

Complete genome sequences of 96 strains of *Ralstonia solanacearum* species complex phylotype I isolated from solanaceous vegetables in Japan

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ABSTRACT Bacterial wilt disease, caused by *Ralstonia solanacearum* species complex phylotype I, severely affects the cultivation of solanaceous vegetables (tomato, eggplant, etc.) in Japan. In this study, we report the complete genome sequences of 96 strains of the pathogen isolated from solanaceous vegetables in various parts of Japan.

KEYWORDS bacterial wilt, *Ralstonia solanacearum* species complex, solanaceous vegetables

Bacterial wilt disease, caused by *Ralstonia solanacearum* species complex (RSSC) (1, 2), is a major bacterial disease worldwide (3). In Japan, RSSC belonging to phylotype I causes severe damage to solanaceous vegetables (4). Here, we determined the complete genome sequences of 96 strains of RSSC phylotype I isolated from diseased solanaceous vegetables (tomato, eggplant, peppers, and potatoes) from 32 prefectures of Japan (Table 1).

These strains were preserved as freeze-dried cells at the Genebank of the National Agriculture and Food Research Organization (NARO, Tsukuba, Japan). A single colony isolated on triphenyl tetrazolium chloride medium (5) was cultured in casamino acid-peptone-glucose broth (5) overnight at 30°C. Genomic DNA was extracted using NucleoBond HMW DNA (Macherey-Nagel, Düren, Germany) according to the manufacturer's instructions. The extracted DNA was subjected to short- and long-read sequencing. For short reads, we generated paired-end libraries (fragment size, ~550 bp) using the Colibri ES DNA Library Prep Kit for Illumina Systems (ThermoFisher Scientific, Waltham, MA). For adaptors, the KAPA HyperPrep Kit with KAPA Universal Adapter and KAPA UDI Primer Mixes_1-96 (Nippon Genetics, Tokyo, Japan) was used. The pooled libraries were sequenced on an Illumina NovaSeq 6000 System (Illumina, San Diego, CA), generating 150-bp paired-end reads. Adapter sequences, low-quality reads (reads in which the number of bases with Qphred ≤ 5 accounted for more than 50% of the total reads), and >10% reads with nucleotide sequence unknown were removed by Fastp (ver. 0.23.4) (6). For long reads, genomic DNA was processed using a Rapid Barcoding Kit (SQK-RBK109-96; Oxford Nanopore Technologies, Oxford, UK). The pooled libraries were sequenced using PromethION 24 (Oxford Nanopore Technologies) with R9.4.1 flow cells under a high-accuracy mode of MinkNOW-4.3.1. Quality scores were measured using a logarithmic Phred scale. Reads shorter than 1 kbp or below the mean quality score of 7 were removed by SeqKit2 (ver. 2.8.2) (7) as failed reads. Library preparation and sequencing were performed at the Research Center of Genetic Resources, NARO (Tsukuba, Japan). Hybrid assembly with long and short reads was performed using Flye (ver. 2.9) (8), NECAT (ver. 0.0.1) (9), and Raven (ver. 1.7.0) (10) and phased into a consensus using Tricycler (ver. 0.5.2) (11). Tricycler searched for *dnaA* alleles within each completed

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TABLE 1 List of RSSC phylotype I strain^a

No.	MAFF no. ^b	Host, location, year	BioSample	DRA accession no. (short read) (long read)	No. of reads <i>N</i> ₅₀ value (bp)	Genomic DNA ^c	Accession no.	Genome size (bp)	Coverage (x)	CDS ^d
1	106244	Eggplant, Nara, 1981	SAMD00889216	DRR657716	1,335,612					
				DRR657717	28,068	22,651	Total	5,877,558	85	5,159
							C	AP041399	3,859,863	3,569
2	106251	Eggplant, Osaka, 1981	SAMD01229170	DRR667423	1,553,992					
				DRR667424	16,173	31,826	Total	5,877,554	80	5,161
							C	AP041401	3,859,856	3,571
3	724001	Potato, Nara, 1982	SAMD01229171	DRR667425	1,483,493					
				DRR667426	16,028	34,574	Total	5,951,892	79	5,251
							C	AP041403	3,975,213	3,695
4	724002	Eggplant, Tottori, 1982	SAMD01229172	DRR667427	1,781,508					
				DRR667428	28,389	27,233	Total	5,787,814	101	5,052
							C	AP041405	3,825,018	3,530
5	724003	Eggplant, Okayama, 1982	SAMD01229173	DRR667429	1,905,699					
				DRR667430	20,034	29,362	Total	5,787,820	92	5,055
							C	AP041407	3,825,025	3,533
6	106252	Eggplant, Fukuoka, 1982	SAMD01229174	DRR667431	2,276,757					
				DRR667432	14,847	30,730	Total	5,784,412	88	5,060
							C	AP041409	3,817,949	3,516
7	724004	Tomato, Hyogo, 1982	SAMD01229175	DRR667433	1,678,190					
				DRR667434	13,511	34,538	Total	5,924,327	77	5,206
							C	AP041411	3,930,316	3,641
8	106253	Eggplant, Hiroshima, 1982	SAMD01229176	DRR667435	1,732,297					
				DRR667436	14,323	26,925	Total	5,854,653	71	5,166
							C	AP041413	3,873,661	3,618
9	724005	Eggplant, Osaka, 1982	SAMD01229177	DRR667437	1,950,644					
				DRR667438	28,234	24,903	Total	5,860,690	106	5,145
							C	AP041415	3,859,476	3,565
10	724008	Tomato, Shizuoka, 1982	SAMD01229178	DRR667439	1,431,216					
				DRR667440	14,795	28,872	Total	5,751,182	67	5,000
							C	AP041417	3,748,644	3,431
11	106245	Tomato, Mie, 1982	SAMD01229179	DRR667441	1,530,502					
				DRR667442	27,622	30,653	Total	5,813,616	102	5,083
							C	AP041419	3,750,393	3,452
12	724009	Tomato, Ibaraki, 1982	SAMD01229180	DRR667443	1,689,531					
				DRR667444	17,656	26,052	Total	5,949,963	77	5,244
							C	AP041421	3,889,075	3,599
13	724010	Eggplant, Gunma, 1982	SAMD01229181	DRR667445	1,614,600					
				DRR667446	12,915	37,791	Total	5,830,308	78	5,100
							C	AP041422	2,060,888	1,645

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TABLE 1 List of RSSC phylotype I strain^a (Continued)

No.	MAFF no. ^b	Host, location, year	BioSample	DRA accession no. (short read) (long read)	No. of reads <i>N</i> ₅₀ value (bp)	Genomic DNA ^c	Accession no.	Genome size (bp)	Coverage (x)	CDS ^d
14	311869	Tomato, Kochi, 1982	SAMD01229182	DRR667447	1,833,824	C	AP041423	3,837,594		3,541
				DRR667448	15,500	M	AP041424	1,992,714		1,559
						Total		5,826,993	92	5,111
						C	AP041425	3,864,193		3,588
15	311870	Tomato, Kochi, 1982	SAMD01229183	DRR667449	1,755,668	M	AP041426	1,962,800		1,523
				DRR667450	16,049	Total		5,864,197	91	5,164
					35,638	C	AP041427	3,877,464		3,602
						M	AP041428	1,986,733		1,562
16	311871	Eggplant, Kochi, 1982	SAMD01229184	DRR667451	1,850,141	Total		5,829,152	113	5,111
				DRR667452	29,282	C	AP041429	3,864,274		3,588
					28,965	M	AP041430	1,964,878		1,523
						Total		5,797,396	81	5,069
17	311872	Tomato, Kagoshima, 1982	SAMD01229185	DRR667453	1,866,691	C	AP041431	3,834,609		3,545
				DRR667454	12,733	M	AP041432	1,962,787		1,524
					34,620	Total		5,797,396	81	5,069
						C	AP041431	3,834,609		3,545
18	311873	Eggplant, Saga, 1982	SAMD01229186	DRR667455	1,733,634	M	AP041432	1,962,787		1,524
				DRR667456	16,646	Total		5,864,206	82	5,129
					29,176	C	AP041433	3,901,396		3,604
						M	AP041434	1,962,810		1,525
19	311874	Tomato, Osaka, 1982	SAMD01229187	DRR667457	1,762,344	Total		5,957,112	108	5,265
				DRR667458	25,586	C	AP041435	3,981,626		3,701
					31,318	M	AP041436	1,975,486		1,564
						Total		5,970,545	107	5,229
20	311875	Tomato, Shimane, 1982	SAMD01229188	DRR667459	1,981,995	C	AP041437	3,975,104		3,669
				DRR667460	25,783	M	AP041438	1,995,441		1,560
					28,512	Total		5,970,545	107	5,229
						C	AP041437	3,975,104		3,669
21	106254	Eggplant, Wakayama, 1982	SAMD01229189	DRR667461	1,885,022	M	AP041438	1,995,441		1,560
				DRR667462	33,480	Total		5,859,969	111	5,144
					22,615	C	AP041439	3,866,563		3,583
						M	AP041440	1,993,406		1,561
22	311876	Eggplant, Tokyo, 1982	SAMD01229190	DRR667463	2,270,174	Total		5,733,050	89	4,994
				DRR667464	10,352	C	AP041441	3,746,404		3,434
					43,728	M	AP041442	1,986,646		1,560
						Total		6,072,814	85	5,342
23	311877	Tomato, Gunma, 1982	SAMD01229191	DRR667465	1,988,279	C	AP041443	4,001,663		3,716
				DRR667466	13,138	M	AP041444	2,071,151		1,626
					38,407	Total		6,072,814	85	5,342
						C	AP041443	4,001,663		3,716
24	311878	Eggplant, Saitama, 1982	SAMD01229192	DRR667467	1,947,749	M	AP041444	2,071,151		1,626
				DRR667468	12,913	Total		5,992,854	75	5,242
					41,801	C	AP041445	5,824,784	90	5,099
						M	AP041447	2,072,447		1,628
25	311879	Tomato, Nagano, 1982	SAMD01229193	DRR667469	1,538,210	Total		5,992,854	75	5,242
				DRR667470	13,940	C	AP041446	3,920,407		3,614
					33,140	M	AP041447	2,072,447		1,628
						Total		5,992,854	75	5,242
26	311880	Tomato, Yamaguchi, 1982	SAMD01229194	DRR667471	1,460,559					

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TABLE 1 List of RSSC phylotype I strain^a (Continued)

No.	MAFF no. ^b	Host, location, year	BioSample	DRA accession no. (short read) (long read)	No. of reads <i>N</i> ₅₀ value (bp)	Genomic DNA ^c	Accession no.	Genome size (bp)	Coverage (x)	CDS ^d
27	311881	Tomato, Yamaguchi, 1982	SAMD01229195	DRR667472	27,072	27,382	Total	5,909,876	95	5,176
							C	AP041448		3,619
							M	AP041449		1,557
28	311882	Tomato, Yamaguchi, 1982	SAMD01229196	DRR667473	731,214					
				DRR667474	15,525	33,813	Total	5,870,348	58	5,165
							C	AP041450		3,567
29	311883	Tomato, Kanagawa, 1982	SAMD01229197	DRR667475	772,604					
				DRR667476	22,148	28,922	Total	6,008,490	67	5,259
							C	AP041452		3,626
30	311884	Eggplant, Yamanashi, 1982	SAMD01229198	DRR667477	1,713,409					
				DRR667478	17,798	28,791	Total	5,878,557	81	5,207
							C	AP041454		3,638
31	311885	Tomato, Oita, 1982	SAMD01229199	DRR667479	1,537,854					
				DRR667480	34,306	26,025	Total	5,931,772	109	5,243
							C	AP041456		3,691
32	311886	Tomato, Oita, 1982	SAMD01229200	DRR667481	1,826,051					
				DRR667482	34,214	21,775	Total	6,013,698	108	5,292
							C	AP041458		3,653
33	311887	Pepper, Oita, 1982	SAMD01229201	DRR667483	1,588,115					
				DRR667484	19,490	31,633	Total	5,786,151	87	5,048
							C	AP041460		3,491
34	311888	Tomato, Ehime, 1982	SAMD01229202	DRR667485	1,736,489					
				DRR667486	22,251	34,896	Total	5,778,998	106	5,046
							C	AP041462		3,505
35	106255	Tomato, Kumamoto, 1982	SAMD01229203	DRR667487	1,854,888					
				DRR667488	13,040	32,986	Total	5,762,479	79	5,009
							C	AP041464		3,452
36	311889	Eggplant, Fukuoka, 1982	SAMD01229204	DRR667489	1,937,994					
				DRR667490	19,427	34,883	Total	5,794,303	99	5,067
							C	AP041466		3,524
37	311890	Eggplant, Shizuoka, 1982	SAMD01229205	DRR667491	1,882,112					
				DRR667492	23,983	31,598	Total	5,962,297	107	5,232
							C	AP041468		3,648
38	311891	Tomato, Aichi, 1982	SAMD01229206	DRR667493	1,401,814					
				DRR667494	18,766	30,727	Total	6,063,933	79	5,359
							C	AP041470		3,729
39	311892	Tomato, Aichi, 1982	SAMD01229207	DRR667495	1,650,554					
				DRR667496	13,791	28,985	Total	5,923,037	72	5,198
							C	AP041472		3,663

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TABLE 1 List of RSSC phylotype I strain^a (Continued)

No.	MAFF no. ^b	Host, location, year	BioSample	DRA accession no. (short read) (long read)	No. of reads	<i>N</i> ₅₀ value (bp)	Genomic DNA ^c	Accession no.	Genome size (bp)	Coverage (x)	CDS ^d
39	311892	Potato, Nagasaki, 1982	SAMD01229207	DRR667497 DRR667498	1,801,689 22,324	36,076	M Total C M	AP041473 AP041474 AP041475	1,967,610 5,772,947 3,783,865 1,989,082	105	1,535 5,027 3,465 1,562
40	311893	Tomato, Kanagawa, 1982	SAMD01229208	DRR667499 DRR667500	2,165,272 18,787	32,290	Total C M	 AP041476 AP041477	5,878,666 3,906,727 1,971,939	103	5,198 3,635 1,563
41	311894	Tomato, Shizuoka, 1982	SAMD01229209	DRR667501 DRR667502	1,197,862 11,844	36,345	Total C M	 AP041478 AP041479	5,968,701 3,994,945 1,973,756	64	5,275 3,738 1,537
42	311895	Eggplant, Saga, 1983	SAMD01229210	DRR667503 DRR667504	1,341,336 11,650	38,383	Total C M	 AP041480 AP041481	5,746,959 3,791,116 1,955,843	66	5,025 3,501 1,524
43	311896	Tomato, Shizuoka, 1983	SAMD01229211	DRR667505 DRR667506	1,966,548 21,509	28,928	Total C M	 AP041482 AP041483	5,863,271 3,862,164 2,001,107	96	5,125 3,553 1,572
44	311897	Tomato, Ehime, 1983	SAMD01229212	DRR667507 DRR667508	1,155,976 13,547	36,611	Total C M	 AP041484 AP041485	5,968,507 3,981,713 1,986,794	66	5,249 3,684 1,565
45	311898	Eggplant, Kyoto, 1983	SAMD01229213	DRR667509 DRR667510	1,422,502 13,481	40,538	Total C M	 AP041486 AP041487	5,896,643 3,904,732 1,991,911	77	5,172 3,609 1,563
46	311899	Tomato, Fukui, 1983	SAMD01229214	DRR667511 DRR667512	1,999,562 22,029	38,589	Total C M	 AP041488 AP041489	5,737,741 3,737,704 2,000,037	113	4,989 3,411 1,578
47	106256	Eggplant, Oita, 1983	SAMD01229215	DRR667513 DRR667514	1,309,706 12,824	38,940	Total C M	 AP041490 AP041491	5,816,819 3,818,903 1,997,916	68	5,084 3,512 1,572
48	311900	Eggplant, Kyoto, 1983	SAMD01229216	DRR667515 DRR667516	1,672,113 14,878	26,998	Total C M	 AP041492 AP041493	5,788,130 3,824,157 1,963,973	70	5,057 3,533 1,524
49	311901	Pepper, Kochi, 1983	SAMD01229217	DRR667517 DRR667518	1,590,209 14,606	32,814	Total C M	 AP041494 AP041495	6,167,988 4,104,406 2,063,582	76	5,431 3,811 1,620
50	106257	Tomato, Kochi, 1983	SAMD01229218	DRR667519 DRR667520	1,453,794 23,817	33,865	Total C M	 AP041496 AP041497	5,828,644 3,713,932 2,114,712	96	5,137 3,461 1,676
51	311902	Tomato, Kochi, 1983	SAMD01229219	DRR667521	1,562,679						

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TABLE 1 List of RSSC phylotype I strain^a (Continued)

No.	MAFF no. ^b	Host, location, year	BioSample	DRA accession no. (short read) (long read)	No. of reads <i>N</i> ₅₀ value (bp)	Genomic DNA ^c	Accession no.	Genome size (bp)	Coverage (x)	CDS ^d
52	106204	Eggplant, Kochi, 1983	SAM01229220	DRR667522	11,731	33,581	Total	5,707,225	69	5,003
							C	AP041498		3,407
							M	AP041499		1,596
53	106205	Eggplant, Kochi, 1983	SAM01229221	DRR667523	1,725,633					
				DRR667524	27,196	30,776	Total	5,827,089	108	5,110
							C	AP041500		3,588
54	106206	Eggplant, Kochi, 1983	SAM01229222	DRR667525	1,450,744					
				DRR667526	26,518	29,537	Total	5,825,193	94	5,112
							C	AP041502		3,587
55	106207	Tomato, Hiroshima, 1984	SAM01229223	DRR667527	1,566,992					
				DRR667528	11,251	34,241	Total	5,763,068	68	5,035
							C	AP041504		3,532
56	106208	Eggplant, Hiroshima, 1984	SAM01229224	DRR667529	1,522,992					
				DRR667530	33,363	28,549	Total	5,850,262	88	5,128
							C	AP041506		3,534
57	106209	Tomato, Hiroshima, 1984	SAM01229225	DRR667531	1,226,118					
				DRR667532	21,582	39,106	Total	5,762,977	91	5,033
							C	AP041508		3,531
58	106210	Eggplant, Nara, 1984	SAM01229226	DRR667533	1,987,491					
				DRR667534	20,421	26,959	Total	5,771,297	92	5,016
							C	AP041510		3,458
59	106211	Eggplant, Kyoto, 1984	SAM01229227	DRR667535	1,451,726					
				DRR667536	19,721	27,117	Total	5,959,154	78	5,265
							C	AP041512		3,707
60	106212	Tomato, Kyoto, 1984	SAM01229228	DRR667537	1,709,384					
				DRR667538	13,915	35,260	Total	6,073,546	80	5,294
							C	AP041514		3,684
61	106213	Eggplant, Hyogo, 1985	SAM01229229	DRR667539	1,776,768					
				DRR667540	25,765	28,296	Total	5,788,129	102	5,053
							C	AP041516		3,528
62	106214	Tomato, Tottori, 1985	SAM01229230	DRR667541	1,778,239					
				DRR667542	14,365	29,061	Total	5,763,643	77	5,020
							C	AP041518		3,461
63				DRR667543	2,114,408					
				DRR667544	16,417	35,716	Total	5,887,165	94	5,208
							C	AP041520		3,637
64				DRR667545	1,937,572					
				DRR667546	35,325	29,186	Total	5,947,209	123	5,214
							C	AP041522		3,655

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TABLE 1 List of RSSC phylotype I strain^a (Continued)

No.	MAFF no. ^b	Host, location, year	BioSample	DRA accession no. (short read) (long read)	No. of reads	<i>N</i> ₅₀ value (bp)	Genomic DNA ^c	Accession no.	Genome size (bp)	Coverage (x)	CDS ^d
64	106215	Tomato, Nara, 1985	SAMD01229232	DRR667547 DRR667548	1,688,859 22,723	29,562	M Total C M	AP041523 AP041524 AP041525	1,990,747 5,972,019 3,977,633 1,994,386	95	1,559 5,237 3,675 1,562
65	106216	Eggplant, Kyoto, 1985	SAMD01229233	DRR667549 DRR667550	2,064,695 22,678	30,062	Total C M	 AP041526 AP041527	5,991,520 3,975,237 2,016,283	105	5,289 3,700 1,589
66	106217	Eggplant, Hiroshima, 1987	SAMD01229234	DRR667551 DRR667552	1,702,280 20,557	26,192	Total C M	 AP041528 AP041529	5,682,684 3,718,867 1,963,817	83	4,945 3,404 1,541
67	106218	Eggplant, Mie, 2020	SAMD01229235	DRR667553 DRR667554	1,536,690 31,179	30,994	C	AP041530	5,872,279	113	5,134
68	311908	Pepper, Kyoto, 2007	SAMD01229236	DRR667555 DRR667556	1,838,524 14,702	31,244	Total C M	 AP041531 AP041532	5,983,525 3,913,610 2,069,915	80	5,242 3,615 1,627
69	311931	Pepper, Kyoto, 1995	SAMD01229237	DRR667557 DRR667558	1,858,227 19,055	30,168	Total C M	 AP041533 AP041534	5,951,512 3,955,129 1,996,383	90	5,241 3,666 1,575
70	311910	Pepper, Kochi, 1997	SAMD01229238	DRR667559 DRR667560	1,425,276 42,147	23,109	Total C M	 AP041535 AP041536	6,157,846 4,092,890 2,064,956	113	5,431 3,807 1,624
71	311909	Pepper, Kochi, 1997	SAMD01229239	DRR667561 DRR667562	1,994,216 21,581	40,481	Total C M	 AP041537 AP041538	6,171,365 4,088,548 2,082,817	116	5,431 3,800 1,631
72	211266	Eggplant, Hiroshima, 1973	SAMD01229240	DRR667563 DRR667564	2,082,029 23,416	38,033	Total C M	 AP041539 AP041540	5,861,269 3,852,230 2,009,039	116	5,155 3,577 1,578
73	211282	Eggplant, Kochi, 1993	SAMD01229241	DRR667565 DRR667566	1,584,583 11,578	32,294	Total C M	 AP041541 AP041542	5,827,957 3,865,143 1,962,814	69	5,109 3,586 1,523
74	331041	Tomato, Tochigi, 2011	SAMD01229242	DRR667567 DRR667568	1,892,787 15,629	29,300	Total C M	 AP041543 AP041544	5,801,374 3,878,807 1,922,567	83	5,102 3,586 1,516
75	331042	Eggplant, Tochigi, 2011	SAMD01229243	DRR667569 DRR667570	1,605,001 18,229	35,134	Total C M	 AP041545 AP041546	5,872,477 3,891,892 1,980,585	88	5,149 3,593 1,556
76	331046	Tomato, Tochigi, 2011	SAMD01229244	DRR667571 DRR667572	1,740,081 15,995	30,694	Total		5,901,312	81	5,163

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TABLE 1 List of RSSC phylotype I strain^a (Continued)

No.	MAFF no. ^b	Host, location, year	BioSample	DRA accession no. (short read) (long read)	No. of reads <i>N</i> ₅₀ value (bp)	Genomic DNA ^c	Accession no.	Genome size (bp)	Coverage (x)	CDS ^d
77	311906	Eggplant, Osaka, 1997	SAMD01229245	DRR667573 DRR667574	1,947,361 48,143 27,757	C	AP041547	3,990,785		3,675
						M	AP041548	1,910,527		1,488
						Total		5,796,534	152	5,101
78	311907	Eggplant, Osaka, 1997	SAMD01229246	DRR667575 DRR667576	1,748,226 15,535 38,185	C	AP041549	3,821,023		3,547
						M	AP041550	1,975,511		1,554
						Total		5,795,064	84	5,108
79	311855	Eggplant, Okayama, 2017	SAMD01229247	DRR667577 DRR667578	2,092,244 19,426 30,903	C	AP041551	3,818,341		3,550
						M	AP041552	1,976,723		1,558
						Total		5,793,865	98	5,055
80	107632	Tomato, Nara, 1981	SAMD01229248	DRR667579 DRR667580	1,692,505 17,549 30,948	C	AP041553	3,800,875		3,496
						M	AP041554	1,992,990		1,559
						Total		5,911,011	86	5,192
81	106259	Eggplant, Osaka, 1981	SAMD01229249	DRR667581 DRR667582	1,780,511 17,391 29,151	C	AP041555	3,914,014		3,624
						M	AP041556	1,996,997		1,568
						Total		5,873,679	83	5,148
82	106260	Tomato, Nara, 1982	SAMD01229250	DRR667583 DRR667584	1,760,106 24,795 28,270	C	AP041557	3,879,681		3,587
						M	AP041558	1,993,998		1,561
						Total		5,951,923	98	5,256
83	106261	Tomato, Gunma, 1982	SAMD01229251	DRR667585 DRR667586	1,810,225 30,819 26,464	C	AP041559	3,975,217		3,696
						M	AP041560	1,976,706		1,560
						Total		5,952,484	110	5,242
84	211268	Eggplant, Kochi, 1982	SAMD01229252	DRR667587 DRR667588	1,810,876 19,156 28,445	C	AP041561	3,892,397		3,603
						M	AP041562	2,060,087		1,639
						Total		6,103,685	88	5,384
85	106263	Eggplant, Kochi, 1982	SAMD01229253	DRR667589 DRR667590	1,625,426 19,853 34,224	C	AP041563	4,038,488		3,759
						M	AP041564	2,065,197		1,625
						Total		5,995,488	92	5,258
86	211267	Tomato, Shimane, 1982	SAMD01229254	DRR667591 DRR667592	1,642,696 19,728 27,290	C	AP041565	3,918,289		3,621
						M	AP041566	2,077,199		1,637
						Total		5,882,274	83	5,157
87	106264	Tomato, Hyogo, 1982	SAMD01229255	DRR667593 DRR667594	2,056,662 25,219 26,804	C	AP041567	3,894,796		3,598
						M	AP041568	1,987,478		1,559
						Total		5,986,207	105	5,296
88	106265	Tomato, Nagano, 1982	SAMD01229256	DRR667595 DRR667596	1,924,721 19,146 29,145	C	AP041569	3,853,259		3,539
						M	AP041570	2,132,948		1,757
						Total		5,986,207	105	5,296
89	106266	Tomato, Shizuoka, 1982	SAMD01229257	DRR667597	1,892,494	C	AP041571	5,824,791	93	5,088

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TABLE 1 List of RSSC phylotype I strain^a (Continued)

No.	MAFF no. ^b	Host, location, year	BioSample	DRA accession no. (short read) (long read)	No. of reads	<i>N</i> ₅₀ value (bp)	Genomic DNA ^c	Accession no.	Genome size (bp)	Coverage (x)	CDS ^d
90	106267	Eggplant, Fukuoka, 1983	SAM01229258	DRR667598	14,684	33,562	Total		5,931,771	85	5,241
							C	AP041572	3,950,773		3,693
							M	AP041573	1,980,998		1,548
91	106268	Eggplant, Kochi, 1983	SAM01229259	DRR667599	1,911,990						
				DRR667600	25,670	25,379	Total		5,791,512	101	5,066
							C	AP041574	3,826,834		3,526
92	106269	Tomato, Shiga, 1984	SAM01229260	DRR667601	1,534,680						
				DRR667602	14,826	37,526	Total		6,087,572	83	5,370
							C	AP041576	4,022,743		3,743
93	211269	Eggplant, Nara, 1985	SAM01229261	DRR667603	1,771,150						
				DRR667604	22,614	29,405	Total		5,935,647	97	5,249
							C	AP041578	3,969,107		3,698
94	311771	Tomato, Kumamoto, 2017	SAM01229262	DRR667605	2,042,781						
				DRR667606	14,316	34,211	Total		5,872,513	90	5,157
							C	AP041580	3,853,604		3,566
95	311772	Tomato, Saitama, 2017	SAM01229263	DRR667607	1,044,996						
				DRR667608	23,339	22,171	Total		5,788,974	69	5,056
							C	AP041582	3,826,179		3,534
96	311800	Tomato, Shizuoka, 2018	SAM01229264	DRR667609	1,089,342						
				DRR667610	22,870	24,187	Total		5,833,954	73	5,114
							C	AP041584	3,784,234		3,504
97	311800	Tomato, Shizuoka, 2018	SAM01229264	DRR667611	1,180,068						
				DRR667612	15,130	26,016	Total		5,833,954	73	5,114
							C	AP041584	3,784,234		3,504
98	311800	Tomato, Shizuoka, 2018	SAM01229264	DRR667613	1,180,068						
				DRR667614	15,130	26,016	Total		5,833,954	73	5,114
							C	AP041585	2,049,720		1,610
99	311800	Tomato, Shizuoka, 2018	SAM01229264	DRR667615	1,180,068						
				DRR667616	15,130	26,016	Total		5,833,954	73	5,114
							C	AP041586	5,962,481	62	5,257

^a Based on previous reports (1, 2, 4).

^b Genebank, Research Center of Genetic Resources, NARO (Tsukuba, Japan).

^c C, chromosome; M, megaplasmid.

^d CDS, coding DNA sequences.

replicon and circularized the sequences. The phased assemblies were further polished using medaka-1.7.2 (<https://github.com/nanoporetech/medaka>) with long reads and hypo-1.0.3 (12) with short reads. Genome annotation was performed using the DFAST program (ver. 1.6.0) (13). Unless otherwise stated, default parameters were used, but the expected genome size was set to 6 Mbp.

The characteristics of the sequenced genomes are shown in Table 1. The GC content of the test strains ranged from 66.7% to 67.0%. These results are similar to those previously reported for RSSC strains (3, 14).

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DATA AVAILABILITY

The complete sequences of the 96 RSSC strains have been deposited in the DNA Data Bank of Japan (DDBJ) under BioProject accession number [PRJDB20372](https://www.ncbi.nlm.nih.gov/bioproject/PRJDB20372). The BioSample accession numbers, DRA accession numbers (short- and long-read archives), and genome nucleotide accession numbers of each strain are shown in Table 1.

REFERENCES

- Fegan M, Prior P. 2005. How complex is “the *Ralstonia solanacearum* species complex, p 449–461. In Allen C, Prior P, Hayward AC (ed), Bacterial wilt disease and the *Ralstonia solanacearum* species complex. APS Press, St. Paul, MN.
- Safni I, Cleenwerck I, De Vos P, Fegan M, Sly L, Kappler U. 2014. Polyphasic taxonomic revision of the *Ralstonia solanacearum* species complex: proposal to emend the descriptions of *Ralstonia solanacearum* and *Ralstonia syzygii* and reclassify current *R. syzygii* strains as *Ralstonia syzygii* subsp. *syzygii* subsp. nov., *R. solanacearum* phylotype IV strains as *Ralstonia syzygii* subsp. *indonesiensis* subsp. nov., banana blood disease bacterium strains as *Ralstonia syzygii* subsp. *celebesensis* subsp. nov. and *R. solanacearum* phylotype I and III strains as *Ralstonia pseudosolanacearum* sp. nov. *Int J Syst Evol Microbiol* 64:3087–3103. <https://doi.org/10.1099/ijss.0.066712-0>
- Genin S, Denny TP. 2012. Pathogenomics of the *Ralstonia solanacearum* species complex. *Annu Rev Phytopathol* 50:67–89. <https://doi.org/10.1146/annurev-phyto-081211-173000>
- Horita M, Tsuchiya K, Suga Y, Yano K, Waki T, Kurose D, Furuya N. 2014. Current classification of *Ralstonia solanacearum* and genetic diversity of the strains in Japan. *J Gen Plant Pathol* 80:455–465. <https://doi.org/10.1007/s10327-014-0537-z>
- Denny TP, Hayward AC. 2001. Gram negative bacteria *Ralstonia*, p 151–174. In Schaad NW, Jones JB, Chun W (ed), Laboratory guide for identification of plant pathogenic bacteria. Vol. 3rd. APS Press, St. Paul, MN.
- Chen S. 2023. Ultrafast one-pass FASTQ data preprocessing, quality control, and deduplication using fastp. *Imeta* 2:e107. <https://doi.org/10.1002/imt2.107>
- Shen W, Sipos B, Zhao L. 2024. SeqKit2: a swiss army knife for sequence and alignment processing. *Imeta* 3:e191. <https://doi.org/10.1002/imt2.191>
- Kolmogorov M, Bickhart DM, Behsaz B, Gurevich A, Rayko M, Shin SB, Kuhn K, Yuan J, Polevikov E, Smith TPL, Pevzner PA. 2020. metaFlye: scalable long-read metagenome assembly using repeat graphs. *Nat Methods* 17:1103–1110. <https://doi.org/10.1038/s41592-020-00971-x>
- Chen Y, Nie F, Xie SQ, Zheng YF, Dai Q, Bray T, Wang YX, Xing JF, Huang ZJ, Wang DP, He LJ, Luo F, Wang JX, Liu YZ, Xiao CL. 2021. Efficient assembly of nanopore reads via highly accurate and intact error correction. *Nat Commun* 12:1–10. <https://doi.org/10.1038/s41467-020-20236-7>
- Vaser R, Šikić M. 2021. Time- and memory-efficient genome assembly with raven. *Nat Comput Sci* 1:332–336. <https://doi.org/10.1038/s43588-021-00073-4>
- Wick RR, Judd LM, Cerdeira LT, Hawkey J, Méric G, Vezina B, Wyres KL, Holt KE. 2021. Trycycler: consensus long-read assemblies for bacterial genomes. *Genome Biol* 22:266. <https://doi.org/10.1186/s13059-021-02483-z>
- Kundu R, Casey J, Sung WK. 2019. HyPo: super fast & accurate polisher for long read genome assemblies. *bioRxiv*. <https://doi.org/10.1101/2019.12.19.882506>
- Tanizawa Y, Fujisawa T, Nakamura Y. 2018. DFAST: a flexible prokaryotic genome annotation pipeline for faster genome publication. *Bioinformatics* 34:1037–1039. <https://doi.org/10.1093/bioinformatics/btx713>
- Lowe-Power T, Avalos J, Bai Y, Munoz MC, Chipman K, Elmgreen VN, Prasad N, Ramirez B, Sandhar A, Tom CE, Williams D. 2020. A meta-analysis of the known global distribution and host range of the *Ralstonia* species complex. *bioRxiv*. <https://doi.org/10.1101/2020.07.13.189936>