Table S1. General information of primer sequences used and GenBank accession numbers obtained in this study.

Locus	Primer Name	T_m (°C)	Sequence (5′–3′)	Size of Amplicon (bp)	Reference	GenBank Accession						
						EX1	EX4	EX7	EX8	EX13	EX16	EX21
16SrDNA	27F 1492R	48	AGAGTTTGATCMTGGCTCAG GGTTACCTTGTTACGACTT	1750	[14]	OR461406	OR461407	OR461408	OR461409	OR461410	OR461411	OR461412
gyrB	Gyrb F Gyrb R	55	GTGCGGCGCTGATTC CGTGTCGGGGTTGAC	590	[15]	OR491295	OR491296	OR491297	OR491298	OR491299	OR491300	OR491301
atpD	P-X-ATPD-F P-X-ATPD-R	60	GGGCAAGATCGTTCAGAT GCTCTTGGTCGAGGTGAT	868	[16]	OR567512	OR567513	OR567514	OR567515	OR567516	OR567517	OR567518

Table S2. Bacterial pustule disease severity ratings of twenty-four edamame genotypes across five survey dates.

Entry No.	Genotype Name	Mean Disease Severity Rating (%)				
		23 Jul	30 Jul	15 Aug	30 Aug	8 Sep
1	UA Kirksey	3.8 a	23.8 abcde	36.3 abcd	51.3 a	58.8 a
2	R15-10280	2.5 a	18.8 abcdef	25.0 abcdefg	36.3 abcde	41.3 abcde
3	R17-2750	0 a	7.5 bcdef	11.3 abcdefg	11.3 bcdefg	12.5 bcdef
4	R17-2776	3.8 a	28.8 abcd	31.3 abcde	40.0 abcd	45.0 abc
5	R17-2965	0 a	2.5 def	3.8 efg	3.8 g	8.8 def
6	R18-9725	0 a	0.3 ef	1.3 g	5.0 fg	7.5 ef
7	R18-9770	0 a	2.5 def	7.5 bcdefg	7.5 defg	8.8 def
8	R18-9782	3.8 a	10.0 abcdef	10.0 bcdefg	11.3 bcdefg	12.5 bcdef
9	R18-9794	1.3 a	2.5 def	4.0 defg	5.3 efg	10.0 cdef
10	R18-9808	5 a	31.3 abc	41.3 ab	53.8 a	58.8 a
11	VT Sweet	2.5 a	10.0 abcdef	20.0 abcdefg	30.0 abcdefg	42.5 abcd
12	V16-0293	0 a	2.5 def	2.5 fg	5.0 fg	10.0 cdef
13	V16-0521	0 a	6.3 bcdef	12.5 bcdefg	27.5 abcdefg	37.5 abcdef
14	V16-0523HP	0 a	0 f	1.5 fg	3.8 fg	8.8 f
15	V16-0527	2.5 a	25.0 abcd	33.8 abcd	51.3 a	61.3 a
16	V16-0546	3.8 a	27.8 abcd	34.0 abcde	45.0 abc	53.8 a
17	V16-0688 HP	1.3 a	3.8 cdef	11.3 bcdefg	11.3 cdefg	16.3 bcdef
18	V18-0785	2.5 a	13.8 abcdef	17.5 abcdefg	31.3 abcdef	45.0 abc
19	V18-1025	5.0 a	13.8 abcdef	23.8 abcdefg	45.0 ab	52.5 a
20	V19-0196	3.8 a	36.3 ab	41.3 abc	52.5 a	61.3 a
21	V19-0288	5.0 a	36.3 ab	40.0 abc	53.8 a	60.0 a
22	V19-0290	3.8 a	21.3 abcdef	27.5 abcdef	37.5 abcde	48.8 ab
23	V19-0322	1.3 a	7.5 bcdef	7.8 cdefg	10.0 defg	15.0 bcdef
24	V19-0368	5.0 a	43.8 a	48.8 a	62.5 a	66.3 a

Note: This shows the mean percentage of the diseased leaf surface area for these genotypes at different growth stages. Results reflect means of four replicates. Means followed by the same letters are not significantly different according to Tukey's HSD ($p < 0.05$) within the data collected on the same date.

Table S3. Mean disease severity rating of twenty-four edamame genotypes to the three soilborne diseases studied.

Entry No.	Variety Name	Type	Source	Mean DSR (Round to One Decimal Place)			Mean DSR ± SD (Round to Two Decimal Places)		
				RR	SB	PR	RR	SB	PR
1	UA Kirksey	CV	UA, USA	4.7	5.1	3.8	4.7 ± 1.4	5.1 ± 1.2	3.8 ± 0.4
2	R15-10280	BL	UA, USA	4.7	4.1	3.8	4.7 ± 1.5	4.1 ± 1.7	3.8 ± 0.4
3	R17-2750	BL	UA, USA	3.5	2.4	3.4	3.5 ± 1.2	2.4 ± 1.8	3.4 ± 0.7
4	R17-2776	BL	UA, USA	3.6	2.7	3.6	3.6 ± 1.2	2.7 ± 1.3	3.6 ± 0.5
5	R17-2965	BL	UA, USA	2.6	4.1	3.9	2.6 ± 1.1	4.1 ± 1.1	3.9 ± 0.5
6	R18-9725	BL	UA, USA	3.4	1.8	3.7	3.4 ± 0.7	1.8 ± 1.1	3.7 ± 0.2
7	R18-9770	BL	UA, USA	3.4	3.0	3.4	3.4 ± 0.9	3.0 ± 1.8	3.4 ± 0.4
8	R18-9782	BL	UA, USA	3.8	3.5	3.8	3.8 ± 0.9	3.5 ± 0.9	3.8 ± 0.3
9	R18-9794	BL	UA, USA	3.1	5.2	3.2	3.1 ± 0.8	5.2 ± 0.7	3.2 ± 0.2

10	R18-9808	BL	UA, USA	2.3	5.3	3.7	2.3 ± 0.3	5.3 ± 1.0	3.7 ± 0.4
11	VT Sweet	CV	VT, USA	2.9	4.2	3.9	2.9 ± 0.9	4.2 ± 1.6	3.9 ± 0.3
12	V16-0293	BL	VT, USA	3.0	4.4	3.9	3.0 ± 1.3	4.4 ± 1.6	3.9 ± 0.3
13	V16-0521	BL	VT, USA	2.9	3.9	3.7	2.9 ± 0.9	3.9 ± 1.7	3.7 ± 0.2
14	V16-0523HP	BL	VT, USA	2.7	3.2	3.1	2.7 ± 0.9	3.2 ± 1.8	3.1 ± 0.6
15	V16-0527	BL	VT, USA	3.0	5.1	3.6	3.0 ± 0.7	5.1 ± 0.6	3.6 ± 0.3
16	V16-0546	BL	VT, USA	3.5	4.0	3.5	3.5 ± 1.1	4.0 ± 1.8	3.5 ± 0.8
17	V16-0688HP	BL	VT, USA	2.9	5.0	3.3	2.9 ± 1.2	5.0 ± 0.9	3.3 ± 0.3
18	V18-0785	BL	VT, USA	3.6	4.2	3.5	3.6 ± 1.1	4.2 ± 1.9	3.5 ± 0.4
19	V18-1025	BL	VT, USA	2.8	3.8	3.8	2.8 ± 0.9	3.8 ± 1.6	3.8 ± 0.6
20	V19-0196	BL	VT, USA	2.8	4.4	3.9	2.8 ± 0.7	4.4 ± 1.7	3.9 ± 0.4
21	V19-0288	BL	VT, USA	3.4	4.0	3.0	3.4 ± 0.9	4.0 ± 1.3	3.0 ± 0.4
22	V19-0290	BL	VT, USA	3.3	5.3	3.3	3.3 ± 0.8	5.3 ± 0.9	3.3 ± 0.6
23	V19-0322	BL	VT, USA	2.8	5.4	3.1	2.8 ± 1.2	5.4 ± 0.4	3.1 ± 0.2
24	V19-0368	BL	VT, USA	3.3	3.8	3.1	3.3 ± 0.8	3.8 ± 1.7	3.1 ± 0.2
CK1	Agate	CV	Japan	7.2	5.7	4.9	7.2 ± 1.1	5.7 ± 0.2	4.9 ± 0.2
CK2	Gardensoy21	CV	UI, USA	5.5	5.1	3.3	5.5 ± 1.9	5.2 ± 0.7	3.3 ± 0.4

Note: Disease severity rating (DSR) = ∑ (class frequency × score of rating class)/total number of observations. UA: University of Arkansas; VT: Virginia Tech; UI: Illinois; CV: Commercial variety; BL: Breeding line; RR: Rhizoctonia root and stem rot; SB: Southern blight; PR: Pythium root rot; DSR: Disease severity rating; SD: Standard deviation. The color was highlighted from green to red based on the DSR of each genotype: Score 1, which was highlighted by green, indicated the healthy plants with no symptoms; while the maximum score (i.e., 9 for RR, 6 for SB, and 5 for PR) highlighted by red, indicated complete rot of the seed and no germination. CK1 (Agate, i.e., PI 548296) and CK2 (Gardensoy21, i.e., PI 662954) were used as reference checks of susceptible and tolerant genotypes, respectively, to broad soilborne diseases, according to the study of Williams and Bradley (2017) [3].