

Supplementary Table 1. Ranges of pairwise similarities (%) of the *G* gene sequences among 10 subgenotypes. The nucleotide sequences of the BRSV strains subjected to the phylogenetic analysis were used.

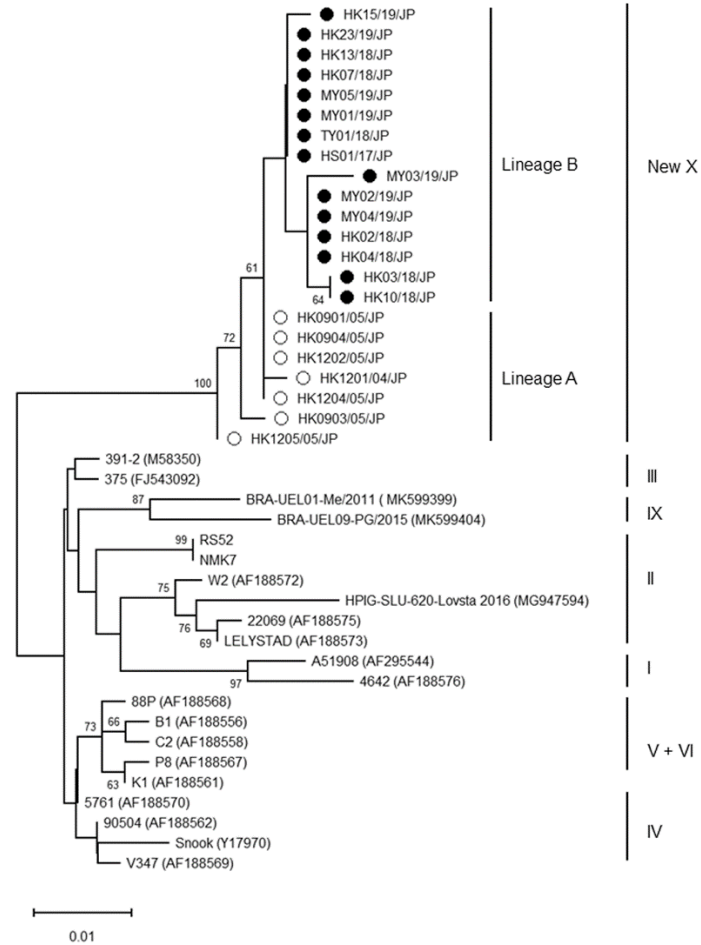
	I	II	III	IV	V	VI	VII	VIII	IX	X-A	X-B
I	94.4–100										
II	87.1–89.6	91.8–100									
III	80.6–85.5	82.7–93.4	83.0–95.3								
IV	84.6–89	86.2–95.9	84.0–92.8	90.3–94.3							
V	84.6–87.7	85.5–90.9	84.9–93.1	88.4–94.3	96.5						
VI	85.6–87.7	84.6–87.7	82.7–87.1	85.8–91.2	93.4–93.7	100					
VII	83.0–85.8	82.6–88.1	82.3–87.1	86.4–90.9	89.6–94.7	88.0–90.3	92.1				
VIII	80.9–83.3	84.9–89.3	83.0–90.3	85.8–89.0	84.0–85.8	81.8–83.3	83–84.6	95.9			
IX	83.4–85.8	84.9–88.4	82.7–89.0	83.6–88.4	82.4–84.9	85.2–86.8	80.1–82.4	82.1–84.6	94		
X-A	81.2–85.2	86.8–92.1	85.5–95.0	85.8–91.8	85.2–88.4	84.0–85.5	82.0–85.5	88.7–92.1	83.6–85.5	94.0–99.7	
X-B	79.0–83.3	84.3–89.0	82.7–92.5	84.6–88.7	83.6–86.5	80.8–83.3	81.1–84.9	87.4–90.3	80.5–82.7	91.2–97.8	95.1–100

Supplementary Table 2. Ranges pairwise similarities (%) of the *F* gene sequences among 10 subgenotypes. The nucleotide sequences of the BRSV strains subjected to the phylogenetic analysis were used.

	I	II	III	IV	V	VI	IX	X-A	X-B
I	98.4								
II	95.8–97.4	96.7–100							
III	96.7–97.2	97.2–98.6	99.5						
IV	95.8–97.4	96.0–98.6	98.4–99.5	98.6–99.8					
V	95.8–96.5	96.3–97.9	98.6–98.8	97.9–99.5	99.1–99.5				
VI	96.0–96.7	96.5–97.4	98.8	98.1–99.5	99.3–99.8	NA			
IX	95.6–96.0	95.3–97.4	97.7–97.9	96.5–97.9	97.4–97.9	97.7–97.9	97.9		
X-A	94.1–95.3	94.2–96.3	96.5–97.2	95.3–97.4	96.0–97.0	96.3–97.0	94.9–95.8	99.3–100	
X-B	93.7–94.6	93.7–95.6	96–96.5	94.9–96.7	95.6–96.3	95.8–96.3	94.4–95.3	98.6–99.8	99.1–100

NA = not available.

New BRSV genotyp in Japan



Supplementary Figure 1. Neighbor-joining phylogenetic tree based on partial nucleotide sequences of BRSV *F* genes.

Numbers are bootstrap values. The scale bar indicates changes per site. Open and closed dots show isolates of lineages A and B, respectively. GenBank accessions of representative BRSV strains are shown in parentheses.

grouped into 10 subgenotypes. The dotted box shows the central hydrophobic region. Solid boxes show 20 unique amino acid substitutions found in the subgenotype X viruses, with which they can be distinguished from the prototypic subgenotype II strain NKM7. Open and closed dots represent the positions of characteristic substitutions in subgenotype X and lineage B, respectively.