

Supplementary Material

Identification and characterization of a novel rodent bocavirus from different rodent species in China

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Supplementary information

Figure S2 (A), Conserved RNA splicing sites of RoBoV and HBoV.

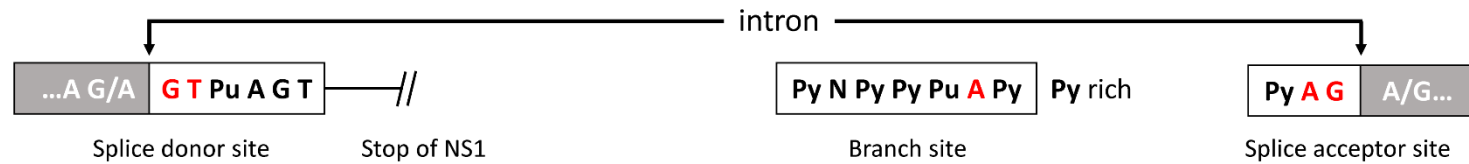
Figure S2 (B), Genomic organization of rodent bocavirus (RoBoV) with possible extended NS1 protein generated by RNA splicing.

Figure S2 (C), Actual reading frames of extended NS1 of RoBoV isolate DL9-RN.

Figure legend

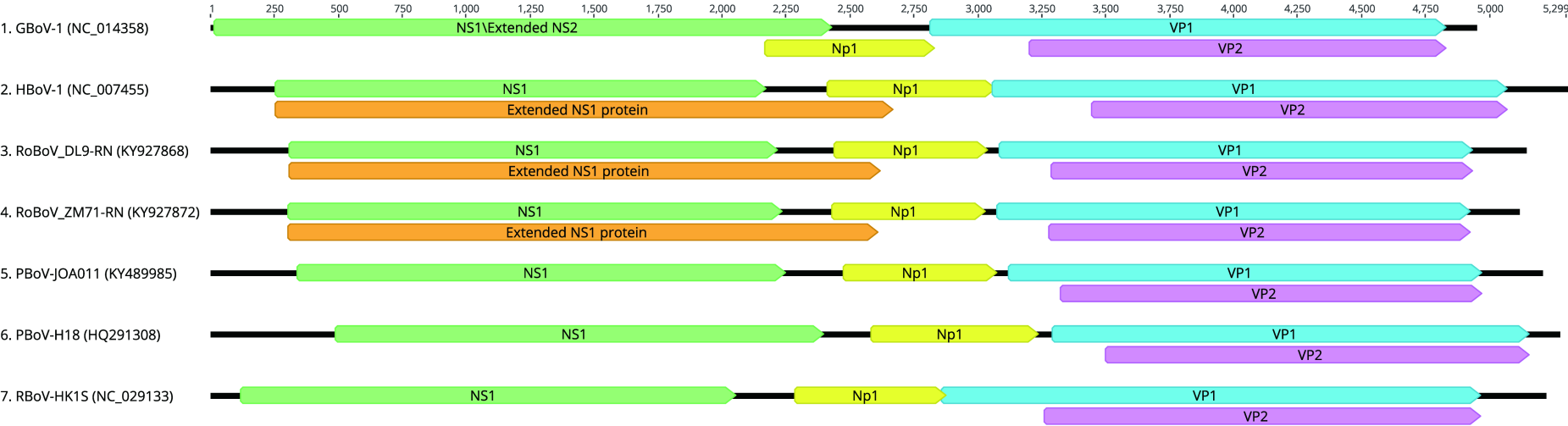
Figure S2. (A) Conserved RNA splicing sites of RoBoV and HBoV. Sequences of RoBoV and HBoV (NC_007455) are aligned to show the conserved RNA splicing sites (sequences in box). The splice donor site (GT) and splice acceptor site (AG) are highlighted in red. Shaded areas on the sequences represent the predicted exons. The stop codons of protein NS1 are underlined. An online tool NetGene 2.4.2 was used to predict the splice sites (<http://www.cbs.dtu.dk/services/NetGene2/>). The score represented the confidence of prediction and “H” means it is a highly confident donor/acceptor site. (B) Genomic organization of rodent bocavirus (RoBoV) compared with that of GBoV, HBoV and PBoV. Different colored boxes represent four ORFs of bocaparvovirus. Orange boxes show the possible extended NS1 protein generated by RNA splicing. The illustration was constructed by geneious software (Biomatters Ltd, Auckland, New Zealand). (C) Predicted reading frames of extended NS1 of RoBoV isolate DL9-RN. Grey shaded areas represent the predicted introns. Yellow shaded areas represent the exons.

(A)



	Splice donor site	Stop of NS1	Branch site	Splice acceptor site	Donor Score	Acceptor Score
DL8-RN	CGGAGGTGAGTA	AAATACATTCAAAAATAAAATTATACATAATATATATATTATATTTAAACAGATATAAAATTAACCTATATTTTCATT-ATATTTAGACGT			0.94 (H)	0.85
DL9-RN	CGGAGGTGAGTA	AAATACATTCAAAAATAAAATTATACATAATATATATATTATATTTAAACAGATATAAAATTAACCTATATTTTCATT-ATATTTAGACGT			0.94 (H)	0.85
DL16-RN	CGGAGGTGAGTA	AAATACATTCAAAAATAAAATTATACATAATATATATATTATATTTAAACAGATATGAAATTAACCTATATTTTCATT-ATATTTAGACGT			0.99 (H)	0.87
DL7-RN	CGGAGGTGAGTA	AAATACATTCAAAAATAAAATTATACATAATATATATATTATATTTAAACAGATATAAAATTAACCTATATTTTCATT-ATATTTAGACGT			0.99 (H)	0.85
DL14-RN	CGGAGGTGAGTA	AAATACATTCAAAAATAAAATTATACATAATATATATATTATATTTAAACAGATATGAAATTAACCTATATTTTCATT-ATATTTAGACGT			0.99 (H)	0.87
DL23-RN	CGGAGGTGAGTA	AAATACATTCAAAAATAAAATTATACATAATATATA--TTATATTTAAACAGATATGGAATTAACCTATATTTAATTTATATTTAGACGT			1.00 (H)	0.83
ZM14-RF	CGGAGGTAAAGTGCTACATTCAAAATATATATATTATG-ATTATAT--TTTATTAATACTTCCAT-AACTTAACATAATTATATTTTTTATTTAGACGT				0.94 (H)	0.85
ZM37-RR	CGGAGGTAAAGTA	AAATACATTCAAAAATAAAGTATACATAATATATA--TTATATTTAAACAAATATGGAATTAACCTATATTTTCATTTATATTTAGACGT			1.00 (H)	0.83
ZM71-RN	CGGAGGTAAAGTGCTACATTCAAAATATATATATTATG-ATTATAT--TTTATTAATACTTCCAT-AACTTAACATAATTATATTTTTTATTTAGACGT				0.94 (H)	0.85
HBoV1	ACCAAAGTAAGTA	AAATACGCATGCGCAAGT-AA-T-T-C-T--TTTACTTTCACCT--C-GCTAT--TTTACCAAT-TTTTA--CT-TTTAGCTGAC			0.99 (H)	1.00 (H)

(B)



(C)

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