

Molecular epidemiology of *Xanthomonas perforans* outbreaks in tomato from transplant to field by single-nucleotide polymorphism analysis

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Supplementary information

Table S1. Genome details of sequenced strains collected from grower A.

Strain	Size (bp)	Coverage	Genes	GC%	Contigs
GEV1989	5,201,369	38.4	4,632	64.70	247
GEV1991	5,192,752	33.9	4,611	64.70	238
GEV1992	5,191,666	38.1	4,642	64.70	262
GEV1993	5,155,078	33.7	4,622	64.69	279
GEV2004	5,057,458	18.9	4,646	64.66	425
GEV2009	5,136,944	43.9	4,620	64.71	324
GEV2010	5,174,097	29.3	4,585	64.67	264
GEV2011	5,115,304	34.2	4,542	64.71	261
GEV2013	5,135,549	28.6	4,561	64.68	345
GEV2015	5,144,994	35.4	4,576	64.70	250
GEV2047	5,185,550	26.7	4,677	64.69	304
GEV2048	5,177,283	47.4	4,655	64.69	304
GEV2049	5,167,720	40.9	4,660	64.70	302
GEV2050	5,165,201	41.5	4,639	64.70	281
GEV2052	5,190,899	36.7	4,619	64.69	249
GEV2055	5,177,880	39.1	4,696	64.70	368
GEV2058	5,210,673	56.9	4,633	64.71	233
GEV2059	5,179,416	45.9	4,686	64.69	331
GEV2060	5,183,330	45.6	4,699	64.71	359
GEV2063	5,128,950	31.1	4,608	64.70	279

Table S2. Genome details of sequenced strains collected from grower B.

Strain	Size (bp)	Coverage	Genes	GC%	Contigs
GEV1911	5,137,800	21.7	4,681	64.67	404
GEV1912	5,167,005	30.4	4,598	64.70	253
GEV1913	5,183,227	25.5	4,678	64.68	340
GEV1914	5,113,830	25.9	4,671	64.61	409
GEV1915	5,174,692	25.2	4,695	64.61	361
GEV1916	5,102,395	30.3	4,591	64.67	311
GEV1917	5,161,255	30.8	4,601	64.67	267
GEV1918	5,092,768	29.7	4,548	64.69	255
GEV1919	5,186,082	46.1	4,658	64.68	286
GEV1920	5,147,727	25.4	4,647	64.61	330
GEV1921	5,172,196	29.4	4,663	64.71	333
GEV2065	5,129,485	31.3	4,603	64.64	328
GEV2067	5,213,895	32.7	4,635	64.64	248
GEV2072	5,203,120	34.3	4,622	64.68	240
GEV2087	5,122,760	34.6	4,582	64.67	272
GEV2088	5,139,743	28.9	4,643	64.69	315
GEV2089	5,102,991	28.1	4,623	64.67	328
GEV2097	5,129,171	32.2	4,560	64.68	299
GEV2098	5,174,608	29.6	4,661	64.70	323
GEV2099	5,110,801	31.0	4,550	64.71	303
GEV2108	5,105,539	37.8	4,566	64.71	345
GEV2109	5,200,764	40.2	4,661	64.67	277
GEV2110	5,120,298	42.9	4,567	64.77	237
GEV2111	5,100,511	52.1	4,481	64.81	181
GEV2112	5,089,796	27.6	4,530	64.64	301
GEV2113	5,163,947	25.2	4,671	64.62	345
GEV2114	5,172,135	28.9	4,648	64.61	314
GEV2115	5,179,887	29.6	4,692	64.66	377
GEV2116	5,153,501	25.6	4,620	64.67	299
GEV2117	5,070,119	26.8	4,539	64.80	272
GEV2118	5,161,403	26.2	4,654	64.68	314
GEV2119	5,114,562	23.9	4,580	64.66	294
GEV2120	5,196,625	25.9	4,647	64.62	276
GEV2121	5,079,594	21.7	4,532	64.64	286
GEV2122	5,127,626	22.0	4,544	64.64	235
GEV2123	5,002,536	19.8	4,592	64.63	420
GEV2124	5,031,454	25.9	4,426	64.71	221
GEV2125	4,944,651	14.0	4,591	64.66	525
GEV2126	5,089,637	30.0	4,475	64.79	204

Strain	Size (bp)	Coverage	Genes	GC%	Contigs
GEV2127	5,031,736	22.3	4,490	64.69	296
GEV2128	5,129,344	33.2	4,517	64.69	247
GEV2129	5,145,947	24.7	4,585	64.66	256
GEV2130	5,120,789	33.1	4,480	64.71	195
GEV2132	5,059,184	33.2	4,452	64.80	193
GEV2133	5,149,660	32.4	4,551	64.71	185
GEV2134	5,106,930	27.6	4,513	64.67	221
GEV2135	5,092,715	28.1	4,474	64.81	175
GEV2384	5,222,248	12.6	4,647	64.69	213
GEV2388	5,236,092	14.1	4,639	64.70	167
GEV2389	5,215,458	16.0	4,554	64.69	132
GEV2390	5,228,216	18.8	4,522	64.67	98
GEV2391	5,179,570	14.7	4,532	64.72	154
GEV2392	5,219,799	13.3	4,569	64.66	155
GEV2393	5,214,977	13.1	4,619	64.69	190
GEV2396	5,221,146	13.6	4,562	64.66	157
GEV2397	5,210,116	12.0	4,622	64.66	238
GEV2398	4,681,733	7.7	4,604	64.56	743
GEV2399	5,188,814	13.8	4,586	64.75	168
GEV2400	5,197,734	12.5	4,609	64.68	226
GEV2403	5,207,841	13.6	4,606	64.69	182
GEV2407	5,234,490	15.0	4,586	64.70	134
GEV2408	5,108,905	12.6	4,496	64.80	193
GEV2410	5,234,631	16.5	4,588	64.69	136
GEV2420	5,239,724	13.7	4,636	64.67	181

Table S3. Single nucleotide polymorphism (SNP) details for individually sequenced strains in this study compared to reference strain Xp91-118.

Strain	#SNP ^a	CDS ^b	Intergenic	Non-synonymous ^c	Synonymous	Nonsense
Group 1						
GEV872	1,348	1,127	221	300	825	2
GEV893	1,339	1,119	220	293	824	2
GEV904	1,337	1,119	218	291	826	2
GEV909	1,344	1,125	219	299	824	2
GEV915	1,349	1,127	222	296	829	2
GEV917	1,335	1,118	217	295	821	2
GEV936	1,342	1,123	219	296	825	2
GEV940	1,352	1,134	218	303	828	3
GEV968	1,346	1,125	221	296	827	2
GEV993	1,348	1,128	220	298	828	2
GEV1026	1,350	1,129	221	300	827	2
GEV2398	1,069	902	164	209	694	1
Group 2						
Xp2010	4,133	3,406	722	874	2,527	8
GEV839	4,249	3,517	727	888	2,624	8
GEV1001	4,118	3,399	714	860	2,535	7
GEV1044	4,136	3,411	720	866	2,540	8
GEV1054	4,140	3,412	723	866	2,542	7
GEV1063	4,115	3,388	722	862	2,522	7
GEV1911	3,982	3,291	686	841	2,446	7
GEV1912	4,093	3,386	702	863	2,519	7
GEV1913	4,060	3,359	696	853	2,502	7
GEV1914	3,972	3,274	693	840	2,430	7
GEV1915	4,044	3,338	701	848	2,486	7
GEV1916	4,098	3,387	706	868	2,515	7
GEV1917	4,088	3,381	702	861	2,516	7
GEV1918	4,077	3,371	701	864	2,503	7
GEV1919	4,117	3,398	714	871	2,522	8
GEV1920	4,003	3,304	695	841	2,458	8
GEV1921	4,087	3,381	701	860	2,516	8
GEV1989	4,135	3,428	702	871	2,550	7
GEV1991	4,120	3,415	702	870	2,540	8
GEV1992	4,142	3,423	714	870	2,549	7
GEV1993	4,108	3,400	703	860	2,535	8
GEV2004	3,669	3,024	641	759	2,260	7
GEV2009	4,130	3,410	715	878	2,528	7
GEV2011	4,090	3,379	706	862	2,513	7
GEV2013	4,062	3,357	700	852	2,501	7
GEV2015	4,126	3,416	705	872	2,539	8
GEV2047	4,052	3,345	702	846	2,495	7
GEV2048	4,148	3,433	711	873	2,554	8
GEV2049	4,132	3,417	710	871	2,542	7
GEV2050	4,124	3,412	707	869	2,539	7
GEV2052	4,133	3,417	711	869	2,544	7
GEV2055	4,122	3,406	710	870	2,532	7
GEV2056	4,164	3,435	723	878	2,522	8
GEV2059	4,135	3,419	711	871	2,544	7
GEV2060	4,144	3,419	719	870	2,544	8
GEV2063	4,120	3,415	699	868	2,542	8

Strain	#SNP ^a	CDS ^b	Intergenic	Non-synonymous ^c	Synonymous	Nonsense
GEV2067	4,106	3,396	705	867	2,525	7
GEV2072	4,105	3,388	712	864	2,520	7
GEV2087	4,120	3,410	705	867	2,539	7
GEV2088	4,094	3,383	706	859	2,520	7
GEV2089	4,076	3,373	698	859	2,510	7
GEV2098	4,100	3,388	707	863	2,521	7
GEV2109	4,124	3,408	711	871	2,532	8
GEV2110	4,103	3,380	718	865	2,511	7
GEV2111	4,119	3,400	714	872	2,523	8
GEV2113	4,027	3,317	705	844	2,468	8
GEV2114	4,089	3,383	701	858	2,520	8
GEV2115	4,076	3,370	701	861	2,505	7
GEV2116	4,067	3,357	705	857	2,495	8
GEV2117	4,030	3,330	695	854	2,472	7
GEV2118	4,038	3,332	701	848	2,480	7
GEV2119	4,013	3,316	692	846	2,465	8
GEV2120	4,049	3,345	699	855	2,486	7
GEV2123	3,864	3,178	681	807	2,367	7
GEV2126	4,059	3,356	698	859	2,492	8
GEV2129	4,057	3,351	701	853	2,494	7
GEV2132	4,093	3,389	699	864	2,520	8
GEV2133	4,089	3,385	699	860	2,521	7
GEV2135	4,068	3,364	699	859	2,501	7
GEV2384	2,796	2,296	520	543	1,723	6
GEV2388	3,039	2,510	525	607	1,900	6
GEV2389	3,571	2,939	626	727	2,208	7
GEV2391	3,387	2,768	614	698	2,066	7
GEV2393	2,910	2,407	499	594	1,810	6
GEV2399	3,156	2,572	579	651	1,917	6
GEV2400	2,764	2,207	552	561	1,643	5
GEV2403	3,169	2,578	586	670	1,905	6
GEV2407	3,349	2,741	603	691	2,045	8
GEV2408	2,955	2,427	521	627	1,796	7
GEV2410	3,583	2,930	648	747	2,179	7
GEV2420	3,035	2,491	540	604	1,883	6
Group 3						
Xp17-12	5,128	4,076	1,043	1,020	3,054	8
GEV2010	4,660	3,903	748	955	2,949	5
GEV2065	4,680	3,910	761	949	2,961	6
GEV2097	4,677	3,915	753	942	2,974	5
GEV2099	4,629	3,874	746	931	2,944	5
GEV2108	4,645	3,887	749	943	2,945	5
GEV2112	4,624	3,861	754	938	2,923	6
GEV2121	4,515	3,778	728	924	2,855	5
GEV2122	4,527	3,779	738	915	2,864	6
GEV2124	4,578	3,834	736	922	2,912	5
GEV2125	3,592	3,016	567	726	2,290	5
GEV2127	4,492	3,752	729	897	2,856	6
GEV2128	4,675	3,911	755	947	2,964	6
GEV2130	4,649	3,892	748	942	2,951	5
GEV2134	4,652	3,887	756	938	2,950	5
GEV2390	4,210	3,539	666	870	2,668	5
GEV2392	3,247	2,701	539	639	2,061	4
GEV2396	3,504	2,927	572	712	2,213	5

GEV2397	2,872	2,399	464	586	1,811	5
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^a Compared to reference genome Xp91-118.

^b CDS: coding DNA sequence. Average number of SNPs in CDS and intergenic non-coding regions.

^c Effect of SNP on coding DNA sequence (CDS) protein product. Non-synonymous: amino acid change; synonymous: no amino acid change; non-sense: early stop codon in CDS.

Table S4. Range of genetic distances between seedling (upper panel) and field (left panel) grower A strains in group 2 based on single-nucleotide polymorphisms compared to Xp2010 reference genome.

	GEV2050 ^a	GEV2059	GEV2049	GEV2048	GEV2047	GEV2052	GEV2060	GEV2058	GEV2055	GEV2063	Range
GEV2009^b	0.060	0.067	0.071	0.064	0.059	0.059	0.057	0.063	0.061	0.055	0.055-0.071
GEV2011	0.052	0.058	0.062	0.055	0.051	0.050	0.048	0.055	0.053	0.046	0.046-0.062
GEV2013	0.050	0.056	0.060	0.053	0.049	0.048	0.046	0.053	0.050	0.044	0.044-0.060
GEV2004	0.016	0.023	0.027	0.019	0.015	0.015	0.013	0.019	0.017	0.011	0.011-0.027
GEV1992	0.016	0.023	0.027	0.019	0.015	0.015	0.013	0.019	0.017	0.011	0.011-0.027
GEV1989	0.011	0.017	0.021	0.014	0.010	0.009	0.016	0.022	0.020	0.014	0.009-0.022
GEV2015	0.013	0.019	0.024	0.016	0.012	0.012	0.016	0.022	0.020	0.014	0.012-0.024
GEV1993	0.015	0.021	0.026	0.018	0.014	0.014	0.012	0.018	0.016	0.010	0.010-0.026
GEV1991	0.017	0.024	0.028	0.020	0.016	0.016	0.014	0.020	0.018	0.012	0.012-0.028
Overall distance between seedling strains^c											0.005-0.035

^a Seedling strains were isolated during 9/2015.

^b Field strains were isolated during 10/2015.

^c The pairwise genetic distance between seedling strains only within grower A strains in group 2.

Table S5. Assignment of group 2 field strains to grower transplant or reference populations using discriminant analysis of principal components. To assess the influence of potential overfitting, posterior probabilities of assignments were calculated using four and three principal components.

Field Strain	Source	Prediction using 4 PCs (posterior probability)	Prediction using 3 PCs (posterior probability)
GEV2420	S. Carolina	Grower B Transplant (1.00)	Grower B Transplant (0.989)
GEV2384	S. Carolina	Grower B Transplant (1.00)	Grower B Transplant (0.989)
GEV2410	S. Carolina	Grower B Transplant (1.00)	Grower B Transplant (0.998)
GEV2408	S. Carolina	Reference (0.77)	Reference (0.969)
GEV2407	S. Carolina	Grower B Transplant (1.00)	Grower B Transplant (0.994)
GEV2403	S. Carolina	Grower B Transplant (1.00)	Grower B Transplant (0.667)
GEV2400	S. Carolina	Grower B Transplant (1.00)	Grower B Transplant (0.990)
GEV2399	S. Carolina	Reference (1.00)	Reference (0.997)
GEV2393	S. Carolina	Grower B Transplant (1.00)	Grower B Transplant (0.667)
GEV2391	S. Carolina	Grower B Transplant (1.00)	Grower B Transplant (0.667)
GEV2389	S. Carolina	Grower B Transplant (1.00)	Grower B Transplant (0.994)
GEV2388	S. Carolina	Reference (1.00)	Reference (0.998)
GEV1991	Grower A	Grower A Transplant (1.00)	Grower A Transplant (1.00)
GEV1989	Grower A	Grower A Transplant (1.00)	Grower A Transplant (1.00)
GEV1992	Grower A	Grower A Transplant (1.00)	Grower A Transplant (1.00)
GEV2004	Grower A	Grower A Transplant (1.00)	Grower A Transplant (1.00)
GEV1993	Grower A	Grower A Transplant (1.00)	Grower A Transplant (1.00)

GEV2009	Grower A	Grower B Transplant (1.00)	Grower B Transplant (0.771)
GEV2011	Grower A	Grower B Transplant (1.00)	Grower B Transplant (0.770)
GEV2013	Grower A	Grower B Transplant (1.00)	Grower B Transplant (0.779)
GEV2015	Grower A	Grower A Transplant (1.00)	Grower A Transplant (1.00)
GEV2109	Grower B	Grower B Transplant (1.00)	Grower B Transplant (0.998)
GEV2110	Grower B	Reference (1.00)	Reference (0.999)
GEV2111	Grower B	Reference (1.00)	Reference (0.999)
GEV2113	Grower B	Grower B Transplant (1.00)	Grower B Transplant (0.784)
GEV2114	Grower B	Grower B Transplant (1.00)	Grower B Transplant (0.894)
GEV2129	Grower B	Grower B Transplant (1.00)	Grower B Transplant (0.997)
GEV2132	Grower B	Reference (1.00)	Reference (0.999)
GEV2133	Grower B	Grower B Transplant (1.00)	Grower B Transplant (0.682)
GEV2135	Grower B	Reference (1.00)	Reference (0.999)
GEV2115	Grower B	Grower B Transplant (1.00)	Grower B Transplant (0.997)
GEV2116	Grower B	Grower B Transplant (1.00)	Grower B Transplant (0.997)
GEV2117	Grower B	Reference (1.00)	Reference (0.999)
GEV2118	Grower B	Grower B Transplant (1.00)	Grower B Transplant (0.998)
GEV2119	Grower B	Grower B Transplant (1.00)	Grower B Transplant (0.661)
GEV2120	Grower B	Grower B Transplant (1.00)	Grower B Transplant (0.873)
GEV2126	Grower B	Reference (1.00)	Reference (0.999)
GEV2123	Grower B	Grower B Transplant (1.00)	Grower B Transplant (0.998)

Table S6. Range of genetic distances between seedling (upper panel) and field (left panel) grower B strains in group 2 based on single-nucleotide polymorphisms compared to Xp2010 reference genome.

	GEV 1911	GEV 1918	GEV 1917	GEV 2072 ^a	GEV 1919	GEV 1921	GEV 1913	GEV 2089 ^a	GEV 1912	GEV 1916	GEV 1915	GEV 2067 ^a	GEV 1914	GEV 1920	GEV 2088 ^a	GEV 2098 ^a	GEV 2087 ^a	Range
GEV 2133 ^b	0.628	0.629	0.626	0.625	0.631	0.628	0.628	0.631	0.627	0.629	0.035	0.038	0.038	0.043	0.043	0.049	0.046	0.035 0.631
GEV 2113	0.612	0.613	0.61	0.609	0.615	0.612	0.612	0.615	0.611	0.613	0.019	0.022	0.022	0.027	0.033	0.039	0.036	0.019 0.615
GEV 2384	0.162	0.163	0.16	0.159	0.165	0.162	0.162	0.165	0.161	0.163	0.447	0.45	0.45	0.455	0.461	0.468	0.464	0.159 0.468
GEV 2420	0.168	0.169	0.166	0.165	0.171	0.168	0.168	0.171	0.167	0.169	0.597	0.6	0.6	0.604	0.611	0.617	0.614	0.165 0.617
GEV 2407	0.087	0.088	0.085	0.084	0.091	0.087	0.087	0.091	0.086	0.088	0.619	0.622	0.622	0.626	0.633	0.639	0.636	0.084 0.639
GEV 2389	0.085	0.086	0.083	0.082	0.088	0.085	0.085	0.088	0.084	0.086	0.653	0.656	0.656	0.661	0.667	0.674	0.67	0.082 0.674
GEV 2123	0.015	0.008	0.005	0.004	0.011	0.007	0.007	0.011	0.006	0.008	0.608	0.612	0.612	0.616	0.622	0.629	0.626	0.004 0.629
GEV 2410	0.016	0.01	0.006	0.005	0.01	0.006	0.006	0.01	0.005	0.007	0.61	0.613	0.613	0.617	0.623	0.63	0.627	0.005 0.63
GEV 2116	0.035	0.029	0.026	0.025	0.027	0.023	0.021	0.029	0.025	0.027	0.629	0.632	0.632	0.636	0.643	0.649	0.646	0.021 0.649
GEV 2115	0.036	0.03	0.027	0.026	0.028	0.025	0.023	0.03	0.026	0.028	0.63	0.633	0.633	0.637	0.644	0.65	0.647	0.023 0.65
GEV 2109	0.019	0.013	0.01	0.008	0.013	0.01	0.01	0.013	0.008	0.011	0.613	0.616	0.616	0.62	0.627	0.633	0.63	0.008 0.633
GEV 2129	0.016	0.01	0.006	0.005	0.01	0.006	0.006	0.01	0.005	0.007	0.609	0.613	0.613	0.617	0.623	0.63	0.627	0.005 0.63
GEV 2118	0.02	0.014	0.011	0.01	0.014	0.011	0.011	0.014	0.01	0.012	0.614	0.617	0.617	0.621	0.628	0.634	0.631	0.01 0.634
GEV 2400	0.127	0.128	0.124	0.123	0.13	0.127	0.127	0.13	0.125	0.128	0.611	0.614	0.614	0.618	0.624	0.631	0.628	0.123 0.631
GEV 2120	0.61	0.611	0.607	0.606	0.613	0.61	0.61	0.613	0.608	0.611	0.004	0.007	0.007	0.012	0.031	0.037	0.034	0.004 0.613
GEV 2114	0.612	0.613	0.609	0.608	0.615	0.612	0.612	0.615	0.611	0.613	0.002	0.005	0.003	0.01	0.033	0.039	0.036	0.002 0.615
GEV 2408	0.667	0.668	0.665	0.664	0.67	0.667	0.667	0.67	0.666	0.668	0.074	0.077	0.077	0.082	0.082	0.088	0.085	0.074 0.67
GEV 2126	0.705	0.706	0.703	0.702	0.708	0.705	0.705	0.708	0.704	0.706	0.113	0.116	0.116	0.12	0.12	0.126	0.123	0.113 0.708

GEV 2132	0.704	0.705	0.702	0.701	0.707	0.704	0.704	0.707	0.703	0.705	0.111	0.115	0.115	0.119	0.119	0.125	0.122	0.111 0.707
GEV 2111	0.714	0.715	0.712	0.71	0.717	0.714	0.714	0.717	0.713	0.715	0.121	0.124	0.124	0.129	0.129	0.135	0.132	0.121 0.717
GEV 2110	0.731	0.732	0.729	0.728	0.735	0.731	0.731	0.735	0.73	0.732	0.139	0.142	0.142	0.146	0.146	0.153	0.149	0.139 0.735
GEV 2399	0.746	0.747	0.744	0.743	0.749	0.746	0.746	0.749	0.745	0.747	0.154	0.157	0.157	0.161	0.161	0.167	0.164	0.154 0.749
GEV 2388	0.744	0.745	0.741	0.74	0.747	0.744	0.744	0.747	0.742	0.745	0.151	0.154	0.154	0.158	0.159	0.165	0.162	0.151 0.747
GEV 2135	0.727	0.728	0.725	0.724	0.73	0.727	0.727	0.73	0.726	0.728	0.134	0.138	0.138	0.142	0.142	0.148	0.145	0.134 0.73
GEV 2117	0.727	0.728	0.725	0.724	0.73	0.727	0.727	0.73	0.726	0.728	0.134	0.138	0.138	0.142	0.142	0.148	0.145	0.134 0.73
GEV 2403	0.621	0.622	0.619	0.618	0.624	0.621	0.621	0.624	0.62	0.622	0.029	0.032	0.032	0.036	0.036	0.043	0.039	0.029 0.624
GEV 2393	0.619	0.62	0.617	0.616	0.622	0.619	0.619	0.622	0.618	0.62	0.027	0.03	0.03	0.034	0.034	0.04	0.037	0.027 0.622
GEV 2391	0.624	0.626	0.622	0.621	0.628	0.624	0.624	0.628	0.623	0.626	0.032	0.035	0.035	0.039	0.039	0.046	0.043	0.032 0.628
GEV 2119	0.616	0.617	0.614	0.613	0.619	0.616	0.616	0.619	0.615	0.617	0.023	0.027	0.027	0.031	0.031	0.037	0.034	0.023- 0.619
Overall distance between seedling strains^b																		0.003- 0.633

^a Seedling strains were isolated at the same time as field strains during 3/2016.

^b Field strains were isolated during 3/2016.

^c The pairwise genetic distance between transplant seedling strains collected during 12/2015 and 3/2016 from grower B in group 2.

Table S7. Range of genetic distances between seedling (upper panel) and field (left panel) of grower B strains in group 3 based on single-nucleotide polymorphisms compared to Xp17-12 reference genome.

	GEV2099^a	GEV2065^a	GEV2097^a	Range
GEV2108	0.063	0.645	0.170	0.063-0.645
GEV2121	0.173	0.541	0.066	0.066-0.541
GEV2010^c	0.194	0.562	0.086	0.086-0.562
GEV2390	0.183	0.551	0.076	0.076-0.551
GEV2392	0.225	0.593	0.117	0.117-0.593
GEV2397	0.262	0.629	0.154	0.154-0.629
GEV2396	0.251	0.619	0.144	0.144-0.619
GEV2134	0.600	0.109	0.493	0.109-0.600
GEV2128	0.738	0.117	0.631	0.117-0.738
GEV2112	0.650	0.053	0.543	0.053-0.650
GEV2122	0.646	0.053	0.539	0.053-0.646
GEV2127	0.114	0.696	0.221	0.114-0.696
GEV2124	0.069	0.651	0.176	0.069-0.651
GEV2125	0.099	0.681	0.206	0.099-0.681
GEV2130	0.053	0.636	0.16	0.053-0.636
Overall distance between seedling strains^d				0.156-0.632

^a Seedling strains were isolated at the same time as field strains during 3/2016.

^b Field strains were isolated during 3/2016.

^c GEV2010 is the only grower A strain in group 3.

^d The pairwise genetic distance between transplant seedling strains in group 3 only.

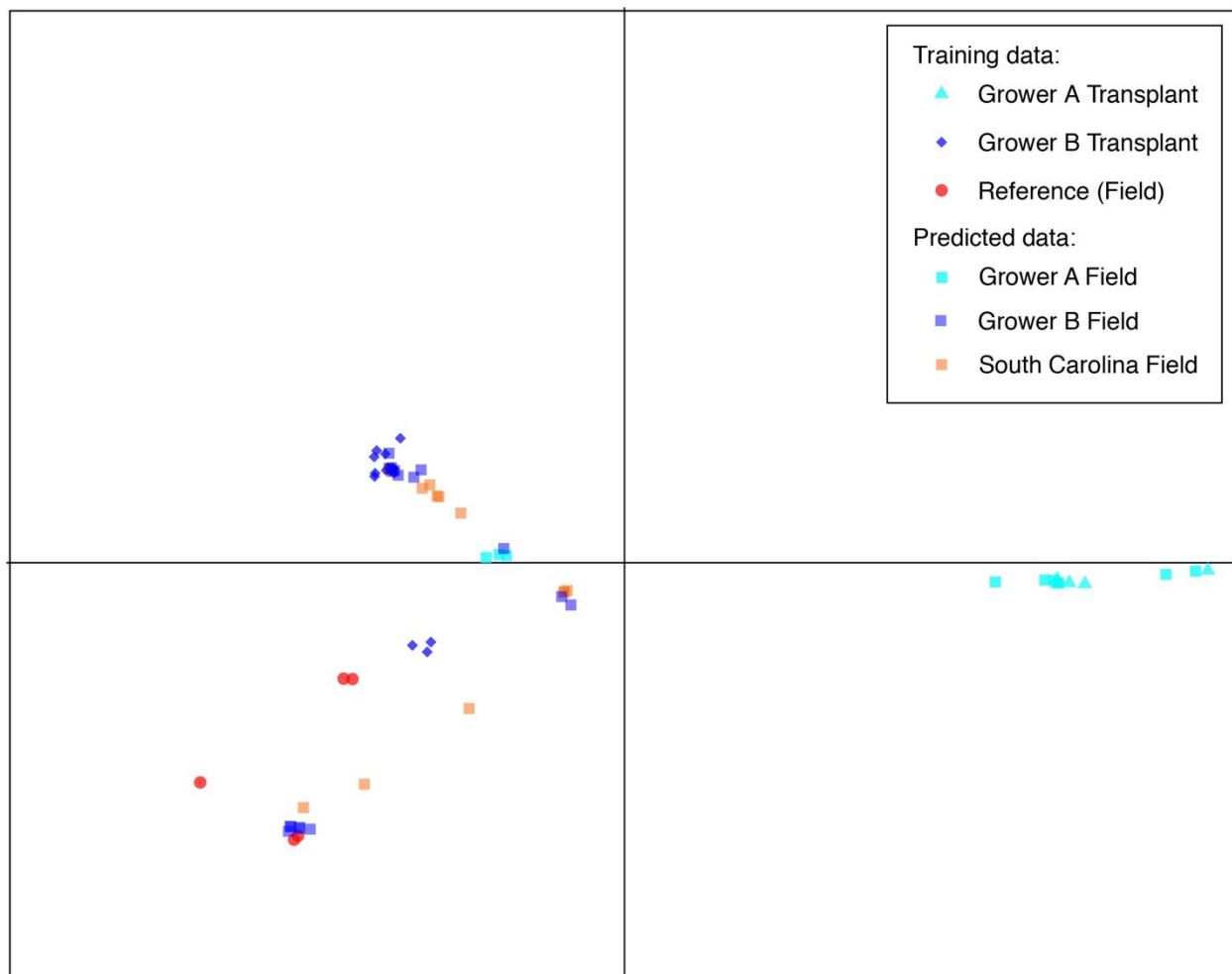


Figure S1. Discriminant analysis of principal components analysis of group 2 SNP data. Three populations were defined as training data: Grower A transplant, Grower B transplant and Reference, which composed of field strains from previous collections. Field strains were mapped on the discriminant functions (Predicted data). This analysis used four principal components and two discriminant functions.