Chapter 3
Exposition of the study
Rotaviruses have been recognized as the major viral agent of acute gastroenteritis known to occur in individuals of all age groups. Rotavirus strains from the groups A, B, C and H have been detected in human infections. Association of RVB with human diarrheal disease was first identified in a large epidemic of adult diarrhea that affected nearly a million people in China during 1982-1983 (Hung et al., 1983, 1984). Infections with the RVB strain, ADRV identified during this epidemic were found to be extremely severe (cholera-like) in all age groups. The mortality resulting from severe dehydration was also reported in some elderly patients (Fang et al., 1989a). Other than China, association of RVB with outbreak cases of gastroenteritis was detected only in Daman, Union territory of India in the year 2000 (Kelkar et al., 2007). Although the epidemic in the early 1980s began in an explosive manner and spread fast, sporadic cases continued to be detected in China (Hung et al., 1984; Yang et al., 2004). Other than this country, RVB was identified at variable levels in sporadic cases of diarrhea from India, Bangladesh, Myanmar and Nepal (Sanekata et al., 2003; Aung et al., 2009; Malik et al., 2011; Alam et al., 2013). In western India, circulation of RVB was reported since 1993 in sporadic diarrheal infections from Pune city (Kelkar and Zade, 2004), while in Kolkata, eastern India, a few cases of severe adult diarrhea due to RVB infection were reported in 1997-1998 (Krishnan et al., 1999). In the latter region, infections with RVB were also detected at a significant level (18.5%) in children hospitalized for diarrhea during 2002-2004 (Barman et al., 2006). These data emphasized the need to undertake a long-term surveillance of RVB infections in India to establish their contribution in causing gastroenteritis.

Among animals, porcine and bovine species hold an important role in economy. RVB infections have been reported in these species residing in different countries. In India, occurrence of RVB infection among calves and adult cows has been reported to vary from 1.7% to 13% in eastern region (Barman et al., 2004; Ghosh et al., 2007; Nataraju et al., 2009). However, no reports were available for pigs from India. Since, approximately 80% of the population in India lives in close contact with domesticated animals and poultry (Chugh, 2008), investigation of RVB infection in animals is necessary to understand the epidemiology, genetic diversity and zoonotic potential of the virus.
Genetic characterization of available RVB strains has been carried out from time to time by different laboratories. At the initiation of the study, analysis of full genome sequences was reported for three human (CAL-1/India, Bang373/Bangladesh, WH-1/China) and single murine (IDIR/USA) RVB strains (Kobayashi et al., 2001, 2003; Ahmed et al., 2004; Yang et al., 2004; Nagashima et al., 2008). Later on, full genome sequences of four RVB strains recovered from sporadic cases of acute gastroenteritis (IDH-084/India, IC-008/India, Bang117/Bangladesh and MMR-B1/Myanmar) have been added by Yamamoto and colleagues (2010). Sequence analysis of the human RVB strains has revealed that all genes were conserved and considered to belong to a single genotype, G2 (Yamamoto et al., 2010). Within the genotype G2, the strains were further categorized into two lineages, i.e. Chinese (Chinese strains) and Indian-Bangladeshi (Indian, Bangladeshi, Myanmarese and Nepalese strains) lineages.

To understand the ecological and epidemiological features of RVB infections, genetic data on more RVBs from different geographic regions are necessary. Moreover, complete understanding of such strains identified locally is essential for development of diagnostic assays and preventive measures of RVB infections.

In view of this background information on RVB infection, a study entitled “Group B rotaviruses: Molecular epidemiology and genomic analyses” was undertaken with the following objectives:

1. To know the contribution of human RVBs in causing acute gastroenteritis in India.
2. To characterize structural (VP1-VP4, VP6, VP7) and non-structural (NSP1-NSP5) genes of human RVB strains isolated from outbreak and sporadic cases of acute gastroenteritis.
3. To identify circulation of RVB in porcine and bovine species in India.

The present study was divided into four parts to achieve the above-mentioned objectives. Part I (Chapter 4) deals with detection of human RVB infections in children, adolescents and adults with acute gastroenteritis in the
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2000s from Pune, western India and Belgaum and Alappuzha, southern India and its comparison with the data obtained from the 1990s. This part also includes detection of RVB in outbreak cases of acute gastroenteritis. Characterization of structural (VP4, VP7, VP6) and non-structural (NSP4) genes of human RVB strains detected as sole viral agent in the outbreaks is described in part II (Chapter 5) while in part III (Chapter 6), full length sequences of all 11 gene segments of 13 human RVB strains identified in both sporadic cases and outbreaks of acute gastroenteritis in western India during 1995-2010, their genetic relatedness with other RVB strains and estimation of evolutionary rates for all gene segments are documented. Part IV (Chapter 7) deals with detection and characterization of RVBs in porcine and bovine species.