Indian Journal of Animal Sciences **84** (10): 1035–1042, October 2014/Review Article

Rotavirus diarrhea in piglets: A review on epidemiology, genetic diversity and zoonotic risks

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Received: 4 February 2014; Accepted: 22 April 2014

ABSTRACT

Pig farming is considered as backbone of rural poor farmers, belonging to lowest socio-economic strata, where mainly unorganized means of pig farming, improper housing, feeding and management are the constraints, and such practices are well known to expose the pig population to a number of infectious and non-infectious disease causing agents. One among those infectious diseases agents is rotavirus (RV), which is the foremost cause of gastrointestinal infections in mammalian and avian species all over the world, also a predominant cause of enteric infections in pigs, and has potential public health concerns. This review provides information on the frequency of RV infection, genotype diversity and zoonotic potential of its emerging reassortants in Indian porcine population. Prevalence studies done so far revealed gruesomely higher porcine RV prevalence in north-eastern region (46.4%) of India. Analysis of available sequence data of VP7 gene (G genotype) and VP4 gene (P genotype) of porcine group A rotaviruses (Po-RVAs) showed the presence of G4, G6, G9, G12 and P[6], P[7], P[13]and P[19] genotypes. Lately, few of the porcine RV strains also exhibited unique genomic constellations with evidence of interspecies transmission events, mainly involving RV strains of human origin. Evolution of rotaviruses is fast due to point mutation and reassortants generation in case of multiple infections. Thus it is imperative to generate the baseline information for formulating better disease preventive and control strategy. At present, nationwide surveillance and monitoring is prerequisite to assess the distribution of common and unusual genotypes of RVs circulating among pig population in India.

Key words: Diarrhea, Genotypic diversity, India, Porcine, Prevalence, Rotavirus, Zoonoses

Viral gastroenteritis is arguably the most significant public health problem today throughout the world, with higher momentous situation in developing countries. Rotavirus (RV) has been identified as an assured cause of severe gastroenteritis in mammalian and poultry species throughout the world. The disease is usually seen in young animals and susceptibility to the disease decreases as the age progress presumably because of change in the animal physiology and/or acquired immunity due to previous exposure (Estes and Kapikian 2007). The RV associated viral gastroenteritis in piglets is of great concern not only because of their economic impact in the livestock sector in terms of mortality and morbidity, but also as potential source of heterologous RV infection in humans and many other animal species (Varghese *et al.* 2006, Chitambar *et al.* 2009, Dhama *et al.* 2009, 2010, Tate *et al.* 2009). Unlike group A, B, C and E rotaviruses reported in porcine population throughout the world so far (Chasey *et al.* 1986, Smitalova *et al.* 2006, Kuga *et al.* 2009), group A rotaviruses (RVA) remain more prominent (Estes and Kapikian, 2007, Miyazaki *et al.* 2013). Further, RVAs are the most important due to their high prevalence and pathogenicity in human as well as in pigs (Papp *et al.* 2013).

RVs are member of the genus *Rotavirus* within the family *Reoviridae*. Its genome entails 11 genomic segments of double stranded RNA (dsRNA) with size from 0.6 to 3.3 kb encoding 6 structural (VP1-VP4, VP6 and VP7) and 6 non-structural proteins (NSP1-NSP6) (Estes and Kapikian 2007). VP1 protein is a RNA-dependent-RNA polymerase and for its correct functioning, VP2 protein is required. VP3 and VP1 forms complex and plays a central role in

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transcription. The outer spike protein is VP4 in the outer capsid, which helps the virus for attachment to the host cells thereby contributing in RV virulence. A non-structural protein NSP3 plays a major role in the process of translation. NSP4 protein acts as an enterotoxin of the virus as well as virulence factor that increases the concentration of calcium ion (Ca^{2+}) intracellularly thus distressing the host cellular homeostasis (Estes 2003). Exploration of the physico-chemical characteristics of RVs revealed higher stability as well as resistance to ether, chloroform, quaternary ammonium compounds and chlorination procedures, but sensitivity to phenol as well as formaldehyde is high (Murphy *et al.* 1999, Song *et al.* 2006).

The convenience of modern biotechnology assays added a newer dual classification system (G and P genotypes) for RVA targeting the outer-layer capsid proteins of virus i.e. VP7 and VP4, which independently elicit neutralizing antibodies (Varghese *et al.* 2004). Thus, RVA strains are classified into VP4 or P types (for protease-sensitive) and VP7 or G types (for glycoprotein) (Estes and Kapikian 2007). Till now, 27 G and 37 P types have been documented in human and animal RVA infections (Mukherjee *et al.* 2013, http://rotac.regatools.be/classificationinfo.html). During a surveillance in New Delhi molecular characterization of several non-typeable strains of rotaviruses have been done and it has been found that most of the strains belong to G1 genotype or P[8] genotype based on sequencing of nucleotide fragments from the VP7 as well as VP4 genes. Acquisition of the VP7 along with VP4 and NSP4 genes can result in generation of new strain of the virus (Sharma *et al.* 2009). Though, several RV genotypes or new genetic variants of a specific genotype have been witnessed in connotation with outbreaks of RV diarrhea in suckling piglets throughout the world (Barreiros *et al.* 2003, Lorenzetti *et al.* 2011, Miyazaki *et al.* 2011), this review presents the information on prevalence of RVs, genotypic distribution in piglets from India and public health concerns of the emerging reassortants pig RV strains.

Epidemiology of porcine RVs

The diversity of RV strains is predominantly increased by accretion of point mutations leading to genetic/antigenic drift and reassortment of cognate genes leading to genetic/antigenic shift. The documentation of emerging RV strains in animals is of utmost prominence for instigating the control measures for the virus infections in both animals and humans. Therefore, more apprehension has been on the information congregation on RV flowing in the environment. In the adult pigs, the rate of sero-conversion due to RV infection is almost 100%. Thus, in 2–4 weeks age group of piglets, the rotaviral outbreak is common (Ramani and Kang 2007). The prompt RV evolution as of a variety of mechanisms offers the foremost challenges in epidemiological surveys of RV infection. Substantial focus has been paid on RV disease in India. Since the very first RV detection in porcine of India (Barman *et al.* 1998, Jhala and Raghavan, 1998, Jain *et al.* 2001a), the porcine RVs have been documented from eastern, north eastern region, northern, central and western parts of the country (Barman *et al.* 1998, 2003, Nath *et al.* 2004, 2007, Bora *et al.* 2007, 2009, 2011, Kusumakar *et al.* 2008, Kumar *et al.* 2011, Dubal *et al.* 2013) as summarized in Table 1.

In India, most of the records on RV epidemiology have originated from north-eastern part of the country where pig farming constitutes major share (40%) of pig population of the country (Fig. 1a), and is directly related to the livelihood of poor farmers in general and tribal farmers in particular. The very first porcine RVAs prevalence study came out from North-eastern part of the country in late 1990's, where 26.9% serum samples were found positive for RV antibodies using sandwich enzyme-linked immunosorbant assay (ELISA) (Barman *et al.* 1998, Kang *et al.* 2005). The highest incidence was recorded in 4-week-old piglets (53.1%) followed by 2-week (46.1%) and 3-week old piglets (48.8%). In a subsequent study, Barman *et al*. (2003) detected RV antibodies in 51.1% of the serum samples by ELISA. The prevalence of RV antibodies was more in

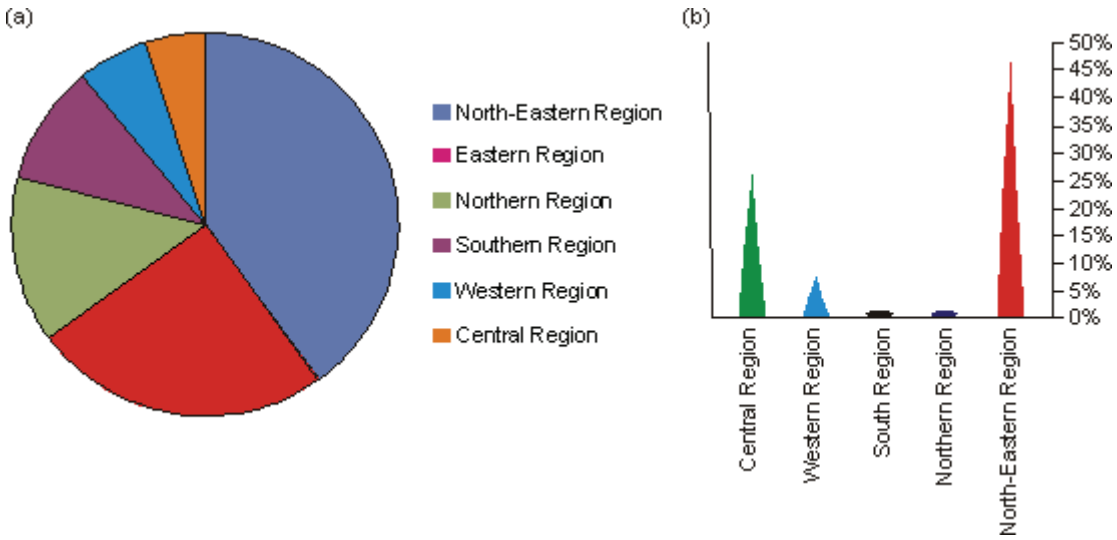

Fig. 1a. Distribution of pig population across the different geographical regions of India (data acquired from 18th Livestock Census, 2007). 1b. Prevalence of porcine RVAs in different parts of India (1998–2013).

Table 1. Descriptive porcine rotavirus surveillance studies done so far in India from 1998–2013.

Authors	Regions surveyed	% Prevalence	Detection methods	Antigen (RV)/antibody (Abs) detected
Barman *et al*. (1998)	North-Eastern Region	26.9% (34/126)	ELISA	Abs
Barman *et al*. (2003)	Asom	51.1% (270/528)	ELISA	Abs
Nath *et al*. (2004)	Asom	73.8% (307/416)	ELISA	Abs
Nath *et al*. (2007)	Asom	22.86% (128/560)	PAGE	RV
Bora *et al*. (2007)	Asom	29.35% (423/1441)	ELISA	RV
Bora *et al*. (2009)	Asom	65.4% (942/1441)	ELISA	RV
Kusumakar *et al*. (2010)	Madhya Pradesh	25.7% (9/35)	PAGE	RV
Kumar *et al*. (2011)	Uttar Pradesh	0% (0/47)	PAGE, PCR	-
Dubal *et al*. (2013)	Western Region	7.4% (10/135)	PAGE, PCR	RV
	Northern Region	0% (0/20)	PAGE, PCR	RV
	Southern Region	0% (0/60)	PAGE, PCR	RV
	North-Eastern hills	30% (18/60)	PAGE, PCR	RV

intensively reared pigs (53.9%) compared to open grazing pigs (45.5%). Later, in a study from the same region, 73.8% (307/416) of pigs were recorded positive for RV infection employing indirect ELISA (Kelkar *et al.* 2004, Nath *et al.* 2004). They established the higher prevalence of RV infection (85.48%) in pigs of more than 8 months age than any other age group, and pigs reared under organized semi-intensive farming were more susceptible to RV infection in comparison to unorganized semi-intensive and open range system of rearing. In a succeeding cross-sectional and cohort work, Nath *et al*. (2007) reported presence of RV in 22.86% (128/560) of the faecal samples with highest incidence in 0–2 month's old piglet (31.25%). Higher per cent of RV infection was recorded in piglets reared under organized semi-intensive system (24.2%), diarrhoeic pigs (38.2%) and during winter (41.1%).

The first report of isolation of porcine RV recovered from diarrhoeic piglets in MA-10^4 cell line came in the year 2007 from Asom (Bora *et al.* 2007) and the same research group detected the porcine RVs in faeces of infected pigs by ELISA (29.35%) and polyacrylamide gel electrophoresis (PAGE) (24.84%). The RV excretion was also demonstrated in healthy as well as clinically affected cases of pigs (Bora *et al.* 2009) during an epidemiological surveillance in 3 organized pig herds of Asom involving 1,441 diarrhoeic and healthy pigs of different age groups. The RV infection was seen higher among diarrhoeic (51.5%) than healthy (13.9%) pigs using ELISA. Also, the RV incidence was highest in 0–2 month age group in diarrhoeic (59%) as well as healthy (26%) piglets, with progressive reduction at later ages. Recently, excretion pattern of RV in the pregnant sows before and after farrowing and their role in disseminating the infection to their newborns was explored by Bora *et al*. (2011) during a longitudinal study. They monitored 6 pregnant sows (3 sows and 3 gilts gilt-farrowing) farrowing on the same day and tested them for presence of RV antigen by sandwich ELISA and PAGE. The average duration of excretion at pre- and post-farrowing in sows was 5.66±0.33 and 5.33±0.33 days, respectively, while in gilts the average duration of excretion in pre- and post-farrowing was 7.33±0.67 days. The excretion of RV in faeces of these piglets was monitored up to 2 months age from the date of farrowing. The piglets excreted RV from eighth day onwards and continued up to sixth week of their life. Some of the studies carried out in past demonstrated that the enteritis in piglets is complicated by secondary pathogens (Das *et al.* 2008, Neog *et al.* 2009). The clinico-pathological and hematological studies conducted in RV infected piglets alone or in combination with bacterial infections have revealed rise in body temperature (103–105°F) followed by profuse diarrhoea and dehydration, along with lymphopenia and neutrophilia. Significant increase in haemoglobin (Hb), packed-cell volume (PCV), erythrocyte sedimentation (ESR) and serum potassium level and decrease in the levels of serum sodium, chloride and bicarbonate in RV infected animals were also documented (Desselberger *et al.* 2001, Das *et al.* 2008, Jain *et al.* 2001b, Neog *et al.* 2009).

On exploitation of the ribonucleic acid-polyacrylamide gel electrophoresis (RNA-PAGE) technique easy separation of all the 11 segments of the RV has become possible and researchers were able to generate an RNA electropherotype, which is a characteristic visual pattern (Chauhan and Singh 1993, Song *et al.* 2006). The prevalence of RV in pigs from Madhya Pradesh was 25.7% (9/35) with detection of long electropherotypes (based on migration of 10^{th} and 11^{th} segment of RV in RNA-PAGE). Surprisingly, in the subsequent year (2008) all the diarrheic piglets (n=34) were found negative for RV infection, which need further evaluation (Kusumakar *et al.* 2008, Malik *et al.* 2013).

The RV infection was more common in piglets of up to 8 week age or weaned piglets (50%) than piglet of above 3 months of age (7.7%). In another study from northern region of the country (Bareilly, Uttar Pradesh), no RV was detected in pig population using RNA-PAGE and reverse transcription polymerase chain reaction (RT-PCR) (Kumar *et al.* 2011).

Recently, the screening for the presence of RV in faeces of piglets from different parts of the India was accomplished by Dubal *et al*. (2013), in which they tested 275 faecal samples (180 diarrheal and 95 non-diarrheal) from piglets from the western, southern, northern and north-eastern hill

(NEH) and found maximum prevalence in NEH region (30%) followed by western region (7.4%) by RNA-PAGE and/or RT-PCR. Surprisingly, all the tested samples from the southern and northern regions were found negative.

Startlingly, the overall porcine RV prevalence rate in India is 44.4% with maximum in north-eastern region (46.4%) followed by central region (25.7%) (Fig. 1b). This high prevalence especially in north-eastern is because of high density of pigs and active research groups monitoring the RV prevalence in pigs. Though porcine RVs have not been reported so far from northern and southern regions of the country, more explicit work is urgently required to confirm the exact scenario of porcine RV prevalence from these regions.

Genotypic diversity among porcine RVs

Based on the antigenic specificity of the viral capsid proteins rotaviruses were classified into 7 serogroups, viz., A – G. This classification is also based on the electrophoretic mobility of the viral RNA segments (11 in number). Out of all these viruses group A-C are known to cause disease in humans and animals. The greatest mass of the virus particle is formed by the VP6 bearing the subgroup (SG) specificities thereby allowing antigenic classification of the viruses. It is easy to derive neutralizing monoclonal antibodies from mouse and thereby have been used extensively in epidemiological surveys (Kang *et al.* 2005). Although extensive epidemiological studies have described the occurrence of RV from humans and cattle in India, few surveillance studies have been conducted on porcine RV, with that only few Indian porcine RV strains have been assessed at molecular level. RV outer capsid layer is made up of a protease sensitive protein designated as VP4 and a glycoprotein designated as VP7. These two outer capsid proteins of the virus, VP4 and VP7, elicits the production of neutralizing antibodies and were used to define the P (protease sensitive VP4) and G (VP7 glycoprotein) serotypes of the virus. In nature the diversity of rotaviruses is provided by all the 11 segments of the viral genome. So it is desired that determination of the genes influencing restriction of host range; replication as well as virulence will influence the construction of a classification system on the basis of all the gene segments of the virus. Determination of the gene segments that encode VP1 to VP3; VP6; NSP1 to NSP5 are required to establish such a classification system for human as well as animal strains of rotaviruses that belong to G as well as P genotypes. Determination of identity cutoff values has been done for each gene on the basis of phylogenetic analysis (Kang *et al.* 2005, Matthijnssens *et al.* 2008a).

However, based on the nucleotide sequence variations in these 2 outer capsid genes (VP4 and VP7), currently, 27 G and 37 P genotypes have been described in human and animals (Kobayashi *et al.* 2007, Marthaler *et al.* 2012, http://rotac.regatools.be/classificationinfo.html). On analysis of the VP1, VP2, VP3, VP4, VP7 and NSP4 genes identification of genetic relatedness has been done in comparison to recent human rotavirus (HRV) strains. These research findings cumulatively points to the facts that there may be evolution of new reassortant viruses (Steele *et al.* 2004, Varghese *et al.* 2004, Mascarenhas *et al.* 2007). By employing RNA electrophoresis several porcine samples were found positive for rotaviral infection between the years 1998–2000 at Kolkata. Genotyping of the G (VP7 genotype) as well as P (VP4 genotype) has been done by reverse transcription as well as multiplex PCR (Gentsch *et al.* 1992). High degree of genetic reassortment was found in samples collected from Manipur (Das *et al.* 2002). It was found that group A rotaviruses (RVAs) of porcine are found in association with weaning as well as post-weaning enteritis in case of piglets both worldwide as well as in India. In piglets aged between 1 and 8 weeks of age RVAs are the viruses most frequently detected and so also they may be detected in non-diarrheic piglets. Both enzootic as well as epizootic forms of diarrhea are caused by RVAs that result in losses commercially in piggeries. The mechanisms of synergism is triggered by other pathogens that worsen the disease condition in piglets. In India more than 50% of the piglets positive for RVA are also found positive for either caliciviruses or rotaviruses belonging to group C (Saif and Fernandez 1996).

Global epidemiologic surveys have identified G3, G4, G5 and G11 as the most common G genotype and P[6] and P[7]) as the most common P genotype associated with diarrhea in pigs. Also rare genotypes (G1, G2-like, G6, G8, G9, G10, and G12) were reported in pigs which are commonly associated with humans and cattle (Bellinzoni *et al.* 1990, Ciarlet and Liprandi 1994, Gouvea *et al.* 1994, Ramos *et al.* 1998, Estes 2001, Steele *et al.* 2004, Martella *et al.* 2005, Varghese *et al.* 2006, Matthijnssens *et al.* 2008b, Prabha and Verghese 2009, Papp *et al.* 2013). Similarly, apart from the common porcine P genotypes (P[6] and P[7]), rare and/or novel P genotypes (P[1], P[5], P[8], P[11], P[13], P[19], P14[23], P[26]) were identified in pigs (Martella *et al.* 2005, Maneekarn *et al.* 2006, Varghese *et al.* 2006, Khamrin *et al.* 2007, Chan-It *et al.* 2008, Matthijnssens *et al.* 2008).

The available information on epidemiological surveys from India clearly indicated that RVAs are the most significant viral contributors to the burden of diarrheal diseases in piglets and huge genetic diversity within porcine RV strains exists. In India, 4 types of G (G4, G6, G9, G12) and 4 types of P genotypes (P [6], P [7], P [13], P[19]) of RVAs have been detected from pigs so far. Hitherto, there is no report till now on occurrence of group B and C RVs in pigs from India. Both the diagnosis as well as molecular typing of RVs are performed at present by using RT-PCR (serotype specific); nested / multiplex RT-PCR as well as restriction fragment length polymorphism (RFLP) (Santos *et al.* 1999, Song *et al.* 2006). Sequencing analysis of the VP6 as well as VP7 genes as well as microarray hybridization (oligonucleotide) are in use for identification of mixed viral infections (Fischer and Gentsch 2004, Ghosh and Kobayashi, 2011). Diarrhea due to RV must be

differentiated from *E. coli* associated infectious diarrhea in pigs, *Clostridium perfringens*, coronavirus, calicivirus or astrovirus infections. For this use of multiplex RT-PCR was found suitable (Santos *et al.* 1999, Smitalova *et al.* 2009, Wang *et al.* 2010). Detection of new/rare genotypes or mixed infection evokes the need for continued surveillance to assess and consider the strain variability in the design of the suitable vaccine candidate.

Zoonotic potential of novel RV strains

Usually the rotaviruses are species-specific but there is a possibility of cross-species transmission. Various case studies worldwide and in India indicated that infection in humans can be caused by the animal rotaviruses. Close identity is often revealed between the human and animal rotaviruses when the genetic sequences are compared. It is suggestive by seeing the incidence of uncommon strains at lower rate that such transmission or at least establishment of animal rotaviruses or a reassortants human/ animal virus in the human population does not occur with a very high frequency. Many researchers therefore suggested that the input of strains of rotaviruses or their genetic sequences from animal to human population may be a continuous process but of course at a very low level (Cook *et al.* 2004, Tate *et al.* 2009).

The evolution of porcine RVs, especially through the exchange of genomic segments among the different host specific RVs, leads to emergence of novel porcine strains having the capability to infect human beings (Fig. 2). Explicit reports are available confirming the reassortment events going on between human and porcine RV strains and emergence of RVs strains with rare genotypes. In one of such study, Varghese *et al*. (2004) characterized a rare genotype with G9P [19] specificity having long

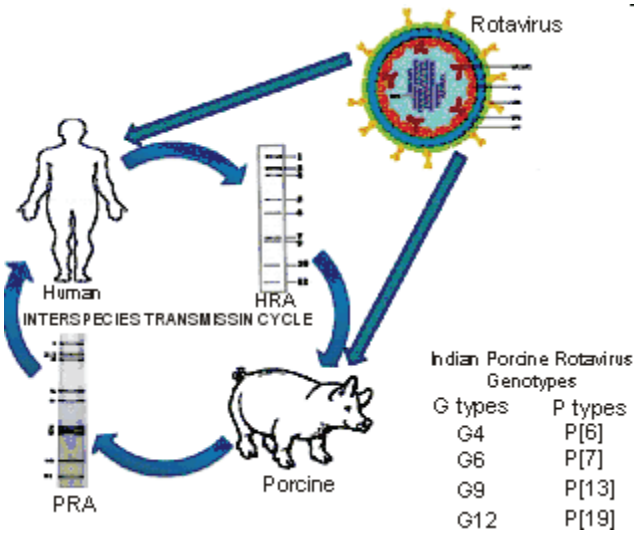

Fig. 2. Porcine rotavirus interspecies transmission cycle. Exchange of genomic segments among different hosts. Specific rotaviruses within the host leads to emergence of new strains/ genotypes. RVA genotypes (G and P) circulating in Indian porcine population are also presented. HRA: Human group A rotavirus; PRA: Porcine group A rotavirus.

electropherotype with subgroup I specificity, isolated from an epidemic (1987–88) of infantile gastroenteritis in Manipur, India. The nucleotide sequences of VP4, VP6, VP7, NSP1, NSP2, NSP3, NSP4 and NSP5 genes of this rare genotype were deciphered and on phylogenetic analysis, all the genes except VP7 were found closely related to porcine RVs, while VP7 gene of this RV strain clustered with human RV strains. Isolation of porcine rotaviral stains like G3 and G5 was done from the human population from various parts of the world (Ra´cz *et al.* 2000, Desselberger *et al.* 2001, Malik *et al.* 2005). In another study, Ghosh *et al*. (2006) reported first time detection of a porcine RVA strain (RU172) with G12P[7] genotype specificity from suburban area of Kolkata city, India and this strain on comparative sequence analysis clustered with human G12 strains with maximum identities of 93.6% to 94.5% at deduced amino acid level. In spite of its G12 genotypic nature, RU172 strain formed a separate lineage with human G12 strains on phylogenetic analysis. The other gene segments (VP4, VP6 and NSP5) of this strain showed porcine origin on analysis. Detection and characterization of strains like RU172 provided dynamic insight into the role of reassortment events in genomic diversity of RVA of man and pigs.

Subsequently, Ghosh *et al*. (2007) characterized 2 porcine RVA strains (HP113 and HP140) from eastern India and these strains were unique in the sense that VP7 gene was closely related to those of human G6P [14] strains, VP4 with a borderline P [13] genotype, and VP6 related to bovine and human sub-group I (SGI) strains rather than porcine SGI and/or SGII RVAs. Both the strains had NSP4 and NSP5 genes of porcine origin. This was the first report of detection of RVA strains with G6P [13] genotype specificities with evidence for independent segregation of the VP6- and NSP4-encoding genes in porcine RVAs. Chitambar *et al*. (2009) characterized a novel human RV strain (NIV929893) with a rare specificity of G1P[19]. The phylogenetic analysis of amino acid sequences of the VP7 and VP4 gene products showed clustering of the VP7 gene with G1 strains of human origin while the VP4 gene with P[19] strains of porcine origin. The findings of this study provide evidence of reassortment between VP7/VP6 genes of humans and VP4/NSP4genes of porcine species. Recently, Dubal *et al*. (2013) reported prevalence of porcine RV of G4, G9 and P[6] specificity with identification of an uncommon strain of G4P[6] specificity. The Indian porcine RV genome sequences retrieved from The National Center for Biotechnology Information (NCBI) database are compiled and presented in Table 2. The sequence data compilation from public domain illustrates that till collation of this review, 19 sequences are available in the sequence databank from India and mostly have been used a partly overlying portion of the RV genes. The HP 113, HP 140 and RU172 PoRV strains isolated from pig farms of Kolkata, India have been elucidated in detail. The VP7 gene of one more PoRV strain (Ro1) was also typed as G4 (EU445113, 1062 bp).

Table 2. Sequence database of porcine rotaviruses circulating in India (retrieved from National Center for Biotechnology Information)

Rotavirus strains	Genes	Accession numbers	Size (bp)	Genotyping using Rota Cv2.0 software
HP140	VP1	AY601117	651bp	R1
	VP2	AY601118	622 bp	C1
	VP3	AY601119	626 bp	M1
	VP4	DQ003291	2341 bp	P13
	VP6	DQ003295	1356 bp	I2
	VP7	DQ003293	1062 bp	G6
	NSP4	DQ003297	589 bp	E1
	NSP5	DQ003299	623 bp	H1
HP113	VP4	DQ003290	2340 bp	P13
	VP6	DQ003294	1356 bp	I2
	VP7	DQ003292	1062 bp	G6
	NSP4	DQ003296	680 bp	E1
	NSP5	DQ003298	616 bp	H1
RU172	VP4	DQ204742	785 bp	P7
	VP6	DQ204741	1236 bp	I5
	VP7	DQ204743	1062 bp	G12
	NSP4	DQ204740	682 bp	E1
	NSP5	DQ204739	631 bp	H1
Ro1	VP7	EU445113	1062 bp	G4

Future perspectives

RVs are well-recognized cause of substantial losses and health problems both in developed and developing countries. Results validate existence of huge genetic diversity among Indian porcine RV strains and present that pig farms may be the plausible source and likely reservoirs for human infections. In India, the rotavirus epidemiological profile is complex in nature thereby highlighting the requirement for a unified surveillance protocol of the strains that are circulating by the laboratories in India. Porcine RV prevalence in India was unexpectedly higher when surveyed, with maximum in the north-eastern region. Overall, epidemiological studies revealed the occurrence of porcine RVA strains with G4, G6, G9, G12 specificity and P types were P[6], P[7], P[13], P[19]. Emergence of some novel/ unusual strains by mechanism of reassortment among the human and porcine RVs highlights their potential of zoonotic infection. The Indian Council of Medical Research (ICMR) along with the Rotavirus Vaccine Project at the Programme for Appropriate Technology in Health have launched a national rotavirus surveillance programme. Appearance of rare combinations of prevailing porcine RV strains showed the need for exhaustive surveillance of RV infection in Indian settings, before entering attempts for a new vaccine. Compiled epidemiological profile of porcine RVs in India will be of considerable importance to both policy makers and vaccine inventors for designing an effective and potent vaccine for safeguarding porcine industry from this important pathogen having public health concerns. Along with monitoring, frequent updating of the methods of virus genotyping are essential on a national scale.

ACKNOWLEDGMENTS

We thank the Director, Indian Veterinary Research Institute, Izatnagar and Department of Biotechnology (DBT), Government of India for infrastructural and financial help. Authors are working under a DBT project (Grant number BT/168/NE/TBP/2011) for North-eastern region on enteric infections of piglets.

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