Supplementary data

Supplemental data 1

Target	Type of markers	Primer name	Primer sequence (5′—3′)	Size of PCR product (bp)
eBSGFV	Integration locus	VM1F	TTGTCCAAAATCTGCTCGTG	481
		VM1R	TGTAATTCCTGCTCCTGCAA	
		VM2F	TTCTCCCTTTTCGATCCGTA	374
		VM2R	TTTTGATGCATCTCCAGCAG	
	Structure	VV1F	ACAGCTCCAGGAGATTGGAA	268
		VV1R	CTGAAGTGTGCCTGTGGAGA	
		VV2F	TCTGAGATCTCCAGCCAGGT	639
		VV2R	GACAGTTCCAGCACAGCAGA	
		VV3F	TTGCCAAGAATTCCTCCAAG	376
		VV3R	AAGTTCTTGTCGGCAAGGTG	
		VV4F	GAGCAACACGAGTCAACGAA	784
		VV4R	TCTCCACAGGCACACTTCAG	
		VV6F	GCATGAAGCATGACTGGAGA	264
		VV6R	AATGCATAAGGGCCTCGAAT	
	Allelic	VV5F	CCATGGAGGTTGACCTGTCT	628
		VV5R	ACCCCTCTGTCTTCCCAACT	
		DifGfF	TTGCAGGAGCAGGAATTACA	670
		DifGfR	GGATGGAAGATGAGCTCTTTG	
eBSOLV	Integration locus	Musa-Ol jonction1 F	TGCATTAGATGGTCTGGGAAA	563
		Musa-Ol jonction1 R	ACTTCACGATGCCCATGTTT	
		Musa-Ol jonction2 F	GAGCTGTTTCCTCCGTGTCT	590
		Musa-Ol jonction2 R	CCTGGAAGAAAGCAGACGAG	
	Structure	sig1 eBSOLV F	TTCGAGGAGTCAACGGAGTC	606
		sig1 eBSOLV R	CCTGGTCTGCACAGAGATGA	
		sig2 eBSOLV F	CTTGCTCTGTGGGCAAGACT	426
		sig2 eBSOLV R	CCATTTTTCTCGCAGATTGTC	
	Allelic	Marker1-BSOLV(2) F	ATACGAAGCCCAACGAATTG	601
		Marker1-BSOLV(2) R	ATGGCTTGCCTTCACAGATT	
		Marker2-BSOLV(2) F	ACTCGCACAAAGTGAACTCG	399
		Marker2-BSOLV(2) R	ACAGTACAAGCCCCACCAAT	
		Marker2-BSOLV(1) F	GTGGTGGTTCTTGATCCGGT	1469
		Marker2-BSOLV(1) R	CACGTGGTAGGGGTCCGCCA	

		Dif-OL(F) (HaeIII)	GAATCATTATTCGAGGAGTCAACGG	337
		Dif-OL(R) (HaeIII)	CGAGTAGAGCGCAAGATCCTAGTTC	
		Dif-OL (F) (AhdI)	TTGGAACAAGACAGATTGACTTCCT	500
		Dif-OL (R) (AhdI)	GGTTCGTTTTTATGGCTTTCATGG	
eBSImV	Integration locus	Musa/F2-F	ACTCAGCAAAGGCAAGCAGT	561
		Musa/F2-R	TCTGGTGTGAGTTTTAATAATACCG	
		F5/Musa-F	GTATGGTTCTTGCCCGATGA	594
		F5/Musa-R	TCGTGCAGACCCCTTACTCT	
	Structure	F1/F3-F	TTCGGTATTATTAAAACTCACACCA	490
		F1/F3-R	GCTGCTAACTGAGGATAATCGAA	
		F3/F4-F	TCCCACGCAAGCTTACTTCT	600
		F3/F4-R	GAAGCTGTCCAAGCCTATATCA	
		F4/F5-F	TGGACAGCTTCTGGTGTGAG	540
		F4/F5-R	AGCAGCTACAACCCTGGAGA	

For eBSGFV:

Primers DifGfF and DifGfR (annealing temperature *Ta*=60°C) amplify a PCR product of 670 bp. This PCR product was digested with the restriction enzyme *Taa*I (Fermentas) in a final volume of 20 µl according to the manufacturer's instructions. Digested DNA was loaded onto a 2.5% agarose gel stained with ethidium bromide, and the bands visualized under UV light. Digestion of the PCR product obtained from eBSGFV9 and eBSGFV7 yields two (442 bp + 227 bp) and three (366 bp + 227 bp + 76 bp) bands, respectively.

The second set of primers (VV5F/VV5R, *Ta*=60°C) hybridizes with eBSGFV9 only and yields a 628-bp amplification product.

For eBSOLV:

Primers Marker1-BSOLV(2) F/Marker1-BSOLV(2) R and Marker2-BSOLV(2) F/Marker2-BSOLV(2) R (Ta=65°C) hybridize with eBSOLV2 only and yield amplification products of 601-bp and a 399-bp, respectively.

The third set (Marker2-BSOLV(1) F/ Marker2-BSOLV(1) R (Ta=65°C) hybridizes with eBSOLV1 only and yields a 1469-bp amplification product.

Primers Dif-OL(F) (HaeIII) and Dif-OL(R) (HaeIII) (*Ta*=65°C) amplify a PCR product of 337 bp. This PCR product was digested with the restriction enzyme *Hae*III (New England Biolabs) in a final volume of 20 µl according to the manufacturer's instructions. Digested DNA was loaded onto a 2.5% agarose gel stained with ethidium bromide, and the bands visualized under UV light. The PCR product

obtained from eBSOLV2 was not digested and that from eBSOLV1 was cut into two bands of 83 and 254 bp.

Primers Dif-OL (F) (AhdI) and Dif-OL (R) (AhdI) (*Ta*=65°C) amplify a PCR product of 500 bp. This PCR product was digested with the restriction enzyme *Ahd*I (New England Biolabs) in a final volume of 20 µl according to the manufacturer's instructions. Digested DNA was loaded onto a 1.5% agarose gel stained with ethidium bromide, and the bands visualized under UV light. The PCR product obtained from eBSOLV1 was not digested and that from eBSOLV2 was cut into two bands of 202 and 298 bp.

For eBSImV:

12 SSR markers defined from the BAC sequence (MBP_68C24) according to the procedure described in the paragraph "eBSV genotyping" were tested on parent *M. balbisiana* PKW in order to check polymorphism for subsequent segregation analysis.

Moreover, two dCaps markers were developed from the BAC sequence (MBP_68C24) and tested on the 23 other BAC clones that hybridized with BSImV probes during the BAC library screening in order to identify a second eBSImV allele. The markers were developed based on point mutations located at position 4,091 and 11,845 of eBSImV, which lead to stop codons. Both point mutations are present in the ORF3 fragment of eBSImV. Primers EPRV-Im 4091 For [5′-AGA AGA ATG AAT AGT CAA GAT TGG AAG ATT GTA CCA T-3′] and EPRV-Im 4091 Rev [5′-GCT TTG CCT TCC ATT TGC AAA-3′] amplify a 158 bp fragment whereas primers EPRV-Im11845 For 2 [5′-AGC CCC ACA TCA TCA AGA AG-3′] and EPRV-Im11845 Rev 2 [5′-ACC TGA GTT TTG ATG TTT TGT ACA ATC CA-3′] amplify a fragment of 217 bp. Both PCRs are performed as described in paragraph "PCR" in the Materials and Methods sections at a *Ta* of 60°C for 35 cycles and PCR product are digested with the restriction enzyme *Bcc*I (New England Biolabs) in a final volume of 20 µl according to the manufacturer's instructions. Digested DNA was loaded onto a 3% agarose gel stained with ethidium bromide, and the bands were visualized under UV light. Digestion of the PCR products yielded two bands (116 bp + 42 bp) and (183 bp + 34 bp) for EPRV-Im 4091 and EPRV-Im 11845, respectively.

Supplemental data 2

Estimates of evolutionary divergence between sequences of eBSVs found in PKW.

For each eBSV species, pairwise distances were computed separately for each virus component (ORF3, IG, ORF1 and ORF2). In the data matrix, the number of base differences per site between sequences is shown. For each virus component, we calculated the average divergence within the

sequence of each allele, between the two alleles and finally between BSV and eBSV sequences (Excel spreadsheet). Overall divergences deduced from these data are listed in Table 5.