

**Figure S1** Colony growth of *Ac* strains in King's B agar medium plates. The typical colony morphology has been observed on strains performed in solid culture media.



**Figure S2** Hypersensitive response (HR) tests of *Ac* strains on tobacco leaves. The strains have caused hypersensitive reaction on six-week-old tobacco (*Nicotiana benthamian*) leaves after pathogen inoculation.



**Figure S3** Oxidase tests of *Ac* strains indicated that oxidase was positive on all tested strains.



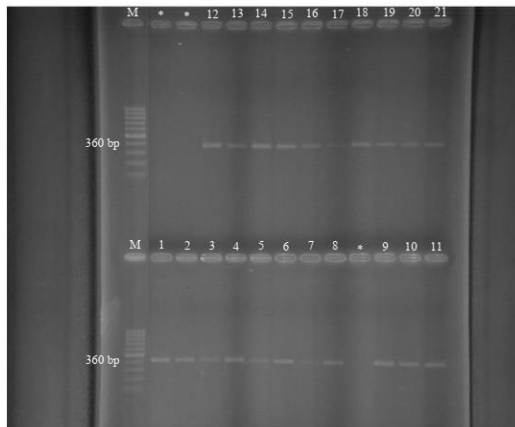
**Figure S4** Pathogenicity tests of *Ac* strains on watermelon seedlings showed typical symptoms of the pathogen on inoculated leaves.



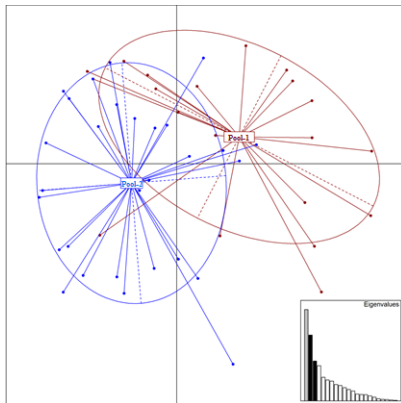
**Figure S5** Watermelon fruits typically appeared the fruit blotch disease symptom in the cultivation areas.



**Figure S6** Serological analysis carried out for the strains (21) collected in Turkey. ELISA tests were performed using an *Ac*-specific antibody (Cat. No. SRA 14800, Loewe).



**Figure S7** Molecular identification performed for the strains collected in Turkey. PCRs were carried out with specific primers for *Ac* strains, generating an expected amplicon at 360 bp according to WALCOTT and GITAITIS (2000). Asterisks (\*) show the deformed wells on gel.



**Figure S8** PCoA analysis based on genetic diversity among strains belonging to the Pool-1 (Red) and Pool-2 (Blue).

**Table S1** ISSR primers tested according to previous *in silico* analyses considering the whole genome sequence (*Acidovorax citrulli* strain NWB SC196).

Amplification(+)		Amplification(-)	
Primer Name	Sequence	Primer Name	Sequence
ENEA34	(ACC)6 CC	ENEA12	CCA(TG)7 T
ENEA13	GCAA(CA)6 C	ENEA36	CCA(TGA)5 TG
ENEA47	AG (CA)8	ENEA7-9	A(GA)7 GYT
ISSR12+12b	(GA)8 YT	ENEA21	(GA)8 GG
ISSR1-6	(CA)8 RG	ISSR8+8b	(GT)8 YG
ISSR2+2b	(AC)8 YG		
ISSR4+4b	(AC)8 YA		

**Table S2** Serological results (plate) for the strains (21) collected in Turkey **(A)** (Figure S6). Strain numbers are given according to Table 1 **(B)**. B blank, - negative control, + positive control.

26.09.2012	18:04:51										(A)
0,633	0,58	0,509	0,48	0,511	0,471	0,506	0,506	0,476			
0,658	0,521	0,497	0,489	0,552	0,489	0,489	0,479	0,536			
0,661	0,572	0,485	0,524	0,544	0,519	0,496	0,564	0,553			
0,69	0,617	0,596	0,581	0,549	0,651	0,592	0,649	0,528			
0,718	0,603	0,568	0,581	0,547	0,634	0,551	0,531	0,516			
0,733	0,664	0,582	0,617	0,639	0,658						
0,709	0,698	0,594	0,711	0,58	0,671				<b>0,108</b>	<b>0,108</b>	<b>0,585</b>
0,798	0,719	0,759	0,703	0,729	0,879				<b>0,108</b>	<b>0,112</b>	<b>0,559</b>
											<b>(B)</b>
30	30	30	38	38	38	46	46	46			
31	31	31	39	39	39	47	47	47			
32	32	32	40	40	40	48	48	48			
33	33	33	41	41	41	49	49	49			
34	34	34	42	42	42	50	50	50			
35	35	35	43	43	43						
36	36	36	44	44	44				<b>B</b>	-	+
37	37	37	45	45	45				<b>B</b>	-	+

**Table S3** BLAST analysis for the tested ISSR markers.

Description <b>(ACC)6 CC</b>	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Acidovorax citrulli</i> strain M6 chromosome, complete genome	34.2	52970	100%	0.006	100.00%	CP029373.1
<i>Acidovorax citrulli</i> strain KACC17005 chromosome, complete genome	34.2	56972	100%	0.006	100.00%	CP023687.1
<i>Acidovorax citrulli</i> AAC00-1, complete genome	34.2	56936	100%	0.006	100.00%	CP000512.1
<i>Acidovorax citrulli</i> strain 148 hypothetical protein gene, partial cds; HrpB1, hypothetical proteins, lytic murein transglycosylase, SAM-dependent methyltransferase, HrcC, HrpD5, hypothetical proteins, HrpK, HrpB2, HrcJ, HrpB4, HrpE, HrcN, hypothetical proteins, GALA, hypothetical proteins, HrcT, HrpB7, HrcU, HrcV, HpaP, HrcQ, HrcR, HrcS, HpaA, HpaB, HrpG, HrpX, and chorismate mutase genes, complete cds; and anthranilate synthase component I gene, partial cds	24.3	319	100%	5.5	100.00%	AY898625.2
<i>Acidovorax citrulli</i> strain MH21 type III secretion system structural protein (hrcR) gene, complete cds	24.3	72.8	90%	5.5	100.00%	GQ202841.1

Description <b>GCAA(CA)6 C</b>	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Acidovorax citrulli</i> AAC00-1, complete genome	22.3	2670	100%	12	100.00%	CP000512.1
<i>Acidovorax citrulli</i> strain KACC17005 chromosome, complete genome	22.3	2670	100%	12	100.00%	CP023687.1
<i>Acidovorax citrulli</i> strain M6 chromosome, complete genome	20.3	1921	100%	49	100.00%	CP029373.1

Description <b>AG (CA)8</b>	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Acidovorax citrulli</i> AAC00-1, complete genome	22.3	2713	100%	15	100.00%	CP000512.1
<i>Acidovorax citrulli</i> strain KACC17005 chromosome, complete genome	22.3	2713	100%	15	100.00%	CP023687.1
<i>Acidovorax citrulli</i> strain M6 chromosome, complete genome	20.3	1713	100%	61	92.86%	CP029373.1

Description (GA)8 CT	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Acidovorax citrulli</i> strain KACC17005 chromosome, complete genome	30.2	5263	100%	0.064	100.00%	CP023687.1
<i>Acidovorax citrulli</i> AAC00-1, complete genome	30.2	5263	100%	0.064	100.00%	CP000512.1
<i>Acidovorax citrulli</i> strain M6 chromosome, complete genome	30.2	3118	100%	0.064	100.00%	CP029373.1

Description (GA)8 TT	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Acidovorax citrulli</i> strain KACC17005 chromosome, complete genome	32.2	5458	100%	0.016	100.00%	CP023687.1
<i>Acidovorax citrulli</i> AAC00-1, complete genome	32.2	5441	100%	0.016	100.00%	CP000512.1
<i>Acidovorax citrulli</i> strain M6 chromosome, complete genome	28.2	3262	100%	0.25	100.00%	CP029373.1

Description (CA)8 AG	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Acidovorax citrulli</i> strain KACC17005 chromosome, complete genome	26.3	2327	100%	0.99	100.00%	CP023687.1
<i>Acidovorax citrulli</i> AAC00-1, complete genome	26.3	2327	100%	0.99	100.00%	CP000512.1

Description (CA)8 GG	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Acidovorax citrulli</i> strain M6 chromosome, complete genome	22.3	2034	100%	15	100.00%	CP029373.1
<i>Acidovorax citrulli</i> strain KACC17005 chromosome, complete genome	22.3	2950	100%	15	100.00%	CP023687.1
<i>Acidovorax citrulli</i> AAC00-1, complete genome	22.3	2950	100%	15	100.00%	CP000512.1

Description (AC)8 CG	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Acidovorax citrulli</i> strain M6 chromosome, complete genome	22.3	2572	100%	15	100.00%	CP029373.1
<i>Acidovorax citrulli</i> AAC00-1, complete genome	22.3	3489	100%	15	100.00%	CP000512.1
<i>Acidovorax citrulli</i> strain KACC17005 chromosome, complete genome	22.3	3489	100%	15	100.00%	CP023687.1

Description (AC)8 TG	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Acidovorax citrulli</i> strain M6 chromosome, complete genome	22.3	1741	100%	15	100.00%	CP029373.1
<i>Acidovorax citrulli</i> AAC00-1, complete genome	22.3	2550	100%	15	100.00%	CP000512.1
<i>Acidovorax citrulli</i> strain KACC17005 chromosome, complete genome	22.3	2536	100%	15	100.00%	CP023687.1

Description (AC)8 CA	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Acidovorax citrulli</i> AAC00-1, complete genome	22.3	3034	100%	15	100.00%	CP000512.1
<i>Acidovorax citrulli</i> strain M6 chromosome, complete genome	22.3	2074	100%	15	100.00%	CP029373.1
<i>Acidovorax citrulli</i> strain KACC17005 chromosome, complete genome	22.3	3034	100%	15	100.00%	CP023687.1

Description (AC)8 TA	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<i>Acidovorax citrulli</i> AAC00-1, complete genome	22.3	2150	100%	15	100.00%	CP000512.1
<i>Acidovorax citrulli</i> strain KACC17005 chromosome, complete genome	22.3	2166	100%	15	100.00%	CP023687.1
<i>Acidovorax citrulli</i> strain M6 chromosome, complete genome	20.3	1402	100%	61	100.00%	CP029373.1



**Table S5** STRUCTURE results. The percentage of different pools (K) was indicated for each *Acidovorax citrulli* strain.

<b>Samples</b>	<b>Origin</b>	<b>group1</b>	<b>group2</b>	<b>group3</b>	<b>K</b>
1_00	USA	0.096	0.499	0.405	Admixture
92_300	USA	0.725	0.179	0.095	K1
92_301	USA	0.217	0.133	0.649	Admixture
92_305	USA	0.465	0.038	0.497	Admixture
94_21	USA	0.219	0.266	0.515	Admixture
94_39	USA	0.085	0.037	0.878	K3
94_48	USA	0.143	0.215	0.643	Admixture
98_17	USA	0.822	0.067	0.111	K1
99_5	USA	0.787	0.108	0.105	K1
200_23	USA	0.733	0.164	0.103	K1
200_30	USA	0.808	0.154	0.038	K1
201_12	USA	0.099	0.105	0.796	K3
202_66	Israel	0.81	0.077	0.113	K1
203_57	USA	0.822	0.04	0.138	K1
204_8	USA	0.067	0.123	0.81	K3
205_22	USA	0.271	0.552	0.178	Admixture
206_1	USA	0.745	0.046	0.208	K1
206_2	USA	0.515	0.219	0.266	Admixture
206_26	USA	0.069	0.04	0.891	K3
206_84	China	0.187	0.182	0.631	Admixture
206_95	China	0.813	0.054	0.133	K1
207_42	USA	0.84	0.03	0.13	K1
208_20	USA	0.149	0.59	0.261	Admixture
210_13	USA	0.592	0.116	0.292	Admixture
210_7	USA	0.114	0.685	0.201	Admixture
211_29	Unknown	0.195	0.362	0.443	Admixture
211_36	USA	0.05	0.042	0.908	K3
211_76	Israel	0.221	0.039	0.74	K3
AU2	Australia	0.766	0.043	0.191	K1
Ac_1	Turkey	0.66	0.231	0.11	Admixture
Ac_2	Turkey	0.146	0.454	0.4	Admixture
Ac_3_1	Turkey	0.05	0.044	0.906	K3
Ac_4	Turkey	0.043	0.921	0.035	K2
Ac_5	Turkey	0.386	0.57	0.044	Admixture
Ac_6_1	Turkey	0.191	0.776	0.032	K2
Ac_9	Turkey	0.043	0.922	0.036	K2
Ac_11	Turkey	0.849	0.043	0.108	K1
Ac_13	Turkey	0.149	0.331	0.519	Admixture
Ac_14	Turkey	0.104	0.426	0.47	Admixture
Ac_16	Turkey	0.155	0.757	0.088	K2
Ac_17	Turkey	0.062	0.846	0.092	K2
Ac_18	Turkey	0.061	0.733	0.205	K2
Ac_19	Turkey	0.445	0.511	0.044	Admixture
Ac_20	Turkey	0.069	0.129	0.802	K3
Ac_21	Turkey	0.11	0.233	0.657	Admixture
Ac_25	Turkey	0.064	0.04	0.897	K3
Ac_27	Turkey	0.175	0.275	0.549	Admixture
Ac_28	Turkey	0.066	0.582	0.352	Admixture
Ac_K1	Turkey	0.105	0.75	0.144	K2
Ac_K2	Turkey	0.071	0.84	0.089	K2