

Table 5. Differential characteristics of biofilm and quorum sensing related genes in ISS *Enterobacter bugandensis* (n=4) and F1-2P MAG (n=1) when compared to other related strains

Gene name	Types of residue	Size (bp)	Numer of variable residues in genes responsible for biofilm formation and quorum sensing in ISS <i>Enterobacter bugandensis</i> strains and MAG when compared to other related strains (Gene bank accession #) that are:										
			EB-247	GN035669	GN02548	GN02283	GN04787	GN03842	GN05729	MNCRE4	IIT-BT-08	MBRL 1077	153 ECLO
			NZ_LT992502.1	NZ_JZB01000066.1	NZ_LEDQ01000032.1	NZ_LEEJ01000039.1	NZ_LVTS01000001.1	NZ_LRCL01000001.1	NZ_LRCV01000001.1	NZ_JZDF01000007.1	NZ_KI911561.1	NZ_CP014280.1	NZ_JVSD01000020.1
<i>LsrA</i>	Nucleotide	1488	NA	25	4	33	27	32	27	35	30	156	21
	Amino acid	495	NA	3	0	7	3	4	2	2	2	22	1
<i>LsrB</i>	Nucleotide	1002	11	18	18	25	11	30	28	22	19	65	8
	Amino acid	333	1	1	0	1	1	1	2	2	2	7	0
<i>LsrC</i>	Nucleotide	1032	23	16	23	90	19	91	21	59	32	85	22
	Amino acid	343	2	4	3	16	2	16	2	8	4	16	2
<i>LsrD</i>	Nucleotide	978	1	17	3	67	12	31	13	29	12	83	3
	Amino acid	325	0	3	0	8	2	3	1	2	1	11	0
<i>LsrF</i>	Nucleotide	888	31	24	29	17	23	47	25	20	27	66	32
	Amino acid	295	2	2	1	1	1	2	2	1	1	12	1
<i>LsrG</i>	Nucleotide	294	11	10	10	21	8	NA	16	98	12	16	5
	Amino acid	97	2	3	1	0	1	NA	3	0	2	2	2
<i>LsrR</i>	Nucleotide	972	22	22	9	51	20	23	22	68	34	58	23
	Amino acid	323	2	1	0	5	1	2	2	5	2	1	1
<i>LsrK</i>	Nucleotide	1581	28	26	23	75	12	42	26	52	16	132	26
	Amino acid	526	4	3	2	12	1	10	3	6	1	20	5
<i>AI-luxS</i>	Nucleotide	516	4	5	3	5	4	6	6	4	5	15	4
	Amino acid	171	0	0	0	0	0	0	0	0	0	0	0
<i>PgaA</i>	Nucleotide	2439	30	24	30	31	30	45	29	NA	34	97	22
	Amino acid	812	13	13	12	15	12	23	14	NA	14	35	13
<i>PgaB</i>	Nucleotide	1938	31	32	28	30	29	46	13	30	15	83	11
	Amino acid	645	7	9	7	6	8	11	4	8	2	18	1
<i>PgaC</i>	Nucleotide	1332	14	13	15	11	16	15	26	11	14	32	14
	Amino acid	443	0	1	2	3	2	2	1	1	1	1	4
<i>PgaD</i>	Nucleotide	435	2	2	4	2	2	3	0	4	4	14	1
	Amino acid	144	0	0	0	0	1	0	0	1	2	3	0

NA indicates that the FASTA data for that gene in that specific strain was not found in any database.