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Burden of disease & molecular epidemiology of group A rotavirus infections in India

Sasirekha Ramani and **Gagandeep Kang**
Department of Gastrointestinal Sciences, Christian Medical College, Vellore, India

Abstract

Rotavirus is the major cause of severe dehydrating diarrhoea in young children worldwide. Considerable research has been carried out on rotavirus disease in India. This review collated data from 46 epidemiological studies to determine rotavirus positivity rates and genotypes of infecting rotavirus strains from various settings in India. Studies on diarrhoea presenting to hospitals, neonatal rotavirus infections, symptomatic and asymptomatic infections in the community and nosocomial enteric infections were included. Rotavirus positivity rates varied greatly between different settings - diarrhoea hospitalizations (20%), neonatal infections (35%), symptomatic and asymptomatic infections in the community (15.1% and 6.3% respectively) and nosocomial enteric infections (22.5%). Among diarrhea hospitalizations, the commonest G types were G1 and G2 while commonest P types were P[8], P[6] and P[4]. Region specific neonatal infections by bovine-human reassortants have been reported, in addition to several recently described unusual strains, which may be evidence of zoonotic infection and/or reassortment. The emergence of several new strains highlights the need for intensive strain surveillance before and after the introduction of a new vaccine.

Keywords

Genotyping; India; rotavirus

Rotaviruses are the major cause of severe gastroenteritis in infants and young children worldwide. Since the first description in humans in 1973, and their subsequent recognition as a major human pathogen, there have been a large number of studies on the structure, pathogenesis and epidemiology of these viruses. Their clinical relevance, structural complexity and unique morphogenesis strategies have prompted extensive research on these viruses in recent years, using molecular biological techniques1.

It is estimated that rotavirus is responsible for 611,000 deaths annually with 80 per cent of these taking place in poorer countries2. Vaccines offer the most promising tool for preventing morbidity and mortality caused by rotavirus. The first licensed rotavirus vaccine was withdrawn due to a temporal association with intussusception3. Efforts to develop new, safer vaccines are now underway with two vaccines having been licensed in Mexico and the United States after extensive safety trials4. Testing of candidate vaccines derived from two rotavirus strains which caused asymptomatic infections in neonates in India are also being carried out. The potential availability of rotavirus vaccines in the near future, including recently licensed vaccines from Merck and Glaxo SmithKline5,6 as well as vaccines currently in development in India highlights the need to better define the epidemiology and

Reprint requests: Dr Gagandeep Kang, Department of Gastrointestinal Sciences, Christian Medical College, Vellore 632004, India, e-mail: gkang@cmcvellore.ac.in.

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disease burden associated with rotavirus. The epidemiological profile of these viruses in India will be of considerable importance to both policy makers and vaccine developers in determining the composition, dosage and schedule for a vaccine to be used in India.

Structure and classification

Rotaviruses are double stranded RNA viruses comprising a genus within the family Reoviridae. The mature virus particles are triple layered, approximately 70 nm in diameter, and possess icosahedral symmetry. The rotavirus genome consists of 11 segments of double-stranded RNA, that code for 6 structural viral proteins (VP1, VP2, VP3, VP4, VP6 and VP7) and 6 non-structural proteins (NSP1 - NSP6)7, with gene segment 11 encoding both NSP5 and 6. The genome is encompassed by an inner core consisting of VP2 with small amounts of VP1 and VP3 proteins. The intermediate layer or inner capsid is made of VP6, which determines group and subgrouping specificities. The outer capsid layer is composed of two proteins, VP7 and VP4 that elicit neutralizing antibody responses (Fig. 1).

Rotaviruses are classified by a scheme of groups and multiple serotypes/genotypes within each group. The classification of rotavirus into seven different groups (A-G) is based on the antigenic specificity of the VP6 capsid proteins, as well as on the pattern of electrophoretic mobility of the 11 RNA segments of the viral genome. Of the seven groups, only groups A, B and C are known to infect humans. Severe, life-threatening disease in children worldwide is caused predominantly by group A rotaviruses. Within group A, four different subgroups (SG); SGI, SGII, SGI and II, and nonI/nonII, have been distinguished on the basis of VP6 diversity, of which human strains are possibly only from SGI or SGII8.

Further typing schemes to describe rotavirus strains are based on the proteins of the outer capsid that elicit neutralizing antibodies- VP7 (G serotypes) and VP4 (P serotypes). G- and P- serotypes were defined based on their reactivity to specific monoclonal antibodies (MAbs). While the use of MAbs for VP7 was relatively easy, cross reactivity between serotypes precluded use of MAbs for VP4 serotyping. Variability in the genes encoding the two outer capsid proteins VP7 and VP4 form the basis of the current strain typing of group A rotaviruses into G and P genotypes respectively. All known G serotypes correspond with genotypes; more P genotypes than serotypes have been identified. Currently, a rotavirus strain is identified by a G genotype, indicated by a number, followed by its P type. To distinguish strains identified by P genotyping from those identified by P serotyping, the dual serotype/genotype nomenclature is used. P genotypes are expressed as P followed by a number in square brackets whereas P serotypes are designated as P with serotype number, followed by corresponding genotype in square brackets (*e.g.*, the same strain could be represented as G9P[6], when both G and P genotypes are used, or G9P2A[6] when G genotype is followed by P serotype/genotype classification). At least 15 G genotypes and 25 P genotypes have been identified to date9.

Rotavirus detection and strain characterization

Laboratory procedures for diagnosis of rotavirus include electron microscopy (EM), passive latex agglutination assays (LA), electropherotyping using polyacylamide gel electrophoresis (PAGE), enzyme-linked immunosorbent assays (ELISA) and reverse transcription - polymerase chain reaction (RT-PCR)10. In recent years, ELISA has become the method of choice for screening. The sensitivity of routine diagnostics is high since the amount of virus excreted by a child with rotavirus diarrhoea (~10^{10} viruses/g of stool) far exceeds the level of detection (~10^{7} viruses/g of stool)11.

Early studies on strain surveillance identified rotavirus serotypes using neutralization assays. Monoclonal antibodies to specific serotypes were used. New methods have greatly improved

data on circulating rotavirus strains and include multiplex RT-PCR based genotyping, hybridization assays and nucleotide sequencing.

The rapid evolution of rotaviruses by a variety of mechanisms provides one of the major challenges in epidemiological studies. Interspecies transmission plays an important role in the diversity of rotaviruses. The ability of rotaviruses to reassort during co-infections results in the exchange of genetic material between human and animal viruses and generates novel viruses. Different mechanisms have been used to describe the evolution of rotaviruses. These include genetic drift, wherein accumulation of point mutations generates genetic lineages leading to the emergence of antibody escape mutants, and genetic shift through gene reassortment during dual infection of a single cell12. Hence methods of virus typing need to be regularly monitored and updated to identify emerging novel strains of epidemiological importance.

Rotavirus epidemiology in India

Considerable research has been carried out on rotavirus disease in India in different settings. Collation of data from these studies is frequently not possible due to the differences in study design, populations examined, and the testing methodologies used. The studies have, however, documented the marked diversity of rotavirus strains circulating in India, as well as the prevalence of unusual strains. Since the introduction and wider use of molecular biology-based typing methods, strains with G and P genotypes other than those considered common have increasingly been reported. G1, G2 and G4 strains are seen in almost all parts of the country, while there are few reports on G3 strains. In the past 5 years, four VP7 (G6, G8, G10 and G12) and one VP4 genotype (P[19]) have been newly identified as causes of diarrhoea in humans13.

A review in 2001 presented data from studies published from India on rotaviral disease14, but provided only the limited genotyping information available at the time. A review published in 2003 described the distribution of rotavirus in various settings in India published till 200215, but does not include a number of very recent publications describing unusual strains, particularly those that are potentially zoonotic in origin. In this review, we included studies published from 1990 to 2005 to collate data on the molecular epidemiology of rotaviruses in India. The studies were categorized as (*i*) rotavirus diarrhoea presenting to hospitals, (*ii*) neonatal rotavirus infections, (*iii*) rotavirus infection in the community, and (*iv*) nosocomial rotavirus infections. Studies in each group were then grouped by city for analysis.

For data on neonatal rotavirus infections and hospitalization due to rotavirus infection, studies published from 1990 to the present time were included. Since limited data are available on rotavirus in the community, all papers published on community rotavirus infections were included. For data on burden of rotavirus disease, all studies were included irrespective of detection technique used. To determine the G and P types circulating in India, only studies that used serotyping, hybridization assays or RT-PCR for G and P characterization of strains were included. Characterization data from studies using electropherotyping were not included, if it was not possible to also obtain data on G and P types from the studies.

Rotavirus diarrhoea in children hospitalized with acute gastroenteritis

A total of 29 studies carried out using samples obtained from children presenting with diarrhoea to a health care facility were included.

Rotavirus disease in hospitalized children

Data from 22 Indian cities are shown in Table I16-43. A total of 15,476 samples have been tested. Rates of rotavirus positivity ranged from 6 to 45 per cent (median 20.8%). The studies were carried out in various geographic locations in India. Most studies used ELISA and/or PAGE for the screening of rotavirus although latex agglutination assay, immunoblot and electron microscopy were also used in a limited number of studies.

Data from a study on the burden of infectious diseases in South Asia published in 2004 showed that an estimated 576,480 deaths occur due to diarrhoea in children in India44. Applying the above figure of 20.8 per cent of all diarrhoeas to be caused by rotavirus, it can be estimated that rotavirus is responsible for approximately 119,908 deaths annually. There are no published prospective studies that have examined rates of diarrhoea and hospitalizations in India. However, recent data from a birth cohort of 452 children in Vellore have shown that, in infancy rates of diarrhoeal episodes/child year (95% CI) is 3.6 (3.3 - 3.9), with a hospitalization rate/100 child years (95% CI) of 5.8 (3.8 - 8.8). Diarrhoea was the second most common cause for both outpatient visits and hospitalization after respiratory infections (unpublished data).

Rotavirus typing of strains obtained from hospitalized children

G- and P- typing was carried out using MAbs, genotyping primers or probes. A total of 1998 and 1108 samples were G- and P-typed respectively. The overall distribution of G and P types is shown in Figs 1 and 2. While most centres used MAbs or primers specific to G1- G4 and G9 types; G6, G8 and G10 were also included in some places. G1 and G2 were the most prevalent (24.7 and 23.4% respectively). However, the overall strain distribution varied from one location to another (Table II, Fig. 2). The commonest P type was P[8] (27%) followed by P[6] (21%) and P[4] (20%) (Table III, Fig. 3).

Unusual strains of rotavirus

A number of unusual strains of rotavirus have been reported in the recent years. Characterization of strains that remained untypable by routine typing methods have resulted in the identification of these unusual strains including G6 strains from Pune46, G8 strains from Vellore37 and Mysore47, G12 from Calcutta (Kolkata)48, G3P[8] from western India49, G9P[19] strains from Manipur50 and G10P[11] strains from Vellore10. Most of these strains are of possible animal origin or animal-human reassortants, containing one or more genes that are highly identical to corresponding genes in animal rotaviruses.

The G6 genotype described from Pune showed >94 per cent identity of VP7 gene with bovine rotavirus RF isolated from France46. The G8 genotype described from Vellore and Mysore showed about 95 per cent similarity in the amino acid sequence of VP7 gene to bovine strain A537,47. The G3P[8] genotype described among tribals in western India showed 100 per cent identity of VP7 gene to simian rotaviruses and 99 per cent identity to human P[8]49. The G9P[19] genotype from Manipur appeared to be a porcine - human reassortant with human VP7 and VP4, VP6 and NSP4 closely related to porcine rotaviruses50. G10P[11] strains described from Vellore appear to be bovine human reassortants with all genes of bovine origin except NSP1 and NSP3 (unpublished data).

Comparison of rotavirus diarrhoea among outpatients and hospitalized patients

One study carried out between 1993 and 1996 in Pune was reviewed51. A total of 489 and 628 faecal samples were collected from inpatient and outpatient children <5 yr with

diarrhoea respectively. The rate of rotavirus detection was higher among in-patients (28.3%) than outpatients (15.5%).

Neonatal rotavirus infections

Studies have reported the association of asymptomatic rotavirus infections in neonates with specific strains. The neonatal rotavirus strain is characterized by its endemicity and persistence in the neonatal ward. Maternal antibodies and physiologic immaturity of the neonatal gut may play a role in majority of neonatal infections being asymptomatic52. Neonatal rotavirus infections are believed to confer protection against subsequent infection and disease. Hence candidate vaccine strains have been derived from strains circulating in neonatal nurseries including two vaccine candidates currently in development in India53. However, symptomatic neonatal infections associated with necrotizing enterocolitis, acute gastroenteritis and feed intolerance have also been reported10.

Studies on neonatal rotavirus infections published before 1990 were reviewed in 200114. Subsequent studies using RT-PCR and genotyping of neonatal rotavirus strains have shown region specific asymptomatic infections by unusual strains (Table IV). This includes G9P[11] in Delhi54 and G10P[11] in Bangalore and Mysore55. Both symptomatic and asymptomatic infections by G10P[11] strain have been reported in Vellore10. Both neonatal strains appear to be bovine-human reassortants. G9P[11] is a human strain with a bovine VP4 while G10P[11] is composed mainly of bovine genes and has gene segments 5 and 7, encoding NSP1 and 3, of human origin53.

Rotavirus infection in the community

Community based studies provide geographically representative information on the disease burden, strain prevalence and rates of rotavirus infection in the community. This is of considerable significance in understanding the natural course of infection and for comparison of symptomatic and asymptomatic infections.

Since no data on rotavirus infection in the community in India have been reviewed so far, all studies have been included. It must be noted that all studies except one from Vellore have been carried out around or before 1990, and hence may not represent the most recent scenario of community rotavirus infections. The studies have been carried out in various settings: rural, semi-urban and urban. All except one study have used ELISA for detection of rotavirus. The studies from four centres include samples from both symptomatic and asymptomatic infections while data from two centres are based only on symptomatic infections in the community (Table V). Rotavirus positivity rate ranges from 4 to 29.3 per cent in symptomatic cases and 2.4 to 12.3 per cent in asymptomatic cases.

Nosocomial rotavirus infections

Nosocomial enteric infections are defined as those occurring more than 72 h after admission to hospital for non diarrhoeal causes or shortly after discharge. Nosocomial rotavirus infection among children results in a significant economic burden, both by prolonging the hospitalization of the affected child and by also serving as a reservoir that propagates additional cases of rotavirus infection.

Three studies on nosocomial rotavirus infection were carried out in the paediatric wards of 2 hospitals in Calcutta (1985-1987) and one in Vellore (1990-1991) (Table VI). A total of 3530 children were screened for nosocomial enteric infections. The mean nosocomial enteric infection rate was 16.16 per cent. Of the nosocomial enteric infections, rotavirus accounted for about 22.5 per cent of cases.

Rotavirus is recognized as the major cause of diarrhoea hospitalizations among children in both developed and developing countries, and it is clear that improvements in hygiene and sanitation alone are not sufficient to decrease or eliminate disease. Based on studies that have shown promising results in prevention of severe gastroenteritis with vaccine candidates, several strains have been identified and tested as potential vaccines. Several vaccines are currently in various stages of development around the world. Two vaccines from the multinational manufacturers Merck and GlaxoSmithKline (GSK) have completed large scale trials and have been recently licensed. The Merck vaccine, *Rotateq*™ is composed of 5 rotavirus strains. Each strain is a single gene reassortant based on parent bovine strain WC3, containing outer capsid gene from a human strain. The vaccine induces immunity to G1- G4 and P[8] genotypes. The GSK vaccine, *Rotarix*™ is derived from a single human rotavirus strain G1P[8] that was attenuated by multiple passages in cell culture. Studies have shown both vaccines to be safe and effective5,6.

In India, candidate vaccines have been derived from strains causing asymptomatic infections in neonatal nurseries. The two India neonatal candidate vaccines are 116E, a G9P[11] rotavirus isolated from neonatal nurseries in Delhi53 and I321, a G10P[11] rotavirus described from Bangalore53. Both strains appear to be natural bovine-human reassortants. The vaccines are being manufactured by Bharat Biotech in India and are in their early phase trials. However, the efficacy of these vaccines has not been tested in developing countries, where previous rotavirus vaccine trials have been shown to evoke a lower seroresponse and be less effective64.

Summary

The rapid evolution of rotavirus strains and the emergence of new strains, possibly through the transmission of viruses across species or through reassortment between animal and human rotaviruses, makes it necessary to include intensive strain surveillance of as an important component of any vaccine implementation programme. This is particularly important in countries such as India where the mortality and economic burden associated with rotavirus is high. The data on the molecular epidemiology of rotaviruses have shown the emergence of interesting strains that may have animal origins. Based on VP7 type, alone G6, G8, G9, G10 and G12 strains have been newly identified in the past few years. The questions raised by these findings are whether this detection is because these strains are ‘emerging’ or because more sophisticated laboratory techniques are now being applied by researchers in India. Even if the latter is true, the collated data indicate that the diversity of rotaviruses in India is greater than found in most other developing countries, and that this will result in challenges for vaccine efficacy that have not been faced elsewhere.

The Cochrane Evidence Database analyses data from 64 trials with three kinds of vaccine, bovine, rhesus and human, and results indicate protection from rotavirus diarrhoea of any severity65. However, the important caveat to this update is that the majority of the trials were carried out in developed countries where the age of first rotavirus infection is later in childhood and where the degree of diversity of circulating strains is limited in comparison to developing countries. Rotavirus vaccines generally have yielded poor efficacy when tested in developing countries has led to concerns about the potential effectiveness of any future live, oral rotavirus vaccine in these settings64. Although rotavirus infection is universal early in childhood, the epidemiology of the disease is quite different in developed and developing countries. Differences in age of first infection, strain distribution, occurrence of mixed infections, seasonality and risk of mortality can affect decisions about vaccine composition and delivery. Higher doses of vaccine or additional doses may be required to overcome the inhibitory effects of competing intestinal flora, concomitant use of oral polio vaccine and high levels of humorally transferred maternal antibodies against rotavirus.

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Despite a recommendation by the World Health Organization that all rotavirus vaccines be tested early in developing countries, no data from the current vaccines are available in Africa or poor Asian countries. These data will be critical to determining the probability of success of the current rotavirus vaccines and to establish requirements for vaccines in pre-clinical and clinical development.

In summary, rotavirus epidemiology is complex as would be expected for a virus with multiple modes of transmission, and this complexity is amply illustrated in studies from India demonstrating the diversity of the virus in different settings. The new hope for prevention of morbidity and mortality due to this agent is the use of oral vaccines, which are effective in developed countries, but we need evidence from developing countries with the highest disease burden and virus diversity before accepting their efficacy in all settings.

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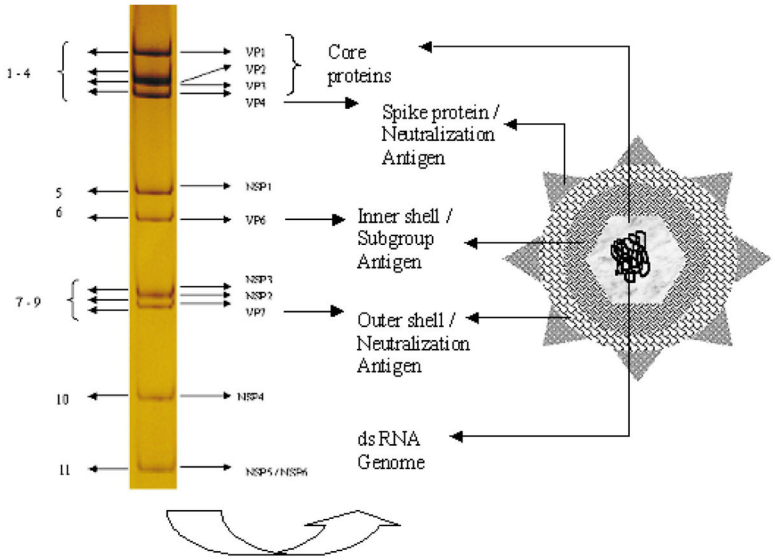

Fig. 1.

Structure of rotavirus. Coding assignments of 11 RNA segment (left) and schematic diagram of ratavirus (right).

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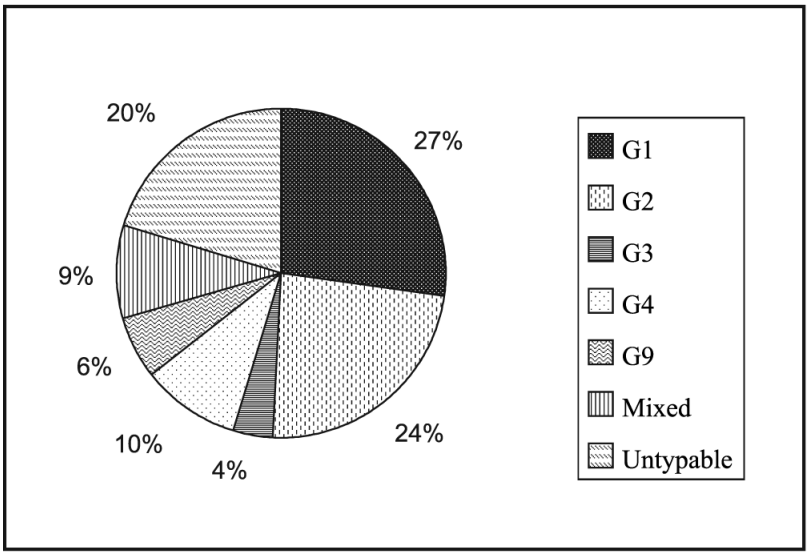

Fig. 2.
Overall distribution of G types in India (studies from 1990-2004). [*Source*: Table II].

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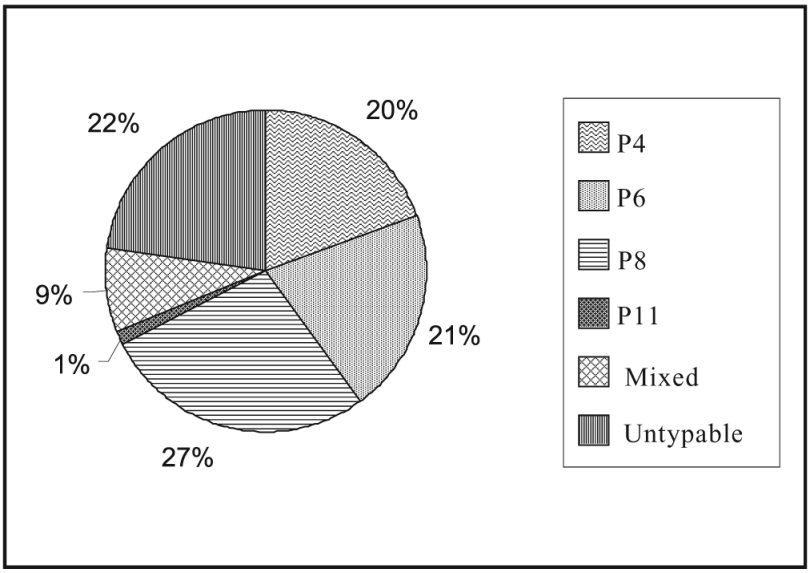

Fig. 3.
Overall distribution of P types in India (studies from 1990-2004). [*Source*: Table III].

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Table I

Burden of rotavirus disease in hospitalized children

Centre	Year of study	Age (yr)	Testing method	Samples		
				Tested	Positive	
				n	n	%
North India:						
Chandigarh16	1982 - 1985	<5	ELISA	694	111	15.9
Delhi17	1987 - 1989	<5	ELISA	978	176	18.0
Delhi18	1987 - 1988	<5	ELISA	288	44	15.3
Delhi19	1988 - 1990	<5	ELISA	990	104	10.5
Delhi20	1989 - 1990	<3	Immunodot	400	23	6.0
Delhi21	1990 - 1991	<5	ELISA/PAGE	450	60	13.3
Delhi22	1990	<5	ELISA	157	71	45.0
Delhi23	1998 - 2000	<5	ELISA/PAGE	1172	158	13.5
Delhi24	2000 - 2001	<5	ELISA	584	137	23.5
Delhi25	1998 - 2000	<3	ELISA/PAGE	560	100	17.8
North India26	NK	NK	ELISA	172	32	19.0
Western India:						
Bombay27	1984 - 1986	NK	LA /EM / ELISA	273	63	21.0
Pune28	1990 - 1993	children	ELISA	722	188	26.0
Pune29	1992 - 1996	<5	ELISA	945	266	28.2
Eastern India:						
Dibrugarh30	1999 - 2000	<5	ELISA	202	47	23.3
South India:						
Bangalore31	1988 - 1994	NK	PAGE	694	150	21.6
Chennai32	1997 - 1999	0 - 2, >2	ELISA	245	51	20.8
Chennai33	1995 - 1999	<3	ELISA	745	168	22.6
Hyderabad34	1998 - 1999	<2	PAGE	352	57	16.2
Manipal35	NK	<5	LA	106	19	18
Mysore31	1993 - 1994	NK	PAGE	447	50	11.2
Tirupati36	1991	<2	ELISA	170	40	23.5
Vellore37	1995 - 1998	<5	ELISA / LA	602	126	20.9

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Centre	Year of study	Age (yr)	Testing method	Samples		
				Tested	Positive	
				n	n	%
Vellore38	2002 - 2004	<5	ELISA/ LA	343	94	27.1
Multiple[**]:						
Multiple 139	1993	6m to <5	ELISA	458	63	13.7
Multiple 240	1996 - 1998	<5	ELISA	1502	313	20.8
Multiple 341	1998 - 1999	<5	LA /EM / ELISA	365	82	22.5
Multiple 442[@]	1998 - 2000	<4	PAGE	406	141	34.7
Multiple 543[#]	2001	<4/all[#]	PAGE	454	161	35.4
Total				15476	3095	

NK, not known

LA, latex agglutination; EM, electron microscopy; PAGE, polyacrylamide gel electrophoresis; ELISA, enzyme linked immunosorbent assay.

Multiple 1: Shimla, Lucknow, Bhopal, Nagpur, Davengere

Multiple 2: Shimla, Lucknow, Bhopal, Nagpur, Davengere, Delhi, Hyderabad

Multiple 3: Vellore, Mysore, Jalandhar, Yamunagar

Multiple 4: Kolkata, Imphal, [@] Data on disease burden from Kolkata only

Multiple 5: Kolkata, Dibrugarh, Bhuvaneshwar, Chandigarh

[#]<4/all: Samples collected from two groups: children <4 yr, patients of all age groups

[**]Multiple studies in which samples were collected from more than one city.

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Table II

Distribution of G types in various geographic locations in India

Centre	Year of study	Age (yr)	No. tested	G1	G2	G3	G4	G9	Mixed	UT
North India:										
Delhi21	1990 - 1991	<5	51	17	13	5	4	—	5	7
Delhi25	1998 - 2000	<3	100	31	12	18	5	—	—	34
Delhi24	2000 - 2001	<5	135	32	18	8	—	21	10	46
Western India:										
Pune28	1990 - 1993	children	205	15	49	1	9	—	33	98
Eastern India:										
Calcutta45	1999 - 2000	NK	150	49	27	—	30	—	18	16
South India:										
Bangalore31	1988 - 1994	NK	150	15	20	53	7	—	—	55
Chennai32	1997 - 1999	0 - 2, >2	48	7	33	1	—	—	7	—
Chennai33	1995 - 1999	<3	118	11	78	2	16	—	11	—
Hyderabad34	1998 - 1999	<2	46	16	—	—	8	—	5	17
Mysore31	1993 - 1994	NK	50	23	—	12	—	—	—	15
Vellore37	1995 - 1998	<5	126	50	24	1	30	5	10	25
Vellore38	2002 - 2004	<5	94	44	8	—	—	18	4	19
Multiple:										
Multiple 139	1993	6 m to <5	63	7	14	7	6	15	7	7
Multiple 240	1996 - 1998	<5	287	51	99	2	32	50	31	22
Multiple 341	1998 - 1999	<5	82	33	7	9	12	7	—	14
Multiple 442	1998 - 2000	<4	159	61	38	—	20	—	11	29
Multiple 543	2001	<4/all	126	62	17	—	6	—	26	15
Total			1998	524	457	119	185	116	178	419

*UT, untypable; NK, not known

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Table III

Distribution of P types in various geographic locations in India

Centre	Year of study	Age (yr)	No. tested	P[4]	P[6]	P[8]	P[11]	Mixed	UT
Delhi21	1990 - 1991	<5	57	14	4	23	—	3	14
Delhi24	2000 - 2001	<5	135	16	29	32	1	7	50
Multiple 139	1993	6m to <5	63	13	27	8	—	7	7
Multiple 240	1996 - 1998	<5	287	63	88	69	10	33	24
Multiple 341	1998 - 1999	<5	82	19	2	31	—	—	30
Multiple 442	1998 - 2000	<4	138	35	8	51	—	26	19
Multiple 543	2001	<4/all	126	19	61	—	—	19	27
Vellore37	1995 - 1998	<5	126	32	7	39	—	—	48
Vellore38	2002 - 2004	<5	94	5	2	52	2	—	32
			1108	216	228	305	13	95	251

*UT, untypable

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Table IV

Neonatal rotavirus infections in India

Centre	Year	Symptoms	Screening	No. Tested	Positive		Predominant strain
				n	n	%	
Delhi54	1993	Asymptomatic	ELISA PAGE	169	38	33	G9P[11]
Bangalore55	1988 - 1997	Asymptomatic	ELISA	882	321	39	G10P[11]
Vellore10	1999 - 2000	Symptomatic/ asymptomatic	ELISA	NK	43	NK	G10P[11]

NK, not known; PAGE, polyacrylamide gel electrophoresis; ELISA, enzyme linked immunosorbent assay

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Table V

Rotavirus infection in the community

Centre	Community	Year of study	Screening	Symptoms	No. Tested		Positive
					n[#]	n[#]	%
Delhi56	Semi urban	NK	ELISA	Symptomatic	212	45	21.2
				Asymptomatic	82	2	2.4
North India57	Urban/rural	1982 - 1983	ELISA	Symptomatic	150	44	29.3
				Asymptomatic	350[*]	43	12.3
Chandigarh58	Urban/peri-urban/rural	1988 - 1991	ELISA	Symptomatic	218	25	11.5
Haryana59	Rural	1985 - 1986	ELISA	Symptomatic	346	14	4
				Asymptomatic	211	14	6.6
Varanasi60	Urban	1988 - 1989	LA	Symptomatic			17.7
				Asymptomatic			4
Vellore38	Urban	2002 - 2004	ELISA	Symptomatic	1152	82	7.1

NK, not known;

[#]No. of samples;

[*]No. of children tested positive for rotavirus; No. of samples collected per child not given LA, latex agglutination; ELISA, enzyme linked immunosorbent assay

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Table VI

Nosocomial rotavirus infections

Centre	Year of study	Age (yr)	No. tested	%	Nosocomial infection no.	RV Positive	
						No.	%
Vellore61	1990 - 1991	<3	194	20.1	39	13	6.7
Calcutta62	1985 - 1986	<12	198	18.2	36	29	14.6
Calcutta63	1987	<5	3138	10.2	320	15*	8.4

*15 of 178 tested