, 5.6	> 54
S. 1,4,5,12:i:- AB37	AApCGNSSuSxtT	NT	8.6, 8, 5.6, 5.1, 4, 3	-
S. 1,4,5,12:i:- AB44	AApCGNSSuSxtT	NT	8, 5.1	-
S. 1,4,5,12:i:- AB51	AApCGNSSuSxtT	NT	8.6, 8, 5.6, 5.1, 4, 3	-
S. 1,4,5,12:i:- AB87	AApCGNSSuSxtT	NT	8.6, 8, 5.6, 5.1, 4, 3	-
S. 1,4,5,12:i:- AB93	AApCGNSSuSxtT	NT	8, 5.1	-
S. 1,4,5,12:i:- AB116	AApCGNSSuSxtT	NT	8, 5.1	-
S. 1,4,5,12:i:- AB117	AApCGNSSuSxtT	NT	8.6, 8, 5.6, 5.1, 4, 3	-
S. 1,4,5,12:i:- AB139	AApCGNSSuSxtT	NT	8, 5.1	-
S. 1,4,5,12:i:- AB141	AApCGNSSuSxtT	NT	8, 5.1	-
S. 1,4,5,12:i:- AB144	AApCGNSSuSxtT	NT	8.6, 8, 5.6, 5.1, 4, 3	-

Note: [a] Isolates name: 1st letter A = *Salmonella* isolated from pigs of Farm A, 2nd letter B or C = *Salmonella* serogroup B or C, number = Lab number of the isolates.

[b] A = ampicillin, Ap = apramycin, C = chloramphenicol, G = gentamicin, K = kanamycin, N = nalidixic acid, S = streptomycin, T = tetracycline, Su = sulfamethoxazole and Sxt = sulfamethoxazole/trimethoprim.

[c] Plasmid profile and size of donor cells were represented in Figure 18.

[d] Conjugative plasmid size were illustrated in Figure 19.

NT = Not transferred.

Table 10 Antimicrobial resistance phenotype of *Salmonella* donor strains containing class 1 integrons, *E. coli* transconjugants and the size of conjugative plasmid.

Salmonella donor strain[a]	Resistance pattern[b]		Class 1 integron carried *aadA* gene	Conjugative plasmid size (kbp)
	Donor	Transconjugant		
S. Stanley CC1	ACGSSuSxtT	ACSSuT	*aadA1*	> 54
S. Panama CB2	ACSSuSxtT	not transfer	*aadA4*	-
S. Panama CB3	ACSSuSxtT	not transfer	*aadA4*	-
S. Anatum EC3	AAmApCSSuSxtT	not transfer	*aadA2*	-

Note: [a] Isolates name: 1st letter C or E = *Salmonella* isolated from pigs of Farm C or E, 2nd letter B or C = *Salmonella* serogroup B or C, number = Lab number of isolates.

[b] A = ampicillin, Am = amoxicillin/clavulanic acid, Ap = apramycin, C = chloramphenicol, G = gentamicin, S = streptomycin, T = tetracycline, Su = sulfamethoxazole and Sxt = sulfamethoxazole/trimethoprim.

Table 11 Comparison of resistance patterns, RFLP-PCR and plasmid profiles of MDR *Salmonella* strains isolated from pigs of Farm A.

Salmonella strain[a]	Source	Resistance pattern[b]	RFLP pattern[c]	Plasmid profiles size (kbp)[d]	Plasmid profiles pattern
S. Corvallis AC11	Dam	AGSSuT	E1, X1	54, 10	M1
S. Corvallis AC23	Suckling period	AGSSuT	E1, X1	54, 10, 4.3	M2
S. Corvallis AC26	Suckling period	AGSSuT	E1, X1	54, 10	M1
S. Corvallis AC30	Suckling period	AGSSuT	E1, X1	54, 10	M1
S. Corvallis AC74	Dam	AGSSuT	E1, X1	54, 10, 4.3	M2
S. Corvallis AC119	Dam	AGSSuT	E1, X1	54, 10	M1
S. Corvallis AC125	Dam	AGSSuT	E1, X1	54, 10	M1
S. Corvallis AC138	Dam	AGSSuT	E1, X1	54, 10	M1
S. Corvallis AC149	Lizard	AGSSuT	E1, X1	54, 10	M1
S. Corvallis AC151	Lizard	AGSSuT	E1, X1	54, 10	M1
S. Rissen AC40	Nursing	ACKSSuSxtT	E4, X4	> 54, 10, 9, 5.6	N1
S. Rissen AC41	Nursing	ACKSSuSxtT	E4, X4	> 54, 10, 9, 5.6	N1
S. Rissen AC46	Nursing	ACKSSuSxtT	E4, X4	> 54, 10, 9, 5.6	N1
S. Rissen AC49	Nursing	ACKSSuSxtT	E4, X4	> 54, 10, 9, 8, 5.1, 4	N2
S. Rissen AC50	Nursing	ACKSSuSxtT	E4, X4	> 54, 10, 9, 8, 5.1, 4	N2
S. Rissen AC69	Nursing	ACKSSuSxtT	E4, X4	> 54, 10, 9, 8, 5.1, 4	N2
S. Rissen AC80	Dam	ACKSSuSxtT	E4, X4	> 54, 10, 9, 5.6	N1
S. Rissen AC105	Fattening	ACKSSuSxtT	E4, X4	> 54, 10, 9, 5.6	N1
S. Rissen AC106	Fattening	ACKSSuSxtT	E4, X4	> 54, 10, 9, 5.6	N1
S. Rissen AC108	Fattening	ACKSSuSxtT	E4, X4	> 54, 10, 9, 5.6	N1
S. 1,4,5,12:i:- AB37	Nursing	AApCGNSSuSxtT	E3, X3	8.6, 8, 5.6, 5.1, 4, 3	P1
S. 1,4,5,12:i:- AB44	Nursing	AApCGNSSuSxtT	E3 , X3	8, 5.1	P2
S. 1,4,5,12:i:- AB51	Fattening	AApCGNSSuSxtT	E3 , X3	8.6, 8, 5.6, 5.1, 4, 3	P1
S. 1,4,5,12:i:- AB87	Fattening	AApCGNSSuSxtT	E3 , X3	8.6, 8, 5.6, 5.1, 4, 3	P1
S. 1,4,5,12:i:- AB93	Fattening	AApCGNSSuSxtT	E3 , X3	8, 5.1	P2
S. 1,4,5,12:i:- AB116	Suckling period	AApCGNSSuSxtT	E3, X3	8, 5.1	P2
S. 1,4,5,12:i:- AB117	Suckling period	AApCGNSSuSxtT	E3 , X3	8.6, 8, 5.6, 5.1, 4, 3	P1
S. 1,4,5,12:i:- AB139	Feed	AApCGNSSuSxtT	E3 , X3	8, 5.1	P2
S. 1,4,5,12:i:- AB141	Feed	AApCGNSSuSxtT	E3 , X3	8, 5.1	P2
S. 1,4,5,12:i:- AB144	Water	AApCGNSSuSxtT	E3 , X3	8.6, 8, 5.6, 5.1, 4, 3	P1

Note: [a] Isolates name: 1st letter A = *Salmonella* isolated from pigs of Farm A, 2nd letter B or C = *Salmonella* serogroup B or C, number = Lab number of the isolates

[b] A = ampicillin, Ap = apramycin, C = chloramphenicol, G = gentamicin, K = kanamycin, N = nalidixic acid, S = streptomycin, T = tetracycline, Su = sulfamethoxazole and Sxt = sulfamethoxazole/trimethoprim. NT = not transferred.

[c] E = RFLP-PCR pattern of *fliC* gene digested with *Mbo*I and X = RFLP-PCR pattern of *fliC* gene digested with *Hha*I.

[d] Plasmid profiles and plasmid size of *Salmonella* donor strains were represented in Figure 18, conjugative plasmid size were illustrated in Figure 19.

Table 12 Combination of antimicrobial resistance and RFLP-PCR patterns of MDR *Salmonella* isolates from pigs of Farm A.

Resistance pattern[a] / RFLP-PCR pattern[b]	Number of *Salmonella* isolates																Total	
	Fecal sample										Environmental sample							
	Sire		Dam		Suckling period		Nursing		Fattening		Feed		Water		Lizard			
	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C	B	C
AGSSuT[a]		1		17(5)		9(3)										4(2)	0	31(10)
E1, X1[b]				**5**		**3**										**2**		**10**
ACKSSuSxtT[a]				1(1)				8(6)		3(3)							0	12(10)
E4, X4[b]				**1**				**6**		**3**								**10**
AApCGNSSuSxtT[a]					4(2)		4(2)	2	5(3)		4(2)		2(1)				19(10)	2
E3, X3[b]					**2**		**2**		**3**		**2**		**1**				**10**	
Total	2	1	11	34	4	15	22	12	21	6	4	0	2	0	4	4	142	

Note: [a] A = ampicillin, Ak = amikacin, Am = amoxicillin/clavulanic acid, Ap = apramycin, C = chloramphenicol, Ct = cephalothin, G = gentamicin, K = kanamycin, N = nalidixic acid, S = streptomycin, T = tetracycline, Su = sulfamethoxazole and Sxt = sulfamethoxazole/trimethoprim.

[b] E = RFLP-PCR pattern of *fliC* gene digested with *Mbo*I and X = RFLP-PCR pattern of *fliC* gene digested with *Hha*I.

Numbers in blanket were the isolates using in RFLP-PCR analysis.

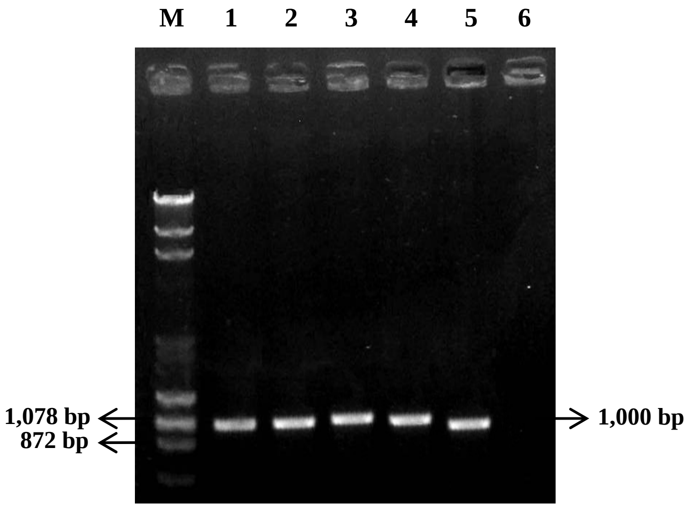
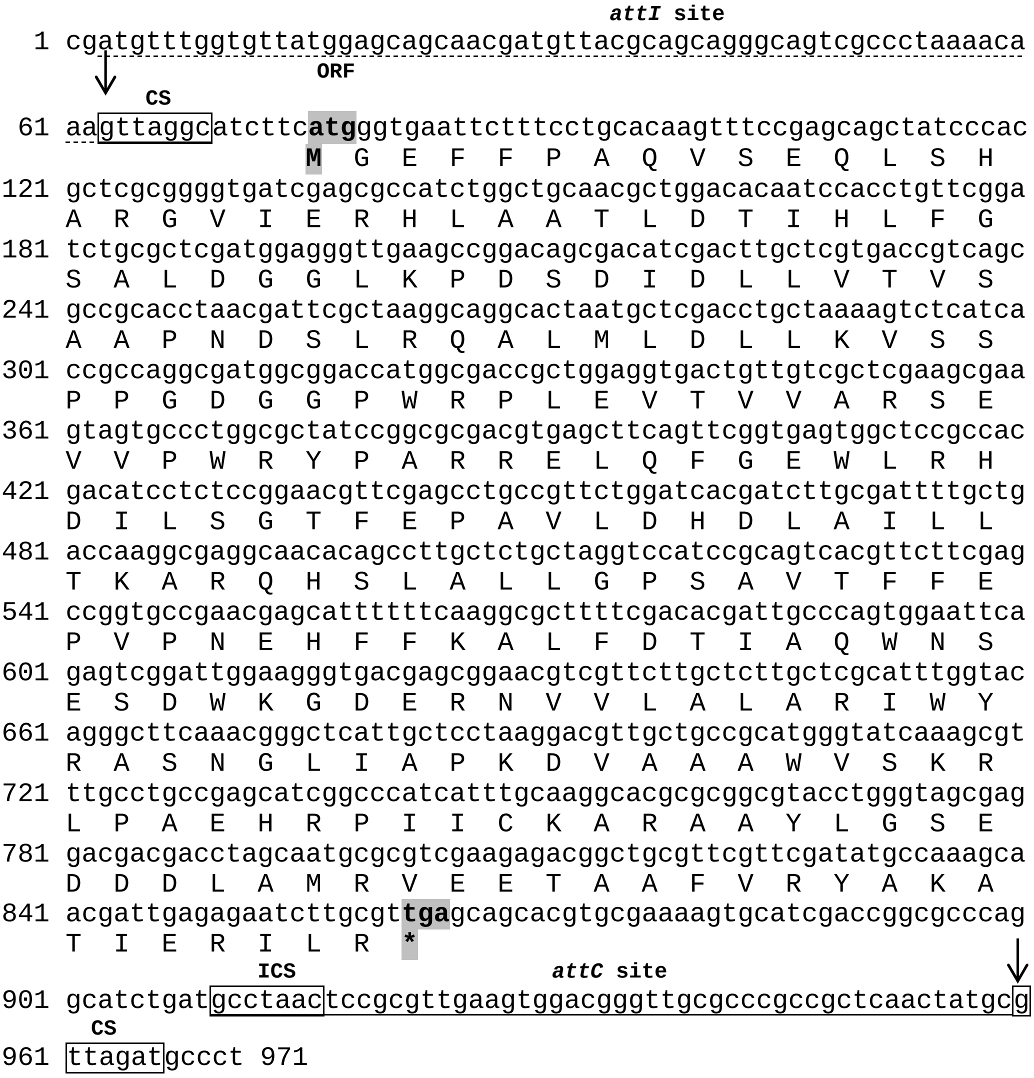


Figure 5 Agarose gel electrophoresis of PCR amplification of class 1 integron. Lane M = standard marker (λ/*Hin*dIII + ϕx/*Hae*III), lane 1 = *S.* Typhimuruim DT104 containing class1 integron was used as positive control, lane 2 = *S.* Stanley CC1, lane 3 = *S.* Panama CB2, lane 4 = *S.* Panama CB3, lane 5 = *S.* Anatum EC3 and lane 6 = negative control.

```
                                      attI site
  1 cgatgtttggtgttatggagcagcaacgatgttacgcagcagggcagtcgccctaaaaca
      ↓             ORF
         CS
 61 aagttaggcatcttcatgagggaagcggtgatcgccgaagtatcgactcaactatcagag
                   M  R  E  A  V  I  A  E  V  S  T  Q  L  S  E
121 gtagttggcgtcatcgagcgccatctcgaaccgacgttgctggccgtacatttgtacggc
    V  V  G  V  I  E  R  H  L  E  P  T  L  L  A  V  H  L  Y  G
181 tccgcagtggatggcggcctgaagccacacagtgatattgatttgctggttacggggacc
    S  A  V  D  G  G  L  K  P  H  S  D  I  D  L  L  V  T  G  T
241 gtaaggcttgatgaaacaacgcggcgagctttgatcaacgaccttttggaaacttcggct
    V  R  L  D  E  T  T  R  R  A  L  I  N  D  L  L  E  T  S  A
301 tcccctggagagagcgagattctccgcgctgtagaagtcaccattgttgtgcacgacgac
    S  P  G  E  S  E  I  L  R  A  V  E  V  T  I  V  V  H  D  D
361 atcattccgtggcgttatccagctaagcgcgaactgcaatttggagaatggcagcgcaat
    I  I  P  W  R  Y  P  A  K  R  E  L  Q  F  G  E  W  Q  R  N
421 gacattcttgcaggtatcttcgagccagccacgatcgacattgatctggctatcttgctg
    D  I  L  A  G  I  F  E  P  A  T  I  D  I  D  L  A  I  L  L
481 acaaaagcaagagaacatagcgttgccttggtaggtccagcggcggaggaactctttgat
    T  K  A  R  E  H  S  V  A  L  V  G  P  A  A  E  E  L  F  D
541 ccggttcctgaacaggatctatttgaggcgctaaatgaaaccttaacgctatggaactcg
    P  V  P  E  Q  D  L  F  E  A  L  N  E  T  L  T  L  W  N  S
601 ccgcccgactgggctggcgatgagcgaaatgtagtgcttacgttgtcccgcatttggtcc
    P  P  D  W  A  G  D  E  R  N  V  V  L  T  L  S  R  I  W  S
661 agcgcagaaaccggcaaaatcgcgccgaaggatgtcgctgccgactgggcaaaagagcgc
    S  A  E  T  G  K  I  A  P  K  D  V  A  A  D  W  A  K  E  R
721 ctgccggcccagtatcagcccgtcatacttgaagctagacaggcttatcttggacaagaa
    L  P  A  Q  Y  Q  P  V  I  L  E  A  R  Q  A  Y  L  G  Q  E
781 gaagatcgcttggcctcccgcgcagatcagttggaagaatttgttcactacgtgaaaggc
    E  D  R  L  A  S  R  A  D  Q  L  E  E  F  V  H  Y  V  K  G
                                  ICS          attC site
841 gagatcaccaaggtagtcggcaaataatgtctaacaattcgttcaagtcgaacccgcttc
    E  I  T  K  V  V  G  K  *
                          ↓
                            CS
901 gcggcgcggcttaactcaagcgttagaagc 930
```

Figure 6 Nucleotide sequence and coding region of *aadA1* gene cassette in class 1 integron of *S.* Stanley CC1 strain. The conserved core site (CS) and inverse core site (ICS) were boxed. The *attI* site was underlined with a dotted line and the *attC* site was underlined. ORF = open reading frame, * = stop codon. The cassette boundaries were indicated by vertical arrow.

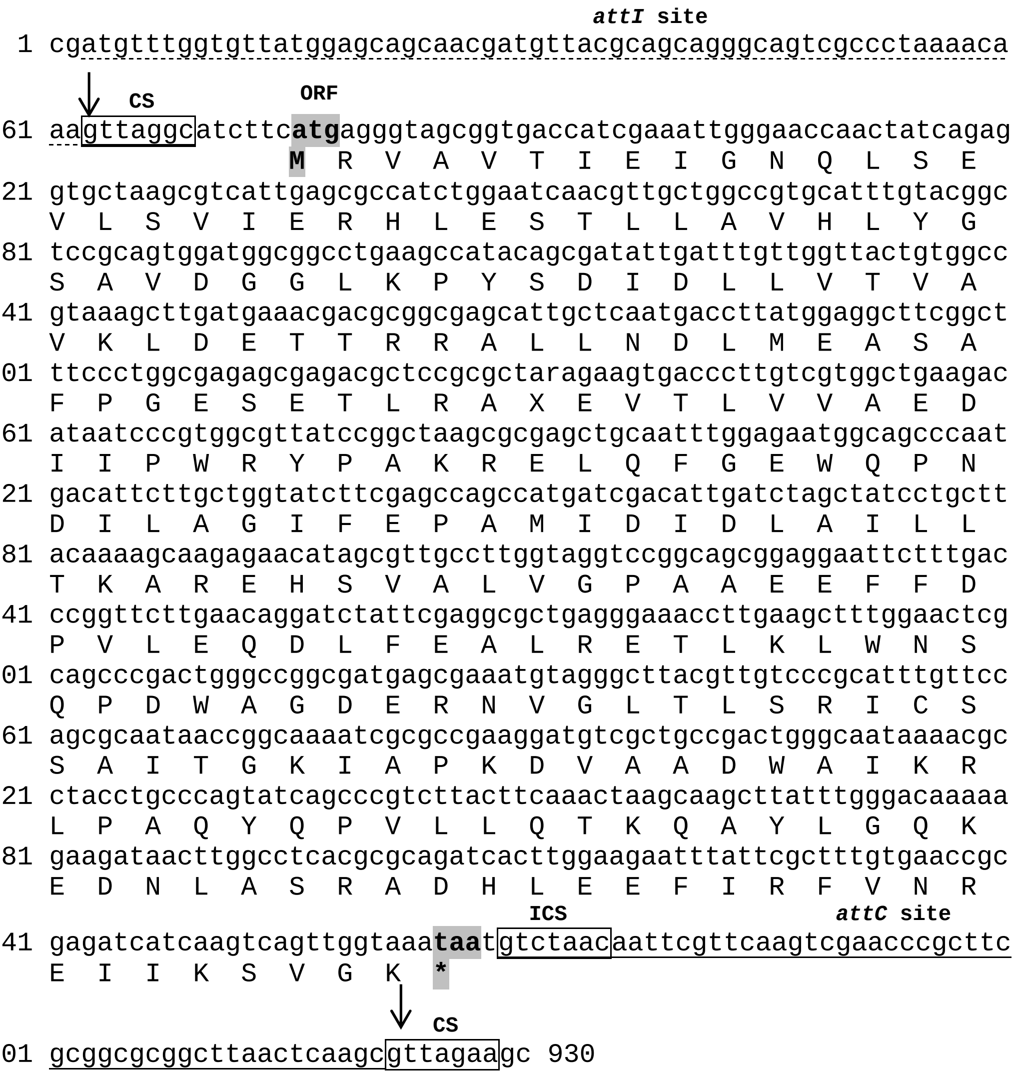


```
                                      attI site
  1 cgatgtttggtgttatggagcagcaacgatgttacgcagcagggcagtcgccctaaaaca
      ↓             ORF
         CS
 61 aagttaggcatcttcatgggtgaattctttcctgcacaagtttccgagcagctatcccac
                   M  G  E  F  F  P  A  Q  V  S  E  Q  L  S  H
121 gctcgcggggtgatcgagcgccatctggctgcaacgctggacacaatccacctgttcgga
    A  R  G  V  I  E  R  H  L  A  A  T  L  D  T  I  H  L  F  G
181 tctgcgctcgatggagggttgaagccggacagcgacatcgacttgctcgtgaccgtcagc
    S  A  L  D  G  G  L  K  P  D  S  D  I  D  L  L  V  T  V  S
241 gccgcacctaacgattcgctaaggcaggcactaatgctcgacctgctaaaagtctcatca
    A  A  P  N  D  S  L  R  Q  A  L  M  L  D  L  L  K  V  S  S
301 ccgccaggcgatggcggaccatggcgaccgctggaggtgactgttgtcgctcgaagcgaa
    P  P  G  D  G  G  P  W  R  P  L  E  V  T  V  V  A  R  S  E
361 gtagtgccctggcgctatccggcgcgacgtgagcttcagttcggtgagtggctccgccac
    V  V  P  W  R  Y  P  A  R  R  E  L  Q  F  G  E  W  L  R  H
421 gacatcctctccggaacgttcgagcctgccgttctggatcacgatcttgcgattttgctg
    D  I  L  S  G  T  F  E  P  A  V  L  D  H  D  L  A  I  L  L
481 accaaggcgaggcaacacagccttgctctgctaggtccatccgcagtcacgttcttcgag
    T  K  A  R  Q  H  S  L  A  L  L  G  P  S  A  V  T  F  F  E
541 ccggtgccgaacgagcattttttcaaggcgcttttcgacacgattgcccagtggaattca
    P  V  P  N  E  H  F  F  K  A  L  F  D  T  I  A  Q  W  N  S
601 gagtcggattggaagggtgacgagcggaacgtcgttcttgctcttgctcgcatttggtac
    E  S  D  W  K  G  D  E  R  N  V  V  L  A  L  A  R  I  W  Y
661 agggcttcaaacgggctcattgctcctaaggacgttgctgccgcatgggtatcaaagcgt
    R  A  S  N  G  L  I  A  P  K  D  V  A  A  A  W  V  S  K  R
721 ttgcctgccgagcatcggcccatcatttgcaaggcacgcgcggcgtacctgggtagcgag
    L  P  A  E  H  R  P  I  I  C  K  A  R  A  A  Y  L  G  S  E
781 gacgacgacctagcaatgcgcgtcgaagagacggctgcgttcgttcgatatgccaaagca
    D  D  D  L  A  M  R  V  E  E  T  A  A  F  V  R  Y  A  K  A
841 acgattgagagaatcttgcgttgagcagcacgtgcgaaaagtgcatcgaccggcgcccag
    T  I  E  R  I  L  R  *
                ICS               attC site                    ↓
901 gcatctgatgcctaactccgcgttgaagtggacgggttgcgcccgccgctcaactatgcg
      CS
961 ttagatgccct 971
```

Figure 7 Nucleotide sequence and coding region of *aadA4* gene cassette in class 1 integron of *S.* Panama CB2 strain. The conserved core site (CS) and inverse core site (ICS) were boxed. The *attI* site was underlined with a dotted line and the *attC* site was underlined. ORF = open reading frame, * = stop codon. The cassette boundaries were indicated by vertical arrow.

```
                                      attI site
  1 cgatgtttggtgttatggagcagcaacgatgttacgcagcagggcagtcgccctaaaaca
      ↓             ORF
         CS
 61 aagttaggcatcttcatgggtgaattctttcctgcacaagtttccgagcagctatcccac
                     M  G  E  F  F  P  A  Q  V  S  E  Q  L  S  H
121 gctcgcggggtgatcgagcgccatctggctgcaacgctggacacaatccacctgttcgga
    A  R  G  V  I  E  R  H  L  A  A  T  L  D  T  I  H  L  F  G
181 tctgcgctcgatggagggttgaagccggacagcgacatcgacttgctcgtgaccgtcagc
    S  A  L  D  G  G  L  K  P  D  S  D  I  D  L  L  V  T  V  S
241 gccgcacctaacgattcgctaaggcaggcactagtgctcgacctgctaaaagtctcatca
    A  A  P  N  D  S  L  R  Q  A  L  V  L  D  L  L  K  V  S  S
301 ccgccaggcgatggcggaccatggcgaccgctggaggtgactgttgtcgctcgaagcgaa
    P  P  G  D  G  G  P  W  R  P  L  E  V  T  V  V  A  R  S  E
361 gtagtgccctggcgctatccggcgcgacgtgagcttcagttcggtgagtggctccgccac
    V  V  P  W  R  Y  P  A  R  R  E  L  Q  F  G  E  W  L  R  H
421 gacatcctctccggaacgttcgagcctgccgttctggatcacgatcttgcgattttgctg
    D  I  L  S  G  T  F  E  P  A  V  L  D  H  D  L  A  I  L  L
481 accaaggcgaggcaacacagccttgctctgctaggtccatccgcagtcacgttcttcgag
    T  K  A  R  Q  H  S  L  A  L  L  G  P  S  A  V  T  F  F  E
541 ccggtgccgaacgagcatttttcaaggcgctttcgacacgattgcccagtggaattca
    P  V  P  N  E  H  F  F  K  A  L  F  D  T  I  A  Q  W  N  S
601 gagtcggattggaagggtgacgagcggaacgtcgttcttgctcttgctcgcatttggtac
    E  S  D  W  K  G  D  E  R  N  V  V  L  A  L  A  R  I  W  Y
661 agggcttcaaacgggctcattgctcctaaggacgttgctgccgcatgggtatcaaagcgt
    R  A  S  N  G  L  I  A  P  K  D  V  A  A  A  W  V  S  K  R
721 ttgcctgccgagcatcggcccatcatttgcaaggcacgcgcggcgtacctgggtagcgag
    L  P  A  E  H  R  P  I  I  C  K  A  R  A  A  Y  L  G  S  E
781 gacgacgacctagcaatgcgcgtcgaagagacggctgcgttcgttcgatatgccaaagca
    D  D  D  L  A  M  R  V  E  E  T  A  A  F  V  R  Y  A  K  A
841 acgattgagagaatcttgcgttgagcagcacgtgcgaaaagtgcatcgaccggcgcccag
    T  I  E  R  I  L  R  *                                     ↓
                ICS                 attC site
901 gcatctgatgcctaactccgcgttgaagtggacgggttgcgcccgccgctcaactatgcg
     CS
961 ttagatgccct 971
```

Figure 8 Nucleotide sequence and coding region of *aadA4* gene cassette in class 1 integron of *S.* Panama CB3 strain. The conserved core site (CS) and inverse core site (ICS) were boxed. The *attI* site was underlined with a dotted line and the *attC* site was underlined. ORF = open reading frame, * = stop codon. The cassette boundaries were indicated by vertical arrow.



```
                                      attI site
  1 cgatgtttggtgttatggagcagcaacgatgttacgcagcagggcagtcgccctaaaaca

      ↓  CS          ORF
 61 aagttaggcatcttcatgagggtagcggtgaccatcgaaattgggaaccaactatcagag
                   M  R  V  A  V  T  I  E  I  G  N  Q  L  S  E
121 gtgctaagcgtcattgagcgccatctggaatcaacgttgctggccgtgcatttgtacggc
    V  L  S  V  I  E  R  H  L  E  S  T  L  L  A  V  H  L  Y  G
181 tccgcagtggatggcggcctgaagccatacagcgatattgatttgttggttactgtggcc
    S  A  V  D  G  G  L  K  P  Y  S  D  I  D  L  L  V  T  V  A
241 gtaaagcttgatgaaacgacgcggcgagcattgctcaatgaccttatggaggcttcggct
    V  K  L  D  E  T  T  R  R  A  L  L  N  D  L  M  E  A  S  A
301 ttccctggcgagagcgagacgctccgcgctaragaagtgacccttgtcgtggctgaagac
    F  P  G  E  S  E  T  L  R  A  X  E  V  T  L  V  V  A  E  D
361 ataatcccgtggcgttatccggctaagcgcgagctgcaatttggagaatggcagcccaat
    I  I  P  W  R  Y  P  A  K  R  E  L  Q  F  G  E  W  Q  P  N
421 gacattcttgctggtatcttcgagccagccatgatcgacattgatctagctatcctgctt
    D  I  L  A  G  I  F  E  P  A  M  I  D  I  D  L  A  I  L  L
481 acaaaagcaagagaacatagcgttgccttggtaggtccggcagcggaggaattctttgac
    T  K  A  R  E  H  S  V  A  L  V  G  P  A  A  E  E  F  F  D
541 ccggttcttgaacaggatctattcgaggcgctgagggaaaccttgaagctttggaactcg
    P  V  L  E  Q  D  L  F  E  A  L  R  E  T  L  K  L  W  N  S
601 cagcccgactgggccggcgatgagcgaaatgtagggcttacgttgtcccgcatttgttcc
    Q  P  D  W  A  G  D  E  R  N  V  G  L  T  L  S  R  I  C  S
661 agcgcaataaccggcaaaatcgcgccgaaggatgtcgctgccgactgggcaataaaacgc
    S  A  I  T  G  K  I  A  P  K  D  V  A  A  D  W  A  I  K  R
721 ctacctgcccagtatcagcccgtcttacttcaaactaagcaagcttatttgggacaaaaa
    L  P  A  Q  Y  Q  P  V  L  L  Q  T  K  Q  A  Y  L  G  Q  K
781 gaagataacttggcctcacgcgcagatcacttggaagaatttattcgctttgtgaaccgc
    E  D  N  L  A  S  R  A  D  H  L  E  E  F  I  R  F  V  N  R
                                  ICS                  attC site
841 gagatcatcaagtcagttggtaaataatgtctaacaattcgttcaagtcgaacccgcttc
    E  I  I  K  S  V  G  K  *
                          ↓  CS
901 gcggcgcggcttaactcaagcgttagaagc 930
```

Figure 9 Nucleotide sequence and coding region of *aadA2* gene cassette in class 1 integron of *S.* Anatum EC3 strain. The conserved core site (CS) and inverse core site (ICS) were boxed. The *attI* site was underlined with a dotted line and the *attC* site was underlined. ORF = open reading frame, * = stop codon. The cassette boundaries were indicated by vertical arrow.

```
DQ141317        ATGAGGGAAGCGGTGATCGCCGAAGTATCGACTCAACTATCAGAGGTAGTTGGCGTCATC 60
AY126947        ATGAGGGAAGCGGTGATCGCCGAAGTATCGACTCAACTATCAGAGGTAGTTGGCGTCATC 60
DQ388123        ATGAGGGAAGCGGTGATCGCCGAAGTATCGACTCAACTATCAGAGGTAGTTGGCGTCATC 60
AY887066        ATGAGGGAAGCGGTGATCGCCGAAGTATCGACTCAACTATCAGAGGTAGTTGGCGTCATC 60
S. Stanley CC1  ATGAGGGAAGCGGTGATCGCCGAAGTATCGACTCAACTATCAGAGGTAGTTGGCGTCATC 60
                ************************************************************

DQ141317        GAGCGCCATCTCGAACCGACGTTGCTGGCCGTACATTTGTACGGCTCCGCAGTGGATGGC 120
AY126947        GAGCGCCATCTCGAACCGACGTTGCTGGCCGTACATTTGTACGGCTCCGCAGTGGATGGC 120
DQ388123        GAGCGCCATCTCGAACCGACGTTGCTGGCCGTACATTTGTACGGCTCCGCAGTGGATGGC 120
AY887066        GAGCGCCATCTCGAACCGACGTTGCTGGCCGTACATTTGTACGGCTCCGCAGTGGATGGC 120
S. Stanley CC1  GAGCGCCATCTCGAACCGACGTTGCTGGCCGTACATTTGTACGGCTCCGCAGTGGATGGC 120
                ************************************************************

DQ141317        GGCCTGAAGCCACACAGTGATATTGATTTGCTGGTTACGGTGACCGTAAGGCTTGATGAA 180
AY126947        GGCCTGAAGCCACACAGTGATATTGATTTGCTGGTTACGGTGACCGTAAGGCTTGATGAA 180
DQ388123        GGCCTGAAGCCACACAGTGATATTGATTTGCTGGTTACGGTGACCGTAAGGCTTGATGAA 180
AY887066        GGCCTGAAGCCACACAGTGATATTGATTTGCTGGTTACGGTGACCGTAAGGCTTGATGAA 180
S. Stanley CC1  GGCCTGAAGCCACACAGTGATATTGATTTGCTGGTTACGGGGACCGTAAGGCTTGATGAA 180
                **************************************** *******************

DQ141317        ACAACGCGGCGAGCTTTGATCAACGACCTTTTGGAAACTTCGGCTTCCCCTGGAGAGAGC 240
AY126947        ACAACGCGGCGAGCTTTGATCAACGACCTTTTGGAAACTTCGGCTTCCCCTGGAGAGAGC 240
DQ388123        ACAACGCGGCGAGCTTTGATCAACGACCTTTTGGAAACTTCGGCTTCCCCTGGAGAGAGC 240
AY887066        ACAACGCGGCGAGCTTTGATCAACGACCTTTTGGAAACTTCGGCTTCCCCTGGAGAGAGC 240
S. Stanley CC1  ACAACGCGGCGAGCTTTGATCAACGACCTTTTGGAAACTTCGGCTTCCCCTGGAGAGAGC 240
                ************************************************************

DQ141317        GAGATTCTCCGCGCTGTAGAAGTCACCATTGTTGTGCACGACGACATCATTCCGTGGCGT 300
AY126947        GAGATTCTCCGCGCTGTAGAAGTCACCATTGTTGTGCACGACGACATCATTCCGTGGCGT 300
DQ388123        GAGATTCTCCGCGCTGTAGAAGTCACCATTGTTGTGCACGACGACATCATTCCGTGGCGT 300
AY887066        GAGATTCTCCGCGCTGTAGAAGTCACCATTGTTGTGCACGACGACATCATTCCGTGGCGT 300
S. Stanley CC1  GAGATTCTCCGCGCTGTAGAAGTCACCATTGTTGTGCACGACGACATCATTCCGTGGCGT 300
                ************************************************************

DQ141317        TATCCAGCTAAGCGCGAACTGCAATTTGGAGAATGGCAGCGCAATGACATTCTTGCAGGT 360
AY126947        TATCCAGCTAAGCGCGAACTGCAATTTGGAGAATGGCAGCGCAATGACATTCTTGCAGGT 360
DQ388123        TATCCAGCTAAGCGCGAACTGCAATTTGGAGAATGGCAGCGCAATGACATTCTTGCAGGT 360
AY887066        TATCCAGCTAAGCGCGAACTGCAATTTGGAGAATGGCAGCGCAATGACATTCTTGCAGGT 360
S. Stanley CC1  TATCCAGCTAAGCGCGAACTGCAATTTGGAGAATGGCAGCGCAATGACATTCTTGCAGGT 360
                ************************************************************

DQ141317        ATCTTCGAGCCAGCCACGATCGACATTGATCTGGCTATCTTGCTGACAAAAGCAAGAGAA 420
AY126947        ATCTTCGAGCCAGCCACGATCGACATTGATCTGGCTATCTTGCTGACAAAAGCAAGAGAA 420
DQ388123        ATCTTCGAGCCAGCCACGATCGACATTGATCTGGCTATCTTGCTGACAAAAGCAAGAGAA 420
AY887066        ATCTTCGAGCCAGCCACGATCGACATTGATCTGGCTATCTTGCTGACAAAAGCAAGAGAA 420
S. Stanley CC1  ATCTTCGAGCCAGCCACGATCGACATTGATCTGGCTATCTTGCTGACAAAAGCAAGAGAA 420
                ************************************************************

DQ141317        CATAGCGTTGCCTTGGTAGGTCCAGCGGCGGAGGAACTCTTTGATCCGGTTCCTGAACAG 480
AY126947        CATAGCGTTGCCTTGGTAGGTCCAGCGGCGGAGGAACTCTTTGATCCGGTTCCTGAACAG 480
DQ388123        CATAGCGTTGCCTTGGTAGGTCCAGCGGCGGAGGAACTCTTTGATCCGGTTCCTGAACAG 480
AY887066        CATAGCGTTGCCTTGGTAGGTCCAGCGGCGGAGGAACTCTTTGATCCGGTTCCTGAACAG 480
S. Stanley CC1  CATAGCGTTGCCTTGGTAGGTCCAGCGGCGGAGGAACTCTTTGATCCGGTTCCTGAACAG 480
                ************************************************************

DQ141317        GATCTATTTGAGGCGCTAAATGAAACCTTAACGCTATGGAACTCGCCGCCCGACTGGGCT 540
AY126947        GATCTATTTGAGGCGCTAAATGAAACCTTAACGCTATGGAACTCGCCGCCCGACTGGGCT 540
DQ388123        GATCTATTTGAGGCGCTAAATGAAACCTTAACGCTATGGAACTCGCCGCCCGACTGGGCT 540
AY887066        GATCTATTTGAGGCGCTAAATGAAACCTTAACGCTATGGAACTCGCCGCCCGACTGGGCT 540
S. Stanley CC1  GATCTATTTGAGGCGCTAAATGAAACCTTAACGCTATGGAACTCGCCGCCCGACTGGGCT 540
                ************************************************************

DQ141317        GGCGATGAGCGAAATGTAGTGCTTACGTTGTCCCGCATTTGGTACAGCGCAGTAACCGGC 600
AY126947        GGCGATGAGCGAAATGTAGTGCTTACGTTGTCCCGCATTTGGTACAGCGCAGTAACCGGC 600
DQ388123        GGCGATGAGCGAAATGTAGTGCTTACGTTGTCCCGCATTTGGTACAGCGCAGTAACCGGC 600
AY887066        GGCGATGAGCGAAATGTAGTGCTTACGTTGTCCCGCATTTGGTACAGCGCAGTAACCGGC 600
S. Stanley CC1  GGCGATGAGCGAAATGTAGTGCTTACGTTGTCCCGCATTTGGTCCAGCGCAGAAACCGGC 600
                ****************************************** ********* *******
```

```
DQ141317        AAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAATGGAGCGCCTGCCGGCCCAGTAT 660
AY126947        AAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAATGGAGCGCCTGCCGGCCCAGTAT 660
DQ388123        AAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAATGGAGCGCCTGCCGGCCCAGTAT 660
AY887066        AAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAATGGAGCGCCTGCCGGCCCAGTAT 660
S. Stanley CC1  AAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAAAAGAGCGCCTGCCGGCCCAGTAT 660
                ************************************  **********************

DQ141317        CAGCCCGTCATACTTGAAGCTAGACAGGCTTATCTTGGACAAGAAGAAGATCGCTTGGCC 720
AY126947        CAGCCCGTCATACTTGAAGCTAGACAGGCTTATCTTGGACAAGAAGAAGATCGCTTGGCC 720
DQ388123        CAGCCCGTCATACTTGAAGCTAGACAGGCTTATCTTGGACAAGAAGAAGATCGCTTGGCC 720
AY887066        CAGCCCGTCATACTTGAAGCTAGACAGGCTTATCTTGGACAAGAAGAAGATCGCTTGGCC 720
S. Stanley CC1  CAGCCCGTCATACTTGAAGCTAGACAGGCTTATCTTGGACAAGAAGAAGATCGCTTGGCC 720
                ************************************************************

DQ141317        TCCCGCGCAGATCAGTTGGAAGAATTTGTTCACTACGTGAAAGGCGAGATCACCAAGGTA 780
AY126947        TCCCGCGCAGATCAGTTGGAAGAATTTGTTCACTACGTGAAAGGCGAGATCACCAAGGTA 780
DQ388123        TCCCGCGCAGATCAGTTGGAAGAATTTGTTCACTACGTGAAAGGCGAGATCACCAAGGTA 780
AY887066        TCCCGCGCAGATCAGTTGGAAGAATTTGTTCACTACGTGAAAGGCGAGATCACCAAGGTA 780
S. Stanley CC1  TCCCGCGCAGATCAGTTGGAAGAATTTGTTCACTACGTGAAAGGCGAGATCACCAAGGTA 780
                ************************************************************

DQ141317        GTCGGCAAATAA 792
AY126947        GTCGGCAAATAA 792
DQ388123        GTCGGCAAATAA 792
AY887066        GTCGGCAAATAA 792
S. Stanley CC1  GTCGGCAAATAA 792
                ************
```

Figure 10 Multiple nucleotide sequence alignment of *aadA1* gene between *S.* Stanley CC1 strain and reference strains in GenBank database. AY887066 = *Acinetobacter baumannii*, DQ388123 = *S.* Typhimurium strain H8, DQ141317 = *Klebsiella pneumoniae* and AY126947 *Salmonella enterica* strain iSG001.

```
AY138986        ATGGGTGAATTCTTTCCTGCACAAATTTCCGAGCAGCTATCCCACGCTCGCGGGGTGATC 60
AF364344        ATGGGTGAATTCTTTCCTGCACAAATTTCCGAGCAGCTATCCCACGCTCGCGGGGTGATC 60
Z50802          ATGGGTGAATTCTTTCCTGCACAAATTTCCGAGCAGCTATCCCACGCTCGCGGGGTGATC 60
S. Panama CB2   ATGGGTGAATTCTTTCCTGCACAAGTTTCCGAGCAGCTATCCCACGCTCGCGGGGTGATC 60
AY214164        ATGGGTGAATTTTTCCCTGCACAAGTTTTCAAGCAGCTGTCCCACGCTCGCGCGGTGATC 60
                *********** ** ********* *** * ******* ************* *******

AY138986        GAGCGCCATCTAGCTGCAACGCTGGACACAATCCACCTGTTCGGATCTGCGCTCGATGGA 120
AF364344        GAGCGCCATCTAGCTGCAACGCTGGACACAATCCACCTGTTCGGATCTGCGCTCGATGGA 120
Z50802          GAGCGCCATCTGGCTGCAACGCTGGACACAATCCACCTGTTCGGATCTGCGCTCGATGGA 120
S. Panama CB2   GAGCGCCATCTGGCTGCAACGCTGGACACAATCCACCTGTTCGGATCTGCGCTCGATGGA 120
AY214164        GAGCGCCATCTGGCTGCGACACTGGACACAATCCACCTGTTCGGATCTGCGATCGATGGA 120
                *********** ***** ** ****************************** ********

AY138986        GGGTTGAAGCCGGACAGCAACATCGACTTGCTCGTGACCGTCAGCGCCGCACCTAACGAT 180
AF364344        GGGTTGAAGCCGGACAGCAACATCGACTTGCTCGTGACCGTCAGCGCCGCACCTAACGAT 180
Z50802          GGGTTGAAGCCGGACAGCGACATCGACTTGCTCGTGACCGTCAGCGCCGCACCTAACGAT 180
S. Panama CB2   GGGTTGAAGCCGGACAGCGACATCGACTTGCTCGTGACCGTCAGCGCCGCACCTAACGAT 180
AY214164        GGGCTGAAGCCGGACAGCGACATAGACTTGCTCGTGACCGTCAGCGCCGCACCTAACGAT 180
                *** ************** **** ************************************


AY138986        TCGCTCCGGCAGGCACTAATGCTCGACCTGCTAAAAGTCTCATCACCGCCAGGCAATGGC 240
AF364344        TCGCTCCGGCAGGCACTAATGCTCGACCTGCTAAAAGTCTCATCACCGCCAGGCAATGGC 240
Z50802          TCGCTCCGGCAGGCACTAATGCTCGACCTGCTAAAAGTCTCATCACCGCCAGGCGATGGC 240
S. Panama CB2   TCGCTAAGGCAGGCACTAATGCTCGACCTGCTAAAAGTCTCATCACCGCCAGGCGATGGC 240
AY214164        TCGCTCCGGCAGGCGCTAATGCTCGATTTGCTGAAAGTCTCATCACCGCCAGGCGATGGC 240
                *****  ******* ***********  **** ********************* *****

AY138986        GGACCATGGCGACCGCTGGAGGTGACTGTTGTCGCTCGAAGCGAAGTAGTGCCCTGGCGC 300
AF364344        GGACCATGGCGACCGCTGGAGGTGACTGTTGTCGCTCGAAGCGAAGTAGTGCCCTGGCGC 300
Z50802          GGACCATGGCGACCGCTGGAGGTGACTGTTGTCGCTCGAAGCGAAGTAGTGCCCTGGCGC 300
S. Panama CB2   GGACCATGGCGACCGCTGGAGGTGACTGTTGTCGCTCGAAGCGAAGTAGTGCCCTGGCGC 300
AY214164        GGAACATGGCGACCGCTGGAGCTAACTGTTGTCGCTCGAAGCGAAGTAGTGCCTTGGCGC 300
                *** ***************** * ***************************** ******
```

```
AY138986        TATCCGGCGCGACGTGGGCTTCAGTTCGGTGAGTGGCTCCGCCACGACATCCTCTCCGGA 360
AF364344        TATCCGGCGCGACGTGGGCTTCAGTTCGGTGAGTGGCTCCGCCACGACATCCTCTCCGGA 360
Z50802          TATCCGGCGATACGTGAGCTTCAGTTCGGTGAGTGGCTCCGCCACGACATCCTCTCCGGA 360
S. Panama CB2   TATCCGGCGCGACGTGAGCTTCAGTTCGGTGAGTGGCTCCGCCACGACATCCTCTCCGGA 360
AY214164        TATCCGGCGCGGCGTGAGCTTCAGTTCGGTGAGTGGCTCCGCCACGACATCCTTTCCGGA 360
                *********   **** ************************************ ******

AY138986        ACGTTCGAGCCTGCCGTTCTGGATCACGATCTTGCGATTTTGCTGACCAAGGCGAGGCAA 420
AF364344        ACGTTCGAGCCTGCCGTTCTGGATCACGATCTTGCGATTTTGCTGACCAAGGCGAGGCAA 420
Z50802          ACGTTCGAGCCTTCCGTTCTGGATCACGATCTTGCGATTTTGCTGACCAAGGCGAGGCAA 420
S. Panama CB2   ACGTTCGAGCCTGCCGTTCTGGATCACGATCTTGCGATTTTGCTGACCAAGGCGAGGCAA 420
AY214164        ACGTTCGAGCCTGCCGTTCTGGATCACGATCTTGCGATTTTGCTGACCAAGGCGAGGCAA 420
                ************ ***********************************************

AY138986        CACAGCCTTGCACTGCTAGGTCCATCCGCAGTCACGTTCTTCGAGCCGGTGCCGAACGAG 480
AF364344        CACAGCCTTGCACTGCTAGGTCCATCCGCAGTCACGTTCTTCGAGCCGGTGCCGAACGAG 480
Z50802          CACAGCCTTGCTCTGCTAGGTCCATCCGCAGTCACGTTCTTCGAGCCGGTGCCGAACGAG 480
S. Panama CB2   CACAGCCTTGCTCTGCTAGGTCCATCCGCAGTCACGTTCTTCGAGCCGGTGCCGAACGAG 480
AY214164        CACAGCCTTGCGCTTCTAGGCCCATCCGCAGCCACGTTTTTCGAGCCGGTGCCGAAGGAG 480
                *********** ** ***** ********** ****** ***************** ***

AY138986        CATTTTTCCAAGGCGCTTTTCGACACGATTGCCCAGTGGAATTCAGAGTCGGATTGGAAG 540
AF364344        CATTTTTCCAAGGCGCTTTTCGACACGATTGCCCAGTGGAATTCAGAGTCGGATTGGAAG 540
Z50802          CATTTTTCCAAGGCGCTTTTCGACACGATTGCCCAGTGGAATTCAGAGTCGGATTGGAAG 540
S. Panama CB2   CATTTTTTCAAGGCGCTTTTCGACACGATTGCCCAGTGGAATTCAGAGTCGGATTGGAAG 540
AY214164        CATTTCTCCAAGGCGCTTTTCGACACTATTGCCCAGTGGAATGCAGAGTCGGATTGGAAG 540
                ***** * ****************** *************** *****************

AY138986        GGTGACGAGCGGAACGTCGTTCTTGCTCTTGCTCGCATTTGGTACAGTGCTTCAACGGGT 600
AF364344        GGTGACGAGCGGAACGTCGTTCTTGCTCTTGCTCGCATTTGGTACAGTGCTTCAACGGGT 600
Z50802          GGTGACGAGCGGAACGTCGTTCTTGCTCTTGCTCGCATTTGGTACAGTGCTTCAACGGGT 600
S. Panama CB2   GGTGACGAGCGGAACGTCGTTCTTGCTCTTGCTCGCATTTGGTACAGGGCTTCAAACGGG 600
AY214164        GGTGACGAGCGGAACGTCGTTCTTGCTCTTGCTCGCATTTGGTACAGCGCTTCAACTGGT 600
                *********************************************** *******  **

AY138986        CTCATTGCTCCTAAGGACGTTGCTGCCGCATGGGTATCGGAGCGTTTGCCTGCCGAGCAT 660
AF364344        CTCATTGCTCCTAAGGACGTTGCTGCCGCATGGGTATCGGAGCGTTTGCCTGCCGAGCAT 660
Z50802          CTCATTGCTCCTAAGGACGTTGCTGCCGCATGGGTATCGGAGCGTTTGCCTGCCGAGCAT 660
S. Panama CB2   CTCATTGCTCCTAAGGACGTTGCTGCCGCATGGGTATCAAAGCGTTTGCCTGCCGAGCAT 660
AY214164        CTCATTGCTCCTAAGGACGTTGCTGCCGCATGGGTATCGGAGCGTTTGCCTGCCGAGCAT 660
                **************************************  ********************

AY138986        CGGCCCATCATTTGCAAGGCACGCGCGGCGTACCTGGGTAGCGAGGACGACGACCTAGCA 720
AF364344        CGGCCCATCATTTGCAAGGCACGCGCGGCGTACCTGGGTAGCGAGGACGACGACCTAGCA 720
Z50802          CGGCCCATCATTTGCAAGGCACGCGCGGCGTACCTGGGTAGCGAGGACGACGACCTAGCA 720
S. Panama CB2   CGGCCCATCATTTGCAAGGCACGCGCGGCGTACCTGGGTAGCGAGGACGACGACCTAGCA 720
AY214164        CGGCCCCTCATCTGCAAGGCACGCGCGGCGTACCTGGGTAGCGAGGACGACGACCTAGCA 720
                ****** **** ************************************************

AY138986        ATGCGCGTCGAAGAGACGGCTGCGTTCGTTCGATATGCCAAAGCAACGATTGAGAGAATC 780
AF364344        ATGCGCGTCGAAGAGACGGCTGCGTTCGTTCGATATGCCAAAGCAACGATTGAGAGAATC 780
Z50802          ATGCGCGTCGAAGAGACGGCTGCGTTCGTTCGATATGCCAAAGCAACGATTGAGAGAATC 780
S. Panama CB2   ATGCGCGTCGAAGAGACGGCTGCGTTCGTTCGATATGCCAAAGCAACGATTGAGAGAATC 780
AY214164        ATGCGCGTCGAAGAGACGGCCGCGTTCGTTCGATATGCCAAAGCAACGATTGAGAGAATC 780
                ******************** ***************************************

AY138986        TTGCGTTGA 789
AF364344        TTGCGTTGA 789
Z50802          TTGCGTTGA 789
S. Panama CB2   TTGCGTTGA 789
AY214164        TTGCGTTGA 789
                *********
```

Figure 11 Multiple nucleotide sequence alignment of *aadA4* gene between *S.* Panama CB2 strain and reference strains in GenBank database. Z50802 = *E. coli*, AY138986 = *A. baumannii*, AF364344 = *A. baumannii* and AY214164 = *E. coli*.

```
AY138986        ATGGGTGAATTCTTTCCTGCACAAATTTCCGAGCAGCTATCCCACGCTCGCGGGGTGATC 60
AF364344        ATGGGTGAATTCTTTCCTGCACAAATTTCCGAGCAGCTATCCCACGCTCGCGGGGTGATC 60
Z50802          ATGGGTGAATTCTTTCCTGCACAAATTTCCGAGCAGCTATCCCACGCTCGCGGGGTGATC 60
S. Panama CB3   ATGGGTGAATTCTTTCCTGCACAAGTTTCCGAGCAGCTATCCCACGCTCGCGGGGTGATC 60
AY214164        ATGGGTGAATTTTTCCCTGCACAAGTTTTCAAGCAGCTGTCCCACGCTCGCGCGGTGATC 60
                *********** ** ********* *** * ******* ************* *******

AY138986        GAGCGCCATCTAGCTGCAACGCTGGACACAATCCACCTGTTCGGATCTGCGCTCGATGGA 120
AF364344        GAGCGCCATCTAGCTGCAACGCTGGACACAATCCACCTGTTCGGATCTGCGCTCGATGGA 120
Z50802          GAGCGCCATCTGGCTGCAACGCTGGACACAATCCACCTGTTCGGATCTGCGCTCGATGGA 120
S. Panama CB3   GAGCGCCATCTGGCTGCAACGCTGGACACAATCCACCTGTTCGGATCTGCGCTCGATGGA 120
AY214164        GAGCGCCATCTGGCTGCGACACTGGACACAATCCACCTGTTCGGATCTGCGATCGATGGA 120
                *********** ***** ** ****************************** ********

AY138986        GGGTTGAAGCCGGACAGCAACATCGACTTGCTCGTGACCGTCAGCGCCGCACCTAACGAT 180
AF364344        GGGTTGAAGCCGGACAGCAACATCGACTTGCTCGTGACCGTCAGCGCCGCACCTAACGAT 180
Z50802          GGGTTGAAGCCGGACAGCGACATCGACTTGCTCGTGACCGTCAGCGCCGCACCTAACGAT 180
S. Panama CB3   GGGTTGAAGCCGGACAGCGACATCGACTTGCTCGTGACCGTCAGCGCCGCACCTAACGAT 180
AY214164        GGGCTGAAGCCGGACAGCGACATAGACTTGCTCGTGACCGTCAGCGCCGCACCTAACGAT 180
                *** ************** **** ************************************

AY138986        TCGCTCCGGCAGGCACTAATGCTCGACCTGCTAAAAGTCTCATCACCGCCAGGCAATGGC 240
AF364344        TCGCTCCGGCAGGCACTAATGCTCGACCTGCTAAAAGTCTCATCACCGCCAGGCAATGGC 240
Z50802          TCGCTCCGGCAGGCACTAATGCTCGACCTGCTAAAAGTCTCATCACCGCCAGGCGATGGC 240
S. Panama CB3   TCGCTAAGGCAGGCACTAGTGCTCGACCTGCTAAAAGTCTCATCACCGCCAGGCGATGGC 240
AY214164        TCGCTCCGGCAGGCGCTAATGCTCGATTTGCTGAAAGTCTCATCACCGCCAGGCGATGGC 240
                *****  ******* *** *******  **** ********************* *****

AY138986        GGACCATGGCGACCGCTGGAGGTGACTGTTGTCGCTCGAAGCGAAGTAGTGCCCTGGCGC 300
AF364344        GGACCATGGCGACCGCTGGAGGTGACTGTTGTCGCTCGAAGCGAAGTAGTGCCCTGGCGC 300
Z50802          GGACCATGGCGACCGCTGGAGGTGACTGTTGTCGCTCGAAGCGAAGTAGTGCCCTGGCGC 300
S. Panama CB3   GGACCATGGCGACCGCTGGAGGTGACTGTTGTCGCTCGAAGCGAAGTAGTGCCCTGGCGC 300
AY214164        GGAACATGGCGACCGCTGGAGCTAACTGTTGTCGCTCGAAGCGAAGTAGTGCCTTGGCGC 300
                *** ***************** * ***************************** ******

AY138986        TATCCGGCGCGACGTGGGCTTCAGTTCGGTGAGTGGCTCCGCCACGACATCCTCTCCGGA 360
AF364344        TATCCGGCGCGACGTGGGCTTCAGTTCGGTGAGTGGCTCCGCCACGACATCCTCTCCGGA 360
Z50802          TATCCGGCGATACGTGAGCTTCAGTTCGGTGAGTGGCTCCGCCACGACATCCTCTCCGGA 360
S. Panama CB3   TATCCGGCGCGACGTGAGCTTCAGTTCGGTGAGTGGCTCCGCCACGACATCCTCTCCGGA 360
AY214164        TATCCGGCGCGGCGTGAGCTTCAGTTCGGTGAGTGGCTCCGCCACGACATCCTTTCCGGA 360
                *********   **** ************************************ ******

AY138986        ACGTTCGAGCCTGCCGTTCTGGATCACGATCTTGCGATTTTGCTGACCAAGGCGAGGCAA 420
AF364344        ACGTTCGAGCCTGCCGTTCTGGATCACGATCTTGCGATTTTGCTGACCAAGGCGAGGCAA 420
Z50802          ACGTTCGAGCCTTCCGTTCTGGATCACGATCTTGCGATTTTGCTGACCAAGGCGAGGCAA 420
S. Panama CB3   ACGTTCGAGCCTGCCGTTCTGGATCACGATCTTGCGATTTTGCTGACCAAGGCGAGGCAA 420
AY214164        ACGTTCGAGCCTGCCGTTCTGGATCACGATCTTGCGATTTTGCTGACCAAGGCGAGGCAA 420
                ************ ***********************************************

AY138986        CACAGCCTTGCACTGCTAGGTCCATCCGCAGTCACGTTCTTCGAGCCGGTGCCGAACGAG 480
AF364344        CACAGCCTTGCACTGCTAGGTCCATCCGCAGTCACGTTCTTCGAGCCGGTGCCGAACGAG 480
Z50802          CACAGCCTTGCTCTGCTAGGTCCATCCGCAGTCACGTTCTTCGAGCCGGTGCCGAACGAG 480
S. Panama CB3   CACAGCCTTGCTCTGCTAGGTCCATCCGCAGTCACGTTCTTCGAGCCGGTGCCGAACGAG 480
AY214164        CACAGCCTTGCGCTTCTAGGCCCATCCGCAGCCACGTTTTTCGAGCCGGTGCCGAAGGAG 480
                *********** ** ***** ********** ****** ***************** ***

AY138986        CATTTTTCCAAGGCGCTTTTCGACACGATTGCCCAGTGGAATTCAGAGTCGGATTGGAAG 540
AF364344        CATTTTTCCAAGGCGCTTTTCGACACGATTGCCCAGTGGAATTCAGAGTCGGATTGGAAG 540
Z50802          CATTTTTCCAAGGCGCTTTTCGACACGATTGCCCAGTGGAATTCAGAGTCGGATTGGAAG 540
S. Panama CB3   CATTTTTTCAAGGCGCTTTTCGACACGATTGCCCAGTGGAATTCAGAGTCGGATTGGAAG 540
AY214164        CATTTCTCCAAGGCGCTTTTCGACACTATTGCCCAGTGGAATGCAGAGTCGGATTGGAAG 540
                ***** * ****************** *************** *****************

AY138986        GGTGACGAGCGGAACGTCGTTCTTGCTCTTGCTCGCATTTGGTACAGTGCTTCAACGGGT 600
AF364344        GGTGACGAGCGGAACGTCGTTCTTGCTCTTGCTCGCATTTGGTACAGTGCTTCAACGGGT 600
Z50802          GGTGACGAGCGGAACGTCGTTCTTGCTCTTGCTCGCATTTGGTACAGTGCTTCAACGGGT 600
S. Panama CB3   GGTGACGAGCGGAACGTCGTTCTTGCTCTTGCTCGCATTTGGTACAGGGCTTCAAACGGG 600
AY214164        GGTGACGAGCGGAACGTCGTTCTTGCTCTTGCTCGCATTTGGTACAGCGCTTCAACTGGT 600
                *********************************************** *******  ** 
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AY138986        CTCATTGCTCCTAAGGACGTTGCTGCCGCATGGGTATCGGAGCGTTTGCCTGCCGAGCAT 660
AF364344        CTCATTGCTCCTAAGGACGTTGCTGCCGCATGGGTATCGGAGCGTTTGCCTGCCGAGCAT 660
Z50802          CTCATTGCTCCTAAGGACGTTGCTGCCGCATGGGTATCGGAGCGTTTGCCTGCCGAGCAT 660
S. Panama CB3   CTCATTGCTCCTAAGGACGTTGCTGCCGCATGGGTATCAAAGCGTTTGCCTGCCGAGCAT 660
AY214164        CTCATTGCTCCTAAGGACGTTGCTGCCGCATGGGTATCGGAGCGTTTGCCTGCCGAGCAT 660
                **************************************  ********************

AY138986        CGGCCCATCATTTGCAAGGCACGCGCGGCGTACCTGGGTAGCGAGGACGACGACCTAGCA 720
AF364344        CGGCCCATCATTTGCAAGGCACGCGCGGCGTACCTGGGTAGCGAGGACGACGACCTAGCA 720
Z50802          CGGCCCATCATTTGCAAGGCACGCGCGGCGTACCTGGGTAGCGAGGACGACGACCTAGCA 720
S. Panama CB3   CGGCCCATCATTTGCAAGGCACGCGCGGCGTACCTGGGTAGCGAGGACGACGACCTAGCA 720
AY214164        CGGCCCCTCATCTGCAAGGCACGCGCGGCGTACCTGGGTAGCGAGGACGACGACCTAGCA 720
                ****** **** ************************************************

AY138986        ATGCGCGTCGAAGAGACGGCTGCGTTCGTTCGATATGCCAAAGCAACGATTGAGAGAATC 780
AF364344        ATGCGCGTCGAAGAGACGGCTGCGTTCGTTCGATATGCCAAAGCAACGATTGAGAGAATC 780
Z50802          ATGCGCGTCGAAGAGACGGCTGCGTTCGTTCGATATGCCAAAGCAACGATTGAGAGAATC 780
S. Panama CB3   ATGCGCGTCGAAGAGACGGCTGCGTTCGTTCGATATGCCAAAGCAACGATTGAGAGAATC 780
AY214164        ATGCGCGTCGAAGAGACGGCCGCGTTCGTTCGATATGCCAAAGCAACGATTGAGAGAATC 780
                ******************** ***************************************

AY138986        TTGCGTTGA 789
AF364344        TTGCGTTGA 789
Z50802          TTGCGTTGA 789
S. Panama CB3   TTGCGTTGA 789
AY214164        TTGCGTTGA 789
                *********
```

Figure 12 Multiple nucleotide sequence alignment of *aadA4* gene between *S.* Panama CB3 strain and reference strains in GenBank database. Z50802 = *E. coli*, AY138986 = *A. baumannii*, AF364344 = *A. baumannii* and AY214164 = *E. coli*.

```
PAU12338        ------------GTGACCATCGAAATTTCGAACCAACTATCAGAGGTGCTAAGCGTCATT 48
L06822          ------------GTGACCATCGAAATTTCGAACCAACTATCAGAGGTGCTAAGCGTCATT 48
AY125352        ATGAGGGTAGCGGTGACCATCGAAATTTCGAACCAACTATCAGAGGTGCTAAGCGTCATT 60
DQ219465        ATGAGGGTAGCGGTGACCATCGAAATTTCGAACCAACTATCAGAGGTGCTAAGCGTCATT 60
S. Anatum EC3   ATGAGGGTAGCGGTGACCATCGAAATTGGGAACCAACTATCAGAGGTGCTAAGCGTCATT 60
                            ***************  *******************************

PAU12338        GAGCGCCATCTGGAATCAACGTTGCTGGCCGTGCATTTGTACGGCTCCGCAGTGGATGGC 108
L06822          GAGCGCCATCTGGAATCAACGTTGCTGGCCGTGCATTTGTACGGCTCCGCAGTGGATGGC 108
AY125352        GAGCGCCATCTGGAATCAACGTTGCTGGCCGTGCATTTGTACGGCTCCGCAGTGGATGGC 120
DQ219465        GAGCGCCATCTGGAATCAACGTTGCTGGCCGTGCATTTGTACGGCTCCGCAGTGGATGGC 120
S. Anatum EC3   GAGCGCCATCTGGAATCAACGTTGCTGGCCGTGCATTTGTACGGCTCCGCAGTGGATGGC 120
                ************************************************************

PAU12338        GGCCTGAAGCCATACAGCGATATTGATTTGTTGGTTACTGTGGCCGTAAAGCTTGATGAA 168
L06822          GGCCTGAAGCCATACAGCGATATTGATTTGTTGGTTACTGTGGCCGTAAAGCTTGATGAA 168
AY125352        GGCCTGAAGCCATACAGCGATATTGATTTGTTGGTTACTGTGGCCGTAAAGCTTGATGAA 180
DQ219465        GGCCTGAAGCCATACAGCGATATTGATTTGTTGGTTACTGTGGCCGTAAAGCTTGATGAA 180
S. Anatum EC3   GGCCTGAAGCCATACAGCGATATTGATTTGTTGGTTACTGTGGCCGTAAAGCTTGATGAA 180
                ************************************************************

PAU12338        ACGACGCGGCGAGCATTGCTCAATGACCTTATGGAGGCTTCGGCTTTCCCTGGCGAGAGC 228
L06822          ACGACGCGGCGAGCATTGCTCAATGACCTTATGGAGGCTTCGGCTTTCCCTGGCGAGAGC 228
AY125352        ACGACGCGGCGAGCATTGCTCAATGACCTTATGGAGGCTTCGGCTTTCCCTGGCGAGAGC 240
DQ219465        ACGACGCGGCGAGCATTGCTCAATGACCTTATGGAGGCTTCGGCTTTCCCTGGCGAGAGC 240
S. Anatum EC3   ACGACGCGGCGAGCATTGCTCAATGACCTTATGGAGGCTTCGGCTTTCCCTGGCGAGAGC 240
                ************************************************************

PAU12338        GAGACGCTCCGCGCTATAGAAGTCACCCTTGTCGTGCATGACGACATCATCCCGTGGCGT 288
L06822          GAGACGCTCCGCGCTATAGAAGTCACCCTTGTCGTGCATGACGACATCATCCCGTGGCGT 288
AY125352        GAGACGCTCCGCGCTATAGAAGTCACCCTTGTCGTGCATGACGACATCATCCCGTGGCGT 300
DQ219465        GAGACGCTCCGCGCTATAGAAGTCACCCTTGTCGTGCATGACGACATCATCCCGTGGCGT 300
S. Anatum EC3   GAGACGCTCCGCGCTARAGAAGTGACCCTTGTCGTGGCTGAAGACATAATCCCGTGGCGT 300
                **************** ****** ************  *** ***** ************
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PAU12338        TATCCGGCTAAGCGCGAGCTGCAATTTGGAGAATGGCAGCGCAATGACATTCTTGCGGGT 348
L06822          TATCCGGCTAAGCGCGAGCTGCAATTTGGAGAATGGCAGCGCAATGACATTCTTGCGGGT 348
AY125352        TATCCGGCTAAGCGCGAGCTGCAATTTGGAGAATGGCAGCGCAATGACATTCTTGCGGGT 360
DQ219465        TATCCGGCTAAGCGCGAGCTGCAATTTGGAGAATGGCAGCGCAATGACATTCTTGCGGGT 360
S. Anatum EC3   TATCCGGCTAAGCGCGAGCTGCAATTTGGAGAATGGCAGCCCAATGACATTCTTGCTGGT 360
                **************************************** *************** ***

PAU12338        ATCTTCGAGCCAGCCATGATCGACATTGATCTAGCTATCCTGCTTACAAAAGCAAGAGAA 408
L06822          ATCTTCGAGCCAGCCATGATCGACATTGATCTAGCTATCCTGCTTACAAAAGCAAGAGAA 408
AY125352        ATCTTCGAGCCAGCCATGATCGACATTGATCTAGCTATCCTGCTTACAAAAGCAAGAGAA 420
DQ219465        ATCTTCGAGCCAGCCATGATCGACATTGATCTAGCTATCCTGCTTACAAAAGCAAGAGAA 420
S. Anatum EC3   ATCTTCGAGCCAGCCATGATCGACATTGATCTAGCTATCCTGCTTACAAAAGCAAGAGAA 420
                ************************************************************

PAU12338        CATAGCGTTGCCTTGGTAGGTCCGGCAGCGGAGGAATTCTTTGACCCGGTTCCTGAACAG 468
L06822          CATAGCGTTGCCTTGGTAGGTCCGGCAGCGGAGGAATTCTTTGACCCGGTTCCTGAACAG 468
AY125352        CATAGCGTTGCCTTGGTAGGTCCGGCAGCGGAGGAATTCTTTGACCCGGTTCCTGAACAG 480
DQ219465        CATAGCGTTGCCTTGGTAGGTCCGGCAGCGGAGGAATTCTTTGACCCGGTTCCTGAACAG 480
S. Anatum EC3   CATAGCGTTGCCTTGGTAGGTCCGGCAGCGGAGGAATTCTTTGACCCGGTTCTTGAACAG 480
                **************************************************** *******

PAU12338        GATCTATTCGAGGCGCTGAGGGAAACCTTGAAGCTATGGAACTCGCAGCCCGACTGGGCC 528
L06822          GATCTATTCGAGGCGCTGAGGGAAACCTTGAAGCTATGGAACTCGCAGCCCGACTGGGCC 528
AY125352        GATCTATTCGAGGCGCTGAGGGAAACCTTGAAGCTATGGAACTCGCAGCCCGACTGGGCC 540
DQ219465        GATCTATTCGAGGCGCTGAGGGAAACCTTGAAGCTATGGAACTCGCAGCCCGACTGGGCC 540
S. Anatum EC3   GATCTATTCGAGGCGCTGAGGGAAACCTTGAAGCTTTGGAACTCGCAGCCCGACTGGGCC 540
                *********************************** ************************

PAU12338        GGCGATGAGCGAAATGTAGTGCTTACGTTGTCCCGCATTTGGTACAGCGCAATAACCGGC 588
L06822          GGCGATGAGCGAAATGTAGTGCTTACGTTGTCCCGCATTTGGTACAGCGCAATAACCGGC 588
AY125352        GGCGATGAGCGAAATGTAGTGCTTACGTTGTCCCGCATTTGGTACAGCGCAATAACCGGC 600
DQ219465        GGCGATGAGCGAAATGTAGTGCTTACGTTGTCCCGCATTTGGTACAGCGCAATAACCGGC 600
S. Anatum EC3   GGCGATGAGCGAAATGTAGGGCTTACGTTGTCCCGCATTTGTTCCAGCGCAATAACCGGC 600
                ******************* ********************* * ****************

PAU12338        AAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAATAAAACGCCTACCTGCCCAGTAT 648
L06822          AAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAATAAAACGCCTACCTGCCCAGTAT 648
AY125352        AAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAATAAAACGCCTACCTGCCCAGTAT 660
DQ219465        AAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAATAAAACGCCTACCTGCCCAGTAT 660
S. Anatum EC3   AAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAATAAAACGCCTACCTGCCCAGTAT 660
                ************************************************************

PAU12338        CAGCCCGTCTTACTTGAAGCTAAGCAAGCTTATCTGGGACAAAAAGAAGATCACTTGGCC 708
L06822          CAGCCCGTCTTACTTGAAGCTAAGCAAGCTTATCTGGGACAAAAAGAAGATCACTTGGCC 708
AY125352        CAGCCCGTCTTACTTGAAGCTAAGCAAGCTTATCTGGGACAAAAAGAAGATCACTTGGCC 720
DQ219465        CAGCCCGTCTTACTTGAAGCTAAGCAAGCTTATCTGGGACAAAAAGAAGATCACTTGGCC 720
S. Anatum EC3   CAGCCCGTCTTACTTCAAACTAAGCAAGCTTATTTGGGACAAAAAGAAGATAACTTGGCC 720
                *************** ** ************** ***************** ********

PAU12338        TCACGCGCAGATCACTTGGAAGAATTTATTCGCTTTGTGAAAGGCGAGATCATCAAGTCA 768
L06822          TCACGCGCAGATCACTTGGAAGAATTTATTCGCTTTGTGAAAGGCGAGATCATCAAGTCA 768
AY125352        TCACGCGCAGATCACTTGGAAGAATTTATTCGCTTTGTGAAAGGCGAGATCATCAAGTCA 780
DQ219465        TCACGCGCAGATCACTTGGAAGAATTTATTCGCTTTGTGAAAGGCGAGATCATCAAGTCA 780
S. Anatum EC3   TCACGCGCAGATCACTTGGAAGAATTTATTCGCTTTGTGAACCGCGAGATCATCAAGTCA 780
                *****************************************  *****************

PAU12338        GTTGGTAAATGA 780
L06822          GTTGGTAAATGA 780
AY125352        GTTGGTAAATGA 792
DQ219465        GTTGGTAAATGA 792
S. Anatum EC3   GTTGGTAAATAA 792
                ********** *
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Figure 13 Multiple nucleotide sequence alignment of *aadA4* gene between *S.* Anatum EC3 strain and reference strains in GenBank database. DQ219465 = *Pseudomonas aeruginosa*, PAU12338 = *P. aeruginosa*, L06822 = *E. coli* and AY125352 = *S. enterica* subsp. *enterica*.

```
CAA26199          MREAVIAEVSTQLSEVVGVIERHLEPTLLAVHLYGSAVDGGLKPHSDIDLLVTVTVRLDE 60
BAE66662          MREAVIAEVSTQLSEVVGVIERHLEPTLLAVHLYGSAVDGGLKPHSDIDLLVTVTVRLDE 60
AAA93350          MREAVIAEVSTQLSEVVGVIERHLEPTLLAVHLYGSAVDGGLKPHSDIDLLVTVTVRLDE 60
AAX97761          MGEAVIAEVSTQLSEVVGVIERHLEPTLLAVHLYGSAVDGGLKPHSDIDLLVTVTVRLDE 60
S. Stanley CC1    MREAVIAEVSTQLSEVVGVIERHLEPTLLAVHLYGSAVDGGLKPHSDIDLLVTGTVRLDE 60
                  * *************************************************** ******

CAA26199          TTRRALINDLLETSASPGESEILRAVEVTIVVHDDIIPWRYPAKRELQFGEWQRNDILAG 120
BAE66662          TTRRALINDLLETSASPGESEILRAVEVTIVVHDDIIPWRYPAKRELQFGEWQRNDILAG 120
AAA93350          TTRRALINDLLETSASPGESEILRAVEVTIVVHDDIIPWRYPAKRELQFGEWQRNDILAG 120
AAX97761          TTRRALINDLLETSASPGESEILRAVEVTIVVHDDIIPWRYPAKRELQFGEWQRNDILAG 120
S. Stanley CC1    TTRRALINDLLETSASPGESEILRAVEVTIVVHDDIIPWRYPAKRELQFGEWQRNDILAG 120
                  ************************************************************

CAA26199          IFEPATIDIDLAILLTKAREHSVALVGPAAEELFDPVPEQDLFEALNETLTLWNSPPDWA 180
BAE66662          IFEPATIDIDLAILLTKAREHSVALVGPAAEELFDPVPEQDLFEALNETLTLWNSPPDWA 180
AAA93350          IFEPATIDIDLAILLTKAREHSVALVGPAAEELFDPVPEQDLFEALNETLTLWNSPPDWA 180
AAX97761          IFEPATIDIDLAILLTKAREHSVALVGPAAEELFDPVPEQDLFEALNETLTLWNSPPDWA 180
S. Stanley CC1    IFEPATIDIDLAILLTKAREHSVALVGPAAEELFDPVPEQDLFEALNETLTLWNSPPDWA 180
                  ************************************************************


CAA26199          GDERNVVLTLSRIWYSAVTGKIAPKDVAADWAMERLPAQYQPVILEARQAYLGQEEDRLA 240
BAE66662          GDERNVVLTLSRIWYSAVTGKIAPKDVAADWAMERLPAQYQPVILEARQAYLGQEEDRLA 240
AAA93350          GDERNVVLTLSRIWYSAVTGKIAPKEVAADWAMERLPAQYQPVIREARQAYLGQEEDRLA 240
AAX97761          GDERNVVLTLSRIWYSAVTGKIAPKDVAADWAMERLPAQYQPVILEARQAYLGQEEDRLA 240
S. Stanley CC1    GDERNVVLTLSRIWSSAETGKIAPKDVAADWAKERLPAQYQPVILEARQAYLGQEEDRLA 240
                  ************** ** *******:****** *********** ***************

CAA26199          SRADQLEEFVHYVKGEITKVVGK 263
BAE66662          SRADQLEEFVHYVKGEITKSVGK 263
AAA93350          SRADQLEEFVHYVKGEITKVVGK 263
AAX97761          SRADQLEEFVHYVKGEITKVVGK 263
S. Stanley CC1    SRADQLEEFVHYVKGEITKVVGK 263
                  ******************* ***
```

Figure 14 Comparison of amino acid sequence of AadA1 between *S.* Stanley CC1 strain and reference strains in GenBank database. Identical amino acid residues were indicated by asterisks. Functionally equivalent amino acid substitution were indicated by colons. The highlight letters were different amino acid of AadA1 from others.

```
CAB41476            MGEFFPAQISEQLSHARGVIERHLAATLDTIHLFGSALDGGLKPDSDIDLLVTVSAAPND 60
AAN34365            MGEFFPAQISEQLSHARGVIERHLAATLDTIHLFGSALDGGLKPDSNIDLLVTVSAAPND 60
S. Panama CB2       MGEFFPAQVSEQLSHARGVIERHLAATLDTIHLFGSALDGGLKPDSDIDLLVTVSAAPND 60
AAT36683            MGEFFPAQVFKQLSHARAVIERHLAATLDTIHLFGSAIDGGLKPDSDIDLFVTVSAAPND 60
AAN41432            MGEFFPAQVFKQLSHARAVVERHLAATLDTIHLFGSAIDGGLKPDSDIDLLVTVSAAPND 60
                    ********: :******.*:*****************:********:***:*********

CAB41476            SLRQALMLDLLKVSSPPGDGGPWRPLEVTVVARSEVVPWRYPAIRELQFGEWLRHDILSG 120
AAN34365            SLRQALMLDLLKVSSPPGNGGPWRPLEVTVVARSEVVPWRYPARRGLQFGEWLRHDILSG 120
S. Panama CB2       SLRQALMLDLLKVSSPPGDGGPWRPLEVTVVARSEVVPWRYPARRELQFGEWLRHDILSG 120
AAT36683            SLRQALMLDLLKVSSPPGDGGTWRPLELTVVARSEVVPWRYPARRELQFGEWLRHDILSG 120
AAN41432            SLRQALMLDLLKVSSPPGDGGTWRPLELTVVARSEVVPWRYPARRELQFGEWLRHDILSG 120
                    ******************:**.*****:*************** * **************

CAB41476            TFEPSVLDHDLAILLTKARQHSLALLGPSAVTFFEPVPNEHFSKALFDTIAQWNSESDWK 180
AAN34365            TFEPAVLDHDLAILLTKARQHSLALLGPSAVTFFEPVPNEHFSKALFDTIAQWNSESDWK 180
S. Panama CB2       TFEPAVLDHDLAILLTKARQHSLALLGPSAVTFFEPVPNEHFFKALFDTIAQWNSESDWK 180
AAT36683            TFEPAVLDHDLAILLTKARQHSLALLGPSAATFFEPVPKEHFSKALFDTIAQWNAESDWK 180
AAN41432            TFEPAVLDHDLAILLTKARQHSLALLGPSAATFFEPVPKEHFSKALFDTIAQWNAESDWK 180
                    ****:*************************.*******:*** ***********:*****
CAB41476            GDERNVVLALARIWYSASTGLIAPKDVAAAWVSERLPAEHRPIICKARAAYLGSEDDDLA 240
AAN34365            GDERNVVLALARIWYSASTGLIAPKDVAAAWVSERLPAEHRPIICKARAAYLGSEDDDLA 240
S. Panama CB2       GDERNVVLALARIWYRASNGLIAPKDVAAAWVSKRLPAEHRPIICKARAAYLGSEDDDLA 240
AAT36683            GDERNVVLALARIWYSASTGLIAPKDVAAAWVSERLPAEHRPLICKARAAYLGSEDDDLA 240
AAN41432            GDERNVVLALARIWYSASTGLIAPKDVAAAWVSERLPAEHRPLICKARAAYLGSEDDDLA 240
                    *************** **.**************:********:*****************

CAB41476            MRVEETAAFVRYAKATIERILR 262
AAN34365            MRVEETAAFVRYAKATIERILR 262
S. Panama CB2       MRVEETAAFVRYAKATIERILR 262
AAT36683            MRVEETAAFVRYAKATIERILR 262
AAN41432            MRVEETAAFVRYAKATIERILR 262
                    **********************
```

Figure 15 Comparison of amino acid sequence of AadA4 between *S.* Panama CB2 strain and reference strains in GenBank database. Identical amino acid residues were indicated by asterisks. Functionally equivalent amino acid substitution were indicated by colons. The highlight letters were different amino acid of AadA4 from others.

```
CAB41476           MGEFFPAQISEQLSHARGVIERHLAATLDTIHLFGSALDGGLKPDSDIDLLVTVSAAPND 60
AAN34365           MGEFFPAQISEQLSHARGVIERHLAATLDTIHLFGSALDGGLKPDSNIDLLVTVSAAPND 60
S. Panama CB3      MGEFFPAQVSEQLSHARGVIERHLAATLDTIHLFGSALDGGLKPDSDIDLLVTVSAAPND 60
AAN41432           MGEFFPAQVFKQLSHARAVVERHLAATLDTIHLFGSAIDGGLKPDSDIDLLVTVSAAPND 60
AAT36683           MGEFFPAQVFKQLSHARAVIERHLAATLDTIHLFGSAIDGGLKPDSDIDLFVTVSAAPND 60
                   ********: :******.*:*****************:********:***:*********

CAB41476           SLRQALMLDLLKVSSPPGDGGPWRPLEVTVVARSEVVPWRYPAIRELQFGEWLRHDILSG 120
AAN34365           SLRQALMLDLLKVSSPPGNGGPWRPLEVTVVARSEVVPWRYPARRGLQFGEWLRHDILSG 120
S. Panama CB3      SLRQALVLDLLKVSSPPGDGGPWRPLEVTVVARSEVVPWRYPARRELQFGEWLRHDILSG 120
AAN41432           SLRQALMLDLLKVSSPPGDGGTWRPLELTVVARSEVVPWRYPARRELQFGEWLRHDILSG 120
AAT36683           SLRQALMLDLLKVSSPPGDGGTWRPLELTVVARSEVVPWRYPARRELQFGEWLRHDILSG 120
                   ******:***********:**.*****:*************** * **************

CAB41476           TFEPSVLDHDLAILLTKARQHSLALLGPSAVTFFEPVPNEHFSKALFDTIAQWNSESDWK 180
AAN34365           TFEPAVLDHDLAILLTKARQHSLALLGPSAVTFFEPVPNEHFSKALFDTIAQWNSESDWK 180
S. Panama CB3      TFEPAVLDHDLAILLTKARQHSLALLGPSAVTFFEPVPNEHFFKALFDTIAQWNSESDWK 180
AAN41432           TFEPAVLDHDLAILLTKARQHSLALLGPSAATFFEPVPKEHFSKALFDTIAQWNAESDWK 180
AAT36683           TFEPAVLDHDLAILLTKARQHSLALLGPSAATFFEPVPKEHFSKALFDTIAQWNAESDWK 180
                   ****:*************************.*******:*** ***********:*****

CAB41476           GDERNVVLALARIWYSASTGLIAPKDVAAAWVSERLPAEHRPIICKARAAYLGSEDDDLA 240
AAN34365           GDERNVVLALARIWYSASTGLIAPKDVAAAWVSERLPAEHRPIICKARAAYLGSEDDDLA 240
S. Panama CB3      GDERNVVLALARIWYRASNGLIAPKDVAAAWVSKRLPAEHRPIICKARAAYLGSEDDDLA 240
AAN41432           GDERNVVLALARIWYSASTGLIAPKDVAAAWVSERLPAEHRPLICKARAAYLGSEDDDLA 240
AAT36683           GDERNVVLALARIWYSASTGLIAPKDVAAAWVSERLPAEHRPLICKARAAYLGSEDDDLA 240
                   *************** **.**************:********:*****************

CAB41476           MRVEETAAFVRYAKATIERILR 262
AAN34365           MRVEETAAFVRYAKATIERILR 262
S. Panama CB3      MRVEETAAFVRYAKATIERILR 262
AAN41432           MRVEETAAFVRYAKATIERILR 262
AAT36683           MRVEETAAFVRYAKATIERILR 262
                   **********************
```

Figure 16 Comparison of amino acid sequence of AadA4 between *S.* Panama CB3 strain and reference strains in GenBank database. Identical amino acid residues were indicated by asterisks. Functionally equivalent amino acid substitution were indicated by colons. The highlight letters were different amino acid of AadA4 from others.

```
ZP_00717087        MRVAVTIEISNQLSEVLSVIERHLESTLLAVHLYGSAVDGGLKPYSDIDLLVTVAVKLDE 60
ZP_01175305        MRVAVTIEISNQLSEVLSVIERHLESTLLAVHLYGSAVDGGLKPYSDIDLLVTVAVKLDE 60
BAE71360           MRVAVTIEISNQLSEVLSVIERHLESTLLAVHLYGSAVDGGLKPYSDIDLLVTVAVKLDE 60
YP_449022          MREAVTIEISNQLSEVLSVIERHLESTLLAVHLYGSAVDGGLKPYSDIDLLVTVAVKLDE 60
S. Anatum EC3      MRVAVTIEIGNQLSEVLSVIERHLESTLLAVHLYGSAVDGGLKPYSDIDLLVTVAVKLDE 60
                   ** ****** **************************************************

ZP_00717087        TTRRALLNDLMEASAFPGESETLRAIEVTLVVHDDIIPWRYPAKRELQFGEWQRNDILAG 120
ZP_01175305        TTRRALLNDLMEASAFPGESETLRAIEVTLVVHDDIIPWRYPAKRELQFGEWQRNDILAG 120
BAE71360           TTRRALLNDLMEASAFPGESETLRAIEVTLVVHDDIIPWRYPAKRELQFGEWQRNDILAG 120
YP_449022          TTRRALLNDLMEASAFPGESETLRAIEVTLVVHDDIIPWRYPAKRELQFGEWQRNDILAG 120
S. Anatum EC3      TTRRALLNDLMEASAFPGESETLRAXEVTLVVAEDIIPWRYPAKRELQFGEWQPNDILAG 120
                   ************************* ****** :******************* ******

ZP_00717087        IFEPAMIDIDLAILLTKAREHSVALVGPAAEEFFDPVPEQDLFEALRETLKLWNSQPDWA 180
ZP_01175305        IFEPAMIDIDLAILLTKAREHSVALVGPAAEEFFDPVPEQDLFEALRETLKLWNSQPDWA 180
BAE71360           IFEPAMIDIDLAILLTKAREHSVALVGPAAEEFFDPVPEQDLFEALRETLKLWNSQPDWA 180
YP_449022          IFEPAMIDIDLAILLTKAREHSVALVGPAAEEFFDPVPEQDLFEALRETLKLWNSQPDWA 180
S. Anatum EC3      IFEPAMIDIDLAILLTKAREHSVALVGPAAEEFFDPVLEQDLFEALRETLKLWNSQPDWA 180
                   ************************************* **********************

ZP_00717087        GDERNVVLTLSRIWYSAITGKIAPKDVAADWAIKRLPAQYQPVLLEAKQAYLGQKEDHLA 240
ZP_01175305        GDERNVVLTLSRIWYSAITGKIAPKDVAADWAIKRLPAQYQPVLLEAKQAYLGQKEDHLA 240
BAE71360           GDERNVVLTLSRIWYSAITGKIAPKDVAADWAIKRLPAQYQPVLLEAKQAYLGQKEDHLA 240
YP_449022          GDERNVVLTLSRIWYSAITGKIAPKDVAADWAIKRLPAQYQPVLLEAKQAYLGQKEDHLA 240
S. Anatum EC3      GDERNVGLTLSRICSSAITGKIAPKDVAADWAIKRLPAQYQPVLLQTKQAYLGQKEDNLA 240
                   ****** ******  ******************************::**********:**

ZP_00717087        SRADHLEEFIRFVKGEIIKSVGK 263
ZP_01175305        SRADHLEEFIRFVKGEIIKSVGK 263
BAE71360           SRADHLEEFIRFVKGEIIKSVGK 263
YP_449022          SRADHLEEFIRFVKGEIIKSVGK 263
S. Anatum EC3      SRADHLEEFIRFVNREIIKSVGK 263
                   *************: ********
```

Figure 17 Comparison of amino acid sequence of AadA2 between *S.* Anatum EC3 strain and reference strains in GenBank database. Identical amino acid residues were indicated by asterisks. Functionally equivalent amino acid substitution were indicated by colons. The highlight letters were different amino acid of AadA2 from others.

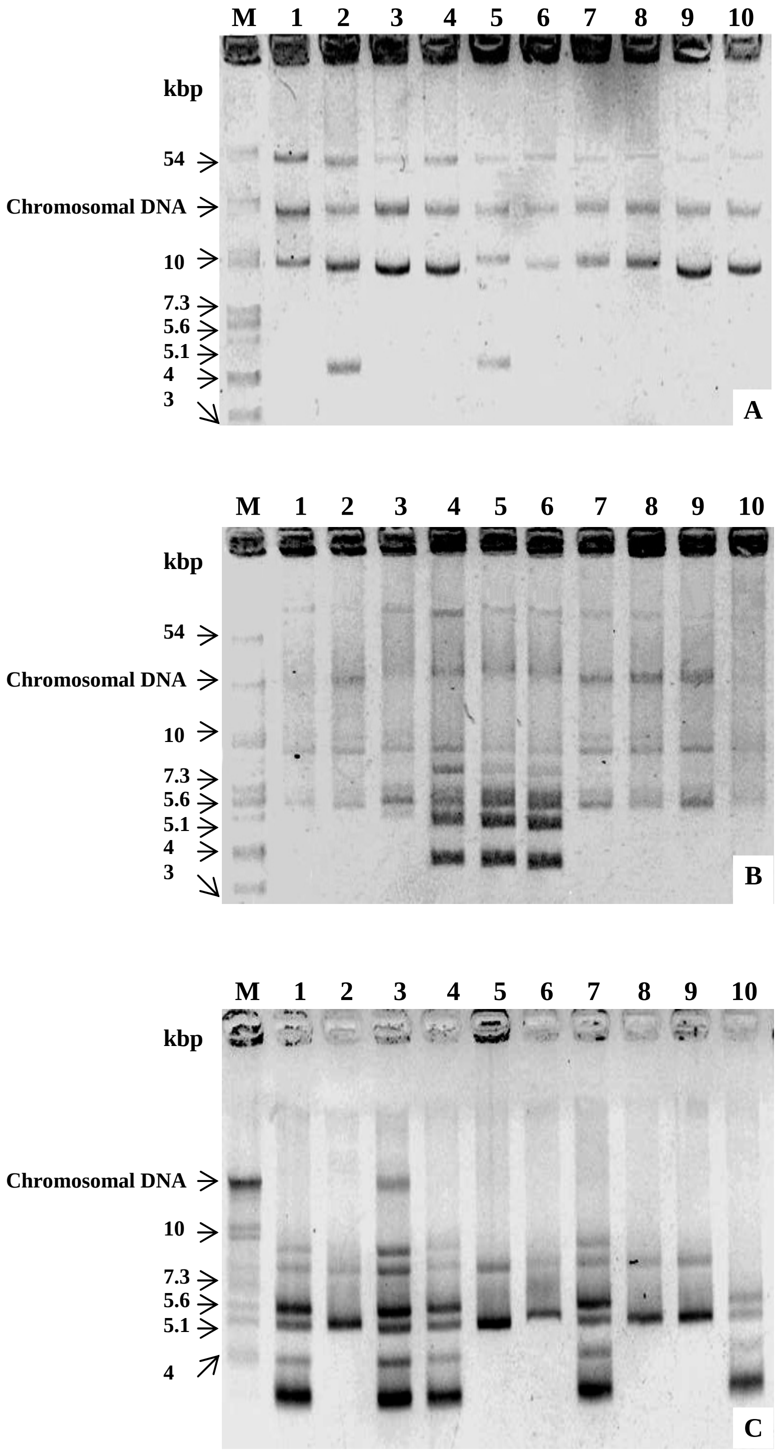

Figure 18 Agarose gel electrophoresis of plasmid profiles of *Salmonella* donor strains. Lane M = plasmid size marker from *E. coli* V517, lane 1-10 (Fig. 18A) = *S.* Corvallis exhibited AGSSuT resistance pattern. Lane 1-10 (Fig. 18B) = *S.* Rissen exhibited ACKSSuSxtT resistance pattern. Lane 1-10 (Fig. 18C) = *S.* 1,4,5,12,:i:- exhibited AApCGNSSuSxtT resistance pattern.

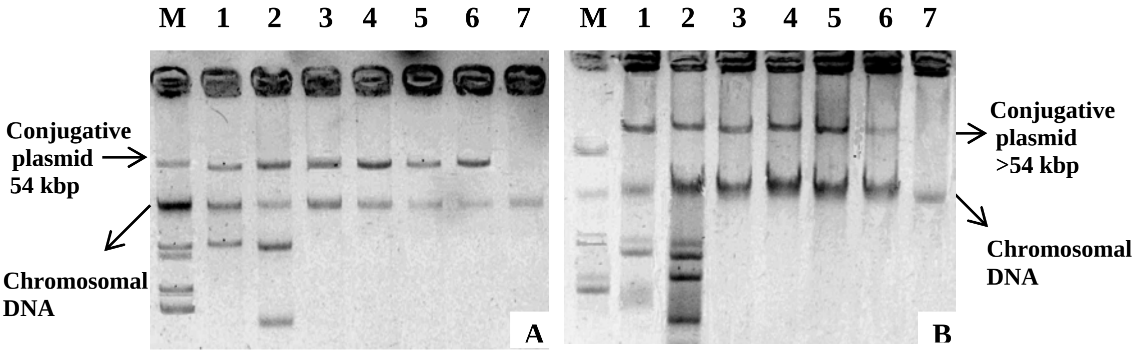

Figure 19 Agarose gel electrophoresis of conjugative plasmid of *Salmonella* donors transferred to *E. coli* transconjugants by conjugation. Lane M = plasmid size marker from *E. coli* V517 and lane 7 = recipient *E. coli* DH5α. Fig. 19A: lane 1 = *S.* Corvallis AC11 donor, lane 2 = *S.* Corvallis AC74 donor, lane 3-4 = transconjugants of *S.* Corvallis AC11 donor (isolates 1 and 2 respectively) and lane 5-6 = transconjugants of *S.* Corvallis AC74 donor (isolates 1 and 2 respectively). Fig. 19B: lane 1 = *S.* Rissen AC40 donor, lane 2 = *S.* Rissen AC50 donor, lane 3-4 = transconjugants of *S.* Rissen AC40 donor (isolates 1 and 2 respectively) and lane 5-6 = transconjugants of *S.* Rissen AC50 donor (isolates 1 and 2 respectively).

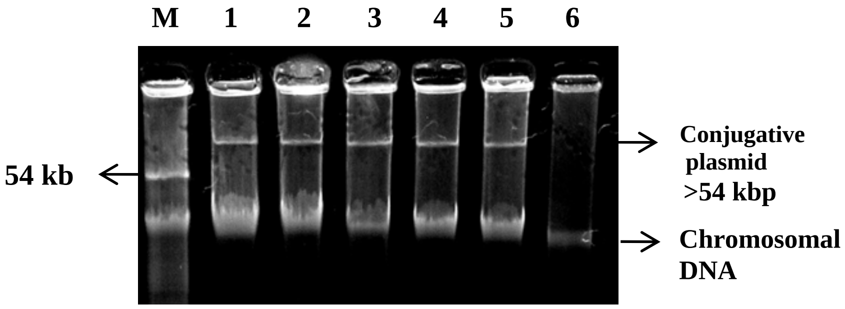

Figure 20 Agrose gel electrophoresis of conjugative plasmid of *S.* Stanley CC1 donor transferred to *E. coli* transconjugants by conjugation. Lane M = *E. coli* V517, lane 1 = *S.* Stanley CC1 donor strain, lane 2-5 = transconjugants (isolates 1-4 respectively) and lane 6 = recipient *E. coli* DH5α.

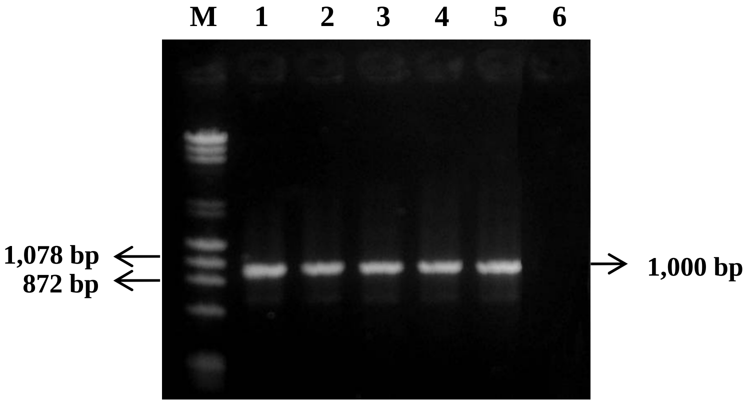

Figure 21 Agarose gel electrophoresis of PCR amplification of class 1 integrons in transconjugants of *S.* Stanley CC1 strain. Lane M = standard marker (λ/*Hin*dIII + Φx/*Hae*III), lane 1 = *S.* Stanley CC1 donor strain, lane 2-5 = transconjugants (isolates 1-4 respectively) and lane 6 = recipient *E. coli* DH5α.

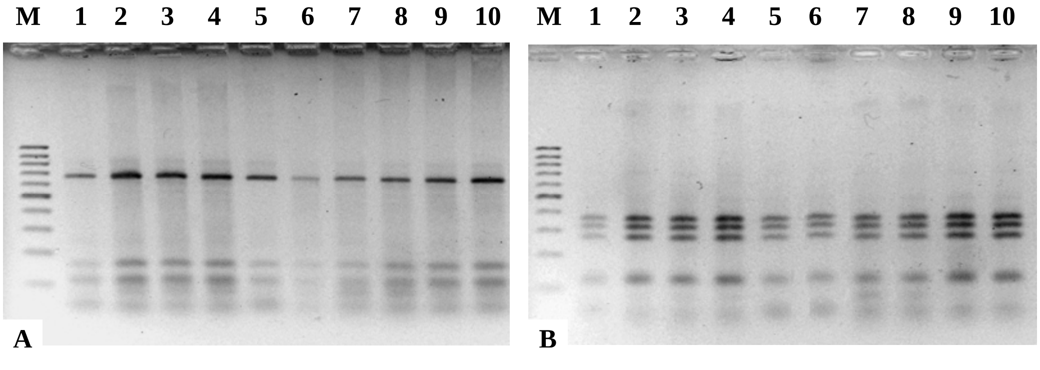

Figure 22 RFLP-PCR analysis of flagellin genes in *S.* Corvallis exhibited AGSSuT resistance pattern. Fig 22A: *fliC* gene digested with *Hha*I and Fig. 22B: *fljC* gene digested with *Mbo*I. Lane M = 100 bp ladder, lane 1-10 = *S.* Corvallis strains AC11, AC23, AC26, AC30, AC74, AC119, AC125, AC138, AC149 and AC151 respectively.

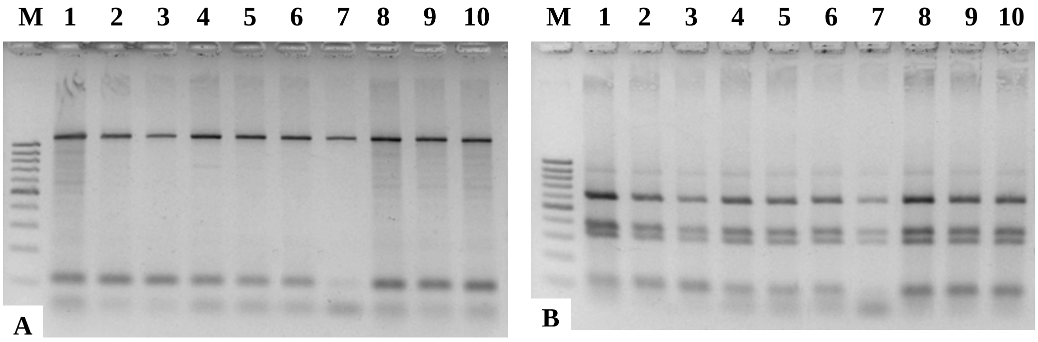

Figure 23 RFLP-PCR analysis of flagellin genes in *S.* Rissen exhibited ACKSSu-SxtT resistance pattern. Fig 23A: *fliC* gene digested with *Hha*I and Fig. 23B: *fljC* gene digested with *Mbo*I. Lane M = 100 bp ladder, lane 1-10 = *S.* Rissen strains AC40, AC41, AC46, AC49, AC50, AC69, AC80, AC105, AC106 and AC108 respectively.

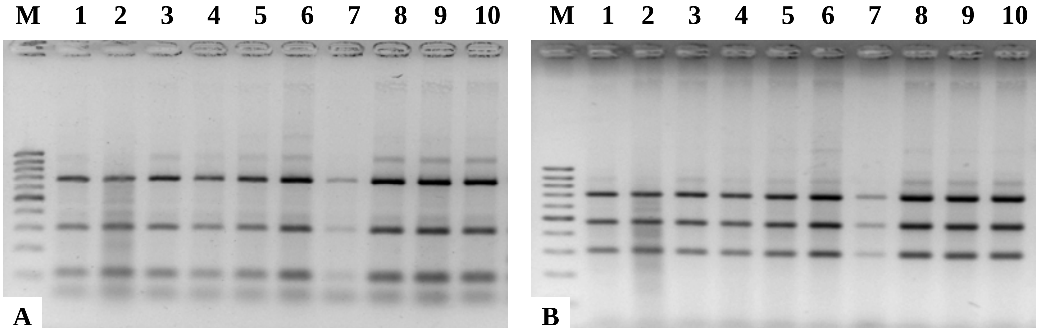

Figure 24 RFLP-PCR analysis of flagellin genes in *S.* 1,4,5,12:i:- exhibited AApC-GNSSuSxtT resistance pattern. Fig. 24A: *fliC* gene digested with *Hha*I and Fig. 24B: *fliC* gene digested with *Mbo*I. Lane M = 100 bp ladder, lane 1-10 = *S.* 1,4,5,12:i:- strains AB37, AB44, AB51, AB87, AB93, AB116, AB117, AB139, AB141 and AB144 respectively.