WEB TABLE I RESULTS OF LITERATURE SEARCH

Q. No.	Research Question	Search engine	Total	After title screening	After abstract screening	After reading full text	From cross reference	Additional search	Finally included
1	Epidemiology of rotavirus diarrhea in under-5 hospitalized children from different parts of India	(epidemiology* OR burden OR morbidity OR mortality or incidence OR prevalence OR profile OR hospital) AND (rotavirus OR rotavirus diarrhea OR rotavirus gastroenteritis OR rotavirus disease) AND India	171	97	87	48	4	0	54
2	Epidemiology of rotavirus diarrhea in under-5 children in community from different parts of India	(epidemiology* OR burden OR morbidity OR mortality or incidence OR prevalence OR profile OR community) AND (rotavirus OR rotavirus diarrhea OR rotavirus gastroenteritis OR rotavirus disease) AND India	152	82	27	15	0	0	16
3	Demographic profile of rotavirus diarrhea in under-5 Indian children	(epidemiology* OR demography OR profile OR hospital OR community) AND (rotavirus OR rotavirus diarrhea OR rotavirus gastroenteritis OR rotavirus disease) AND India	138	95	46	35	0	0	35
4	Molecular epidemiology of rotavirus diarrhea in under-five children of India	(classification* OR genetics OR phylogeny OR virology OR genotype OR polymerase chain reaction OR classification OR genetic variation OR molecular epidemiology) AND (rotavirus OR rotavirus diarrhea OR rotavirus gastroenteritis OR rotavirus disease) AND India	137	100	54	47	2	1	49
5	Incidence of rotavirus infection as a cause of nosocomial diarrhea	(epidemiology* OR burden OR morbidity OR mortality or incidence OR prevalence OR profile OR hospital OR nosocomial) AND (rotavirus OR rotavirus diarrhea OR rotavirus gastroenteritis OR rotavirus disease) AND India	122	18	9	5	0	0	5
6	Mortality from rotavirus infection in under-5 children from different parts of India	(epidemiology* OR burden OR morbidity OR morbidity OR mortality or incidence OR prevalence OR profile OR hospital OR community OR case fatality) AND (rotavirus OR rotavirus diarrhea OR rotavirus gastroenteritis OR rotavirus disease) AND India	168	38	22	14	0	1	15

WEB TABLE II ROTAVIRUS SEROTYPES DETECTED FROM VARIOUS PARTS OF INDIA

Reference	*Place of study*	*Study period (year)*	*Age group (yr)*	*Detection method*	*Total stool samples tested for G strains (n)*	*Total stool samples positive for G strains (n)*	*G strains not tested*	*Total stool samples tested for P strains (n)*	*Total stool samples tested positive for P strains(n)*
Northern India									
Husain, *et al.* [19]	Delhi	1990-1991	<5	RT-PCR	51	44	G9, G12	57	45
Chakravarti, *et al.* [77]	Delhi	1998 -2000	<3	RT-PCR	100	66	G9, G12	134	84
Sharma, *et al.* [78]	Delhi	2000 - 2001	<5	RT-PCR	465	437	None	457	428
Bahl, *et al.* [23]	Delhi	2000 - 2004	<5	RT-PCR	135	89	G12	NT	0
Chakravarti, *et al.* [22]	Delhi	2005-2007	<2	RT-PCR	100	100	None	100	100
Mishra, *et al.* [26]	Lucknow	2004 - 2008	<3	ELISA,PAGE	79	75	G12	79	75
Western India									
Awachat, *et al.* [81]	Pune	1993-1994	<2	RT-PCR	Examined 35 nontypeable specimens of Rotavirus. 10 (28.57%) were identified as rotavirus serotype G9. The results indicate that serotype G9 may represent significant proportion of specimens, which were previously nontypeable.				
Kelkar, *et al.* [29]	Pune	1992-1996	<5	ELISA	205	107	G9, G12	NT	NT
Kelkar, *et al.*[30]	Pune	1990-1997	<5	PAGE	111	111	G12	None	None
Desai, *et al.*[28]	Thane	2000-2001	<5	RT-PCR	7	7	-	-	-
Zade, *et al.* [79]	Pune	1990- 1994, 2000-2002	Children	RT-PCR	90	90	G9, G12	89	89
Awachat, *et al.* [81]	Thane	2000-2001	Children	RT-PCR	Simian G3, SA11 like strains are isolated for the first time as etiological agents of diarrhea in humans				
Chitambar, *et al.* [82]	Surat	2004	NK	RT-PCR	Group B Rotavirus (*NSP*2 gene) was detected in 295 (100%) cases				
Chitambar, *et al.* [82]	Sangli, Maharashtra		2009	NK	RT-PCR Group B Rotavirus (*NSP*2 gene) was detected in 5 (17.2%) cases				
Eastern India									
Samajdar, *et al.* [83]	Kolkata	2000 - 2004	<4	RT-PCR	147	147	None	140	140
Khetawat, *et al.* [84]	Kolkata	2000 - 2004	<4	RT-PCR	140	124	G12	NT	0
Barman, *et al.* [85]	Kolkata	2002-2004	<3	RT- PCR	37 (18.5%) sporadic cases of human group B rotavirus infection was detected of which 15 (7.5%) showed mixed infection with group A rotaviruses				
Mukherjee, *et al.* [86]	Kolkata	2004-2006	<4	RT- PCR	60	31	None	60	31
Samajdar, *et al.* [97]	Kolkata and Orissa		2004-2006	<4	RT-PCR P[8] strains were isolated in 317 (43.2%) children. Phylogenetic analysis of VP8* amino acid sequences of 16 of these strains with other P[8] strains revealed four distinct lineages, clustered within rare OP354-like and Hun9-like lineages, pointing towards co-prevalence of divergent P[8] strains.				
Samajdar, *et al.* [40]	Kolkata	2005 - 2006	Children	RT- PCR	249	197	None	249	204

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Reference	*Place of study*	*Study period (year)*	*Age group (yr)*	*Detection method*	*Total stool samples tested for G strains (n)*	*Total stool samples positive for G strains (n)*	*G strains not tested*	*Total stool samples tested for P strains (n)*	*Total stool samples tested positive for P strains(n)*
Mukherjee, *et al.* [88]	Manipur	2005-2006	<5	RT- PCR	244	244	None	244	244
Southern India									
Jain, *et al.* [89]	Vellore	1984	Children	PAGE/ELISA	46	32	G9, G12	NT	NT
Aijaz, *et al.* [46]	Mysore	1988-1994	Children	PAGE/ELISA	200	130	G9, G12	NT	NT
Jain, *et al.* [89]	Chennai	1995 - 1999	Children	PAGE/ELISA	90	70	G9, G12	NT	NT
Saravanan, *et al.* [48]	Chennai (21)	1995 - 1999	<3	PAGE/ELISA	118	118	G9, G12	NT	NT
Ananthan, *et al.* [47]	Chennai	1995 - 1999	Children	NK	48	48	G12	NT	NT
Kang, *et al.* [53]	Vellore	1995 - 1999	<5	RT-PCR	126	101	G12	126	78
Anand, *et al.* [90]	Hyd	1995 - 1999	Children	PAGE	46	29	G9, G12	NT	0
Mukhopadhya, *et al.* [92]	Vellore[2]	1999-2000	<10	RT-PCR	20	20	None	20	20
Ramani, *et al.* [91]	Vellore	2002 - 2006	Children	RT-PCR	452	282	None	NT	0
Banerjee, *et al.* [54]	Vellore (26)[1]	2000 - 2004	Children	RT-PCR	161	129	G12	166	100
Gladstone, *et al.*[3]	Vellore	2002-2004	<5	RT-PCR	472	472	None	472	472
Banerjee, *et al.*[93]	Vellore	2005	<5	RT-PCR	13	13	Only G12 strains were taken for sequencing and phylogenetic analysis		
Sowmyanarayanan, *et al.* [55]	Vellore	2005-2008	<5	RT-PCR	354	341	None	354	296
Multiple locations									
Ramachandran, *et al.* [94]	Multiple	1993	Children	RT-PCR	63	56	G12	62	55
Jain, *et al.*[89]	Multiple	1995	Children	PAGE/ELISA	93	74	G9, G12	91	72
Jain, *et al.* [57]	Multiple	1995 - 1999	Children	RT-PCR	287	265	G12	277	253
Das, *et al.* [59]	Multiple	1995 - 1999	Children	RT-PCR	159	130	None	139	120
Kang, *et al.* [58]	Multiple	1998 - 1999	Children	RT-PCR	82	68	G12	82	52
Das, *et al.* [60]	Multiple	2001	<4	RT-PCR	161	126	G12	126	109
Kang, *et al.* [61]	Multiple	2005 - 2009	<4	RT-PCR	1375	1177	None	1375	1166

NT: not typeable.

[1] *Rotavirus was detected in 82/1,152 (7.1%) episodes of diarrhea in the community and 94/343 (27.4%) cases in the hospital. In the community, the genotypes identified in symptomatic patients, in order of frequency, were G1 (36.5%), G10 (17.1%), G2 (15.9%), and G9 (7.3%) and mixed infections (7.3%). The most common G-P combinations were G1P[8], G2P[4], G1P[4], and G10P[11]. The distribution of G types from hospitalized children was G1 (46.8%), G9 (19.1%), G2 (8.5%), G10 (1.1%), and 4.3% mixed infections. The most common G-P combinations were G1P[8] and G9P[8].*

[2] *Anti-group C VP6 antibodies were detected in 237 of 936 samples with a seroprevalence for group C of 16.79%in children aged <10 years.*

WEB TABLE III G SEROTYPES ISOLATED FROM DIFFERENT PARTS OF INDIA

Reference	*Place of study*	*G1*	*G2*	*G3*	*G4*	*G9*	*G12*	*G-mixed*	*G UT/*	*G Novel(n) Other*
Northern India										
Husain, *et al.* [19]	Delhi	17	13	5	4	NT	NT	5	7	G6 (3)
Chakravarti, *et al.* [77]	Delhi	31	12	18	5	NT	NT	NR	34	-
Sharma, *et al.* [78]	Delhi	120	116	11	2	67	67	54G2P[11], G3P[11]	28	-
Bahl, *et al.* [23]	Delhi	32	18	8	0	21	NT	10P[8]G1,P[4]G2, P[8]G9, P[6]G1, P[6]G9, P[6]G3	46	-
Chakravarti, *et al.* [25]	Delhi	60	16	3	-	8	2	G1P[8], G1P[4], G1P[6]	-	
Mishra, *et al.* [26]	Lucknow	30	12	13	4	8	NT	8G1P[8], G3P[6], G1P[6], G2P[8]	4	-
Western India										
Desai, *et al.*[28]	Thane	-	-	7	-	-	-	-	-	-
Kelkar, *et al.* [30]	Pune	15	49	1	9	NT	NT	33	98	-
Zade, *et al.* [79]	Pune	43	32	7	6	2	NT	(G1P[8], G2P[4], G3P[8], G4P[8]) -79.2% in 1990-1994 and 92.3% in 2000-2002.G9P[8] -1.3% in 1990-1994 and 7.7% in 2000-2002. Unusual strains (G1P[6],G1P[4], G1P[19], G2P[8], G3P[4], G4P[6]) detected in 19.5%	0	-
Kelkar, *et al.*[32]	Pune	35	34	16	12	NT	NT	0	0	G6(6), G8(4), G10(4)
Kelkar, *et al* [95]	Pune	Isolated nucleotide sequences of cDNA derived from the gene encoding VP7 of two strains indicating >94% identity with G6, the serotype, generally associated with cattle. The isolates were more close to G6 RF strain, which is a bovine rotavirus, reported from France.								
Eastern India										
Samajdar, *et al.* [83]	Kolkata	79	33	0	0	3	25	7	NR	-
Khetawat, *et al.* [84]	Kolkata	49	27	0	30	0	NT	18	16	-
Samajdar, *et al.* [41]	Kolkata[a]	82	65	0	0	20	28	G1P[8], G2P[4], G9P[8], G12P[8], G12P[6]	-	-
Mukherjee, *et al.* [86]	Kolkata	0	0	0	0	0	0	G9P[4](8), G12P[8](8), G1P[8](6), G10P[4](6), G2P[4](3)	-	G10(6)

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Reference	*Place of study*	*G1*	*G2*	*G3*	*G4*	*G9*	*G12*	*G-mixed*	*G UT/*	*G Novel(n)*
Jain, *et al.*[89]	Manipur	126	57	0	2	11	20	23G10[4](36%), G2P[4](22%), G12P[6](8%), G9P[6](3%)	4	G10(1) G(1+2) P[6](4), G(1+2) P[8](5), G(2+9) P[4](8), G(2+9) P[6](4), G(1+12) P[4](1), G(1+12) P[6](1)
Southern India										
Aijaz, *et al.* [46]	Mysore	38	20	65	7	0	NT	NR	70	-
Ananthan, *et al.* [47]	Chennai	0	0	0	0	0	0	G[2,1], P[4,8](7). G2P[4]-P[8](12)	NR	-
Saravanan, *et al.* [48]	Chennai	11	78	2	16	0	NT	G2P[4,8], G1-G2P[4,8]	NR	-
Kang, *et al.* [53]	Chennai	7	33	1	0	0	NT	7	NR	-
Mathew, *et al.*[45]	Kerala	-	-	-	-	-	-	88G1P[8] (49.7%) G9P[8] (26.4%), G2P[4] (5.5%), G9P[4] (2.6%) G12P[6] (1.3%)		
Kang, *et al.* [58]	Vellore	50	24	1	30	5	NT	G1P1A[8], G1P1B[4], G2P1B[4], G4P1A[8]	25	-
Anand, *et al.* [90]	Hyderabad	16	0	0	8	NT	NT	5 17	-	
Ramani, *et al.*[91]	Vellore	155	91	1	2	59	9	31G12P[6](10), G12P[8](3)	101	G8 (1) and G10 (69)
Banerjee, *et al.* [54]	Vellore[1]	74	21	0	0	24	NT	10 32	-	
Sowmyanarayanan, *et al.* [55]	Vellore[*]	0	0	0	0	0	0	G2P [4] (30.8%), G1P [8] (17.8%) and G9P [8] (15.8%)	-	-
Mukhopadhya, *et al.* [92]	Vellore	0	0	0	0	0	0	G1P[8], G2P[4], G10P[11]	-	-
Banerjee, *et al.*[93]	Vellore	0	0	0	0	0	13	0 -	-	
Gladstone, *et al.*[3]	Vellore	The most common types were G1P[8] (15.9%), G2P[4] (13.6%), G10P[11](8.7%), G9P[8] (7.2%), G1P[4] (4.4%), G10P[4] (1.7%), G9P[4] (1.5%), G12P[6] (1.1%), and G1P[6] (0.6%).								
Multiple locations										
Ramachandran, *et al.* [94]	Multiple	7	14	7	6	15	NT	7 7	-	
Jain, *et al.*[89]	Multiple	15	3	2	12	NT	NT	NR 14	-	
Jain, *et al.* [57]	Multiple	51	99	2	32	50	NT	31 22	G8 (1)	
Das *et al.* [59]	Multiple	61	38	0	20	0	0	11 29	-	
Kang, *et al.* [58]	Multiple	33	7	9	12	7	NT	NR 14	-	

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Reference	*Place of study*	*G1*	*G2*	*G3*	*G4*	*G9*	*G12*	*G-mixed*	*G UT/*	*G Novel(n)*
Das *et al.* [60]	Multiple	62	17	0	6	0	NT	G1P[6],G2P[8], G2P[6],G4P[4], G4P[6]	15	-
Kang *et al.*[61]	Multiple*	G2P[4] (354 strains [25.7%]), G1P[8] (304 [22.1%]), and G9P[8] (117 [8.5%]), G1[P4](11), G1P[6](15), G2P[6](15), G2P[8](16), G9P[4](3), G9P[6](7), G3P[8], G4P[4](1), G10P[6](2), and G2P[10](1), G10P[11](1)								
Kang, *et al.*[62]	Multiple*	G1[P4] (14), G1[P6] (21), G1[P8] (545), G1[P untyped] (114), G1[P Mixed] (22), G2[P4] (489), G2[P6] (17), G2[P8] (26), G2[P untyped] (48), G2[P Mixed] (15), G9[P4] (25), G9[P6] (16), G9[P8] (176), G9[P untyped] (150), G9[P Mixed] (4), G12[P4] (2), G12[P6] (2), G12[P8] (4), G12[P untyped] (4)								

Only detected combination of strains; NT - Not typed; NR - Not reported; UT - Untypeable; [a]Phylogenetic analysis of 13 G9 strains revealed clustering within G9 lineage III. Nine of 28 G12 strains were sequenced and exhibited phylogenetic clustering with previously reported G12 strains from Kolkata.

WEB TABLE IV P SEROTYPES ISOLATED FROM DIFFERENT PARTS OF INDIA

StudyGroup [reference]	*Place*	*P[4]*	*P[6]*	*P[8]*	*P mixed*	*P UT/Other*
Northern India						
Husain, *et al.* [19]	Delhi	14	4	23	2	14
Chakravarti, *et al.* [77]	Delhi	16	29	32	7	50
Sharma, *et al.* [78]	Delhi	90	104	162	72	29
Chakravarti, *et al.* [22]	Delhi	26	17	40	G1P[8] (26%), G1P[4] G1P[6]	0
Mishra, *et al.* [26]	Lucknow	11	24	35	5	4
Western India						
Zade, *et al.* [79]	Pune	38	11	40	0	0
Eastern India						
Samajdar, *et al.* [83]	Kolkata	45	14	31	50	0
Samajdar, *et al.* [40]	Kolkata	64	15	111	14	-
Southern India						
Kang, *et al.* [53]	Vellore	32	7	39	NR	-
Sowmyanarayanan, *et al.* [55]	Vellore	28	3	65	4	66
Multiple locations						
Ramachandran, *et al.* [108/94]	Multiple	13	27	8	7	7
Jain, *et al.* [57]	Multiple	63	88	69	33	24
Kang, *et al.* [58]	Multiple	19	2	31	NR	22
Das, *et al.* [59]	Multiple	35	8	51	26	19
Das *et al.* [60]	Multiple	19	61	19	-	27

NT : Not typed; NR: Not reported; UT : Untypeable.