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Complete genome sequence of the biocontrol agent *Serratia marcescens* strain N4–5 uncovers an assembly artefact

Ferreira, Larissa Carvalho; Maul, Jude E.; Viana, Marcus Vinicius Canário; de Sousa, Thiago Jesus; de Carvalho Azevedo, Vasco Ariston; Roberts, Daniel P.; de Souza, Jorge Teodoro

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tel: +44 1970 62 2400

email: is@aber.ac.uk

Supplementary Material

Table S1. Genomic relatedness values between the strain N4-5 and other *Serratia* spp. genomes calculated with genomic metrics.

Organism	DDH	ANI	AAI
<i>S. marcescens</i> B3R3	74.2	96.41	97.66
<i>S. marcescens</i> U36365	74.3	96.58	97.82
<i>S. marcescens</i> UMH8	90.3	98.68	99.06
<i>S. marcescens</i> WW4	72.8	96.40	96.15
<i>S. liquefaciens</i> ATCC 27592 ^T	34.8	82.88	85.77
<i>S. ficaria</i> NCTC12148 ^T	24.8	87.06	87.65
<i>S. fonticola</i> DSM4567 ^T	27.2	79.91	79.61

Values in percentage. ANI was calculated based on BLAST and DDH on formula 2. Values in bold indicate they are above the threshold to be classified in the same species, namely 70, 95 and 95%.

Table S2. List of completely sequenced genomes of *Serratia* and the presence of extra copies of the 5S rRNA gene until April 25, 2019.

Species	Strain	Accession No.	Source	Coverage	Position	Assembler	Sequencing technology**
<i>S. marcescens</i>	N4-5	NZ_CP031316.1	This study	664x	no artefact	SPAdes	1
<i>S. marcescens</i>	B3R3	CP013046.2	[1]	430x	operon 5 C*	AllPaths	1, 2
<i>S. marcescens</i>	CAV1492	CP011642.1	Sheppard et al., 2015, unpublished	74x	operon 6	HGAP	2
<i>S. marcescens</i>	CAV1761	CP029449.1	Mathers et al., 2018, unpublished	36x	operon 6	HGAP	2
<i>S. marcescens</i>	Db11	NZ_HG326223.1	[2]	11x	operon 3 C	Phrap	3
<i>S. marcescens</i>	RSC-14	CP012639.1	[3]	175x	operon 6	SMRT	2
<i>S. marcescens</i>	SM39	NZ_AP013063.1	[2]	12.6x	operon 3 C	phred/phrap/c	4
<i>S. marcescens</i>	SMB2099	NZ_HG738868.1	Yao et al., 2017, unpublished	167x	operon 3 C	NI	NI
<i>S. marcescens</i>	SmUNAM836	CP012685.1	[4]	172x	operon 3 C	HGAP	2
<i>S. marcescens</i>	U36365	CP016032.1	[5]	490x	operon 5 C	HGAP	2
<i>S. marcescens</i>	UMH1	NZ_CP018915.1	[6]	NI	operon 3 C	HGAP	2
<i>S. marcescens</i>	UMH2	NZ_CP018924.1	[6]	244.4x	operon 3 C	HGAP	2
<i>S. marcescens</i>	UMH3	NZ_CP018925.1	[6]	241.8x	operon 3 C	HGAP	2
<i>S. marcescens</i>	UMH5	NZ_CP018917.1	[6]	303.2x	operon 3 C	HGAP	2
<i>S. marcescens</i>	UMH6	NZ_CP018926.1	[6]	328.6x	operon 3 C	HGAP	2
<i>S. marcescens</i>	UMH7	NZ_CP018919.1	[6]	245.7x	operon 3 C	HGAP	2
<i>S. marcescens</i>	UMH8	NZ_CP018927.1	[6]	317x	operon 3 C	HGAP	2
<i>S. marcescens</i>	UMH9	NZ_CP018923.1	[6]	284.3x	operon 3 C	HGAP	2
<i>S. marcescens</i>	UMH10	NZ_CP018928.1	[6]	279.2x	operon 3 C	HGAP	2
<i>S. marcescens</i>	UMH11	NZ_CP018929.1	[6]	253.8x	operon 3 C	HGAP	2
<i>S. marcescens</i>	UMH12	NZ_CP018930.1	[6]	320x	operon 3 C	HGAP	2
<i>S. marcescens</i>	WW4	NC_020211.1	[7]	NI	operon 5 C	Velvet	1
<i>S. marcescens</i>	FDAARGOS_6	NZ_CP026050.1	Sichtig et al., 2018, unpublished	636.2x	operon 6	Celera	1,2
<i>S. marcescens</i>	AR_0027	NZ_CP026702.1	Conlan et al., 2018, unpublised	138x	operon 6 C	HGAP	2
<i>S. marcescens</i>	AR_0091	NZ_CP027533.1	Conlan et al., 2018, unpublised	141x	operon 3 C	HGAP	2
<i>S. marcescens</i>	AR_0099	NZ_CP027539.1	Conlan et al., 2018, unpublised	177x	operon 6 C	HGAP	2

<i>S. marcescens</i>	AR_0124	NZ_CP028946.1	Conlan et al., 2018, unpublished	120x	operon 2 C	HGAP	2
<i>S. marcescens</i>	AR_0130	NZ_CP028947.1	Conlan et al., 2018, unpublished	225x	operon 5 C	HGAP	2
<i>S. marcescens</i>	AR_0123	NZ_CP028948.1	Conlan et al., 2018, unpublished	137x	operon 6	HGAP	2
<i>S. marcescens</i>	AR_0121	NZ_CP028949.1	Conlan et al., 2018, unpublished	140x	operon 6	HGAP	2
<i>S. marcescens</i>	AR_0131	NZ_CP029715.1	Conlan et al., 2018, unpublished	213x	operon 2 C	HGAP	2
<i>S. marcescens</i>	AR_0122	NZ_CP029746.1	Conlan et al., 2018, unpublished	156x	operon 2 C	HGAP	2
<i>S. marcescens</i>	AS-1	NZ_AP019009.1	Sakuraoka et al., 2018, unpublished	258x	operon 5 C	Canu	2
<i>S. marcescens</i>	322	NZ_CP021164.1	Hoffman et al., 2018, unpublished	305x	operon 5 C	HGAP	2
<i>S. marcescens</i>	SGAir0764	NZ_CP027300.1	[8]	520.9x	operon 5 C	HGAP	2
<i>S. ficaria</i>	NCTC12148	NZ_LT906479.1	NCTC, unpublished	228x	operon 5 C	NI	2
<i>S. fonticola</i>	DSM 4576	NZ_CP011254.1	[9]	217.2x	operon 2 C	HGAP	2
<i>S. fonticola</i>	FDAARGOS_4	NZ_CP023956.1	Minogue et al., 2017, unpublished	863.5x	operon 6 C	Celera	1,2
<i>S. fonticola</i>	GS2	CP013913.1	Jung et al., 2016, unpublished	64x	operons 1/8 C	SMRT	2
<i>S. fonticola</i>	NCTC13193	LR134492.1	NCTC, unpublished	100x	operon 5 C	NI	2
<i>S. liquefaciens</i>	ATCC 27592	CP006252.1	[10]	127x	operon 4 C	Celera	2
<i>S. liquefaciens</i>	FDAARGOS_1	CP014017.1	Goldberg et al., 2016, unpublished	433.6x	operon 6	HGAP	2
<i>S. liquefaciens</i>	HUMV-21	NZ_CP011303.1	[11]	100x	operon 1	Celera	2
<i>S. plymuthica</i>	3Re4-18	CP012097.1	[12]	110x	operon 6C	HGAP	2
<i>S. plymuthica</i>	3Rp8	CP012096.1	[12]	81x	operon 6	HGAP	2
<i>S. plymuthica</i>	4Rx13	CP006250.1	[13]	NI	operon 5 C	Newbler	4,5
<i>S. plymuthica</i>	AS9	CP002773.1	[14]	30x	operon 5 C	Newbler	1,5
<i>S. plymuthica</i>	PRI-2c	NZ_CP015613.1	[15]	211x	operon 5 C	SMRT	2
<i>S. plymuthica</i>	S13	CP006566.1	[16]	35x	operon 5 C	Newbler	5
<i>S. plymuthica</i>	NCTC12961	NZ_LS483469.1	WTSI, 2018, unpublished	75x	operon 5 C	NI	2
<i>S. plymuthica</i>	NCTC8900	NZ_LR134151.1	WTSI, 2018, unpublished	100x	operon 5 C	NI	2
<i>S. plymuthica</i>	NCTC8015	NZ_LR134478.1	WTSI, 2018, unpublished	100x	operon 5 C	NI	NI
<i>S. odorifera</i>	NCTC11214	NZ_LR134117.1	WTSI, 2019, unpublished	100x	operon 6	NI	2
<i>S. proteamaculans</i>	568	CP000826.1	Copeland et al., 2007, unpublished	NI	operon 5 C	NI	NI
<i>S. rubidaea</i>	1122	CP014474.1	[17]	139x	operon 5 C	Newbler	1,6
<i>S. quinivorans</i>	NCTC13188	NZ_LR134494.1	WTSI, 2018, unpublished	100x	operon 5 C	NI	NI

<i>S. quinivorans</i>	PKL:12	CP038467.1	Kumar and Mukhia, 2019, unpublished	90x	operon 6	HGAP	2
<i>Serratia</i> sp.	FGI94	CP003942.1	[18]	NI	operon 5 C	Velvet/Allpath	1
<i>S. rubidaea</i>	NCTC10848	NZ_LS483492.1	WTSI, 2018, unpublished	113x	operon 2	NI	2
<i>S. rubidaea</i>	NCTC9419	NZ_LR134155.1	WTSI, 2019, unpublished	100x	operon 2C	NI	2
<i>S. rubidaea</i>	NCTC10036	NZ_LR134493.1	WTSI, 2018, unpublished	100x	operon 6	NI	NI
<i>Serratia</i> sp.	AS12	CP002774.1	[19]	30x	operon 5 C	Newbler	1,5
<i>Serratia</i> sp.	AS13	CP002775.1	[20]	30x	operon 5 C	Newbler	1,5
<i>Serratia</i> sp.	YD25	NZ_CP016948.1	[21]	15x	operon 3 C	Velvet	1
<i>Serratia</i> sp.	1D1416	NZ_CP032738.1	Alabed et al., 2018, unpublished	110x	operon 2 C	HGAP	2
<i>Serratia</i> sp.	3ACOL1	NZ_CP033055.1	Bekkelund et al., 2018, unpublished	173.5x	operon 2 C	HGAP	2
<i>Serratia</i> sp.	ATCC39006	NZ_CP025084.1	[22]	330x	operon 7	Canu/Pilon	1,2
<i>Serratia</i> sp.	ATCC39006	NZ_CP025085.1	Hampton et al., 2017, unpublished	465x	operon 7	Pilon	1
<i>Serratia</i> sp.	FDAARGOS_5	NZ_CP033831.1	Goldberg et al., 2018, unpublished	2,026x	operon 2 C	Canu	1,2
<i>Serratia</i> sp.	FS14	NZ_CP005927.1	[23]	25x	no extra copies	Newbler	4,5
<i>Serratia</i> sp.	LS-1	NZ_CP033504.1	Guan et al., 2018, unpublished	30x	operon 3 C	SOAPdenovo	1
<i>Serratia</i> sp.	Myb239	NZ_CP023268.1	Zimmermann et al., 2018, unpublished	254x	operon 5 C	SPAdes	1
<i>Serratia</i> sp.	P2ACOL2	NZ_CP033162.1	Bekkelund et al., 2018, unpublished	164.8x	operon 5 C	HGAP	2
<i>Serratia</i> sp.	SCBI	NZ_CP003424.1	Abebe-Akele et al., 2017, unpublished	NI	no extra copies	Newbler	5
<i>Serratia</i> sp.	SSNIH1	NZ_CP026383.1	[24]	115x	operon 1 C	HGAP	2

* Complementary strand.

** 1) Illumina; 2) PacBio; 3) Shotgun (ABI3730 or ABI3700 capillary automated sequencers (Applied Biosystems)); 4) Standard Sanger; 5) 454; 6) IonTorrent

Table S3. Number of copies of the ribosomal genes 5S, 16S and 23S, respectively, in genomes of four bacterial genera. All completely sequenced genomes of these genera until April 25, 2009 were included.

Genera/ patterns	<i>Serratia</i>		<i>Vibrio</i>		<i>Yersinia</i>		<i>Proteus</i>	
	Patterns#	Frequency	Patterns	Frequency	Patterns	Frequency	Patterns	Frequency
1	10, 8, 8	1	16, 15, 15	1	9, 9, 8	3	8, 7, 7	24
2	8, 7, 7	70	15, 14, 14	2	8, 7, 7	84	8, 6, 7	1
3	7, 7, 7	3	15, 13, 13	2	7, 6, 6	11		
4	5, 6, 2	1	14, 13, 13	3	6, 6, 6	2		
5			14, 13, 14	1				
6			14, 12, 13	1				
7			14, 11, 11	1				
8			13, 12, 12	49				
9			12, 12, 11	1				
10			12, 11, 11	28				
11			11, 11, 10	1				
12			11, 10, 11	1				
13			11, 10, 10	26				
14			11, 8, 9	1				
15			10, 10, 10	1				
16			10, 9, 9	32				
17			9, 8, 8	18				
18			9, 9, 7	1				
19			8, 8, 8	1				
20			8, 7, 7	12				
21			8, 7, 6	2				
22			7, 6, 6	2				
Total n. genomes		75		187		100		25
With artefact (%)		96		99		98		100

#Patterns of occurrence of the genes 5S, 23S and 16S.

Legend to supplementary Figures

Fig. S1. Phylogenetic tree of whole genomes indicating the current taxonomic placement of strain N4-5. Phylogenomic tree constructed with *Serratia* spp. complete genome sequences. The tree was constructed with the Phylogenetic Tree Building Service available at PATRIC, using the RAxML programme [26]. The scale indicates the expected number of substitutions per site. Branch support values are gene-wise jackknifing as implemented in PATRIC.

Fig. S2. The phylogenetic tree was constructed in MEGA 6.06 [25] based on 1,479-bp nucleotide sequences of the 16S gene aligned in MAFFT [27]. The tree construction method was Maximum Likelihood with the Kimura 2-parameter model. Bootstrap values were calculated with 1,000 resamplings and values higher than 70% are shown on the appropriate branching points. The scale indicates the number of substitutions per site.

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