Table S1. Bacterial strains of the *Ralstonia solanacearum* Species Complex (RSSC) tested for presence of *ripAX2* coding sequence. Phylotype I and III strains belong to the species *R. pseudosolanacearum*, Phylotype IIA and IIB to the species *R. solanacearum*.

RUN	Strain Code	Phyl.[a]	Seqv.[a]	eST[b]	mST[b]	Clade[c]	Host of isolation	Country / Region	Location	Year of isolation	Virulence on E6[d]	Genomic sequence
17	CFBP6783	IIB	4NPB	16	3	4	*Heliconia caribea*	Martinique	Morne Rouge	2002	2	(Ailloud et al., 2015)
36	CFBP2957	IIA	36	33	1	2	*Solanum lycopersicum*	Martinique	Case Pilote	1987	2	(Remenant et al., 2010)
39	CFBP3059	III	23	2	5	6	*Solanum melongena*	Burkina Faso	Vallée du Kou	1990	4	(Guinard et al., 2016)
47	CIP365	I	45	42	11	1	*Solanum tuberosum*	Philippines	NA	1989	2	
54	GMI1000	I	18	60	22	1	*Solanum lycopersicum*	French Guiana	Kourou	1978	0	(Salanoubat et al., 2002)
58	JQ1143	IIA	39	78	1	2	*Solanum tuberosum*	Reunion Isl.	Bois Court	NA	1	
59	JT510	IIB	1	10	7	5	*Solanum tuberosum*	Reunion Isl.	Notre Dame de La Paix	1993	0	
85	PSS190	I	15	15	22	1	*Solanum lycopersicum*	Taïwan	Taipei	1995	NA	RalstoT3E
104	UW395	I	31	43	22	1	*Solanum lycopersicum*	South Africa	Transvaal	1986	1	

RUN	Strain Code	Phyl.[a]	Seqv.[a]	eST[b]	mST[b]	Clade[c]	Host of isolation	Country / Region	Location	Year of isolation	Virulence on E6[d]	Genomic sequence
106	UW397	I	31	43	22	1	*Solanum melongena*	South Africa	Transvaal	1986	1	
108	UW399	I	31	43	22	1	*Nicotinia tabacum*	South Africa	Transvaal	1986	3	
133	CMR15	III	29	59	47	6	*Solanum lycopersicum*	Cameroon	Obala	2005	5	(Remenant et al., 2010)
145	CFBP6942	III	29	9	25	6	*Solanum scabrum*	Cameroon	Dschang	2005	0	
147	CFBP7029	IIB	1	10	26	5	*Solanum lycopersicum*	Cameroon	Baham	2005	4	
150	CFBP7032	IIA	41	11	27	2	*Solanum lycopersicum*	Cameroon	Dschang	2005	1	
155	PSS366	I	15	15	22	1	*Solanum lycopersicum*	Taïwan	Yunlin	2003	1	
156	PSS216	I	15	15	11	1	*Solanum lycopersicum*	Taïwan	Hsinchu	1996	NA	RalstoT3E
157	PSS4	I	15	15	28	1	*Solanum lycopersicum*	Taïwan	Tainan	1988	4	(Guinard et al., 2016)
158	ACH92	I	16	91	9	1	*Zingiber officinale*	Australia	Queensland	1966	1	

RUN	Strain Code	Phyl.[a]	Seqv.[a]	eST[b]	mST[b]	Clade[c]	Host of isolation	Country / Region	Location	Year of isolation	Virulence on E6[d]	Genomic sequence
159	PSS358	I	15	15	22	1	*Solanum lycopersicum*	Taïwan	Yunlin	2003	NA	
215	CFBP7058	I	13	19	30	1	*Solanum scabrum*	Cameroon	Bafia	2005	2	(Guinard et al., 2016)
353	02-035	I	18	60	22	1	*Capsicum annuum*	Martinique	Marigot	2002	NA	
356	02-045	I	18	60	22	1	*Solanum melongena*	Martinique	Morne-des-Esses	2002	NA	
523	CFBP4963	III	19	29	14	6	*Solanum tuberosum*	Reunion Isl.	NA	NA	0	
657	CFBP2146	III	19	29	14	6	*Pelargonium asperum*	Reunion Isl.	NA	1980	1	
811	02-048	I	18	60	22	1	*Solanum melongena*	Martinique	Morne-des-Esses	2002	NA	
928	JQ1023	IIB	1	10	7	5	*Solanum lycopersicum*	Reunion Isl.	Mont Vert	1993	3	
941	JQ1131	IIB	1	10	7	5	*Solanum tuberosum*	Reunion Isl.	Piton Hyacinthe	1992	4	
969	TO10	I	47	50	22	1	*Solanum lycopersicum*	Indonesia	Magelang	2003	4	(Guinard et al., 2016)
994	RS82	I	18	60	22	1	*Solanum lycopersicum*	Indonesia	Magelang	1998	NA	

RUN	Strain Code	Phyl.[a]	Seqv.[a]	eST[b]	mST[b]	Clade[c]	Host of isolation	Country / Region	Location	Year of isolation	Virulence on E6[d]	Genomic sequence
996	JCRS23	I	17	30	22	1	*Solanum lycopersicum*	Thailand	Chiang Rai	NA	NA	
997	JCRS35	I	13	119	22	1	*Solanum melongena*	Thailand	Chiang Rai	NA	1	
999	JCRS01	I	17	30	22	1	*Solanum lycopersicum*	Thailand	Chiang Rai	NA	NA	
1002	RS67	I	14	72	46	1	*Solanum melongena*	India	Chikballapur, Karnataka	1998	2	
1008	RS70	I	14	72	46	1	*Solanum melongena*	India	Chikballapur, Karnataka	1998	NA	
1013	RS53	I	48	32	22	1	*Solanum lycopersicum*	India	Hazaribagh,,Bihar	1997	NA	
1029	RS22	I	48	32	22	1	*Capsicum sp.*	India	Bhubaneshwar, Orissa	1996	4	
1032	JCRS26	I	18	60	22	1	*Solanum lycopersicum*	Thailand	Chiang Rai	NA	2	
1039	RS15	I	48	120	22	1	*Solanum lycopersicum*	Thailand	Chiang Rai	1995	NA	
1040	RS32	I	14	72	46	1	*Solanum lycopersicum*	India	Bangalore, Karnataka	1997	NA	

RUN	Strain Code	Phyl.[a]	Seqv.[a]	eST[b]	mST[b]	Clade[c]	Host of isolation	Country / Region	Location	Year of isolation	Virulence on E6[d]	Genomic sequence
1042	RS14	I	48	120	22	1	*Solanum lycopersicum*	Thailand	Chiang Rai	1995	NA	
1047	RS51	I	48	32	22	1	*Solanum lycopersicum*	India	Hazaribagh, Bihar	1997	NA	
1050	RS48	I	17	121	22	1	*Solanum lycopersicum*	Indonesia	Magelang, Centr. Java	1997	1	
1109	RS43	I	47	50	22	1	*Solanum lycopersicum*	Indonesia	Magelang, Centr. Java	1997	NA	
1114	RS66	I	14	14	22	1	*Solanum lycopersicum*	Indonesia	Magelang, Centr. Java	1998	1	
1143	02-047	I	18	60	22	1	*Solanum melongena*	Martinique	Morne-des-Esses	2002	NA	
1216	RS79	I	18	60	22	1	*Solanum lycopersicum*	Indonesia	Magelang, Centr. Java	1998	NA	
1234	RS35	I	31	43	22	1	*Solanum melongena*	India	Bangalore, Karnataka	1997	NA	
1240	RS44	I	47	50	22	1	*Solanum lycopersicum*	Indonesia	Magelang, Centr. Java	1997	2	
1251	RS69	I	14	72	46	1	*Solanum melongena*	India	Chikballapur, Karnataka	1998	NA	

RUN	Strain Code	Phyl.[a]	Seqv.[a]	eST[b]	mST[b]	Clade[c]	Host of isolation	Country / Region	Location	Year of isolation	Virulence on E6[d]	Genomic sequence
1533	CIV3	I	46	28	39	1	*Solanum lycopersicum*	Ivory Coast	Songon	2010	1	
1538	CIV8	I	14	14	22	1	*Solanum lycopersicum*	Ivory Coast	Songon	2010	1	
1539	CIV9	I	31	43	22	1	*Solanum lycopersicum*	Ivory Coast	Songon	2010	2	
1546	CIV16	I	13	19	22	1	*Solanum melongena*	Ivory Coast	Anguédédou	2010	3.1	
1739	CIV18	I	18	63	39	1	*Solanum lycopersicum*	Ivory Coast	Bonoufla	2010	2	
1740	CIV19	I	31	43	22	1	*Solanum melongena*	Ivory Coast	Daloa	2010	2	
1743	CIV22	I	31	43	22	1	*Solanum melongena*	Ivory Coast	Daloa	2010	2	
1744	CIV23	I	31	43	22	1	*Solanum melongena*	Ivory Coast	Man	2010	2	(Guinard et al., 2016)
1747	CIV26	I	46	28	39	1	*Solanum lycopersicum*	Ivory Coast	Sinfra	2010	4	
1753	CIV32	IIA	35	27	1	2	*Solanum lycopersicum*	Ivory Coast	Sinfra	2010	5	

RUN	Strain Code	Phyl.[a]	Seqv.[a]	eST[b]	mST[b]	Clade[c]	Host of isolation	Country / Region	Location	Year of isolation	Virulence on E6[d]	Genomic sequence
1756	CIV35	I	14	14	22	1	*Solanum lycopersicum*	Ivory Coast	Sinfra	2010	3.2	
1761	CIV40	IIA	35	27	1	2	*Solanum lycopersicum*	Ivory Coast	Datta	2010	4	
1762	CIV41	IIA	35	27	1	2	*Solanum lycopersicum*	Ivory Coast	Datta	2010	1	
1771	CIV49	I	18	63	39	1	*Solanum lycopersicum*	Ivory Coast	Souandala	2010	2	
1792	CIV55	I	13	122	22	1	*Solanum lycopersicum*	Ivory Coast	Djebonoua-Kondoukro	2010	5	
1793	CIV56	III	48	67	5	6	*Solanum melongena*	Ivory Coast	Djebonoua-Kondoukro	2010	2	
1802	CIV65	I	31	43	22	1	*Solanum lycopersicum*	Ivory Coast	Agnibilekro-Attobro	2010	1	
1854	CIV98	I	14	14	22	1	*Solanum lycopersicum*	Ivory Coast	Yamoussoukro Nanan	2011	2	
1861	CIV105	IIA	35	27	1	2	*Solanum lycopersicum*	Ivory Coast	Datta Houphouékro	2011	1	

RUN	Strain Code	Phyl.[a]	Seqv.[a]	eST[b]	mST[b]	Clade[c]	Host of isolation	Country / Region	Location	Year of isolation	Virulence on E6[d]	Genomic sequence
1867	CIV111	I	13	19	22	1	*Solanum lycopersicum*	Ivory Coast	Datta Houphouékro	2011	1	
1884	CIV128	IIA	35	27	1	2	*Solanum lycopersicum*	Ivory Coast	Pakobo (Tiassalé)	2011	1	
1898	CIV142	I	31	43	22	1	*Solanum lycopersicum*	Ivory Coast	Sinfra	2011	1	
1900	CIV144	I	18	63	39	1	*Solanum lycopersicum*	Ivory Coast	Sinfra	2011	5	
1916	CIV160	I	14	14	22	1	*Capsicum annuum*	Ivory Coast	Bassam	2011	1	
1924	CIV168	I	13	123	22	1	*Croton hirsutum*	Ivory Coast	Bassam	2011	2	
1947	CIR011-076	IIB	4NPB	16	3	4	*Capsicum annuum*	French Guiana	Cacao	2011	3,2	
1966	CIR011-152	IIB	4NPB	16	3	4	*Solanum melongena*	French Guiana	Wayabo	2011	2	
1976	CIR011-187	IIB	38	39	4	2	*Solanum melongena*	French Guiana	Corossoni	2011	2	
1984	CIR011-206	I	17	30	22	1	*Capsicum annuum*	French Guiana	Javouhey	2011	NA	
1985	CIR011-208	I	17	30	22	1	*Solanum melongena*	French Guiana	Javouhey	2011	5	(Guinard et al., 2016)

RUN	Strain Code	Phyl.[a]	Seqv.[a]	eST[b]	mST[b]	Clade[c]	Host of isolation	Country / Region	Location	Year of isolation	Virulence on E6[d]	Genomic sequence
1986	CIR011-209	I	17	30	22	1	*Solanum melongena*	French Guiana	Javouhey	2011	NA	
1987	CIR011-219	I	17	30	22	1	*Solanum melongena*	French Guiana	Javouhey	2011	2	
1992	CIR011-239	IIB	4NPB	16	3	4	*Cucurbita pepo*	French Guiana	Cacao	2011	2	
1994	CIR011-242	IIA	41	75	4	2	*Solanum lycopersicum*	French Guiana	Montsinéry	2011	2	
2004	CIR011-253	IIB	4NPB	16	3	4	*Solanum lycopersicum*	French Guiana	Corossoni	2011	2	
2174	012-011	I	14	80	22	1	*Solanum melongena*	French Guiana	Saint Laurent du Maroni	2012	4	
2175	012-012	I	14	80	22	1	*Solanum melongena*	French Guiana	Saint Laurent du Maroni	2012	4	
2176	012-013	I	14	80	22	1	*Solanum melongena*	French Guiana	Saint Laurent du Maroni	2012	3.1	
3012	TD1301	I	31	43	22	1	*Solanum melongena*	Reunion Isl.	Saint Pierre, Le Vallon	2013	2	(Guinard et al., 2016)
3013	RD1301	I	31	43	22	1	*Solanum melongena*	Reunion Isl.	Saint Pierre, Le Vallon	2013	1	(Guinard et al., 2016)

RUN	Strain Code	Phyl.[a]	Seqv.[a]	eST[b]	mST[b]	Clade[c]	Host of isolation	Country / Region	Location	Year of isolation	Virulence on E6[d]	Genomic sequence
3014	TF3108	I	31	43	22	1	*Solanum melongena*	Reunion Isl.	Saint Pierre, Le Vallon	2013	2	(Guinard et al., 2016)

[a] Phylotype and *egl*-based sequevar (Fegan & Prior, 2005, Wicker *et al.*, 2012)

[b] egl-Sequence Type (eST) and mutS-Sequence Type (mST) (Wicker et al., 2012, Wicker *et al.*, 2016)

[c] Clade, determined from *egl* and *mutS* phylogenetic trees, as defined in (Wicker et al., 2012)

[d] E6 is the code name of the eggplant accession AG91-25. The number assigned to each strain x accession combination represents the phenotype score, defined by the combination of final wilting incidence and colonization index and calculated as defined by Lebeau et al. (2011): 1, highly resistant; 2, moderately resistant; 3.1, partially resistant; 3.2, latent infection; 4, moderately susceptible; 5, highly susceptible. 0 is a incompatible interaction (no symptom and no colonization).

Fegan, M. and Prior, P. (2005) How complex is the "*Ralstonia solanacearum* species complex". In: *Bacterial wilt disease and the Ralstonia solanacearum species complex.* (Allen, C., Prior, P. and Hayward, A. C., eds.). Madison: APS Press, pp. 449-462.

Lebeau, A., Daunay, M. C., Frary, A., Palloix, A., Wang, J. F., Dintinger, J., Chiroleu, F., Wicker, E. and Prior, P. (2011) Bacterial wilt resistance in tomato, pepper, and eggplant: genetic resources respond to diverse strains in the *Ralstonia solanacearum* species complex. *Phytopathology,* **101,** 154-165.

Wicker, E., Lefeuvre, P., Cambiaire, J. C. d., Lemaire, C., Poussier, S. and Prior, P. (2012) Contrasting recombination patterns and demographic histories of the plant pathogen *Ralstonia solanacearum* inferred from MLSA. *ISME Journal,* **6,** 961-974.

Wicker, E., N'Guessan, A. C., Le Roux-Nio, A.-C., Deberdt, P., Sujeeun, L., Rivière, P. and Vinatzer, B. A. (2016) A reference database of *Ralstonia solanacearum* egl-mutS haplotypes for global epidemiological surveillance of bacterial wilts. Toulouse, The Laboratory for PLant -Microbes Interactions.

Table S2. Distribution of *ripAX2* within the 74 RSSC genomes harbored in the RalstoT3E database. Strains are ranked by Phylotype and code. Phylotypes I and III are grouped within *R.pseudosolanacearum*, Phylotype IIA and IIB within *R.solanacearum*, Phylotype IV within *R.syzygii*. The *ripAX2* type III effector is either present as a complete sequence (PROT), frameshifted (FS), pseudogenized (PS), or absent (NO).

Phylotype	Strain	RipAX2
I	161	PROT
I	244	FS
I	CMR134	PROT
I	FJAT-452	NO
I	FJAT-462	NO
I	FJAT-91	NO
I	FJAT1458	PS
I	FQY_4	NO
I	GMI1000	PROT
I	KACC10709	PROT
I	OE1-1	NO
I	PSS1308	NO
I	PSS190	NO
I	PSS216	NO
I	PSS4	NO
I	RD1301	PROT
I	RD15	FS
I	RUN1744	PROT
I	RUN1985	NO
I	Rs-T02	NO
I	SD54	NO
I	TD1301	PROT
I	TF3108	PROT
I	TO10	FS
I	Y45	PROT
I	YC40-M	FS
I	YC45	NO
III	CFBP3059	NO
III	CMR15	NO
IIA	B50	NO
IIA	CFBP2957	NO
IIA	Grenada91	PROT
IIA	IBSBF1900	NO
IIA	K60	NO
IIA	UW181	NO
IIB	23_10BR	PROT
IIB	CFBP1416	NO

Phylotype	Strain	RipAX2
IIB	CFBP3858	NO
IIB	CFBP6783	NO
IIB	CFBP7014	NO
IIB	CFIA906	NO
IIB	CIP417	PROT
IIB	IBSBF1503	NO
IIB	IPO1609	NO
IIB	KACC10722	NO
IIB	Molk2	PROT
IIB	NCPPB909	NO
IIB	NCPPB_282	FS
IIB	P673	PROT
IIB	POPS2	NO
IIB	Po82	NO
IIB	R52B	NO
IIB	UW163	PROT
IIB	UW179	NO
IIB	UW349B	PROT
IIB	UW365B	PROT
IIB	UW491B	NO
IIB	UW551	NO
IIB	UY031	NO
IV	BDBR229	NO
IV	BDB_RUN1314	NO
IV	BDB_RUN1347	NO
IV	BDB_RUN1348	NO
IV	BDB_RUN1349	NO
IV	BDB_RUN1350	NO
IV	BDB_RUN1351	NO
IV	Psi07	NO
IV	RUN1302	NO
IV	RUN1308	NO
IV	RUN1311	NO
IV	RUN1313	NO
IV	RUN702	NO
IV	RUN84	NO
IV	R24	NO

Table S3. Comparison of *ripAX2* distribution assessed by PCR amplification, or genome sequencing, on the 15 strains common to our collection and the RalstoT3E database. The gene was present (1), frameshifted (FS), or absent (0).

RUN code	Strain ID	Genome ID	Phylotype	Sequevar	Year	PCR	Genome
17	CFBP6783	CFBP6783	IIB	4NPB	2002	0	0
36	CFBP2957	CFBP2957	IIA	36	1987	0	0
39	CFBP3059	CFBP3059	III	23	1990	0	0
54	GMI1000	GMI1000	I	18	1978	1	1
85	PSS190	PSS190	I	15	1995	0	0
133	CMR15	CMR15	III	29	2005	0	0
156	PSS216	PSS216	I	15	1996	0	0
157	PSS4	PSS4	I	15	1988	0	0
215	CFBP7058	CMR134	I	13	2005	1	1
969	TO10	TO10	I	47	2003	1	FS
1744	CIV23	RUN1744	I	31	2010	1	1
1985	E16A2	RUN1985	I	17	2011	0	0
3012	TD13.01	TD1301	I	31	2013	1	1
3013	RD13.01	RD1301	I	31	2013	1	1
3014	TF31.08	TF3108	I	31	2013	1	1

Table S4. External and internal primers designed to amplify the *ripAX2*-coding sequence. Both external and internal primers were designed on the alignment of GM1000 and RS1000 *ripAX2* gene and neighbouring regions.

Target	Primer name	Sequence (5'->3')	Tm (°C)	Annealing temperature (°C)	PCR cycles	Expected size (pb)	Reference
Flanking regions	ripAX2-ph1_309F	TGTACTCGCCCCATCAGTTG	59.8	57	30	858	This study
	ripAX2-ph1_1167R	TTCAGGCGAGCCATTGACAA	60.3				
Internal sequence	RSp0572_60F	CGAAGCTGACCGTTATGCGGG	58.8	55	30	468	(Pensec et al., 2015)
	RSp0572_527R	CCTGCCTCGCTGGTTTCGTTG	59.3				

PCR reactions consisted in 5 min of initial denaturation at 96° ; 30 cycles of (i) 30 s at 94°, (ii) 60 s at the annealing temperature, (iii), 60 s at 72°; 10 min of final elongation at 72°.

Table S5. Bacterial strains of the *Ralstonia solanacearum* Species Complex (RSSC) with their host of isolation, nucleotidic and proteic RipAX2 alleles, GenBank accession numbers.

RUN ID	Phylotype	Sequevar[a]	Clade egl[b]	Clade mutS[b]	eST[c]	mST[c]	Year	Region	Country	Host	Nucleotide allele[d]	Proteic allele[e]	PROT[f]	GENBANK number
RUN 0017	IIB	4NPB	4	4	16	NA	2002	South America	Martinique	*Heliconia caribea*	NA	NA	NA	
RUN 0036	IIA	36	2	2	33	1	1987	South America	Martinique	*Solanum lycopersicum*	NA	NA	NA	
RUN 0039	III	23	6	6	2	5	1990	Africa	Burkina Faso	*Solanum melongena*	NA	NA	NA	
RUN 0047	I	45	1	1	42	11	1989	Asia	Philippines	*Solanum tuberosum*	hapng01	HapAA22	PROT	MF055715
RUN 0054	I	18	1	1	60	22	1978	South America	French Guiana	*Solanum lycopersicum*	hapng02	HapAA22	PROT	MF055716
RUN 0058	IIA	39	2	2	78	1	NA	Africa	Reunion	*Solanum tuberosum*	hapng01	HapAA22	PROT	
RUN 0059	IIB	1	5	5	10	7	1993	Africa	Reunion	*Solanum tuberosum*	NA	NA	NA	
RUN 0085	I	15	1	1	15	22	1995	Asia	Taiwan	*Solanum lycopersicum*	NA	NA	NA	
RUN 0104	I	31	1	1	43	22	1986	Africa	South Africa	*Solanum lycopersicum*	NA	NA	NA	

RUN ID	Phylotype	Sequevar[a]	Clade egl[b]	Clade mutS[b]	eST[c]	mST[c]	Year	Region	Country	Host	Nucleotide allele[d]	Proteic allele[e]	PROT[f]	GENBANK number
RUN 0106	I	31	1	1	43	22	1986	Africa	South Africa	*Solanum melongena*	hapng02	HapAA22	PROT	
RUN 0108	I	31	1	1	43	22	1986	Africa	South Africa	*Nicotinia tabacum*	hapng02	HapAA22	PROT	
RUN 0133	III	29	6	6	59	47	2005	Africa	Cameroon	*Solanum lycopersicum*	NA	NA	NA	
RUN 0145	III	29	6	6	9	25	2005	Africa	Cameroon	*Solanum scabrum*	Hapng05	HapAA08	PROT	MF055719
RUN 0147	IIB	1	5	5	10	26	2005	Africa	Cameroon	*Solanum lycopersicum*	NA	NA	NA	
RUN 0150	IIA	41	2	2	11	27	2005	Africa	Cameroon	*Solanum lycopersicum*	Hapng06	HapAA06	PROT	MF055720
RUN 0155	I	15	1	1	15	22	2003	Asia	Taiwan	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 0156	I	15	1	1	15	11	1996	Asia	Taiwan	*Solanum lycopersicum*	NA	NA	NA	
RUN 0157	I	15	1	1	15	28	1988	Asia	Taiwan	*Solanum lycopersicum*	NA	NA	NA	
RUN 0158	I	16	1	1	91	9	1966	Asia	Australia	*Zingiber officinale*	NA	NA	NA	

RUN ID	Phylotype	Sequevar[a]	Clade egl[b]	Clade mutS[b]	eST[c]	mST[c]	Year	Region	Country	Host	Nucleotide allele[d]	Proteic allele[e]	PROT[f]	GENBANK number
RUN 0159	I	15	1	1	15	22	2003	Asia	Taiwan	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 0215	I	13	1	1	19	30	2005	Africa	Cameroon	*Solanum scabrum*	hapng02	HapAA22	PROT	
RUN 0353	I	18	1	1	60	22	2002	South America	Martinique	*Capsicum annuum*	hapng02	HapAA22	PROT	
RUN 0356	I	18	1	1	60	22	2002	South America	Martinique	*Solanum melongena*	hapng02	HapAA22	PROT	
RUN 0523	III	19	6	6	29	14	NA	Africa	Reunion	*Solanum tuberosum*	Hapng09	HapAA13	NF	MF055723
RUN 0657	III	19	6	6	29	14	1980	Africa	Reunion	*Pelargonium asperum*	Hapng10	HapAA14	NF	MF055724
RUN 0811	I	18	1	1	60	22	2002	South America	Martinique	*Solanum melongena*	Hapng11	HapAA20	PROT	MF055725
RUN 0928	IIB	1	5	5	10	7	1993	Africa	Reunion	*Solanum lycopersicum*	NA	NA	NA	
RUN 0941	IIB	1	5	5	10	7	1992	Africa	Reunion	*Solanum tuberosum*	NA	NA	NA	
RUN 0969	I	47	1	1	50	22	2003	Asia	Indonesia	*Solanum lycopersicum*	Hapng13	HapAA17	NF	MF055727

RUN ID	Phylotype	Sequevar[a]	Clade egl[b]	Clade mutS[b]	eST[c]	mST[c]	Year	Region	Country	Host	Nucleotide allele[d]	Proteic allele[e]	PROT[f]	GENBANK number
RUN 0994	I	18	1	1	60	22	1998	Asia	Indonesia	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 0996	I	17	1	1	30	22	NA	Asia	Thailand	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 0997	I	13	1	1	119	22	NA	Asia	Thailand	*Solanum melongena*	hapng02	HapAA22	PROT	
RUN 0999	I	17	1	1	30	22	NA	Asia	Thailand	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 1002	I	14	1	1	72	46	1998	Asia	India	*Solanum melongena*	Hapng14	HapAA22	PROT	MF055728
RUN 1008	I	14	1	1	72	46	1998	Asia	India	*Solanum melongena*	Hapng14	HapAA22	PROT	
RUN 1013	I	48	1	1	32	22	1997	Asia	India	*Solanum lycopersicum*	Hapng15	HapAA19	NF	MF055729
RUN 1029	I	48	1	1	32	22	1996	Asia	India	*Capsicum sp.*	Hapng15	HapAA19	NF	
RUN 1032	I	18	1	1	60	22	NA	Asia	Thailand	*Solanum lycopersicum*	hapng02	HapAA22	PROT	

RUN ID	Phylotype	Sequevar[a]	Clade egl[b]	Clade mutS[b]	eST[c]	mST[c]	Year	Region	Country	Host	Nucleotide allele[d]	Proteic allele[e]	PROT[f]	GENBANK number
RUN 1039	I	48	1	1	120	22	1995	Asia	Thailand	*Solanum lycopersicum*	Hapng16	HapAA22	PROT	MF055730
RUN 1040	I	14	1	1	72	46	1997	Asia	India	*Solanum lycopersicum*	Hapng14	HapAA22	PROT	
RUN 1042	I	48	1	1	120	22	1995	Asia	Thailand	*Solanum lycopersicum*	Hapng17	HapAA07	PROT	MF055731
RUN 1047	I	48	1	1	32	22	1997	Asia	India	*Solanum lycopersicum*	Hapng15	HapAA19	NF	
RUN 1050	I	17	1	1	121	22	1997	Asia	Indonesia	*Solanum lycopersicum*	NA	NA	NA	
RUN 1109	I	47	1	1	50	22	1997	Asia	Indonesia	*Solanum lycopersicum*	Hapng13	HapAA17	NF	
RUN 1114	I	14	1	1	14	22	1998	Asia	Indonesia	*Solanum lycopersicum*	Hapng18	HapAA18	NF	MF055732
RUN 1143	I	18	1	1	60	22	2002	South America	Martinique	*Solanum melongena*	hapng02	HapAA22	PROT	
RUN 1216	I	18	1	1	60	22	1998	Asia	Indonesia	*Solanum lycopersicum*	hapng02	HapAA22	PROT	

RUN ID	Phylotype	Sequevar[a]	Clade egl[b]	Clade mutS[b]	eST[c]	mST[c]	Year	Region	Country	Host	Nucleotide allele[d]	Proteic allele[e]	PROT[f]	GENBANK number
RUN 1234	I	31	1	1	43	22	1997	Asia	India	*Solanum melongena*	hapng02	HapAA22	PROT	
RUN 1240	I	47	1	1	50	22	1997	Asia	Indonesia	*Solanum lycopersicum*	Hapng19	HapAA16	NF	MF055733
RUN 1251	I	14	1	1	72	46	1998	Asia	India	*Solanum melongena*	Hapng14	HapAA22	PROT	
RUN 1533	I	46	1	1	28	39	2010	Africa	Ivory Coast	*Solanum lycopersicum*	Hapng20	hapAA02	PROT	MF055734
RUN 1538	I	14	1	1	14	22	2010	Africa	Ivory Coast	*Solanum lycopersicum*	Hapng21	HapAA22	PROT	MF055735
RUN 1539	I	31	1	1	43	22	2010	Africa	Ivory Coast	*Solanum lycopersicum*	Hapng21	HapAA22	PROT	
RUN 1546	I	13	1	1	19	22	2010	Africa	Ivory Coast	*Solanum melongena*	Hapng29	HapAA23	NF	MF055743
RUN 1739	I	18	1	1	63	39	2010	Africa	Ivory Coast	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 1740	I	31	1	1	43	22	2010	Africa	Ivory Coast	*Solanum melongena*	Hapng30	HapAA24	NF	MF055744

RUN ID	Phylotype	Sequevar[a]	Clade egl[b]	Clade mutS[b]	eST[c]	mST[c]	Year	Region	Country	Host	Nucleotide allele[d]	Proteic allele[e]	PROT[f]	GENBANK number
RUN 1743	I	31	1	1	43	22	2010	Africa	Ivory Coast	*Solanum melongena*	Hapng31	HapAA25	NF	MF055745
RUN 1744	I	31	1	1	43	22	2010	Africa	Ivory Coast	*Solanum melongena*	Hapng21	HapAA22	PROT	
RUN 1747	I	46	1	1	28	39	2010	Africa	Ivory Coast	*Solanum lycopersicum*	Hapng21	HapAA22	PROT	
RUN 1753	IIA	35	2	2	27	1	2010	Africa	Ivory Coast	*Solanum lycopersicum*	Hapng22	hapAA03	PROT	MF055736
RUN 1756	I	14	1	1	14	22	2010	Africa	Ivory Coast	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 1761	IIA	35	2	2	27	1	2010	Africa	Ivory Coast	*Solanum lycopersicum*	NA	NA	NA	
RUN 1762	IIA	35	2	2	27	1	2010	Africa	Ivory Coast	*Solanum lycopersicum*	NA	NA	NA	
RUN 1771	I	18	1	1	63	39	2010	Africa	Ivory Coast	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 1792	I	13	1	1	122	22	2010	Africa	Ivory Coast	*Solanum lycopersicum*	hapng02	HapAA22	PROT	

RUN ID	Phylotype	Sequevar[a]	Clade egl[b]	Clade mutS[b]	eST[c]	mST[c]	Year	Region	Country	Host	Nucleotide allele[d]	Proteic allele[e]	PROT[f]	GENBANK number
RUN 1793	III	48	6	6	67	5	2010	Africa	Ivory Coast	*Solanum melongena*	Hapng23	HapAA05	PROT	MF055737
RUN 1802	I	31	1	1	43	22	2010	Africa	Ivory Coast	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 1854	I	14	1	1	14	22	2011	Africa	Ivory Coast	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 1861	IIA	35	2	2	27	1	2011	Africa	Ivory Coast	*Solanum lycopersicum*	NA	NA	NA	
RUN 1867	I	13	1	1	19	22	2011	Africa	Ivory Coast	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 1884	IIA	35	2	2	27	1	2011	Africa	Ivory Coast	*Solanum lycopersicum*	NA	NA	NA	
RUN 1898	I	31	1	1	43	22	2011	Africa	Ivory Coast	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 1900	I	18	1	1	63	39	2011	Africa	Ivory Coast	*Solanum lycopersicum*	hapng02	HapAA22	PROT	
RUN 1916	I	14	1	1	14	22	2011	Africa	Ivory Coast	*Capsicum annuum*	Hapng24	HapAA15	NF	MF055738

RUN ID	Phylotype	Sequevar[a]	Clade egl[b]	Clade mutS[b]	eST[c]	mST[c]	Year	Region	Country	Host	Nucleotide allele[d]	Proteic allele[e]	PROT[f]	GENBANK number
RUN 1924	I	13	1	1	123	22	2011	Africa	Ivory Coast	*Croton hirsutum*	hapng02	HapAA22	PROT	
RUN 1947	IIB	4NPB	4	4	16	3	2011	South America	French Guiana	*Capsicum annuum*	NA	NA	NA	
RUN 1966	IIB	4NPB	4	4	16	3	2011	South America	French Guiana	*Solanum melongena*	NA	NA	NA	
RUN 1976	IIB	38	2	2	39	4	2011	South America	French Guiana	*Solanum melongena*	NA	NA	NA	
RUN 1984	I	17	1	1	30	22	2011	South America	French Guiana	*Capsicum annuum*	NA	NA	NA	
RUN 1985	I	17	1	1	30	22	2011	South America	French Guiana	*Solanum melongena*	NA	NA	NA	
RUN 1986	I	17	1	1	30	22	2011	South America	French Guiana	*Solanum melongena*	NA	NA	NA	
RUN 1987	I	17	1	1	30	22	2011	South America	French Guiana	*Solanum melongena*	hapng02	HapAA22	PROT	
RUN 1992	IIB	4NPB	4	4	16	3	2011	South America	French Guiana	*Cucurbita pepo*	NA	NA	NA	
RUN 1994	IIA	41	2	2	75	4	2011	South America	French Guiana	*Solanum lycopersicum*	Hapng32	HapAA26	NF	MF055746
RUN 2004	IIB	4NPB	4	4	16	3	2011	South America	French Guiana	*Solanum lycopersicum*	NA	NA	NA	

RUN ID	Phylotype	Sequevar[a]	Clade egl[b]	Clade mutS[b]	eST[c]	mST[c]	Year	Region	Country	Host	Nucleotide allele[d]	Proteic allele[e]	PROT[f]	GENBANK number
RUN 2174	I	14	1	1	80	22	2012	South America	French Guiana	*Solanum melongena*	NA	NA	NA	
RUN 2175	I	14	1	1	80	22	2012	South America	French Guiana	*Solanum melongena*	NA	NA	NA	
RUN 2176	I	14	1	1	80	22	2012	South America	French Guiana	*Solanum melongena*	NA	NA	NA	
RUN 3012	I	31	1	1	43	22	2013	Africa	Reunion	*Solanum melongena*	hapng02	HapAA22	PROT	
RUN 3013	I	31	1	1	43	22	2013	Africa	Reunion	*Solanum melongena*	hapng02	HapAA22	PROT	
RUN 3014	I	31	1	1	43	22	2013	Africa	Reunion	*Solanum melongena*	hapng02	HapAA22	PROT	

[a]Phylotype was determined based on *egl* and *mutS* partial sequence analysis, and sequevar based on *egl* only, based on reference sequences deposited on PAMDB (Wicker *et al.*, 2016).

[b]Clades determined as described in Wicker et al. (2012) (http://dx.doi.org/10.1038/ismej.2011.160)

[c]**eST**: egl-Sequence Type; **mST**: mutS-Sequence Type (N'Guessan et al., 2012, Deberdt *et al.*, 2014, Wicker et al., 2016), as deposited in PAMDB (http://genome.ppws.vt.edu/cgi-bin/MLST/home.pl)

[d] Nucleotide alleles were determined using DNASPv5 (Librado & Rozas, 2009), with sites with gaps/missing being considered. 32 alleles were thus determined.

[e]Proteic alleles were translated from the nucleotide alleles (Bacterial, Archeal and Plant Plastid Code), using Geneious v8.1.

[f] Amino-acid sequences were scored as PROT if their length was above 80% of the reference RipAX2 protein ($RipAX2_{GMI1000}$). Sequences with early stop codons were considered non-functional (NF).

Table S6. Specificities in distributions of the RipAX2 protein alleles (Hap_AA) across regions, as assessed by Chi-Square tests. **A**: distribution of each allele across regions. Status is either "absence" (ABS), "functional" (PROT), or "not functional" (NF). **B**: Distribution of each region across alleles.

A.

Hap_AA	All phylotypes (n=91)			Phylotype I (n=66)	
	Status	Chi-square, P-value		Chi-square, P-value	
ABS	ABS	0.000606198	***	0.008138687	*
hapAA_02	PROT	0.927097065	NS	0.463369369	NS
hapAA_03	PROT	0.100558869	NS	NA	
HapAA_05	PROT	0.048295195	NS	NA	
HapAA_06	PROT	0.100558869	NS	NA	
HapAA_07	PROT	0.944718345	NS	0.507341248	NS
HapAA_08	PROT	0.048295195	NS	NA	
HapAA_13	NF	0.048295195	NS	NA	
HapAA_14	NF	0.048295195	NS	NA	
HapAA_15	NF	0.927097065	NS	0.463369369	NS
HapAA_16	NF	0.944718345	NS	0.507341248	NS
HapAA_17	NF	0.720717274	NS	0.257395142	NS
HapAA_18	NF	0.944718345	NS	0.507341248	NS
HapAA_19	NF	0.455365742	NS	0.130587173	NS
HapAA_20	PROT	0.473511317	NS	0.105399225	NS
HapAA_22	PROT	0.025831442	NS	0.353270235	NS
HapAA_23	NF	0.927097065	NS	0.463369369	NS
HapAA_24	NF	0.927097065	NS	0.463369369	NS
HapAA_25	NF	0.927097065	NS	0.463369369	NS
HapAA_26	NF	1.70983E-07	***	NA	

B.

All phylotypes (n=91)				Phylotype I (n=66)	
Phylotype	Region	Chi-square, P-value		Chi-square, P-value	
Phylotype I	Africa	0.1368124	NS	0.42279989	NS
	Asia	0.4803289	NS	0.70064089	NS
	South America	0.9616814	NS	0.33805894	NS
Phylotype IIA	Africa	0.11711797	NS		

All phylotypes (n=91)				Phylotype I (n=66)
Phylotype	Region	Chi-square, P-value		Chi-square, P-value
	South America	0.00067032	**	
Phylotype IIB	Africa	0.98020688	NS	
	South America	0.847279	NS	
Phylotype III	Africa	<0.0001	***	