JVDI Supplementary material

Kumagai A, et al. Sequence and unique phylogeny of G genes of bovine respiratory syncytial viruses circulating in Japan

Supplementary Table 1. Ranges of pairwise similarities (%) of the G gene sequences among 10 subgenotypes. The nucleotide

seq	uences of the	BRSV	strains s	subjected	to the	phylog	genetic a	analysis	were us	sed.

	Ι	II	III	IV	V	VI	VII	VIII	IX	X-A	X-B
Ι	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

	Ι	II	III	IV	V	VI	IX	X-A	Х-В
Ι	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	
Х-В	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

sequences of the BRSV strains subjected to the phylogenetic analysis were used.

NA = not available.



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.

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Supplementary Figure 2. Alignment of the deduced amino acid sequences of the BRSV G genes. The 53 BRSV strains are

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 NMK7. Open and closed dots represent the positions of characteristic substitutions in subgenotype X and lineage B, respectively.