

## **Full genome sequence analysis of Group B human rotaviruses**

### **Abstract**

**Background:** Rotavirus is a major causative pathogen of severe diarrhea in humans and animals. On the basis of VP6 antigen, Rotaviruses are classified into seven groups (A-G), among which only groups A-C rotaviruses cause infection in humans. Group B rotavirus (GBR) was first detected in China in 1982 as a cause of adult diarrheal outbreaks. Although the detection of GBR had been limited in China, GBR has been found in India since 1998, in Bangladesh since 2000, and in Myanmar in 2007. Because of limited data, genetic characteristics of GBR have not been well known so far.

**Methods:** GBRs detected recently in India (IDH-084 in 2007, IC-008 in 2008), Bangladesh (Bang117 in 2003), and Myanmar (MMR-B1 in 2007) were analyzed genetically. Full genome sequences of these strains were determined by RT-PCR and direct sequencing methods. Sequence data was analyzed phylogenetically by MEGA4 program with those of GBRs reported previously.

**Results:** Sequences of all genes of GBRs, including those of animals, were classified into three clusters, i.e., Chinese lineage, India-Bangladeshi-Myanmar lineage, and animal (bovine and murine) lineages. Each strain showed high sequence identity among the same lineage (e.g., 95.6-100% among India-Bangladeshi-Myanmar lineage). The evolutionary rate of all segment genes of GBRs was estimated to be 1.89-2.05310<sup>-3</sup> nucleotide substitutions per site per year, using the synonymous substitutions between CAL-1(1998 in India) and IDH-084, CAL-1 and IC-008, and Bang373(2000 in Bangladesh) and Bang117.

**Conclusion:** Full genome sequences of recent group B human rotaviruses were determined and revealed the presence of two major lineages in human GBRs by phylogenetic analysis. Compared to the strains detected in different years, the substitution rate was estimated for the first time for all the gene segments. It was similar to those from partial sequence data reported previously and was comparable to the rate of other rapidly evolving RNA viruses. Further accumulation of genetic data is needed for resolution of ecological features of group B rotaviruses.