

Distribution of Secretion System Type VI (T6SS) among *Aeromonas* spp. genome sequences.

Species	Strains	Accession number	Size (Mb)	GC%	T6SS RAST	T6SS selected
<i>A. allosaccharophila</i> (2 genomes)	<i>A. allosaccharophila</i> BVH88	CDCB01	4.70859	58.60		
	<i>A. allosaccharophila</i> CECT 4199	CDBR01	4.66384	58.40		
<i>A. aquatica</i> (1 genome)	<i>A. aquatica</i> AE235	JRGL01	4.5823	61.20	•	
<i>A. australiensis</i> (1 genome)	<i>A. australiensis</i> CECT 8023	CDDH01	4.11003	58.10		
<i>A. bestiarum</i> (2 genomes)	<i>A. bestiarum</i> CBA 100	JPWL01	4.78811	60.50	•	
	<i>A. bestiarum</i> CECT 4227	CDDA01	4.69082	60.60	•	•
<i>A. bivalvium</i> (1 genome)	<i>A. bivalvium</i> CECT 7113	CDBT01	4.30259	62.20	•	•
<i>A. caviae</i> (14 genomes)	<i>A. caviae</i> 429865	LIHX01	4.70059	61.00		
	<i>A. caviae</i> 8LM	CP024198	4.47748	61.80	•	•
	<i>A. caviae</i> A23	LFXO01	4.52123	61.30		
	<i>A. caviae</i> Ae398	CACP01	4.43922	61.40		
	<i>A. caviae</i> BWH65	LESK01	4.44564	61.80	•	•
	<i>A. caviae</i> CECT 838	CDBK01	4.4714	61.70	•	
	<i>A. caviae</i> CECT 4221	CDBS01	4.5792	61.10		
	<i>A. caviae</i> FDAARGOS 72	CP026055	4.51752	61.70	•	•
	<i>A. caviae</i> FDAARGOS 75	JTBH02	4.55501	61.60	•	•
	<i>A. caviae</i> FDAARGOS 76	JTBG02	4.87779	61.00		
	<i>A. caviae</i> L12	JWJP01	4.37672	61.70	•	
	<i>A. caviae</i> YL12	JOVP01	4.84757	61.50	•	
	<i>A. sp. (caviae)</i> HZM	JEMQ01	4.45136	61.70		
	<i>A. sp. (caviae)</i> ZOR0002	JRQJ01	4.57807	61.10		
<i>A. dhakensis</i> (14 genomes)	<i>A. dhakensis</i> AAK1	BAFL01	4.76769	61.80	•	•
	<i>A. dhakensis</i> CECT 7289	CDBP01	4.69234	61.90	•	•
	<i>A. dhakensis</i> CIP 107500	CDBH01	4.71188	61.80	•	•
	<i>A. dhakensis</i> SSU	JH815591	4.87787	61.60	•	
	<i>A. hydrophila</i> (<i>dhakensis</i>) 14	AOBM01	4.67332	62.00	•	•
	<i>A. hydrophila</i> (<i>dhakensis</i>) 116	ANPN01	4.67704	62.00	•	•
	<i>A. hydrophila</i> (<i>dhakensis</i>) 145	JEMK01	4.8641	61.50		
	<i>A. dhakensis</i> 173	AOBN01	4.78635	61.60		
	<i>A. hydrophila</i> (<i>dhakensis</i>) 187	AOBO01	4.78391	61.60	•	•
	<i>A. hydrophila</i> (<i>dhakensis</i>) 259	AOBP01	4.70069	61.70	•	•
	<i>A. dhakensis</i> 277	AOBQ01	4.7901	61.60	•	•
	<i>A. hydrophila</i> KOR1	LJOE01	4.78317	61.80	•	•
	<i>A. hydrophila</i> (<i>dhakensis</i>) YL17	CP007518	4.80627	61.60		
	<i>A. sp. (dhakensis)</i> MDS8	AOTK01	4.84175	61.60	•	
<i>A. diversa</i> (2 genomes)	<i>A. diversa</i> 2478-85	APVG01	4.02642	61.70		
	<i>A. diversa</i> CECT 4254	CDCE01	4.06251	61.60		
<i>A. encheleia</i> (1 genome)	<i>A. encheleia</i> CECT 4342	CDDI01	4.47253	62.00	•	•
<i>A. enteropelogenes</i> (4 genomes)	<i>A. enteropelogenes</i> 1999lcr	JMGO02	4.05408	60.20	•	
	<i>A. enteropelogenes</i> CECT 4255T	CDDE01	4.33725	60.10	•	
	<i>A. enteropelogenes</i> CECT 4487	CDCG01	4.47474	59.70	•	
	<i>A. enteropelogenes</i> LK14	LDWG01	4.67835	62.00	•	•
<i>A. eucrenophila</i> (1 genome)	<i>A. eucrenophila</i> CECT 4224	CDDF01	4.54006	61.10	•	•
<i>A. finlandiensis</i> (1 genome)	<i>A. finlandiensis</i> 4287D	JRKG01	4.71751	58.60	•	
<i>A. fluvialis</i> (1 genome)	<i>A. fluvialis</i> LMG 24681	CDBO01	3.90423	58.30		
<i>A. hydrophila</i> (27 genomes)	<i>A. hydrophila</i> 226	JEML01	5.11106	60.90		
	<i>A. hydrophila</i> 48 AHYD	JVFM01	4.70016	61.60	•	•
	<i>A. hydrophila</i> 4AK4	CP006579	4.52799	62.00	•	•
	<i>A. hydrophila</i> 50 AHYD	JVES01	4.66846	61.60	•	
	<i>A. hydrophila</i> 52 AHYD	JVDW01	4.68345	61.60	•	
	<i>A. hydrophila</i> 53 AHYD	JVDL01	4.67151	61.60	•	
	<i>A. hydrophila</i> 56 AHYD	JVCD01	4.68375	61.60	•	
	<i>A. hydrophila</i> AD9	JFJO01	4.90707	61.30	•	
	<i>A. hydrophila</i> Ae34	BAXY01	4.7051	61.60		
	<i>A. hydrophila</i> AH10	CP011100	4.90827	61.10	•	•
	<i>A. hydrophila</i> AL06-06	CP010947	4.90139	61.37		
	<i>A. hydrophila</i> AL09-71	CP007566	5.02386	60.80		
	<i>A. hydrophila</i> FDAARGOS 78	JTBD02	4.9262	61.00	•	
	<i>A. hydrophila</i> J-1	CP006883	5.00081	60.90	•	•
	<i>A. hydrophila</i> L14f	JWJQ01	4.68278	61.70	•	
	<i>A. hydrophila</i> M013	JRWS01	4.96772	61.00	•	

Species	Strains	Accession number	Size (Mb)	GC%	T6SS RAST	T6SS selected
<i>A. hydrophila</i> (27 genomes)	<i>A. hydrophila</i> M023	JSWA01	4.91453	60.90		
	<i>A. hydrophila</i> M062	JSXE01	4.97435	61.10	•	
	<i>A. hydrophila</i> ML09-119	CP005966	5.0245	60.80		
	<i>A. hydrophila</i> NF1	JDWB01	4.80653	61.10	•	•
	<i>A. hydrophila</i> NF2	JDWC01	4.78711	61.30	•	
	<i>A. hydrophila</i> NJ-35	CP006870	5.27964	60.50	•	•
	<i>A. hydrophila</i> pc104A	CP007576	5.02383	60.80		
	<i>A. hydrophila</i> RB-AH	JPEH01	5.08893	60.80		
	<i>A. hydrophila</i> SNUFPC-A8	AMQA01	4.96909	60.80	•	•
	<i>A. hydrophila</i> subsp. <i>hydrophila</i> ATCC7966	CP000462	4.74445	61.50	•	•
	<i>A. hydrophila</i> subsp. <i>ranae</i> CIP 107985	CDDC01	4.68256	61.60		
<i>A. jandaei</i> (3 genomes)	<i>A. jandaei</i> CECT 4228	CDBV01	4.50035	59.00	•	
	<i>A. jandaei</i> L14h	JWJR01	4.67694	61.70	•	
	<i>A. jandaei</i> Riv2	JFDL01	4.47809	59.00	•	
<i>A. lacus</i> (1 genome)	<i>A. lacus</i> AE122	JRGM01	4.39437	59.00	•	•
<i>A. media</i> (4 genomes)	<i>A. media</i> ARB13	JRBF01	4.61236	61.00		
	<i>A. media</i> ARB20	JRBG01	4.6201	61.00		
	<i>A. media</i> CECT 4232	CDBZ01	4.48434	61.10		
	<i>A. media</i> WS	CP007567	4.78843	60.69		
<i>A. molluscorum</i> (1 genome)	<i>A. molluscorum</i> 848	AQGQ01	4.23617	59.20		
<i>A. piscicola</i> (1 genome)	<i>A. piscicola</i> LMG 24783	CDBL01	5.17797	59.20	•	•
<i>A. popoffii</i> (1 genome)	<i>A. popoffii</i> CIP 105493	CDBI01	4.76247	58.60	•	
<i>A. rivuli</i> (1 genome)	<i>A. rivuli</i> DSM 22539	CDBJ01	4.53415	60.00	•	
<i>A. salmonicida</i> (9 genomes)	<i>A. salmonicida</i> subsp. <i>achromogenes</i> AS03	AMQG02	4.95838	58.30		
	<i>A. salmonicida</i> subsp. <i>masoucida</i> NBRC 13784	BAWQ01	4.50226	58.80		
	<i>A. salmonicida</i> subsp. <i>pectinolytica</i> 34mel	ARYZ02	4.76707	58.50		
	<i>A. salmonicida</i> subsp. <i>salmonicida</i> 01-B526	AGVO01	4.92793	58.40	•	•
	<i>A. salmonicida</i> subsp. <i>salmonicida</i> 2004-05MF26	JRYW01	5.02109	58.20	•	•
	<i>A. salmonicida</i> subsp. <i>salmonicida</i> 2009-144K3	JRYV01	4.95883	58.40	•	•
	<i>A. salmonicida</i> subsp. <i>salmonicida</i> A449	CP000644	5.04054	58.17	•	•
	<i>A. salmonicida</i> subsp. <i>salmonicida</i> CIP 103209	CDDW01	4.74015	58.50	•	•
	<i>A. salmonicida</i> subsp. <i>salmonicida</i> JF3224	JXTA01	4.80617	58.49	•	•
<i>A. sanarellii</i> (1 genome)	<i>A. sanarellii</i> LMG 24682	CDBN01	4.1869	63.10		
<i>A. schubertii</i> (1 genome)	<i>A. schubertii</i> CECT 4240	Cddb01	4.12625	61.70	•	
<i>A. simiae</i> (1 genome)	<i>A. simiae</i> CIP 107798	CDBY01	3.98769	61.30	•	•
<i>A. sobria</i> (1 genome)	<i>A. sobria</i> CECT 4245	CDBW01	4.68367	57.60	•	•
<i>A. sp.</i> (3 genomes)	<i>A. sp.</i> 159	ALOT01	3.36084	58.20	•	
	<i>A. sp.</i> L_1B5_3	JXIR01	4.8067	58.70	•	
	<i>A. sp.</i> ZOR0001	JRJY01	4.45737	58.60		
<i>A. taiwanensis</i> (1 genome)	<i>A. taiwanensis</i> LMG 24683	BAWK01	4.23059	62.80		
<i>A. tecta</i> (1 genome)	<i>A. tecta</i> CECT 7082	CDCA01	4.75522	60.10	•	•
<i>A. veronii</i> (12 genomes)	<i>A. veronii</i> AER39	AGWT01	4.42059	58.90		
	<i>A. veronii</i> AER397	AGWV01	4.49666	58.90		
	<i>A. veronii</i> AMC34	AGWU01	4.57873	58.50	•	•
	<i>A. veronii</i> AMC35	AGWW01	4.56561	58.60		
	<i>A. veronii</i> ARB3	JRBE01	4.54266	58.80	•	
	<i>A. veronii</i> B565	CP002607	4.55178	58.70		
	<i>A. veronii</i> CECT 4486	CDBU01	4.4108	58.90	•	
	<i>A. veronii</i> CIP 107763	CDDU01	4.43081	58.80		
	<i>A. veronii</i> Hm21	ATFB01	4.68496	58.70	•	•
	<i>A. veronii</i> PhIn2	ANNT01	4.30055	58.80	•	
	<i>A. veronii</i> bv. <i>sobria</i> LMG 13067	CDBQ01	4.73561	58.40		
	<i>A. veronii</i> bv. <i>veronii</i> CECT 4257	CDDK01	4.51642	58.90		

Genome sequences available in Genome NCBI database, release 210; in bold the *Aeromonas* strains with complete genomes. The • in the T6SS RAST column indicates that the strain contains this system and in the T6SS selected column the • exhibits the strains selected for analysis.