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Short Communication

The first caprine rotavirus detected in Argentina displays genomic features resembling virus strains infecting members of the *Bovidae* and *Camelidae*



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ABSTRACT

Rotavirus group A (RVA) is a major cause of diarrhea in humans and young animals including small ruminants. The purpose of this study was to identify RVA in dairy goat kids, and to characterize the complete genomic constellation and genetic relatedness with other RVA strains. Four out of twenty fecal samples from diarrheic and non-diarrheic goat kids were positive for RVA by ELISA. A representative sample was selected for further genome analyses. The RVA strain RVA/Goat-wt/ARG/0040/2011/G8P[1] displayed the following genomic constellation: G8-P[1]-I2-R5-C2-M2-A3-N2-T6-E12-H3, reminiscent to guanaco and other bovine-like RVA strains detected in Argentina. Phylogenetic analyses revealed that most of the genome segments had a rather close relatedness with RVA strains typically obtained from cattle, sheep, South American camelids and goats. Interestingly, strain 0040 possessed the R5 and E12 genotypes which have up to date only been found in different animal species from Argentina. Overall, these findings suggest that strain 0040 could represent a typical goat RVA genome constellation similar to those previously found in other animal species within the order *Artiodactyla*.

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1. Introduction

Goat production is an important economic activity of small farmers, mainly in poor rural areas in Argentina

where the goat population is approximately 4,257,000 animals. Goat husbandry systems can have different production purposes including meat, fiber, skin for leather, milk and cheese (Smith and Sherman, 2009).

Rotaviruses (RVs) belong to the family *Reoviridae* and are a leading cause of diarrhea in both humans and animals worldwide (Estes and Kapikian, 2007). RVs are classified into at least eight serological species or groups (A–H) (Matthijnsens et al., 2012), and rotavirus group A (RVA) and B (RVB) are associated with diarrhea in young goats (Smith and Sherman, 2009; Alkan et al., 2012). The RVA

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genome comprises 11 segments of dsRNA encoding 6 structural (VP1, VP2, VP3, VP4, VP6 and VP7) and 5 or 6 non-structural proteins (NSP1–NSP6) (Estes and Kapikian, 2007; Matthijssens et al., 2008b).

A classification system of RVA has been generated to assign genotypes to the 11 genome segments based on identity cut-off percentages and phylogenetic analyses. The schematic nomenclature Gx-P[x]-Ix-Rx-Cx-Mx-Ax-Nx-Tx-Ex-Hx represents the genotypes for the VP7-VP4-VP6-VP1-VP2-VP3-NSP1-NSP2-NSP3-NSP4-NSP5/6 encoding genes, respectively (Matthijssens et al., 2008b).

Worldwide information regarding caprine RVA is scarce and only the complete genome constellation of strain RVA/Goat-tc/BGD/GO34/1999/G6P[1] has been characterized. Further analyses of caprine RVA strains around the world are still needed to properly understand their genetic diversity (Ghosh et al., 2010). The purpose of this study was to identify RVA strains in dairy goat kids, and to characterize the complete genomic constellation and genetic relatedness with other RVA strains.

2. Materials and methods

The study was conducted with Saanen goat kids (300 animals, approximately) in a commercial dairy farm located in General Pueyrredon, a county from Buenos Aires province, Argentina. Production of goat cheese and milk were the main activities but Jersey cattle were also reared in the farm. During an episode of diarrhea, a total of 20 fecal samples were collected (March 2011) from diarrheic ($n=5$) and non-diarrheic ($n=15$) goat kids corresponding to different age groups: (i) 60- to 90-day-old ($n=11$) and (ii) younger than 35-day-old ($n=9$). A double sandwich ELISA was performed to detect RVA (Badaracco et al., 2013) and positive samples were selected for RT-PCR and sequence analyses.

Viral dsRNA extraction (QIAamp Viral RNA mini kit; Qiagen/Westburg), RT-PCR procedure (Qiagen OneStep RT-PCR kit; Qiagen/Westburg), cycle conditions and sequencing reactions (BigDye Terminator Cycle Sequencing Reaction kit; Applied Biosystems Group) were performed as described previously (Badaracco et al., 2013). Specific primers were used for RT-PCR and sequencing reactions on both strands, and primer walking was conducted to cover the sequence of the respective genome fragments (Table 1).

Genotype assignments of the 11 genome segments were carried out with the RotaC online classification tool (Maes et al., 2009), following the recommendations of the RCWG (Matthijssens et al., 2011a). Phylogenetic and molecular evolutionary analyses were conducted using MEGA 5 (Tamura et al., 2011). Genetic distances were calculated with the Kimura-2 correction parameter at the nucleotide level, and phylogenetic trees were constructed using the neighbor-joining method (1000 bootstrap replicates).

The nucleotide sequences for each genome segment (VP1–VP4, VP6, VP7, and NSP1–NSP5) of strain RVA/Goat-wt/ARG/0040/2011/G8P[1] were deposited in GenBank under the accession numbers KF577838 to KF577848 (Table 1).

3. Results

The ELISA screening allowed the detection of RVA in 4 samples (20%) corresponding to one diarrheic and three non-diarrheic goat kids within the 60- to 90-day-old group. By RT-PCR and sequence analyses, 3 ELISA-positive samples displayed amplification products for the VP7 (strains RVA/Goat-wt/ARG/0040/2011/G8P[1], RVA/Goat-wt/ARG/0076/2011/G8P[X] and RVA/Goat-wt/ARG/0096/2011/G8P[X]), VP6 and NSP4 (strains 0040 and 0076) encoding genes, corresponding to the G8, I2 and E12 genotypes, respectively. The nucleotide sequence identity for VP7 (100% identical), VP6 (99.9% identical) and NSP4 (100% identical) indicated a clonal origin, so only strain 0040 was further analyzed.

Nucleotide sequencing of the different genome segments of the strain 0040 (Table 1) revealed the genotype constellation: G8-P[1]-I2-R5-C2-M2-A3-N2-T6-E12-H3. All these genotypes have been previously reported and comparisons with other known RVA genotype constellations are shown in Table 2. Strain 0040 possessed 10 or 9 genotypes in common with the Argentinean guanaco strains RVA/Guanaco-wt/ARG/Rio_Negro/1998/G8P[1] and RVA/Guanaco-wt/ARG/Chubut/1999/G8P[14] (Matthijssens et al., 2009), and with the macaque strain RVA/Macaque-tc/USA/PTRV/1990/G8P[1], believed to be of bovine origin (Matthijssens et al., 2010). Likewise, strain 0040 shared 8 genotypes with different bovine RVA strains (including RVA/Cow-wt/ARG/B383/1998/G15P[11]), and 7 genotypes were identical to those from the caprine strain GO34 (G6P[1]) detected in Bangladesh (Ghosh et al., 2010) (Table 2).

Interestingly, strain 0040 exhibited the R5 (VP1) and E12 (NSP4) genotypes which have up to date only been found in Argentinean RVA strains from a calf (strain B383 G15P[11]) and guanacos (strains Rio Negro G8P[1] and Chubut G8P[14]) (Matthijssens et al., 2009). In addition, the E12 genotype has also been reported in equine RVA strains circulating in thoroughbred foals from Argentina (Garai-coechea et al., 2011; Matthijssens et al., 2012) (Table 2).

Phylogenetic analyses of the VP1, VP2, VP3, NSP2 and NSP4 genome segments showed a consistent close clustering with cognate genes from the bovine strain B383 (G15P[11]) (Matthijssens et al., 2009) (Figs. 1 and 3). Moreover, the goat strain 0040 was phylogenetically related to the guanaco strain Chubut (G8P[14]) (Matthijssens et al., 2009) for the VP1, VP3 and NSP4 genome segments, and also with the guanaco strain Rio_Negro (G8P[1]) (Matthijssens et al., 2009) for the VP1, NSP4 and NSP5 genes (Figs. 1 and 3). The NSP1 and NSP3 genome segments of strain 0040 were rather distantly related to other known RVA strains (Figs. 2 and 3), although they belonged to the characteristic bovine-like genotypes A3 and T6, respectively (Table 2).

The VP6 genome segment of the caprine strains 0040 and 0076 clustered together within the genotype I2, forming a distinct phylogenetic branch together with the Asian bovine RVA strains RVA/Cow-xx/IND/RUBV51/2001-5/G15P[21] (Ghosh et al., 2008), RVA/Cow-wt/JPN/Azuk-1/2006/G21P[29] and RVA/Cow-tc/JPN/Dai-10/2007/G24P[33] (Abe et al., 2011) (Fig. 2).

Table 1

Gene fragments, genotype assignments, and primers used for RT-PCR and sequencing reactions of the different genome segments of strain RVA/Goat-wt/ARG/0040/2011/G8P[1].

Viral proteins	Gene fragment (bp)	Genotype	Position ^a	Acc. number	Primer name	(Degenerate) Primer sequences (5'–3') ^b	Reference
VP1	3267	R5	19–3285	KF577838	GEN_VP1Fb	GGC TAT TAA AGC TRT ACA ATG GGG AAG	Matthijnsens et al. (2008a)
					Lama_VP1_1009R	GAA AYG ACC AYG AAT ATA TTT TAG CC	Matthijnsens et al. (2009)
					G8_VP1_843F	CGT AAA AGC GAT AGT CCC AG	This study
					G8_VP1_2121R	CCA TTG TGT GCT TTG ACC C	This study
					G8_VP1_1962F	GCA AGA CGT GTC AAA TGA CG	This study
G8_VP1_3285R	GGT CAC ATC TAA GCG CTC	This study					
VP2	870	C2	1790–2659	KF577839	GEN_VP2Fb	GGC TAT TAA AGG YTC AAT GGC GTA TCG	Matthijnsens et al. (2008a)
					FR5_VP2_23F	TAC AGG AAA CGT GGA GCG	This study
					GEN_VP2_Rbc	GTC ATA TCT CCA CAR TGG GGT TGG	Matthijnsens et al. (2008a)
					Lama-VP2_917R	GYC TTA TRT ATC TAG CYG TTG ATG G	Matthijnsens et al. (2009)
					B383-VP2_1747F	GTT AAC TTC GGT TAC ATC GC	Matthijnsens et al. (2009)
B383-VP2_2689R	GTC ATA TCT CCA CAA TGG GG	Matthijnsens et al. (2009)					
VP3	2367	M2	191–2557	KF577840	GEN_VP3-24F	TGY GTT TTA CCT CTG ATG GTG	This study
					B383-VP3_1959R	GGT GAG TGT AAG TAT ATC CAT CG	Matthijnsens et al. (2009)
					B383-VP3_578F	ATG ACA ACT TCA TTG CCA ATA GC	Matthijnsens et al. (2009)
					NCDV_VP3_2573R	GTG TTA AGT TTT TAG CTC ACT CAG	Matthijnsens et al. (2008a)
					Goat_VP3_1875F	CGG TAT CGG GAC ATG TTT A	This study
AD63_VP3-2590R	GTC ACA TCG TGA CCA GTG TG	This study					
VP4	2058	P[1]	58–2115	KF577841	P1-5-11_12F	TGG CTT CRC TMA TWT AYA GAC AG	This study
					RioN_VP4_285F	AAT ACA AAC AGA TGG TTA GCG AC	Matthijnsens et al. (2009)
					VP4_1083_1099R	TGG GAT GAT TCA CAA GC	This study
					P1-5-11_1106R	CTR AAW GCY TGT GAA TCR TCC C	This study
					GEN_VP4_P1_2345R	GTT GCT YAY AAG CGA CAT TGC	Matthijnsens et al. (2009)
VP6	1176	I2	42–1217	KF577842	GEN_VP6F	GGC TTT WAA ACG AAG TCT TC	Matthijnsens et al. (2006a)
					GEN_VP6R	GGT CAC ATC CTC TCA CT	Matthijnsens et al. (2006a)
VP7	981	G8	49–1029	KF577843	Beg9	GGC TTT AAA AGA GAG AAT TTC CGT CTG G	Gouvea et al. (1990)
					End9	GGT CAC ATC ATA CAA TTC TAA TCT AAG	Gouvea et al. (1990)
NSP1	1344	A3	165–1508	KF577844	26097_NSP1_GENF	CAT GGC GAC TTT YAA RGA TGC	Matthijnsens et al. (2011b)
					26097_NSP1_GENR	YCT AGG CGC TAC TCT AGT G	Matthijnsens et al. (2011b)
					Chu_NSP1_1271F	GAA GTG AAC TGG GAA GTG AG	Matthijnsens et al. (2009)
NSP2	954	N2	47–1000	KF577845	GEN_NSP2F	GGC TTT TAA AGC GTC TCA G	Matthijnsens et al. (2006a)
					GEN_NSP2R	GGT CAC ATA AGC GCT TTC	Matthijnsens et al. (2006a)
					LAP_NSP2_910F	ACT GTT CCA AAA GAT GAA GC	Matthijnsens et al. (2006a)
NSP3	933	T6	35–967	KF577846	GEN_NSP3F	GGC TTT TAA TGC TTT TCA GTG	Matthijnsens et al. (2006a)
					GEN_NSP3R	ACA TAA CGC CCC TAT AGC	Matthijnsens et al. (2006a)
NSP4	528	E12	42–569	KF577847	LAP_NSP4_1F	GGC TTT TAA AAG TTC TGT TCC	Matthijnsens et al. (2006a)
					C4_NSP4_564F	ATG TAA GAG GTT GAG CTG C	Matthijnsens et al. (2006b)
					GEN_NSP4R	GGW YAC RYT AAG ACC RTT CC	Matthijnsens et al. (2006a)
NSP5	597	H3	22–618	KF577848	GEN_NSP5F	GGC TTT TAA AGC GCT ACA G	Matthijnsens et al. (2006a)
					Goat_NSP5_217F	GCT TCA AAC GAC CCA CTC A	This study
					E_NSP5_145R	AAA TGT ACT GTT CAC TCC TAC C	Matthijnsens et al. (2008a)
					POR_NSP5_190R	GAT GGT CCA ATA TCC TCT GG	This study
					LAP_NSP5_314R	CGT GAT TGT GTT GAT GAA TCC	Matthijnsens et al. (2006a)
GEN_NSP5R	GGT CAC AAA ACG GGA GT	Matthijnsens et al. (2006a)					

^a Position with respect to strains RVA/Guanaco-wt/ARG/Rio_Negro/1998/G8P[1] and RVA/Cow-wt/Arg/B383/1998/G15P[11], except for the VP4 and VP7 gene fragments of strain B383.

^b Degenerate primers; R = A/G, W = A/T and Y = C/T.

Table 2

Comparisons of complete genomic constellations between the caprine strain RVA/Goat-wt/ARG/0040/2011/G8P[1] and other selected RVA strains from different animal species and humans.

Rotavirus strain name	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5	Shared genotypes
RVA/Goat-wt/ARG/0040/2011/G8P[1]	G8	P[1]	I2	R5	C2	M2	A3	N2	T6	E12	H3	
RVA/Guanaco-wt/ARG/Rio_Negro/1998/G8P[1]	G8	P[1]	I2	R5	C2	M2	A13	N2	T6	E12	H3	10
RVA/Guanaco-wt/ARG/Chubut/1999/G8P[14]	G8	P[14]	I2	R5	C2	M2	A11	N2	T6	E12	H3	9
RVA/Macaque-tc/USA/PTRV/1990/G8P[1]	G8	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3	9
RVA/Human-tc/KEN/B12/1987/G8P[1]	G8	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3	9
RVA/Cow-wt/ARG/B383/1998/G15P[11]	G15	P[11]	I2	R5	C2	M2	A13	N2	T6	E12	H3	8
RVA/Cow-tc/FRA/RF/1982/G6P[1]	G6	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3	8
RVA/Cow-tc/VEN/BRV033/1990/G6P6[1]	G6	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3	8
RVA/Cow-tc/USA/NCDV/1967/G6P6[1]	G6	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3	8
RVA/Cow-tc/USA/WC3/1981/G6P[5]	G6	P[5]	I2	R2	C2	M2	A3	N2	T6	E2	H3	7
RVA/Cow-tc/KOR/KJ19-2/2004/G6P[7]	G6	P[7]	I2	R2	C2	M2	A3	N2	T6	E2	H3	7
RVA/Sheep-tc/CHN/DQ-75/2008/G10P[11]	G10	P[11]	I2	R2	C2	M2	A3	N2	T6	E2	H3	7
RVA/Sheep-tc/ESP/OVR762/2002/G8P[14]	G8	P[14]	I2	R2	C2	M2	A11	N2	T6	E2	H3	7
RVA/Goat-tc/BGD/GO34/1999/G6P[1]	G6	P[1]	I2	R2	C2	M2	A11	N2	T6	E2	H3	7
RVA/Human-tc/ITA/PA169/1988/G6P[14]	G6	P[14]	I2	R2	C2	M2	A3	N2	T6	E2	H3	7
RVA/Human-wt/HUN/BP1062/2004/G8P[14]	G8	P[14]	I2	R2	C2	M2	A11	N2	T6	E2	H3	7
RVA/Buffalo-XX/ZAF/Buf1442 07SA/2007/G10P[11]	G10	P[11]	I2	R2	C2	M2	A13	N2	T6	E2	H3	6
RVA/Cow-tc/GBR/UK/1973/G6P7[5]	G6	P[5]	I2	R2	C2	M2	A3	N2	T7	E2	H3	6
RVA/Human-wt/HUN/BP1879/2003/G6P[14]	G6	P[14]	I2	R2	C2	M2	A11	N2	T6	E2	H3	6
RVA/Human-wt/EGY/EGY3399/2004/G6P[14]	G6	P[14]	I2	R2	C2	M2	A11	N2	T6	E2	H3	6
RVA/Vicugna-wt/ARG/75/2010/G8P[14]	G8	P[14]	I2	R2	C2	M2		N2	T6	E3		6
RVA/Antelope-wt/ZAF/RC-18/2008/G6P[14]	G6	P[14]	I2	R2	C2	M2	A11	N2	T6	E2	H3	6
RVA/Human-tc/GBR/A64/1987/G10P11[14]	G10	P[14]	I2	R2	C2	M1	A3	N2	T6	E2	H3	6
RVA/Sheep-xx/CHN/CC0812-1/2008/G10P[15]	G10	P[15]	110	R2	C2	M2	A11	N2	T6	E2	H3	5
RVA/Sheep-tc/CHN/Lamb-NT/XXXX/G10P[15]	G10	P[15]	110	R2	C2	M2	A11	N2	T6	E2	H3	5
RVA/Cow-wt/JPN/Azuk-1/2006/G21P[29]	G21	P[29]	I2	R2	C2	M2	A13	N2	T9	E2	H3	5
RVA/Cow-tc/JPN/Dai-10/2007/G24P[33]	G24	P[33]	I2	R2	C2	M2	A13	N2	T9	E2	H3	5
RVA/Human-wt/IND/N155/2003/G10P[11]	G10	P[11]	I2	R2	C2	M2	A1	N1	T1	E2	H3	4
RVA/Horse-wt/ARG/E4040/2008/G4P[12]	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E12	H7	4
RVA/Horse-wt/ARG/E30/1993/G3P[12]	G3	P[12]	16	R2	C2	M3	A10	N2	T3	E12	H7	3
RVA/Goat-tc/TUR/Kirkklareli/2007/G8[1]	G8	P[1]	I2							E2		3

RVA strains highlighted in bold font indicate a goat origin.

Among the outer capsid genes, the VP7 genome segments of the goat strains 0040, 0076 and 0096 grouped very closely together, representing a monophyletic cluster with the macaque strain PTRV (Matthijssens et al., 2010), the human strain RVA/Human-tc/KEN/B12/1987/G8P[1] (Ghosh et al., 2011), and the Argentinean RVA strains from South American camelids (Rio_Negro G8P[1], Chubut G8P[14] and 75 G8P[14]) (Matthijssens et al., 2009; Badaracco et al., 2013). Regarding the VP4 genome segment, the caprine strain 0040 grouped together, within the P[1] genotype, with the macaque strain PTRV (G8P[1]) (Matthijssens et al., 2010) and with prototype bovine G6P[1] RVA strains (Matthijssens et al., 2008a) (Fig. 1).

4. Discussion

The role of RVA as a major cause of diarrhea in young children (Estes and Kapikian, 2007), calves and pigs (Papp et al., 2013) has been widely confirmed, but the relative importance of caprine RVA remains to be established. The current study reports, for the first time in Argentina, the circulation of RVA in goat kids. However, its role during the episodes of diarrhea could not be completely determined because of the small number of diarrheic goat kids available. Nevertheless, a recent study in Turkey confirmed that a G8P[1] RVA was responsible for outbreaks of diarrhea in 1-week-old goat kids (Alkan et al., 2012).

Currently, the classification system of RVA based on the complete genomic constellation enables scientists to evaluate RVA evolutionary relationships, gene reassortment events and emergence of new RVA strains by interspecies transmission (Matthijssens et al., 2008b). The backbone genotype constellation of strain 0040 belongs to the consensus genotype constellation I2-(R2/R5)-C2-M2-(A3/A11/A13)-N2-T6-H3 displayed by RVA strains identified in the *Bovidae* (bovine, caprine and ovine) and *Camelidae* (guanaco and vicugna) families from the order *Artiodactyla* (Matthijssens et al., 2008a,b, 2009; Badaracco et al., 2013). Moreover, this consensus genotype configuration is also displayed by human G8P[1], G10P[11] and G6/G8/G10P[14] strains (Table 2) that seem to be derived from interspecies transmission events from animals to humans (Matthijssens et al., 2008a,b, 2009; Ramani et al., 2009; Bányai et al., 2010; El Sherif et al., 2011; Ghosh et al., 2011).

Taken together, phylogenetic analyses also indicated that 7 (VP1, VP2, VP3, VP4, VP6, NSP2 and NSP4) out of 11 gene sequences of strain 0040 had a close to relatively close relatedness with cognate genes from canonical bovine RVA strains (Figs. 1–3). Interestingly, the VP7 gene sequence of strain 0040 clustered together with G8 strains from Argentinean South American camelids (Rio Negro G8P[1], Chubut G8P[14] and vicugna RVA strain 75 G8P[14]) (Matthijssens et al., 2009; Badaracco et al.,

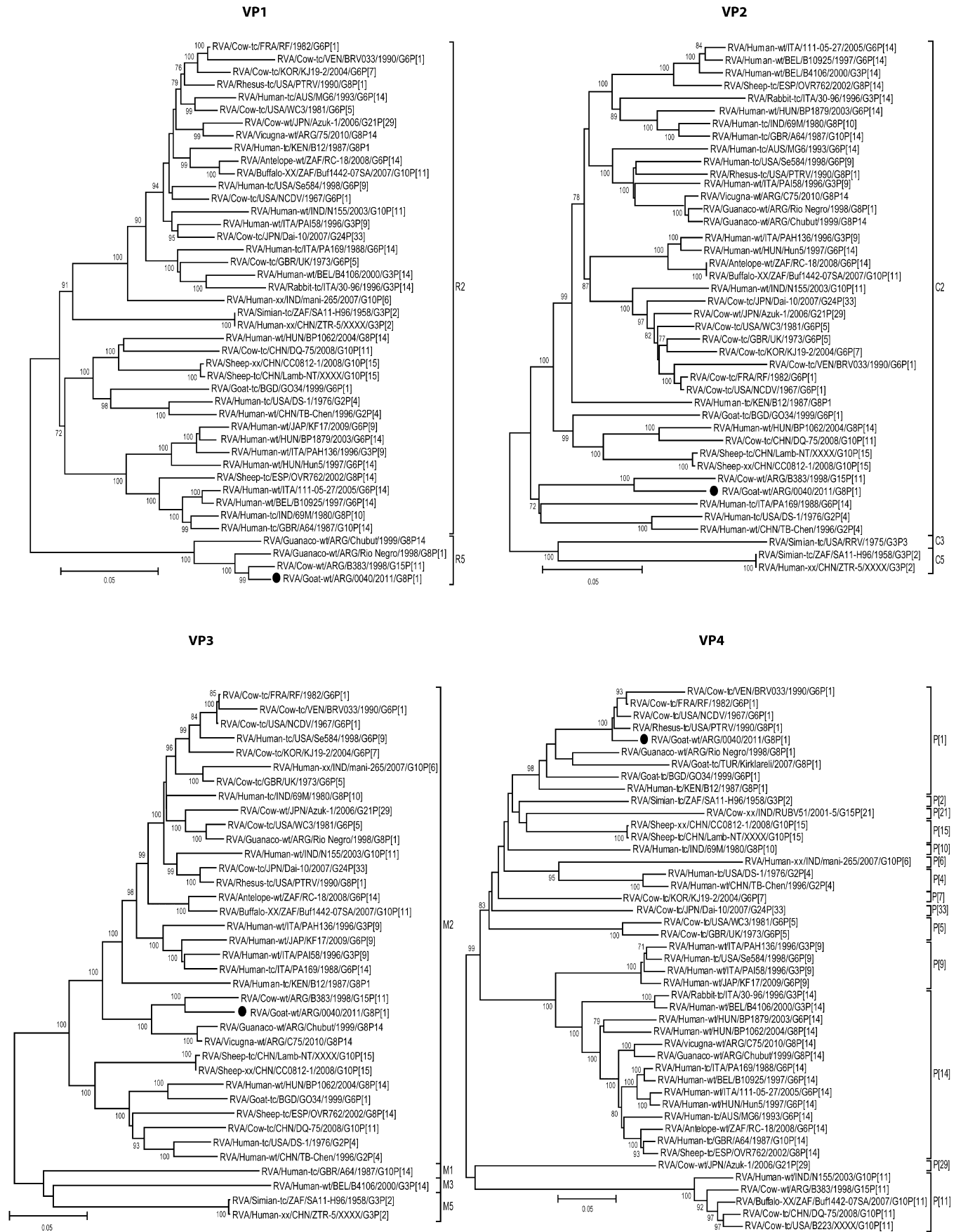


Fig. 1. Phylogenetic trees based on the complete (VP1) and partial (VP2, VP3 and VP4) ORF sequences for the different genome segments (Table 1). Phylogenetic trees were constructed using the neighbor-joining method with the kimura-2-parameter. Bootstrap values (1000 replicates) above 70% are shown. RVA/Goat-wt/ARG/0040/2011/G8P[1] is indicated by a black circle.



Fig. 2. Phylogenetic trees based on the partial (VP6) and complete (VP7 and NSP1) ORF sequences for the different genome segments (Table 1). Phylogenetic trees were constructed using the neighbor-joining method with the kimura-2-parameter. Bootstrap values (1000 replicates) above 70% are shown. RVA/Goat-wt/ARG/0040/2011/G8P[1], RVA/Goat-wt/ARG/0076/2011/G8Px and RVA/Goat-wt/ARG/0096/2011/G8Px are indicated by a black circle.

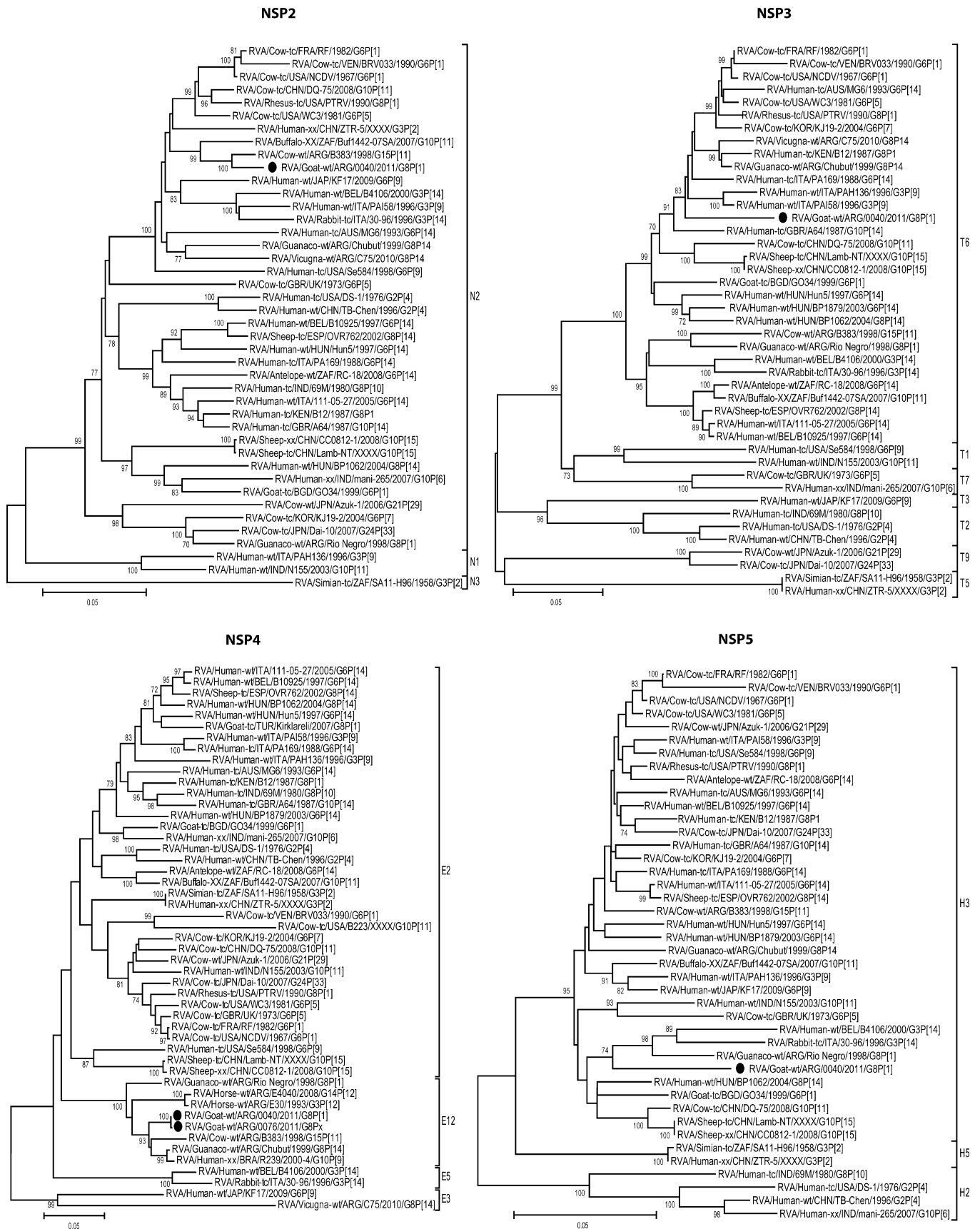


Fig. 3. Phylogenetic trees based on the complete ORF sequences for the genome segments NSP2, NSP3, NSP4 and NSP5 (Table 1). Phylogenetic trees were constructed using the neighbor-joining method with the kimura-2-parameter. Bootstrap values (1000 replicates) above 70% are shown. RVA/Goat-wt/ARG/0040/2011/G8P[1] and RVA/Goat-wt/ARG/0076/2011/G8Px are indicated by a black circle.

2013) and also with G8 bovine-like strains (PTRV G8P[1] and K12 G8P[1]) (Matthijnsens et al., 2010; Ghosh et al., 2011). Altogether, the G8 genotype seems to be frequent among RVA strains infecting different animal species from the order *Artiodactyla* (mainly ruminants and camelids).

Overall, the data presented in this study suggest a number of possible hypotheses. First, the caprine strain 0040 could represent a typical goat RVA genome constellation similar to those previously found in other animal species within the order *Artiodactyla*, but further studies will be needed to confirm this. Secondly, the strain 0040 could be the result of a direct transmission from cattle to goats, or it might be generated by reassortment events between RVA strains during co-infections in these ruminant species. This hypothesis is plausible because cattle were also reared in the dairy farm. Thirdly, the possibility of a recent direct RVA interspecies transmission or multiple segments reassortment events between RVA strains infecting guanacos and goat kids is less plausible because of the geographical distance separating the farm from the natural environment of South American camelids. However, the genetic relatedness for some genome segments in these RVA strains suggests a common ancestor, which is not unexpected given the overlapping geographic distribution of these animals in the past. The data from genotyping and phylogenetic analyses, in addition to previous information, suggest that caprine strains such as 0040 have a zoonotic potential for humans in intimate contact with goats, since artiodactyl-derived human RVA strains have been described frequently in the past.

Conflict of interest statement

None.

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