

## Supplementary Tables

**Table S1. Data generated in this study and summary of the viruses**

Rice samples	Data generated				viruses
	No. of reads	data yield (Gb)	contigs	Novel viruses	Known viruses
Rby1-21	70,923,042	12.69	328,146	FMV	RTV1
				RPeV	RRSV
				FPIV2	
				FNV	
Rby2-45	84,627,146	10.64	586,111	FMV	RTV1
				FPhV	RPIV1
				RPeV	RRSV
				FTV2	NLRV
				FPIV3	RTov
				FTV3	

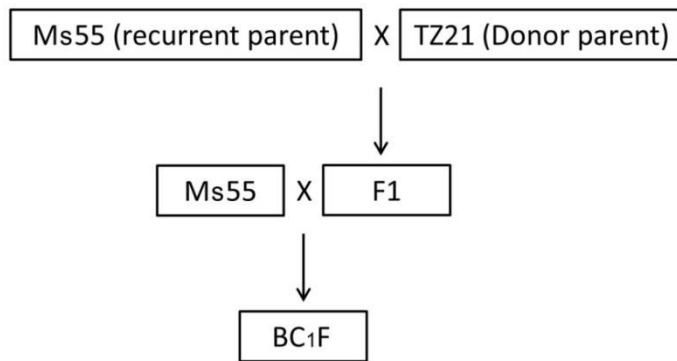
**Table S2. Number of small RNA reads mapped to viruses**

Viruses	No. of small RNA reads mapped to		viruses	
	Rby1-21	Rby2-45		
RPeV	198	3639		8
FMV	69	39		
FPIV2	24			
RTV1	134703	109437		
FNV	43			

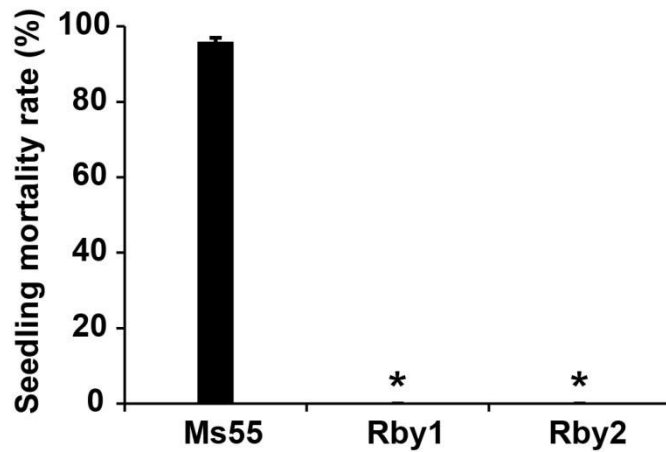
RRSV	7108	23558
FPhV		23
FTV2		84
FPIV3		9
FTV3		76
RPIV1		179
RTov		135
NLRV		15

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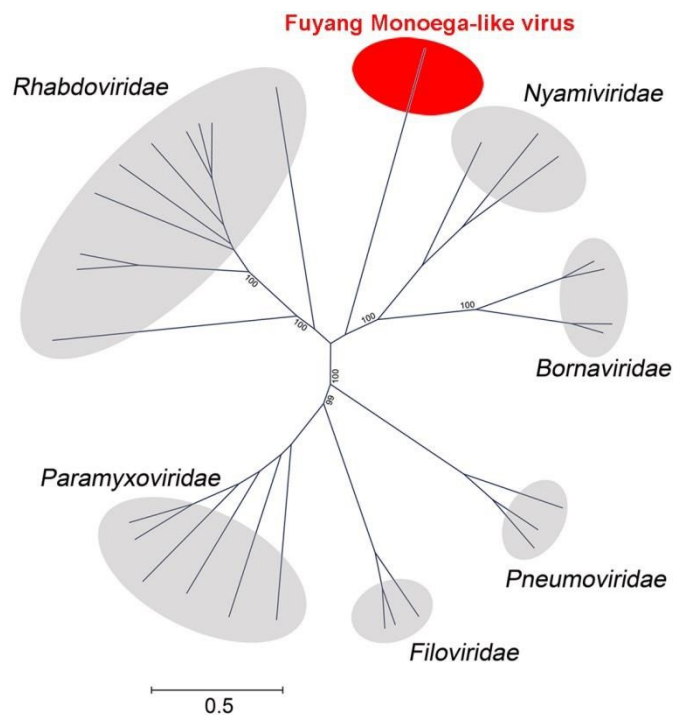
## Supplementary Figures



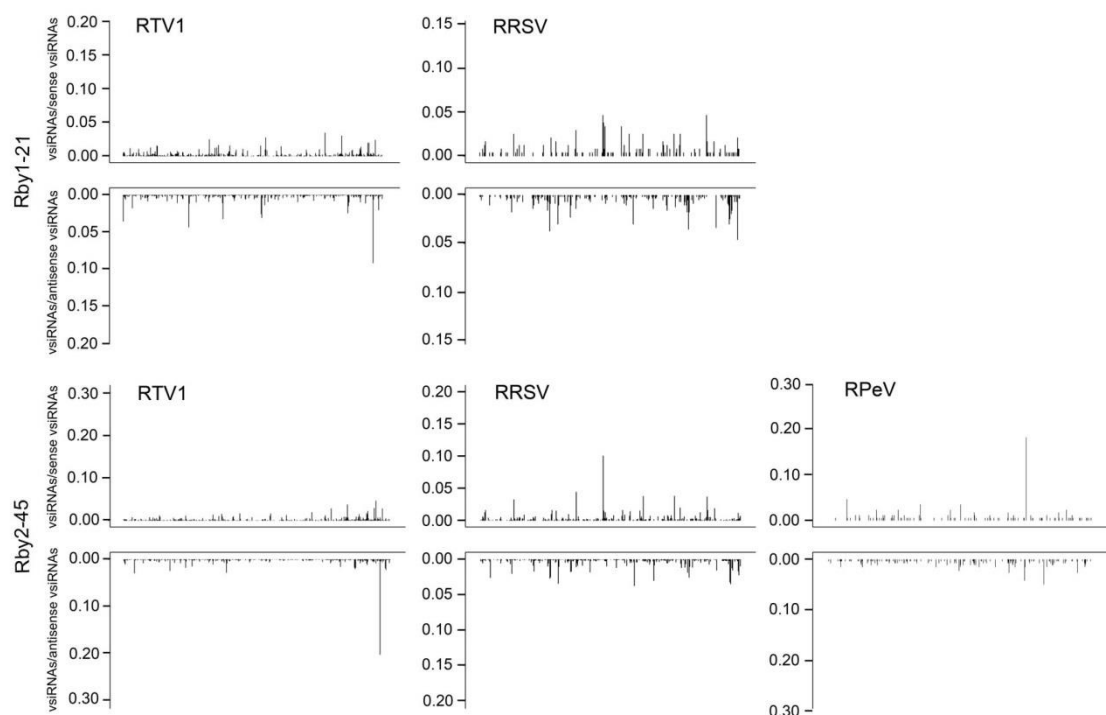
**Figure S1. Scheme of backcross breeding used in the current study.** Ms55 was used as recurrent 12 parent. TZ21 harboring resistance gene *Bph3* served as donor parent. F1: hybrid first generation; BC<sub>1</sub>F: backcross hybrid first generation.



**Figure S2. Seedling mortality rate of Ms55, Rby1, and Rby2 infested with BPH.** Data were collected 23 19 days post infestation (dpi). About 20 seedlings each. (Error bars, mean of three replicates  $\pm$  s.e.m. \*P < 0.01).



**Figure S3. The unrooted ML phylogeny of the novel FMV.** Phylogeny of the FMV to viruses within *Mononegavirales* based on RdRp. Each terminal branch represents a single type species representative of a genus.



**Figure S4. Highly abundance 21-nt vsiRNAs to target the viral genomes.** Mapping of the 21 sense and antisense vsiRNAs to the full-length genomes of RTV1 and RRSV in Rby1-21 as well as RTV1,

RRSV and RPeV in Rby2-45. Lines plotted above the x axis represent vsiRNAs that map to the positive strand, and those plotted below represent those that mapped to the negative strand.