Molecular Characterization of Human and Bovine Rotaviruses in Marathwada Province of Maharashtra State

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Abstract: Rotavirus is the major etiologic agent associated with diarrhoeal diseases of young ones of many farm animals and human infants. Due to segmented nature of the RNA genome and wide host range, vast genetic and antigenic diversity exist amongst different isolates of rotavirus, keeping this point in view, the present study was undertaken to characterize bovine and human rotavirus circulating in Marathwada province of Maharashtra state. Total 211 faecal samples from bovines calves and 55 stool samples from children were collected from various regions of Marathwada. 21 (9.95%) and 6 (10.90%) samples were positive for rotavirus in bovine calves and children respectively. The characteristic RNA migration pattern of group ‘A’ rotavirus was observed in all bovine and human samples through RNA PAGE showing long electropherotype. All the PAGE positive samples tested by RT-PCR for VP7 and VP4 genes of bovine and human were amplified as evidenced by an expected PCR product of 1062bp of VP7 gene, 856bp of bovine VP4 gene and 876bp of human VP4. Nucleotide sequences retrieved after sequencing of PCR products were subjected to sequence analysis of VP7 and VP4 genes for further confirmation which showed 85% to 99% homology with other group ‘A’ rotaviruses after examined by nucleotide BLAST revealing the interspecies transmission.

Keywords: Rotavirus, RNA, RT-PCR, VP4, VP7

1. Introduction

Neonatal calf transience due to diarrhoea is one of the most common animal health concerns for dairy business leads to not only major financial losses but also creation of farm animals for Dairy and Beef (Kapikian, 1996, Tamilmani Suresh et al. 2012, Lorenz et al., 2011). Neonatal calf mortality occurs majorly between 3rd week to one month of age due to calf diarrhoea (Jenny BF et al. 1981). In case of human infants 800,000 deaths occurs between ages of 6 months to 2 years in developing countries a lead to major loss. In India, one of every 250 children death is attributed to rotavirus diarrhea every year. Prevalence of rotavirus diarrhoea in India has been found to vary from 5-71% in hospitalized children below 5yrs of age with acute gastroenteritis (Shoobha broor et al., 2003.)

Rota is a latin word means wheel, As rotavirus has individual wheel like appearance by negative stain electron microscopy and thus have been named Rotavirus (Shoobha broor et al., 2003). Rotavirus belongs to Reoviridae family, characterized by non enveloped triple layered viral particles with a viral genome having 11 double stranded RNA segment (ds RNA). Rotaviruses are classified in 7 groups (A-G) according to the antigenic variability of the inner capsid protein VP6. Group A Rotavirus are further classified into G & P types based on the genetic and antigenic variation of the 2 outer capsid proteins VP7 (Glycoprotein) & VP4 (protease sensitive protein) respectively (Estes, 1996). In India Group A bovine rotaviruses are responsible for neonatal calf diarrhoea, and having characteristic 4:2:3:2 pattern of 11 monocistronic dsRNA segments where segments 7, 8, and 9 were grouped as a triplet, typical of group A rotaviruses. RNA polyacrylamide gel electrophoresis (RNA PAGE) has been employed for detection of rotavirus antigen or viral nucleic acid in faecal samples (Minakshi et al., 2009) and molecular methods by reverse transcriptase PCR (RT-PCR) for the amplification of rotaviruses. As segmented nature viral genome allows re-assortment in mixed infection situation leading to emergence of new strains of the virus. There are also few reports in other countries noticed mixed infection in human infants (Nakagomi et al.1991) and bovine calves. The present study was undertaken with objectives: as screening of faecal samples from calves and children for rotavirus by employing RNA polyacrylamide gel electrophoresis (PAGE) and molecular characterization of rotaviruses.

2. Material and Methods

Total two hundred and sixty six faecal samples were collected in and around Marathwada province in Maharashtra state. 101 samples from cow calves and 110 from buffalo calves less than one month of age. The samples were collected from veterinary dispensaries, Dairy farms, Animal market, Small dairy farmers of various districts in Marathwada region. Along with fifty samples of human neonates were collected from both private and government pediatric hospitals were admitted for acute gastroenteritis in and around marathwada region during winter and prior to summer season in year 2014. All samples are collected in a sterile screw cap vials and keep it at 4°C. The faecal samples were diluted in phosphate buffer Saline (pH7.2) to make 10% suspension, followed by centrifugation at 10,000xg for 15 mins to remove course partials and cellular debris. The clarified supernatant was stored at -20°C until further use (Minakshi et al., 2009).

Extraction of Viral RNA: RNA extraction were done with TRI reagent directly from 10% faecal suspensions, described by World health organization Department of Immunization, Vaccines and biological (www.who.int/vaccines-documents/)

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The sequences obtained were subjected to BLAST analysis to conform the presence of genes specific to rotavirus (Yashpal S. et al. 2013). The nucleotide sequences of VP7 and VP4 gene fragments of rotavirus were aligned using default parameters of muscle alignment implemented in MEGA 7.0 software (http://www.megasoftware.net/). The sequences were further analyzed for identity and differences using Sequence Identity and Similarity Tool available at (http://imed.med.ucm.es/Tools/sias.html).

3. Results and Discussion

This study was mainly aimed at distribution, detection, molecular characterization and sequence analysis of rotaviruses isolated from bovines and humans in faecal samples of diarrheic neonates using RT-PCR.

Detection of bovine and human rotavirus in RNA- PAGE

As shown in plate 1, 21 (9.95%) out of 211 faecal samples tested positive for rotavirus by RNA-PAGE resolved 11 segments with typical migration pattern of 4:2:3:2. This confers that all of them belongs to Group A rotavirus.

All of the positive bovine rotavirus showed ‘long’ electrophoretic migration pattern. Similar migration pattern was recorded by (Broor et al.1993, Kasule et al.2004, Urbina et al 200, Zuridah et al.2004). During the study, out of 55 human stool samples tested, 6 (10.90%) showed a typical migration of dsRNA segments in 4:2:3:2 pattern, indicative of group A rotaviruses shown in plate 2.

However, in a study of rotaviruses in Kolkata, (Barman et al. 2004) detected a total of 18 (10.3%) Group A (4:2:3:2) rotavirus from 175 diarrheic stool samples of calves between 1 to 6 months of age. Group A rotaviruses have been detected worldwide. In India, Group A rotavirus has been detected in different places and the isolates were subjected to genetic characterization at the DNA level. The nucleotide sequences of VP7 and VP4 gene fragments of rotavirus were aligned using default parameters of muscle alignment implemented in MEGA 7.0 software (http://www.megasoftware.net/). The sequences were further analyzed for identity and differences using Sequence Identity and Similarity Tool available at (http://imed.med.ucm.es/Tools/sias.html).
Amplification of VP7 gene of bovine and human 
Rotavirus: Full length (1062 bp) amplification of VP7 gene was transcribed into cDNA by reverse transcription using FalcBeg9 and FalcEnd9 primers. The cDNA was amplified by PCR using same gene specific terminal sequence primers (Table 1).

Samples subjected to full length amplification yield a specific product of 1062 bp as observed in 1% agarose gel (Plate no 3) as per (Isegawa et al.1993 and Deswal et al. 2006). for bovine samples (Gentsch et al.1992, Siwach 2005 and Deswal 2006) for human samples.

Amplification of VP4 gene of bovine and human rotavirus: For partial length Bovine (856bp) and human (876 bp) amplification of VP4 gene was transcribed into cDNA by reverse transcription using gene specific (Falc FP and Falc RP) primers for bovines and (CON 3 and CON 2) primers for human. The cDNA was amplified by PCR using terminal sequence primers (Table 1).

Samples subjected to partial length amplification, yield a specific product of 856 bp for bovine and 876 bp for human as observed in 1% agarose gel. Representative sample are shown in Plate no. 4. Similar findings were recorded by Gentsch et al.(1992), Kumar Harsh Bardhan (2007); Siwach (2005), Deswal (2006).

Nucleotide sequence analysis

Nucleotide sequence analysis of VP7 for bovine and human 
The VP7 sequence homology analysis of bovine and human rotavirus isolates of Marathwada region revealed maximum homology 99% and 97% at nucleotide level in India and around countries for both bovine and human with Accession number (KJ701395, KJ701394.1) and (AB905458.1, JN192109.1 JN192100.1, JN192098.1, JN192096.1, JN192059.1) respectively. Similar findings were recorded by Yashpal S. et al.(2013), Masako Abe et al.(2009), V. Martella et al (2009).

Nucleotide sequence analysis of VP4 for bovine and human 
The VP4 sequence homology analysis of bovine rotavirus isolates of Marathwada region didnot revealed homology with any bovine species so it may be because of reassortment of virus which is frequently detected in developing countries due to close contact of animals and human and inter-species transmission of rotavirus. The maximum homology recorded 87% and 86% at nucleotide level around Asian countries with human rotavirus G4P6 VP4 gene isolated from Argentina (KC412048) and from Japan (AB770153.1). But in human rotavirus isolates of Marathwada region revealed maximum homology 87%, 86% and 86% at nucleotide level with the Rotavirus A isolates G4P6 from (KC412048.1), VP4 gene,G1P[10] from Japan (AB770153.1) and G6P[6] VP4 gene from Belgium (EF554085.1). Similar findings were recorded by William A. Rodriguez et al.(2009), Tung Gia Phan et al.(2007). Masako Abe et al.(2009), V. Martella et al (2009). This indicates cross species transmission among bovine and human rotavirus types (Souvik et al. 2007).

4. Summary and Conclusion
Out of 211 samples collected from cattle calves and buffalo calves, 21(9.95%) samples were positive showing typical long electropherotype pattern (4:2:3:2) indicating group A Rotaviruses. So present study reveals that there was Group A rotavirus was prevalent in Marathwada region and the prevalence was about 9.95% in case of bovines. In case of human neonates 55 stool samples are collected in that 6(10.90%) samples are positive showing long electropherotype pattern (4:2:3:2) indicating of group A rotaviruses. For further conformation with RT-PCR by amplifying VP4 and VP7 gene for both bovines and humans were amplified as evidence by an expected PCR product of 856bp of bovine and 876bp of human for VP4gene and 1062bp for VP7 gene. Representative sample from bovine and human were analyzed by nucleotide sequencing for VP7 and VP4 genes further conformation which showed 85% to 99% homology at nucleotide level with other group ‘A’ rotaviruses when subjected to nucleotide BLAST reveals cross species transmission of bovine rotavirus VP4 gene reveals 87% homology at nucleotide level with human G6P[6] VP4 gene. 

In future, extensive evaluation of serogroup specific nested RT-PCR assays with isolates of different serotypes from varied geographical locations or regions would strengthen
their serogroup specificity. Large scale testing of field samples would be useful in better extending application of these assays at field level. Moreover, due to the ability of the genomes of virus strains to re-assort, other genome segments should also be targeted, to obtain a truly comprehensive picture, which will in turn help to formulate comprehensive control strategies including effective vaccines development.

References


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