

Table S3

Reproducibility of GBS loci identification, allele similarity and allele numbers of biological and technical replicates within and between runs.

	isolate ^a	species	abbreviation	replicates	DNA ^b	number of loci		allele similarity (%) ^d	number of alleles ^e		
						mean	SD ^c		shared	unique	% shared
intra-run	02/001	<i>P. ramorum</i>	RAM	2	=	20942	66	99.99	26986	532	98.1
	10/045	<i>P. cactorum</i>	CAC	3	=	15746	43	100.00 (0.00)	15997 (42)	95 (42)	99.4 (0.3)
	10/051	<i>P. hedraiaandra</i>	HED	2	=	16047	54	100.00	16379	147	99.1
	10/114	<i>P. porri</i>	POR	2	≠	10976	110	99.99	11414	559	95.3
	11/013	<i>P. cactorum</i>	CAC	2	≠	15707	100	99.99	15909	211	98.7
	12/006	<i>P. kernoviae</i>	KER	2	≠	12678	12	100.00	12808	63	99.5
	15/008	<i>P. ×pelgrandis</i>	×PEL	3	=	27868	432	99.99 (0.01)	29589 (328)	1359 (225)	95.6 (0.7)
	CBS109229	<i>P. ipomoeae</i>	IPO	3	≠	18390	188	99.98 (0.00)	20805 (184)	985 (197)	95.5 (0.9)
	CBS581.69	<i>P. botryosa</i>	BOT	2	≠	12097	7	99.94	14373	1135	92.7
	HC21	<i>P. ×serendipita</i>	×SER	3	≠	19251	150	99.99 (0.01)	26039 (146)	653 (121)	97.6 (0.5)
	SW14	<i>P. niederhauseri</i>	NIE	2	≠	30712	177	99.94	38940	3341	92.1
	TJ001	<i>P. ×alni</i>	×ALN	2	≠	43617	139	99.90	60189	7671	88.7
	TJ008	<i>P. uniformis</i>	UNI	2	≠	23022	74	100.00	24352	590	97.6
	TJ027	<i>P. quercina</i>	QUE	2	≠	18541	13	100.00	18816	260	98.6
	TJ091	<i>P. botryosa</i>	BOT	2	≠	12206	15	99.99	14974	151	99.0
inter-run	02/001	<i>P. ramorum</i>	RAM	5	=	21014	63	99.99 (0.01)	26115 (103)	500 (87)	98.1 (0.3)
	10/022	<i>P. kernoviae</i>	KER	2	=	12641	46	100.00	12740	27	99.1
	14/011	<i>P. cryptogea</i>	CRY	2	≠	23572	127	99.99	31036	931	94.8
	15/007	<i>P. ×pelgrandis</i>	×PEL	2	≠	26136	996	99.98	26427	1835	86.0
	15/053	<i>P. cactorum</i>	CAC	3	≠	15653	109	100.00 (0.01)	15855 (105)	117 (103)	98.8 (0.6)
	16/053	<i>P. infestans</i>	INF	2	≠	18819	10	99.93	22306	1163	90.9
	AC10	<i>P. pseudosyringae</i>	PSR	2	=	21843	156	100.00	22044	149	98.5

AC14	<i>P. plurivora</i>	PLV	2	=	15660	66	99.99	15789	44	99.2
AC16	<i>P. pseudosyringae</i>	PSR	2	=	22133	109	99.99	22405	48	98.9
AC22	<i>P. sp. hungarica</i>	HUN	2	=	36365	606	99.99	42259	396	97.0
AC24	<i>P. megasperma</i>	MEG	2	=	32123	1719	99.97	47016	1948	91.2
CBS129.23	<i>P. cryptogea</i>	CRY	2	≠	17069	441	99.96	19502	1129	91.0
CBS200.81	<i>P. humicola</i>	HUM	2	=	24575	20	99.99	32176	246	98.8
CBS235.30/TJ098	<i>P. citrophthora</i> -related	CIPr	2	≠	12675	391	100.00	15820	575	94.6
CBS292.35/SW30	<i>P. drechsleri</i>	DRE	2	≠	24531	704	99.89	31958	3136	82.9
CBS411.96/SW45	<i>P. parvispora</i>	PAS	2	≠	30598	150	99.98	36881	370	97.4
JA06/SW38	<i>P. fragariae</i>	FRA	2	≠	22505	14	100.00	23732	127	99.2
JA07	<i>P. infestans</i>	INF	2	≠	19225	132	99.95	23410	1678	87.7
SW31	<i>P. melonis</i>	MEL	2	≠	29091	11	99.99	31387	260	97.5
TJ021	<i>P. syringae</i>	SYR	2	≠	20553	16	100.00	21284	61	99.3
TJ035	<i>P. castaneae</i>	CAS	2	=	16276	38	99.99	16704	94	99.0
TJ099	<i>P. tropicalis</i>	TRO	2	≠	15342	238	99.99	20302	704	94.8
TJ103	<i>P. ×citrophthora</i> -related1	×CIPr1	2	≠	14941	313	99.99	19801	758	94.4
TJ190	<i>P. pseudosyringae</i>	PSR	2	≠	22032	93	99.99	22299	50	99.1

^a two codes separated by a slash indicate identical isolates with a different isolate code (see Table S1)

^b ≠ : DNA from independent extractions was used for library preparation; = : the same DNA-extract was used for library preparation

^c SD: standard deviation

^d mean value in case of >2 replicates with standard deviation between brackets

^e mean value in case of >2 replicates with standard deviation between brackets; shared = shared alleles between replicates; unique = unique alleles for each replicate