



Research paper

Multispecies reassortant bovine rotavirus strain carries a novel simian G3-like VP7 genotype



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ABSTRACT

Rotavirus-A (RVAs), are the major cause of severe gastroenteritis in the young of mammals and birds. RVA strains possessing G6, G8, and G10 genotypes in combination with P[1] or P[11] have been commonly detected in cattle. During a routine surveillance for enteric viruses in a bovine population on North-Western temperate Himalayan region of India, an uncommon bovine RVA strain, designated as RVA/Cow-wt/IND/M1/09/2009 was detected in a diarrhoeic crossbred calf. The examination of nearly complete genome sequence of this RVA strain revealed an unusual G-P combination (G3P[11]) on a typical bovine RVA genotype backbone (I2-R2-C2-M2-A11-N2-T6-E2-H3). The VP7 gene of M1/09 isolate displayed a maximum nucleotide sequence identity of 73.8% with simian strain (RVA/Simian-tc/USA/RRV/1975/G3P[3]). The VP4 and NSP5 genes clustered with an Indian pig strain, RVA/Pig-wt/IND/AM-P66/2012/G10P[11] (99.6%), and a caprine strain, RVA/Goat-tc/BGD/GO34/1999/G6P[1] (98.9%) from Bangladesh, respectively, whilst the, VP6, NSP1, NSP3 and NSP4 genes were identical or nearly identical to Indian bovine strains (RVA/Cow-wt/IND/B-72/2008/G10P[X], RVA/Cow-wt/IND/B85/2010/GXP[X], and RVA/Cow-wt/IND/C91/2011/G6P[X]). The remaining four genes (VP1, VP2, VP3 and NSP2) were more closely related to RVA/Human-wt/ITA/PAI11/1996/G2P[4] (93.5%), RVA/Sheep-wt/CHN/LLR/1985/G10P[15] (88.8%), RVA/Human-tc/SWE/1076/1983/G2P2A[6] (93.2%) and RVA/Human-wt/AUS/CK20003/2000/G2P[4] (91.2%), respectively. Altogether, these findings are suggestive of multiple independent interspecies transmission and reassortment events between co-circulating bovine, porcine, ovine and human rotaviruses. The complete genome sequence information is necessary to establish the evolutionary relationship, interspecies transmission and ecological features of animal RVAs from different geographical regions.

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1. Introduction

Rotavirus-A (RVAs) are a major cause of severe gastroenteritis in the young of mammals and birds (Malik et al., 2012; Matthijnsens et al.,

Abbreviations: aa, amino acid; NCBI, The National Center for Biotechnology Information; NCDV, Nebraska Calf Diarrhea Virus; nt, nucleotide; PopART, Population Analysis with Reticulate Trees; RVA, Rotavirus Group A; RVs, Rotaviruses; TAE, Tris-acetate-EDTA.

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2012; Papp et al., 2013; Dhama et al., 2015; Mihalov-Kovács et al., 2015). The 11 segmented dsRNA genome of RVAs encodes six structural proteins (VP1–4, VP6 and VP7) and five/six non-structural proteins (NSP1–NSP5/6) (Greenberg and Estes, 2009). Further classification of the 11 RVA gene segments into respective genotypes is based on the nucleotide sequence identity cut-off values (Matthijnsens et al., 2008a). The commonly used dual classification system for RVAs, i.e., P- and G-genotypes, is based on the gene encoding outer capsid proteins, VP4 and VP7, respectively. At least 27 G and 37 P RVA genotypes have been identified so far (Matthijnsens et al., 2011; Papp et al., 2013). Analysis of the VP7 and VP4 genes may not be sufficient to provide conclusive data on the possible origin of a rotavirus strain (Ghosh and Kobayashi, 2011). Therefore, for better understanding of the exact origin as well as the overall genomic diversity among rotaviruses, Rotavirus Classification Working Group (RCWG) recommends a whole

Table 1
Closest nucleotide and amino acid sequence identities of 11 segments of RVA/Cow-wt/IND/M1/2009/G3P[11] along with their individual gene sequenced detailed information and genotypes (nt, nucleotide; aa, amino acid).

Genes	Accession numbers	Sequenced gene length		ORFs positions	Genotypes	Strains from the NCBI database that had highest sequence homology with M1/09 strain	nt (%)	aa (%)
		nt	aa					
VP1	HQ440220	3290	1089	1 to 3267	R2	RVA/Human-wt/ITA/PAI11/1996/G2P[4]	93.5	98.8
VP2	HQ440221	2654	878	19 to 2653	C2	RVA/Sheep-wt/CHN/LLR/1985/G10P[15]	88.8	98.8
VP3	HQ440222	968	323	1 to 968	M2	RVA/Human-tc/SWE/1076/1983/G2P2A[6] RVA/Human-wt/EGY/Egy3399/2004/G6P[14]	93.2 92.5	95.7 96.1
VP4	HM235506	866	289	1 to 866	P[11]	RVA/Pig-wt/IND/AM-P66/2012/G10P[11]	99.6	99.0
VP6	HM235508	1339	398	14 to 1207	I2	RVA/Cow-wt/IND/B-72/2008/G10P[X]	99.9	100
VP7	HM235505	846	282	1 to 846	G3-like	RVA/Simian-tc/USA/RRV/1975/G3P[3] RVA/Mouse-wt/AUS/MelMuRV/2007/G16P[X]	73.8 73.5	87.9 89.1
NSP1	HM363560	1576	499	1 to 1497	A11	RVA/Cow-wt/IND/B85/2010/GXP[X]	97.1	100
NSP2	HM363561	1057	318	47 to 1000	N2	RVA/Human-wt/AUS/CK20003/2000/G2P[4]	91.2	96.1
NSP3	HM363562	1049	314	1 to 942	T6	RVA/Cow-wt/IND/C91/2011/G6P[X]	99.5	99.6
NSP4	HM363563	725	176	27 to 554	E2	RVA/Cow-wt/IND/C91/2011/G6P[X]	100	100
NSP5	HM363564	653	199	14 to 610	H3	RVA/Goat-tc/BGD/GO34/1999/G6P[1]	98.9	99.4

genome classification system that assigns Gx-P[x]-Ix-Rx-Cx-Mx-Ax-Nx-Tx-Ex-Hx genotypes (x-represents genotype number) to the RVA VP7-VP4-VP6-VP1-VP2-VP3-NSP1-NSP2-NSP3-NSP4-NSP5/6 genes, respectively (Matthijssens et al., 2008a).

Some RVA genotypes are commonly associated with particular host species whereas others have been detected in several species. For example, RVA genotypes G3, G6, G8 and G10 in conjunction with P[1], P[5], P[11], P[15], and P[21] have frequently been detected in cattle (Malik et al., 2012; Martella et al., 2010). However, bovine genotypes, derived from interspecies transmission and reassortment events, have also been detected on several occasions (Desselberger et al., 2001; Jeong

et al., 2014; Jere et al., 2012; Matthijssens et al., 2008b). The whole genomic analysis of atypical bovine RVA strains are essential to obtain conclusive data on the complex genomic diversity, cross-species transmission and evolution of rotaviruses. For example, DS-1-like human rotaviruses and bovine rotaviruses share a common origin, while Wa-like human rotaviruses and porcine rotaviruses have a common ancestry (Matthijssens et al., 2008c). Furthermore, several studies on whole genome analysis of rotaviruses have provided evidence for reassortment events between humans and animal strains (Banyai et al., 2009; Doan et al., 2013; Esona et al., 2009; Ghosh et al., 2010; Jere et al., 2012; Masuda et al., 2014; Matthijssens et al., 2008b, 2009, 2010a;

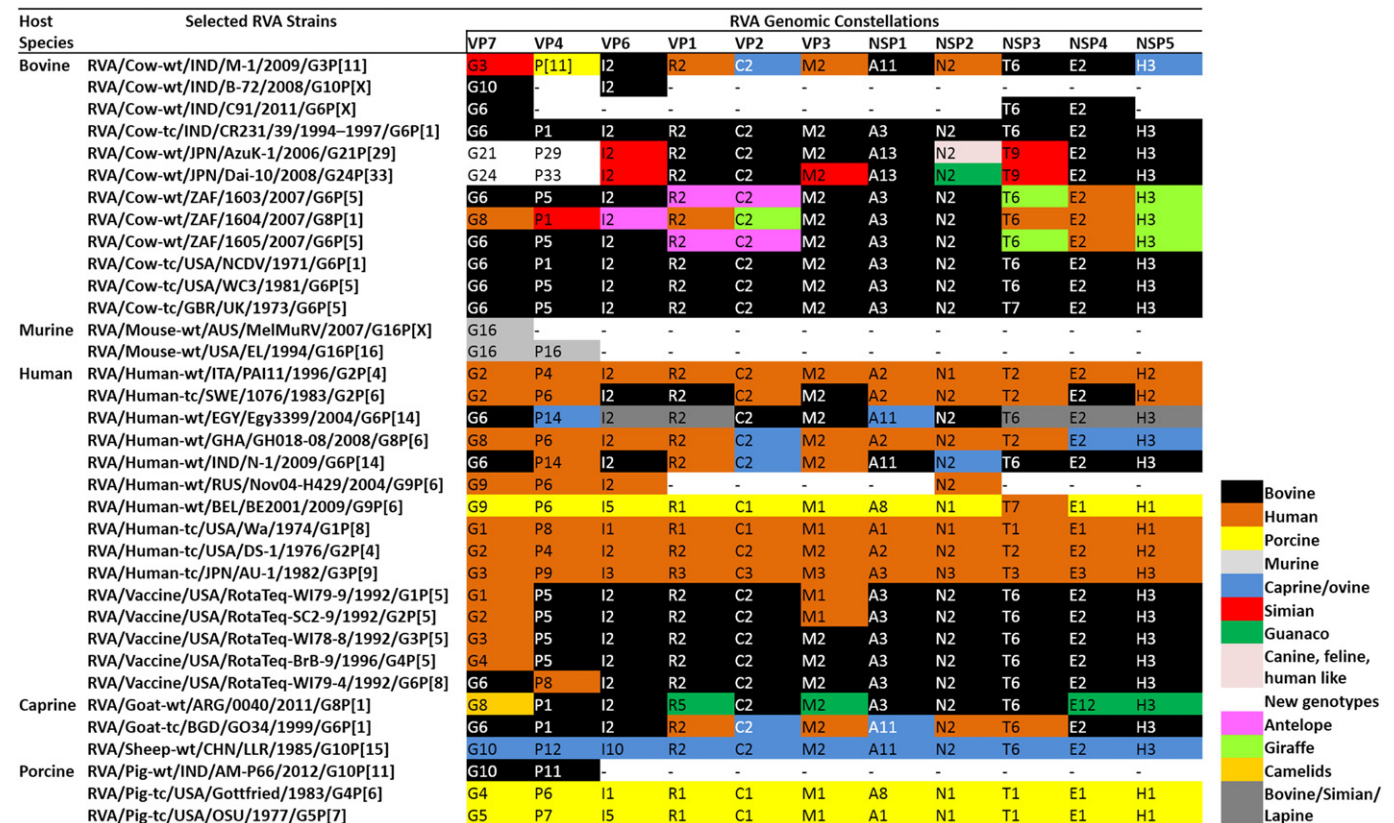


Fig. 1. Comparison of genomic constellations of RVA/Cow-wt/IND/M1/2009/G3P[11] with those of selected human and animal RVA strains with known genomic constellations. Individual gene segments of all strains are colour coded based on the maximum homology with the RVA strains available in the public domain.

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