

		Wild						Domesticated					
		LA1547	LA1589	LA1684	LA2093	LA2176	LA480	LA2706	LA3008	LA3475	LA410	LA4345	LA4355
Wild	LA1547		3256	3975	3069	2228	3006	2165	3478	1847	1253	3942	2970
	LA1589	<0.001		5323	4755	3566	4563	3396	4860	3173	2406	5491	4426
	LA1684	<i>0.086</i>	NS		4020	3008	3926	2885	4194	2627	1959	4776	3810
	LA2093	<0.001	NS	NS		3395	4575	3260	4943	2919	2093	5630	4384
	LA2176	<0.001	0.007	<0.001	0.002		5766	4428	5955	4287	3411	6670	5610
	LA480	<0.001	NS	<i>0.067</i>	NS	0.012		5939	4376	6212	6999	3703	4869
Domesticated	LA2706	<0.001	0.002	<0.001	<0.001	NS	0.003		6071	4564	3785	6716	5794
	LA3008	0.003	NS	NS	<i>0.607</i>	0.003	NS	0.001		3062	2339	5309	4283
	LA3475	<0.001	<0.001	<0.001	<0.001	NS	<0.001	NS	<0.001		3824	7088	6022
	LA410	<0.001	<0.001	<0.001	<0.001	0.002	<0.001	<i>0.030</i>	<0.001	<i>0.037</i>		7779	6820
	LA4345	<i>0.072</i>	<i>0.065</i>	NS	<i>0.030</i>	<0.001	<i>0.018</i>	<0.001	NS	<0.001	<0.001		3601
	LA4355	<0.001	NS	<i>0.034</i>	NS	<i>0.032</i>	NS	0.010	NS	0.002	<0.001	0.009	

Table S1. Rank order shifts of 97 *B. cinerea* isolates by lesion area across all of the tomato accessions.

Wilcoxon signed-rank test comparing mean *B. cinerea* lesion area on tomato accessions. This tests for a change in the rank order of the 97 isolates between each pair of tomato accessions. A significant p-value suggests that the relative performance of individual isolates is altered from one host to the other. The lower left corner of the chart includes FDR-corrected p-values, the upper right corner includes the test statistic (W). Bold text indicates significance at $p < 0.01$ after correction, italicized text indicates suggestive p-values $0.01 < p < 0.1$. NS shows non-significant interactions.

geneID	tot_LA0410	tot_LA0480	tot_LA1547	tot_LA1589	tot_LA1684	tot_LA2093	tot_LA2176	tot_LA2706	tot_LA3008	tot_LA3475	tot_LA4345	tot_LA4355	TotPhenos	PFAM_NAME	PFAM_DESCRIPTION	BCIN
BcT4_8813	1	1	1	1	1	1	1	1	1	1	1	1	1	12 M20_dimer	Peptidase dimerisation domain	Bcin01g10130
BcT4_8803	1	1	1	1	1	1	1	1	1	1	1	1	1	12 HET	Heterokaryon incompatibility protein (HET)	Bcin01g10020
BcT4_6001	1	1	1	1	1	1	1	1	1	1	1	1	1	Pectinesterase 12 se	Pectinesterase	Bcin14g00860
BcT4_6000	1	1	1	1	1	1	1	1	1	1	1	1	1	12 MFS_1	Major Facilitator Superfamily	Bcin14g00870
BcT4_5778	1	1	1	1	1	1	1	1	1	1	1	1	1	12 Pkinase	Protein kinase domain	Bcin15g04110
BcT4_2485	1	1	1	1	1	1	1	1	1	1	1	1	1	12 HET	Heterokaryon incompatibility protein (HET)	NA
BcT4_8805	1	1	1	1	1	1	1	1	0	1	1	1	1	11 DUF3506	Domain of unknown function (DUF3506)	Bcin01g10040
BcT4_8749	1	1	0	1	1	1	1	1	1	1	1	1	1	11 Ecm29	Proteasome stabiliser	Bcin01g09300
BcT4_6975	1	1	1	1	1	1	1	1	1	1	1	1	0	Semialdehyde 11_dh	Semialdehyde dehydrogenase	Bcin12g03680
BcT4_6901	0	1	1	1	1	1	1	1	1	1	1	1	1	11 Thi4	Thi4 family	Bcin12g02910
BcT4_6018	1	1	0	1	1	1	1	1	1	1	1	1	1	11 KR	KR domain	Bcin14g00690
BcT4_6003	1	1	0	1	1	1	1	1	1	1	1	1	1	11 DUF1279	Protein of unknown function (DUF1279)	Bcin14g00840
BcT4_6002	1	1	0	1	1	1	1	1	1	1	1	1	1	Glyco_hydro 11_28	Glycosyl hydrolases family 28	Bcin14g00850
BcT4_5054	1	1	0	1	1	1	1	1	1	1	1	1	1	11 MFS_1	Major Facilitator Superfamily	Bcin01g05010
BcT4_4123	1	1	1	1	1	0	1	1	1	1	1	1	1	11 Ion_trans	Ion transport protein	Bcin11g05810
BcT4_2339	0	1	1	1	1	1	1	1	1	1	1	1	1	11 CorA	CorA-like Mg2+ transporter protein	Bcin04g03640
BcT4_1921	1	1	0	1	1	1	1	1	1	1	1	1	1	11 Sugar_tr	Sugar (and other) transporter	Bcin09g05080
BcT4_1613	1	1	0	1	1	1	1	1	1	1	1	1	1	Methyltrans 11_f_23	Methyltransferase domain	Bcin09g01570
BcT4_10249	1	1	0	1	1	1	1	1	1	1	1	1	1	11 Cyt-b5	Cytochrome b5-like Heme/Steroid binding domain	Bcin01g03790

Function	More Function	Enzyme	fisher.up.All	fisher.up.Do	fisher.up.Wi	fisher.up.Se
PHD-zinc-finger like domain			0.274715652	0.257708474	0.167028635	0.003339128
Pre-mRNA splicing Prp18-interacting factor			0.274715652	0.257708474	0.167028635	0.003339128
Dopa 4	betalain biosynthesis	y	0.274715652	0.257708474	1	0.003339128
Sulfatase	likely miscat: Type I phosphodiesterase/nucleotide pyrophosphatase/phosphate transferase	y	0.474006167	1	1	0.006668033
Indoleamine 2	possibly: trp degradation in tomato. Indoleamine 2,3-dioxygenase		0.337610912	0.647739513	0.47263339	0.011642283
Haloacid dehalogenase-like hydrolase		y	0.216119104	0.412560339	0.064377777	0.014945753
OPT oligopeptide transporter protein			0.141993548	0.264479262	0.282408636	0.018239099
Enoyl-CoA hydratase/isomerase family		y	0.595431476	0.832912721	0.315925912	0.019881985
Aldehyde dehydrogenase family		y	0.027038641	0.048120046	0.180853822	0.024795532
DNA polymerase family B			0.045924725	0.038230181	0.01084408	1
Clr5 domain			0.071670613	0.060134627	0.017756436	1
Protein of unknown function (DUF3445)			0.071670613	0.196627891	0.017756436	1
WSC domain	carbohydrate binding		0.141993548	0.264479262	0.028396574	1
ZOG-Fe(II) oxygenase superfamily		y	0.095566172	0.155098474	0.031354155	1
Phosphotyrosyl phosphate activator (PTPA) protein			0.107344357	0.094811632	0.040557284	1
Ubiquitin fusion degradation protein UFD1			0.107344357	0.094811632	0.040557284	1
C2H2 type zinc-finger (2 copies)			0.107344357	0.360487301	0.040557284	1
ABC-2 type transporter			0.175448052	0.150579732	0.049971041	1
Acetyltransferase (GNAT) family		y	0.970918916	1	0.866412802	1
Alcohol dehydrogenase GroES-like domain		y	0.975244541	1	0.878110635	1
KR domain	kringle, binding		0.933177489	0.990056533	0.913715933	1
Phosphopantetheine attachment site			0.988880644	0.983317719	1	1

Table S2. a) Genes with significant SNPs for Botrytis virulence in 11 or 12 of the tomato accessions. b) functional categories significantly overrepresented in genes linked to Botrytis virulence response to tomato domestication.

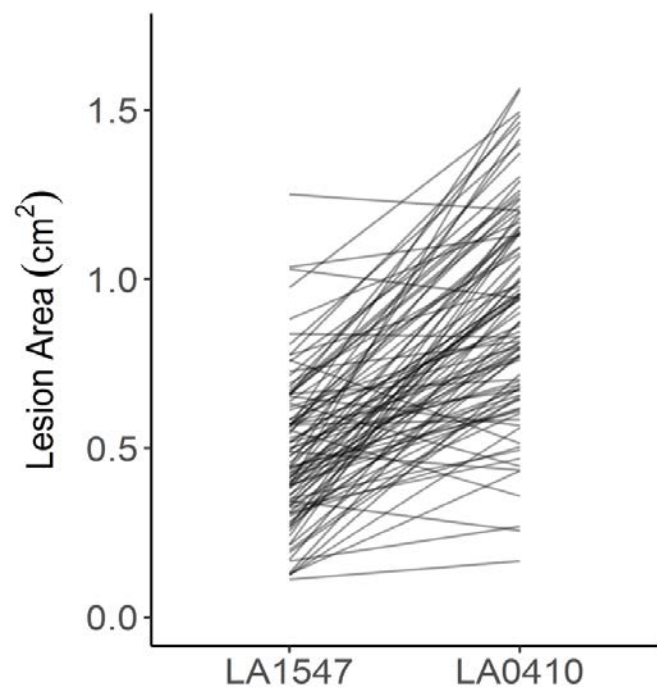


Figure S1. Rank order plot of *B. cinerea* lesion size on two tomato genotypes.

Each *B. cinerea* isolate is a straight line tracing mean lesion size on LA1547 to mean on LA0410, the two host genotypes with the most pronounced effect on the rank order of isolates by lesion size (Wilcoxon signed-rank test with FDR-correction, $p < 7.18e-17$, Table S1).