Wastewater-based Epidemiology in India: Current Status, Prospects, and Recommendations

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16 **Table S1.** Disease/biomarkers investigated and wastewater sampling details for WBE studies

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S. No.	Disease/clinical conditions investigated	Wastewater collection period	Number of wastewater samples collected; sampling frequency	Sampling site	Sampling type; sampling time	Sample transport and storage conditions	Population coverage and city/town served	References
1	COVID-19	February 2020 to September 2022	4924; NS	Sewage treatment plants (STPs)	NS	Refrigerated	NS; Bengaluru	(Kutteyil et al., 2023)
2		July 2020 to August 2021	40; Weekly and Monthly	Drains	Grab; 8 am-8:30 am	Refrigerated	0.25 million; Hyderabad	(Tharak et al., 2022)

3		8th July 2020 to 6th August 2020	30; Weekly	Equalization tanks and secondary clarifiers of 10 STPs, and a collection tank from a community	Grab; 8 am-4 pm	Refrigerated	80% of STP capacity (603.5 MLD); Hyderabad	(Hemalatha et al., 2021)
4		April 2021 to June 2021	162; Weekly	Raw (influent), secondary, and tertiary treated wastewater samples from WWTPs	Grab; 9 am- 10 am	Refrigerated	NS; Mumbai	(Wani et al., 2023)
5		September 3, 2020, to April 12, 2021	287; Weekly	Wastewater pumping stations and STPs	Grab	Refrigerated	NS; Ahmedabad	(Kumar et al., 2023a)
6		One week in September 2020. Hospital wastewater for three weeks during partial	37; Daily	Inlets, primary sludge, and outlets of STPs	Composite Grab sampling; 7 AM, 10 AM, 1 PM, 4 PM, and 7 PM	Refrigerated	0.132-1.16 million; Chennai	(Chakraborty et al., 2021)

		lockdown (n = 15) (August, 2020) and one week during post-lockdown (September 2020) (n = 5)						
7		November 2021 to April 2022	442, Weekly twice	Inlets of 10 STPs	Grab	Refrigerated	92% of Pune city's population (7.4 million population)	(Rajput et al., 2023)
8		December 2020 to April 2021	6; NS	Open drains entering the Mutha river	Grab	Refrigerated	NS; Pune	(Dharmadhikari et al., 2022)
9		3rd May 2020 and 14th June 2020	NS	Six municipal WWTPs and two hospitals	Grab	Refrigerated	NS; Jaipur	(Arora et al., 2020)

10		8 May 2020 and 27 May 2020	NS; only two days	Influent and effluent samples	Grab samples combined into Composite ; 11:30 am	Refrigerated	NS; Ahmedabad	(Kumar et al., 2020)
11		1st week of November 2020	18; weekly	Influent	Grab	Refrigerated	NS; Ahmedabad, Gandhinagar, and Surat	(Srivastava et al., 2021)
12		From the third week of October 2021 to the last week of March 2022	119; weekly	Pumping stations	Grab	Refrigerated	Population of Gandhinagar city, approximately 3 Lakhs	(Kumar et al., 2023b)
13		August 7th to September 30th, 2020	43; Initially biweekly, followed by weekly for two months	Influent wastewater samples from 4 WWTPs	Grab	Refrigerated	NS; Gandhinagar	(Kumar et al., 2021a)
14		September to November 2020	116; Weekly	8 wastewater pumping stations and 1 STP	Grab	Refrigerated	Ahmedabad	(Kumar et al., 2021b)
15		January 31, 2021, to July 9, 2021	983; weekly twice	Sewers within urban municipality zones and open drains/grou	Grab ; morning hours	Refrigerated	NS; Nagpur district, Maharashtra	(Acheampong et al., 2024)

				ndwater sources in rural talukas				
16		May 11-22, 2020, with samples also collected before March 16, 2020	20; NS	Pumping station and open drains	Grab; 10:30 am-11:30 am	Refrigerated	NS; Mumbai	(Sharma et al., 2021)
17		February 19th to June 8th, 2021	164; weekly	110 influent samples and 54 effluent samples	Grab; 11 am & 1 pm	Refrigerated	60-70% of Jaipur's population	(Arora et al., 2022)
18		January 2022 to June 2022	878; Weekly from each of the 28 STPs and twice a week from 14 STPs	Inlet of 28 STPs	Grab; 8 am to 2 pm	Refrigerated	Approximately 11 million inhabitants of Bengaluru city	(Lamba et al., 2023)

19		May 4, 2020 to August 14, 2020	Some sites had 12 samples, while others had fewer based on the collection times; Random (weekly and monthly);	Influent, primary treatment, secondary treatment, and tertiary treatment stages from WWTPs	Grab and composite sampling; 6 am to 10 pm	Refrigerated	NS; Jaipur, Rishikesh, Haridwar, and Roorkee	(Arora et al., 2021)
20		First wave (September/ November 2020) and before the second wave (February 2021)	6; one sampling event	November 2020: Two influent samples from Vinzol wastewater treatment plant, February 2021: Two samples (one untreated and one treated wastewater) from the Vinzol wastewater treatment plant	Grab	Refrigerated	~8.25 million in 2021; Ahmedabad	(Joshi et al., 2022)

21		19 February 2021 to 8 June 2021	110; weekly	Influent water samples from WWTPs	Grab	Refrigerated	500-480,000; Jaipur	(Nag et al., 2022)
22		June and September 2020, May and June 2021	12; Two different days during the earlier and later phases of each COVID-19 wave	Open canals (contaminated with sewage)	Grab	Refrigerated	NS; Bengaluru	(Basu et al., 2022)
23		Ahmedabad: September 3, 2020, to December 28, 2020. Guwahati: October 27, 2020	Ahmedabad: 31 samples (weekly), Guwahati: 10 samples (one sampling event)	Urban water bodies	Grab	Refrigerated	NS; Ahmedabad and Guwahati	(Kumar et al., 2022)
24		April 2022 – December 2022 (India)	41 ; Once from each site	Open canal and lake inlets	Grab	Refrigerated	Hyderabad, Janagaon, Kurnool	(Thompson et al., 2025)
25		Pre-monsoon: March – June 2022 Monsoon: July –	NS; Weekly, seasonally (March–June: pre-monsoon,	Two major wastewater treatment plants (WWTPs) and two	Composite	Refrigerated	60 % of the sewershed of Dehradun city; Dehradun	(Kumar and Mahapatra, 2024)

		September 2022 Post-monsoon: October – November 2022	July–September: monsoon, October–November: post-monsoon)	minor WWTPs in academic institutions				
26		May 2022 – May 2023	1128; Weekly twice	10 Sewage Treatment Plants	Grab	Refrigerated	7.4 million; Pune	(Rajput et al., 2024b)
27		December 2023 to April 2024	628, bi-weekly	10 sewage treatment plants	Grab	Refrigerated	NS; Pune, Maharashtra	(Rajput et al., 2024a)
28		August 2022 – June 2023	728 (72 from open drains, 56 from STPs; Weekly twice	Open drains and STPs	Grab	Refrigerated	NS; Mumbai	(Kadam et al., 2024)
29		June 2022 to May 2023	1548 samples; weekly	Open drains	Grab	Refrigerated	NS; 23 cities across Maharashtra, including Mumbai, Pune, Solapur, Aurangabad, and others	(Matra et al., 2025)

30		October 2021 to July 2022	1,115; weekly	Open drain	Grab	Refrigerated	NS; Pune and Pimpri-Chinchwad, Maharashtra	(Zambre et al., 2024)
31	AMR	Two separate sampling events in 2016 and 2017	2 from India; NS	Influent of WWTPs	Grab	Refrigerated	NS; India, Hong Kong, the Philippines, Sweden, Switzerland, and the US	(Prieto Riquelme et al., 2022)
32	AMR	24th and 26th Jan 2022	17; NS	Open drains	Grab ; 7 am-10 am	Refrigerated	NS; Hyderabad	(Madhukar et al., 2024)
33	AMR	September 2014	Wastewater (2 samples, 12 E. coli isolates); NS	Wastewater influent	NS	Refrigerated	NS; Rural village in Ujjain district, Madhya Pradesh	(Purohit et al., 2017)
34	Poliomyelitis	2004 to 2006	305; weekly	Various sewage collection sites and treatment plants	Grab	Refrigerated	NS; Lucknow	(Chowdhary and Dhole, 2008)
35		January 2001 to December 2001	137; weekly	Wet well of a sewage pumping station and	Grab	Refrigerated	NS; Mumbai	(Deshpande Jagadish et al., 2003)

				large trenches where domestic wastewater is drained				
36	Gastrointestinal (GI) discomfort	September 2016 to August 2019	NS	Major sewage points in and around the hospital and various parts of the city	Grab	Refrigerated	NS; Uttar Pradesh, Madhya Pradesh, Chhattisgarh, Bihar, Jharkhand, and neighboring countries Bangladesh and Nepal	(Singh et al., 2021)
37	Typhoid	May 2021 to April 2022.	In Vellore, 520 grab samples and 517 Moore swabs In Blantyre, 533 grab samples and 594 Moore swabs ; Monthly	Environmental surveillance sites at wastewater confluence points	Grab sampling and Moore swab (trap sampling); 6 am-10 am	Refrigerated	Vellore catchment population ranges from 233 to 28,036	(Uzzell et al., 2024)

38	Population-level disease predictions related to diabetes, obesity, hypertension, and anemia.	23rd November 2017 to 22nd January 2018, 12th June 2017 to 19th June 2017	47; NS	Inlet and Outlet of STPs and main outlets of sewage disposal sites in rivers/water bodies in cities without functioning STPs	Grab	Refrigerated	Tier 1 and 2 cities, including Jammu, Patna, Imphal, Itanagar, Jodhpur, Hyderabad, Chandigarh, Lucknow, Bikaner, Jaipur, Bangalore, Trivendrum, Kolkata, Ahmedabad, Delhi, Dehradun, Guwahati, and Chennai	(Singh et al., 2023)
39	Acute flaccid paralysis and enterovirus-related diseases	July 2007 to September 2009	109; NS	Sewage effluent at STPs	Grab	Refrigerated	Approximately 1,000,000; Lucknow	(Tiwari and Dhole, 2018)
40	Influenza A (H1N1, H3N2), Respiratory Syncytial Virus (RSV), and COVID-19	January 2022 to December 2023	2,232; weekly	11 sewage treatment plants	Grab	Refrigerated	NS; Pune	(Pramanik et al., 2024)

41	Enteric fever (Typhoid fever)	May 2022 – April 2023	1037 total samples (520 grab samples, 517 Moore swabs); monthly	40 sites in open drainage channels	Grab samples (membrane filtration) and Moore swabs (trap sampling)	Refrigerated	280,000 in the southern half of Vellore city	(Abraham et al., 2025)
42	Influenza A and Influenza B	July and August 2023	100 samples (50 in July and 50 in August); alternate days	Inlet of four WWTPs	Grab ; 8 am-11 am	Refrigerated	WWTP 1 & WWTP 2 serve around 15,000 residents and a tertiary hospital (~1000 beds) WWTP 3- Covers around 15,000 residents WWTP 4- Covers a 200-bed hospital	(Panneerselvam et al., 2024)

*NS Non specified

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22 **Table S2.** Wastewater sample processing and analysis details from WBE studies.

S.No.	Disease/ clinical conditions investigated	Sample processing pipeline	QA/QC	Analytical assays	Analytical target	Viral load/number of copies of genes	References
1	COVID-19, Acute respiratory infections	Filtration, centrifugation, and RNA isolation	No	RT-PCR	SARS-CoV-2 RNA, Influenza virus strains, and Respiratory Syncytial Virus	Influenza A (H3N2) positivity (2.7%), Influenza A (H1N1), pdm09 (1.9%) and influenza B/Victoria (7.4%)	(Kutteyil et al., 2023)
2	COVID-19	Gravity filtration, ultrafiltration, and RNA extraction	Heat inactivation followed by target dilution; nanodrop spectrophotometric assay	RT-PCR	SARS-CoV-2 RNA, E-gene, N-gene, ORF1ab	Below detectable limits to 61,160 RNA copies per liter	(Tharak et al., 2022)
3	COVID-19	PEG precipitation followed by	NS	qPCR kit with a real-time RT-PCR	SARS-CoV-2 RNA N1		(Chaudhuri et al., 2023)

		RNA extraction			and N2 genes		
4	COVID-19	PEG precipitation followed by RNA extraction	Surrogate (Phi6) seeding; Nanodrop spectrophotometer assay	qRT-PCR	SARS-CoV-2 RNA N1 (Nucleocapsid), ORF1b-nsp14, and RdRp (RNA dependent RNA polymerase)	Mean N1, ORF1b-nsp14 and RdRp genes copies in were in the range of 10^4-10^5 GC/100 mL	(Wani et al., 2023)
5	COVID-19	Centrifugation, filtration, PEG precipitation, and RNA isolation	Surrogate seeding; Nanodrop spectrophotometer assay	RT-PCR TaqPath™ COVID-19 RT-PCR Kit (ThermoFisher Scientific, USA) includes MS2 phage as an internal control	ORF1ab, N, and S genes	ORF1ab gene: 6.1 x 10^2 copies/mL to 1.4 x 10^4 copies/mL	(Kumar et al., 2023a)
6	COVID-19	Sample concentration was done by four different	EURM-019, obtained from the	qRT-PCR for SARS-CoV-2 and SPE-LC-	SARS-CoV-2 RNA N1 and N2	RNA copies ranged from 9.66×10^4 to 1.99×10^5	(Chakraborty et al., 2021)

		methods: composite, supernatant, sediment, and syringe filtration followed by RNA extraction Sample prep for MS/MS: Filtration followed by SPE-LC-MS/MS	European Commission Joint Research Centre served as an internal positive control. RNA extracted from a buccal swab and amplified with RNaseP gene served as an internal control; Nanodrop spectrophotometer assay	MS/MS was used for analyzing PPCPs	genes, caffeine, carbamazepine, azithromycin, erythromycin, methyl paraben, sulfamethoxazole, ofloxacin, norfloxacin, ciprofloxacin, and triclosan	gc/L in STPs and from 1.41×10^4 to 9.96×10^4 gc/L in sewage Pumping Stations. In hospital wastewater, RNA copies detected ranged from 4.25×10^5 to 1.62×10^6 gc/L	
7	COVID-19	PEG precipitation followed by RNA extraction	NS	RT-qPCR for detecting SARS-CoV-2 and next-generation sequencing	Next-gen SARS-CoV-2 genetic regions: N, RdRp, and E using NGS	SARS-CoV-2 viral load observed in November and December 2021, with an average viral copy of 3.2	(Rajput et al., 2023)

				(NGS). Lineage decomposition for SARS-CoV-2, a model for predicting the lineage composition in a sample was used		gc/ml and 2.2 gc/ml respectively, to a sharp increase in January 2022 with an average detection of 83.9 gc/ml	
8	COVID-19	Heat inactivation, concentration by electronegative membrane filtration, followed by RNA extraction	NS	RT-qPCR and sequencing	SARS-CoV-2 RNA fragment	Novel mutations detected before clinical detection	(Dharmadhikari et al., 2022)
9	COVID-19	Method A: virus inactivation followed by PEG precipitation, Method B: Direct processing	NS	RT-PCR	S, E, ORF1ab, RdRp, and N genes	Ct value less than 40 for all genes tested, indicating the presence of SARS-CoV-2 RNA in untreated WW samples	(Arora et al., 2020)

		after centrifugation					
10	COVID-19	PEG precipitation, and RNA isolation	MS2 added in each sample to verify the efficacy of RNA extraction and the absence of inhibitors in the RT-PCR reaction.	RT-PCR using TaqPath™ COVID-19 RT-PCR Kit	ORF1ab, N gene, and S gene of SARS-CoV-2	CT values were 32.65-35.52 (ORF1ab), 34.28-35.39 (N protein gene), and 34.83-39.56 (S protein gene)	(Kumar et al., 2020)
11	COVID-19	Filtration, PEG concentration, and RNA extraction	MS2 added in each sample; Qubit fluorometer assay	RT-qPCR	N1 and N2 genes of SARS-CoV-2	Effective gene concentration ranged from 0 to 11900 copies/L	(Srivastava et al., 2021)
12	COVID-19	PEG concentration followed by RNA isolation	Surrogate seeding; Qubit fluorometer assay	Digital PCR	N1 and N2 genes of SARS-CoV-2	1766-64,640 gc/L	(Kumar et al., 2023b)
13	COVID-19	Centrifuged, filtered, and RNA isolated RNA concentration	Surrogate seeding (ms2); Qubit	RT-PCR	ORF1ab, N Protein, and S Protein genes	S-gene (~1223 copies/L)>N-gene (~1022 copies/L)> ORF 1 ab-	(Kumar et al., 2021a)

		estimated using fluorometer	fluorometer assay			gene (~485 copies/L). Average Ct values for the S, N, and ORF 1 ab genes were 32.66, 33.03, and 33.95, respectively	
14	COVID-19	Centrifuged, filtered, and the viral RNA was PEG precipitated and extracted using a commercial kit	Surrogate seeding; Qubit fluorometer assay	RT-PCR	N, ORF1ab, and S genes	3,047 copies/L to ~10,729 copies/L	(Kumar et al., 2021b)
15	COVID-19	Filtered, PEG precipitation, RNA extraction with a commercial kit	FAM, HEX probe; Qubit fluorometer assay	RT-qPCR	N gene, E gene, RdRp gene	0.07 x 10^5 copies/L to 14.90 x 10^5 copies/L	(Acheampong et al., 2024)
16	COVID-19	Sewage samples mixed with chloroform, stirred, and centrifuged. The clarified samples underwent	NS	RT-PCR with LabGun COVID-19 real-time RT-PCR kit	E gene and RdRp genes	Lowest Ct Value for E Gene: 31.92, Lowest Ct Value for RdRp Gene: 30.46. The highest Ct value for E	(Sharma et al., 2021)

		phase separation using the PEG-dextran method to concentrate the virus				gene was 40.60 and 41.94 for RdRp gene	
17	COVID-19	Surface sterilized under UV, centrifuged, and RNA extracted using a commercial kit.	Surrogate seeding	RT-PCR using two separate commercially available kits (Allplex)™ 2019-nCoV Assay RT-PCR and InnoDetect One Step COVID-19).	N gene, ORF1ab gene, RdRp gene, and E gene.	log10 4.4 to 6.04 GC/L for the N gene and log10 4.5 to 5.60 GC/L for ORF1ab	(Arora et al., 2022)
18	COVID-19	Heat-inactivated, PEG-precipitated, centrifuged, and viral RNA extracted	Qubit fluorometer assay and high-resolution automated electrophoresis	RT-qPCR	SARS-CoV-2 RNA N-gene, RdRp-gene, and E-gene	Positivity-27%-78%	(Lamba et al., 2023)
19	COVID-19	Heat inactivation, filtration, PEG concentration,	NS	RT-qPCR using Allplex™ 2019-nCoV Assay kit.	Genes E, RdRp, and N	Ct values between 30 and 38	(Arora et al., 2021)

		followed by centrifugation					
20	COVID-19	PEG precipitation, followed by RNA extraction, cDNA synthesis, library preparation, and sequencing	Surrogate seeding	Sequencing using Ion GeneStudio S5 Plus, and data analysis using PRINSEQ-lite and CLC Genomics Workbench.	Key mutations in the SARS-CoV-2 genome and tracking circulating variants	Not applicable	(Joshi et al., 2022)
21	COVID-19	UV sterilization, centrifugation, followed by RNA extraction	Qubit fluorometer assay and high-resolution automated electrophoresis	RT-qPCR	E gene, N gene, and RdRp	Concentrations ranged from 1 × 10^4 to 1 × 10^6 gene copies/L of wastewater	(Nag et al., 2022)
22	COVID-19	UV light for 30 minutes and pasteurized at 60°C for 90 minutes. Ultrafiltration was done using a 0.2 µm filter into a falcon tube containing	NS	Modified TrueNATT M microchip-based rapid method and traditional rRT-PCR	E gene and RdRp gene	5,942 copies/ml to as high as 100,000 copies/ml	(Basu et al., 2022)

		PEG and NaCl. RNA extraction was then performed using the QIAamp Viral RNA Mini Kit.					
23	COVID-19	Centrifuged, Polyethylene glycol (PEG) precipitation followed by RNA isolation	Surrogate seeding (MS2 phage); Qubit fluorometer assay	RT-qPCR using the TaqPath™ COVID-19 RT-PCR Kit	N gene, ORF1ab gene, and S gene	Ahmedabad: 800 copies/L for ORF1ab gene in Sabarmati River Guwahati: 9169 copies/L for N gene in the drain near a COVID care center; positivity 20%-26%	(Kumar et al., 2022)
24	COVID-19	Pasteurization at 60°C for 1 hour before further processing, Filtration using Whatman Grade 1 filter paper and 0.22 µm PES membrane filter,	NS	RT-qPCR using Bio-Rad CFX96 system and GenePath Dx CoViDx One v2.1.1TK kit	N, RdRp, and E	Highest viral load ranged from 2,440 copies/mL to 4,585 copies/mL Seasonal variation in viral load: Monsoon: 1,695 copies/ml	(Kadam et al., 2024)

		PEG (polyethylene glycol) precipitation for viral concentration RNA isolation using a commercial kit				Winter: 72.5 copies/ml Summer: 3,657 copies/ml	
25	COVID-19	Filtration and vacuum pump concentration for viral particles	Surrogate spiked (bovine herpesvirus (BoHV) and bovine respiratory syncytial virus (BRSV); Qubit fluorometer assay and high-resolution automated electrophoresis	RT-qPCR and CovidSeq sequencing	N-gene, E-gene, and RdRP gene detected in Indian samples	Up to 3 million viral copies/L	(Thompson et al., 2025)
26	COVID-19	Concentration followed by qPCR analysis following whole genome	NS	qPCR and Whole Genome Sequencing (WGS)	SARS-CoV-2 RNA (ORF1a, ORF1b, N	Ct values were analyzed, but specific viral load data is not provided	(Kumar and Mahapatra, 2024)

		sequencing (WGS)			gene, and S gene)		
27	COVID-19	PEG precipitation, filtered, centrifuged, and RNA isolated	Qubit fluorometer assay and high-resolution automated electrophoresis	RT-qPCR assay targeting SARS-CoV-2 genes (N, RdRp, and E)	SARS-CoV-2 RNA and specific variants (Omicron BA.2, XBB clades, BA.2.75.X, etc.)	Viral load varied throughout the study, with peaks in June–July 2022 (130,014.24 ± 284,248.056 copies/L) and December 2022 (71,773.35 ± 233,237.6 copies/L)	(Rajput et al., 2024a)
28	COVID-19	Samples processed using RT-qPCR for SARS-CoV-2 RNA quantification. Whole genome sequencing performed on selected positive samples	Qubit fluorometer assay and high-resolution automated electrophoresis	RT-qPCR for SARS-CoV-2 detection and quantification. Whole genome amplicon sequencing for lineage analysis	SARS-CoV-2 RNA (genes: N, RdRp, E)	Viral load trends varied over time with peaks in July 2022, December 2022, and March-April 2023. Solapur recorded the highest viral titer of 314,500 gc/L in June–July 2022	(Matra et al., 2025)

29	COVID-19	Heat inactivation followed by centrifugation and filtration. Concentration using polyethylene glycol (PEG 8000 MW) and sodium chloride (NaCl) Viral RNA isolation using a commercial kit	Qubit fluorometer assay	Quantitative RT-qPCR using the GenePath Dx CoViDx One v2.1.1TK-Quantitative multiplex RT-qPCR kit	N (nucleocapsid) gene, E (envelope) gene, and RdRp (RNA-dependent RNA polymerase) gene of SARS-CoV-2	SARS-CoV-2 RNA detected in 27% of samples	(Zambre et al., 2024)
30	COVID-19	Wastewater samples heat-inactivated, filtered followed by concentration with Amicon Ultra-15 centrifugal filters (30 kDa cutoff)	Qubit fluorometer assay and high-resolution automated electrophoresis	RT-qPCR and sequencing using Illumina NextSeq 550 platform	SARS-CoV-2 genetic material, focusing on the KP.2 variant	P.2 lineage was first detected at low abundance (~5%) in early April 2024. Its abundance increased steadily to over 50% by mid-May 2024, becoming the dominant variant in the	(Rajput et al., 2024a)

						sampled locations. Other co-circulating lineages included XBB.1.16 and JN.1, which showed declining trends as KP.2 rose.	
31	Microbiome	Centrifuged at 30,000 xg for 15 minutes at 4 °C followed by DNA isolation	NS; Qubit fluorometer assay and high-resolution automated electrophoresis	Next-generation sequencing (16S rRNA gene amplicon sequencing)	ARGs	182 ARGs were identified, classified into 12 distinct ARG classes, the overall representation of known gut microbes was low (13.8%), but these represented 98% of the known gut microbiome, indicating sewage as a reliable proxy for gut	(Singh et al., 2023)

						microbiome assessment	
32	AMR	Sewage biomass was concentrated via vacuum filtration, preserved in ethanol, and stored at −20 °C	Qubit fluorometer assay	DNA extraction was carried out using the FastDNA Spin Kit for Soil, and sequencing was performed on the Illumina HiSeq 2500 platform	Targeted ARGs, plasmids, and metal resistance genes (MRGs)	An average of 449 ARGs (range: 309−489) were detected at each site	(Prieto Riquelme et al., 2022)
33	AMR	Metagenomic DNA was extracted from the samples after PEG concentration, followed by sequencing using high-throughput sequencing platforms	NS	Metagenomic sequencing	Antimicrobial resistance genes	Macrolide class of antibiotics exhibited the highest resistance at 40.1%, followed by aminoglycosides at 24.4%, tetracyclines at 11.3%, and lincosamides at 6.7%	(Madhukar et al., 2024)
34	AMR	Water samples were filtered	Qubit fluoromet	Antibiotic susceptibili	coliforms, specifically	Highest ARG relative	(Purohit et al., 2017)

		and then inoculated on agar plates.	er assay and high-resolution automated electrophoresis	ty testing using the Kirby-Bauer disc diffusion method. PCR for genetic confirmation and identification of resistance genes.	E. coli, for phenotyping and genotyping antibiotic resistance.	abundance found in wastewater (0.75 ARG copies per 16S rRNA gene copy). Animal feces had a relative ARG abundance of 0.4; human feces had 0.2–0.3 ARG copies per 16S rRNA gene.	
35	Poliomyelitis	Sewage samples were concentrated and treated with chloroform	NS	Virus isolation using tissue culture methods, intratypic differentiation (ITD) methods including ELISA and RNA probe hybridization, and partial genomic	Poliovirus types 1, 2, and 3	Wild poliovirus type-1 was detected	(Chowdhary and Dhole, 2008)

				sequencing of wild PV.			
36	Poliomyelitis	Sewage samples adjusted to pH 7.2, centrifuged, and processed with chloroform extraction and PEG precipitation. The concentrated virus suspension was stored at -20°C until used for poliovirus isolation	Raw sewage samples were spiked with 10^3 50% tissue culture infective doses (TCID50s) per ml of poliovirus type 1 (Sabin, attenuated vaccine strain).	Virus isolation was performed using L20B and RD cell cultures. Poliovirus typing and differentiation were conducted using neutralization tests, enzyme-linked immunosorbent assays (ELISA), and RNA probe hybridization.	wild poliovirus	10 to 500 TCID50s per liter.	(Deshpande Jagadish et al., 2003)
37	Amoebiasis	Sewage water samples were filtered, washed, concentrated, and separated	commercial DNA extraction kit (QIAamp Fast DNA Stool Mini	Microscopy, Nested multiplex PCR, Conventional PCR	16S-like rRNA gene for E. histolytica, E. dispar, E. moshkovsk		(Singh et al., 2023)

			Kit); DNA quantification by spectrophotometry, and confirmation of PCR product size via agarose gel electrophoresis		ii; 18S small subunit ribosomal RNA gene for E. bangladeshi		
38	Typhoid	DNA was extracted using a commercial kit	Duplex qPCR for HF183, a marker gene from a human-restricted Bacteroides and an extraction/ PCR positive control (Cy5-QXL670; Eurogentec) was spiked into	Multiplex quantitative PCR (qPCR)	Salmonella genes (ttr, staG, and tviB) and a marker of human fecal contamination (HF183)	Grab samples-7.5% positive for S. Typhi. Moore Swabs: 15.3% positive for S. Typhi.	(Uzzell et al., 2024)

			samples before extraction.				
39		Concentrated using a two-phase concentration method	Non-infectious RNA used as positive control and culture supernatant from uninfected cells was used as negative reagent control.	Virus isolation using tissue culture, enterovirus neutralization tests, RT-PCR for enterovirus detection	Enteroviruses, including poliovirus and non-polio enteroviruses (NPEV)	44 out of 109 were positive for enterovirus	(Tiwari and Dhole, 2018)
40	Influenza A (H1N1, H3N2), Respiratory Syncytial Virus (RSV), and COVID-19	PEG precipitation, followed by centrifugation and sequential filtration with Whatman filter paper and 0.22 µm PES filter membranes. The viral pellet was resuspended in TE buffer, and	Qubit fluorometer assay	RT-qPCR	Influenza A (matrix gene), H1N1pdm09 (H1 hemagglutinin gene), H3N2 (H3 hemagglutinin gene), RSV (matrix gene), SARS-CoV-2	H1N1pdm09: First detected on March 8, 2022, in Erandwane STP; highest viral load: 9.73 copies/µL on September 5, 2023, in Bopodi STP. H3N2: First detected on April 26,	(Pramanik et al., 2024)

		RNA was extracted			(RdRP and N-gene)	2022, in Vitthalwadi STP; highest viral load: 8.28 copies/µL on September 5, 2023, in Erandwane STP. Influenza A: First detected on March 8, 2022, in Erandwane STP; highest viral load: 84.1 copies/µL on February 1, 2023, in Kharadi STP. RSV: First detected on February 4, 2022, in New Naidu STP; highest viral load: 8.42 copies/µL on August 21, 2023, in Phytorid STP.	

						SARS-CoV-2: Highest viral load: 10,446 copies/µL on January 16, 2023, in Mundhwa STP	
41	Typhoid	DNA extraction using a commercial kit, stored at −20°C	Duplex qPCR was conducted for HF183,a marker gene from a human-restricted Bacteroides, and an extraction/ PCR positive control (Cy5-QXL670, Eurogentec) that was spiked into samples before extraction; Qubit	Quantitative PCR (qPCR) for Salmonella Typhi genes (ttr, staG, tviB) and fecal biomarker HF183	Salmonella Typhi genes (ttr, staG, tviB)	7.50% (39/520) grab samples were positive for all three S. Typhi genes 15.28% (79/517) Moore swabs were positive for all three S. Typhi genes. Positivity rates increased during monsoon season	(Abraham et al., 2025)

			fluorometer assay				
42	Influenza	Pasteurization followed by centrifugation and filtration. Viral concentration using PEG-NaCl precipitation method Resuspension in elution buffer and nucleic acid extraction	Qubit fluorometer assay	RT-PCR	Influenza A, Influenza B	Influenza A: 1.4×10^2 to 2.2×10^3 gc/L Influenza B: 5.2×10^3 to 7.7×10^3 gc/L	(Panneerselvam et al., 2024)

***NS Non specified**

ABRAHAM, D., KATHIRESAN, L., SASIKUMAR, M., AIEMJOY, K., CHARLES, R. C., KUMAR, D., SRINIVASAN, R., TROMAN, C., GRAY, E., UZZELL, C. B., JOHN, J., VEERARAGHAVAN, B., GRASSLY, N. C. & MOHAN, V. R. 2025. Wastewater surveillance for Salmonella Typhi and its association with seroincidence of enteric fever in Vellore, India. *PLOS Neglected Tropical Diseases,* 19**,** e0012373.

ACHEAMPONG, E., HUSAIN, A. A., DUDANI, H., NAYAK, A. R., NAG, A., MEENA, E., SHRIVASTAVA, S. K., MCCLURE, P., TARR, A. W., CROOKS, C., LADE, R., GOMES, R. L., SINGER, A., KUMAR, S., BHATNAGAR, T., ARORA, S., KASHYAP, R. S. & MONAGHAN, T. M. 2024. Population infection estimation from wastewater surveillance for SARS-CoV-2 in Nagpur, India during the second pandemic wave. *PLOS ONE,* 19**,** e0303529.

ARORA, S., NAG, A., KALRA, A., SINHA, V., MEENA, E., SAXENA, S., SUTARIA, D., KAUR, M., PAMNANI, T., SHARMA, K., SAXENA, S., SHRIVASTAVA, S. K., GUPTA, A. B., LI, X. & JIANG, G. 2022. Successful application of wastewater-based epidemiology in prediction and monitoring of the second wave of COVID-19 with fragmented sewerage systems–a case study of Jaipur (India). *Environmental Monitoring and Assessment,* 194**,** 342.

ARORA, S., NAG, A., RAJPAL, A., TYAGI, V. K., TIWARI, S. B., SETHI, J., SUTARIA, D., RAJVANSHI, J., SAXENA, S., SHRIVASTAVA, S. K., SRIVASTAVA, V., GUPTA, A. B., KAZMI, A. A. & KUMAR, M. 2021. Imprints of Lockdown and Treatment Processes on the Wastewater Surveillance of SARS-CoV-2: A Curious Case of Fourteen Plants in Northern India. *Water* [Online], 13.

ARORA, S., NAG, A., SETHI, J., RAJVANSHI, J., SAXENA, S., SHRIVASTAVA, S. K. & GUPTA, A. B. 2020. Sewage surveillance for the presence of SARS-CoV-2 genome as a useful wastewater based epidemiology (WBE) tracking tool in India. *Water Science and Technology,* 82**,** 2823-2836.

BASU, P., CHOUDHURY, S., SHRIDHAR, V., HUILGOL, P., ROYCHOUDHURY, S., NANDI, I., CHAUDHURI, A. & MITRA, A. 2022. Surveillance of SARS-CoV-2 RNA in open-water sewage canals contaminated with untreated wastewater in resource-constrained regions. *Access Microbiology,* 4.

CHAKRABORTY, P., PASUPULETI, M., JAI SHANKAR, M. R., BHARAT, G. K., KRISHNASAMY, S., DASGUPTA, S. C., SARKAR, S. K. & JONES, K. C. 2021. First surveillance of SARS-CoV-2 and organic tracers in community wastewater during post lockdown in Chennai, South India: Methods, occurrence and concurrence. *Science of The Total Environment,* 778**,** 146252.

CHAUDHURI, A., PANGARIA, A., SODHI, C., KUMAR V, N., HARSHE, S., PARIKH, N. & SHRIDHAR, V. 2023. Building health system resilience and pandemic preparedness using wastewater-based epidemiology from SARS-CoV-2 monitoring in Bengaluru, India. *Frontiers in Public Health,* Volume 11 - 2023.

CHOWDHARY, R. & DHOLE, T. N. 2008. Interrupting wild poliovirus transmission using oral poliovirus vaccine: Environmental surveillance in high-risks area of India. *Journal of Medical Virology,* 80**,** 1477-1488.

DESHPANDE JAGADISH, M., SHETTY SUSHMITHA, J. & SIDDIQUI ZAEEM, A. 2003. Environmental Surveillance System To Track Wild Poliovirus Transmission. *Applied and Environmental Microbiology,* 69**,** 2919-2927.

DHARMADHIKARI, T., RAJPUT, V., YADAV, R., BOARGAONKAR, R., PATIL, D., KALE, S., KAMBLE, S. P., DASTAGER, S. G. & DHARNE, M. S. 2022. High throughput sequencing based direct detection of SARS-CoV-2 fragments in wastewater of Pune, West India. *Sci Total Environ,* 807**,** 151038.

HEMALATHA, M., KIRAN, U., KUNCHA, S. K., KOPPERI, H., GOKULAN, C. G., MOHAN, S. V. & MISHRA, R. K. 2021. Surveillance of SARS-CoV-2 spread using wastewater-based epidemiology: Comprehensive study. *Science of The Total Environment,* 768**,** 144704.

JOSHI, M., KUMAR, M., SRIVASTAVA, V., KUMAR, D., RATHORE, D. S., PANDIT, R., GRAHAM, D. W. & JOSHI, C. G. 2022. Genetic sequencing detected the SARS-CoV-2 delta variant in wastewater a month prior to the first COVID-19 case in Ahmedabad (India). *Environmental Pollution,* 310**,** 119757.

KADAM, P. P., MESTRY, T., MISTRY, N. & NILGIRIWALA, K. S. 2024. Wastewater-based genomic surveillance of SARS-CoV-2 in vulnerable communities in Mumbai. *Indian J Med Res,* 160**,** 570-577.

KUMAR, M., JOSHI, M., JIANG, G., YAMADA, R., HONDA, R., SRIVASTAVA, V., MAHLKNECHT, J., BARCELO, D., CHIDAMBRAM, S., KHURSHEED, A., GRAHAM, D. W., GOSWAMI, R., KURODA, K., TIWARI, A. & JOSHI, C. 2023a. Response of wastewater-based epidemiology predictor for the second wave of COVID-19 in Ahmedabad, India: A long-term data Perspective. *Environmental Pollution,* 337**,** 122471.

KUMAR, M., JOSHI, M., PATEL, A. K. & JOSHI, C. G. 2021a. Unravelling the early warning capability of wastewater surveillance for COVID-19: A temporal study on SARS-CoV-2 RNA detection and need for the escalation. *Environmental Research,* 196**,** 110946.

KUMAR, M., JOSHI, M., PRAJAPATI, B., SIRIKANCHANA, K., MONGKOLSUK, S., KUMAR, R., GALLAGE, T. P. & JOSHI, C. 2023b. Early warning of statewide COVID-19 Omicron wave by sentineled urbanized sewer network monitoring using digital PCR in a province capital city, of Gujarat, India. *Science of The Total Environment,* 905**,** 167060.

KUMAR, M., JOSHI, M., SHAH, A. V., SRIVASTAVA, V. & DAVE, S. 2021b. Wastewater surveillance-based city zonation for effective COVID-19 pandemic preparedness powered by early warning: A perspectives of temporal variations in SARS-CoV-2-RNA in Ahmedabad, India. *Science of The Total Environment,* 792**,** 148367.

KUMAR, M. & MAHAPATRA, D. M. 2024. First reporting of BA.1* and BA.2* recombinant SARS-CoV-2 lineage XAP from Indian wastewaters. *Science of The Total Environment,* 949**,** 174756.

KUMAR, M., PATEL, A. K., SHAH, A. V., RAVAL, J., RAJPARA, N., JOSHI, M. & JOSHI, C. G. 2020. First proof of the capability of wastewater surveillance for COVID-19 in India through detection of genetic material of SARS-CoV-2. *Science of The Total Environment,* 746**,** 141326.

KUMAR, M., SRIVASTAVA, V., MAZUMDER, P., DEKA, J. P., GUPTA, S., GOSWAMI, R., MUTIYAR, P. K., DAVE, S., MAHANTA, C., RAMANATHAN, A. L. & JOSHI, M. 2022. Spectre of SARS-CoV-2 RNA in the ambient urban waters of Ahmedabad and Guwahati: A tale of two Indian cities. *Environmental Research,* 204**,** 112067.

KUTTEYIL, S. S., PATTASSERY, S. A., JAYASWAMY, M. M., POTDAR, V., RAJAGOPAL, P. M. & MUNIVENKATAPPA, A. 2023. Trend of coronavirus disease 2019 pandemic in Bengaluru, Karnataka, India. *Indian J Public Health,* 67**,** 468-470.

LAMBA, S., GANESAN, S., DAROCH, N., PAUL, K., JOSHI, S. G., SREENIVAS, D., NATARAJ, A., SRIKANTAIAH, V., MISHRA, R., RAMAKRISHNAN, U. & ISHTIAQ, F. 2023. SARS-CoV-2 infection dynamics and genomic surveillance to detect variants in wastewater – a longitudinal study in Bengaluru, India. *The Lancet Regional Health - Southeast Asia,* 11.

MADHUKAR, M. K., SINGH, N., IYER, V. R., SOWPATI, D. T., TALLAPAKA, K. B., MISHRA, R. K. & MOHARIR, S. C. 2024. Antimicrobial resistance landscape in a metropolitan city context using open drain wastewater-based metagenomic analysis. *Environ Res,* 252**,** 118556.

MATRA, S., GHODE, H., RAJPUT, V., PRAMANIK, R., MALIK, V., RATHORE, D., KUMAR, S., KADAM, P., TUPEKAR, M., KAMBLE, S., DASTAGER, S., BAJAJ, A., QURESHI, A., KAPLEY, A., KARMODIYA, K. & DHARNE, M. 2025. Wastewater surveillance of open drains for mapping the trajectory and succession of SARS-CoV-2 lineages in 23 cities of Maharashtra state (India) during June 2022 to May 2023. *Heliyon,* 11**,** e42534.

NAG, A., ARORA, S., SINHA, V., MEENA, E., SUTARIA, D., GUPTA, A. B. & MEDICHERLA, K. M. 2022. Monitoring of SARS-CoV-2 Variants by Wastewater-Based Surveillance as a Sustainable and Pragmatic Approach—A Case Study of Jaipur (India). *Water* [Online], 14.

PANNEERSELVAM, S., MANAYAN PARAMBIL, A., JAYARAM, A., VARAMBALLI, P., MUKHOPADHYAY, C. & JAGADESH, A. 2024. Surveillance of influenza A and B viruses from community and hospital wastewater treatment plants. *Environ Microbiol Rep,* 16**,** e13317.

PRAMANIK, R., NANNAWARE, K., MALIK, V., SHAH, P., SANGEWAR, P., GOGATE, N., SHASHIDHARA, L. S., BOARGAONKAR, R., PATIL, D., KALE, S., BHALERAO, A., JAIN, N., KAMBLE, S., DASTAGER, S. & DHARNE, M. 2024. Monitoring Influenza A (H1N1, H3N2), RSV, and SARS-CoV-2 Using Wastewater-Based Epidemiology: A 2-Year Longitudinal Study in an Indian Megacity Covering Omicron and Post-Omicron Phases. *Food and Environmental Virology,* 17**,** 3.

PRIETO RIQUELME, M. V., GARNER, E., GUPTA, S., METCH, J., ZHU, N., BLAIR, M. F., ARANGO-ARGOTY, G., MAILE-MOSKOWITZ, A., LI, A.-D., FLACH, C.-F., AGA, D. S., NAMBI, I. M., LARSSON, D. G. J., BÜRGMANN, H., ZHANG, T., PRUDEN, A. & VIKESLAND, P. J. 2022. Demonstrating a Comprehensive Wastewater-Based Surveillance Approach That Differentiates Globally Sourced Resistomes. *Environmental Science & Technology,* 56**,** 14982-14993.

PUROHIT, M. R., CHANDRAN, S., SHAH, H., DIWAN, V., TAMHANKAR, A. J. & STÅLSBY LUNDBORG, C. 2017. Antibiotic Resistance in an Indian Rural Community: A 'One-Health' Observational Study on Commensal Coliform from Humans, Animals, and Water. *International Journal of Environmental Research and Public Health* [Online], 14.

RAJPUT, V., DAS, R., PRAMANIK, R., NANNAWARE, K., SUSHMA, Y., TAJI, N., RAJPUT, V., RAJKHOWA, R., PACHARNE, P., SHAH, P., GOGATE, N., SANGWAR, P., BHALERAO, A., JAIN, N., KAMBLE, S., DASTAGER, S., SHASHIDHARA, L. S., KARYAKARTE, R. & DHARNE, M. 2024a. Early Detection of KP.2 SARS-CoV-2 Variant using Wastewater-based Genomic Surveillance in Pune, Maharashtra, India. *J Travel Med*.

RAJPUT, V., PRAMANIK, R., MALIK, V., YADAV, R., SAMSON, R., KADAM, P., BHALERAO, U., TUPEKAR, M., DESHPANDE, D., SHAH, P., SHASHIDHARA, L. S., BOARGAONKAR, R., PATIL, D., KALE, S., BHALERAO, A., JAIN, N., KAMBLE, S., DASTAGER, S., KARMODIYA, K. & DHARNE, M. 2023. Genomic surveillance reveals early detection and transition of delta to omicron lineages of SARS-CoV-2 variants in wastewater treatment plants of Pune, India. *Environmental Science and Pollution Research,* 30**,** 118976-118988.

RAJPUT, V., PRAMANIK, R., NANNAWARE, K., MALIK, V., MATRA, S., KUMAR, S., JOSHI, S., KADAM, P., BHALERAO, U., TUPEKAR, M., DESHPANDE, D., SHAH, P., SANGEWAR, P., GOGATE, N., BOARGAONKAR, R., PATIL, D., KALE, S., BHALERAO, A., JAIN, N.,

SHASHIDHARA, L. S., KAMBLE, S., DASTAGER, S., KARMODIYA, K. & DHARNE, M. 2024b. Wastewater surveillance in post-omicron silent phase uncovers silent waves and cryptic transmission of SARS-CoV-2 variants; a yearlong study in Western India. *Science of The Total Environment,* 955**,** 176833.

SHARMA, D. K., NALAVADE, U. P., KALGUTKAR, K., GUPTA, N. & DESHPANDE, J. M. 2021. SARS-CoV-2 detection in sewage samples: Standardization of method & preliminary observations. *Indian J Med Res,* 153**,** 159-165.

SINGH, A., BANERJEE, T., KHAN, U. & SHUKLA, S. K. 2021. Epidemiology of clinically relevant Entamoeba spp. (E. histolytica/dispar/moshkovskii/bangladeshi): A cross sectional study from North India. *PLOS Neglected Tropical Diseases,* 15**,** e0009762.

SINGH, K. S., PAUL, D., GUPTA, A., DHOTRE, D., KLAWONN, F. & SHOUCHE, Y. 2023. Indian sewage microbiome has unique community characteristics and potential for population-level disease predictions. *Science of The Total Environment,* 858**,** 160178.

SRIVASTAVA, V., GUPTA, S., PATEL, A. K., JOSHI, M. & KUMAR, M. 2021. Reflections of COVID-19 cases in the wastewater loading of SARS-CoV-2 RNA: A case of three major cities of Gujarat, India. *Case Studies in Chemical and Environmental Engineering,* 4**,** 100115.

THARAK, A., KOPPERI, H., HEMALATHA, M., KIRAN, U., C. G, G., MOHARIR, S., MISHRA, R. K. & MOHAN, S. V. 2022. Longitudinal and Long-Term Wastewater Surveillance for COVID-19: Infection Dynamics and Zoning of Urban Community. *International Journal of Environmental Research and Public Health* [Online], 19.

THOMPSON, C., LEAL, C. V., DA SILVA FAUSTINO, R., LEOMIL, L., JAGADEESHWARI, U., SHARMA, R., DE OLIVEIRA, M., TSCHOEKE, D., FELIX, T., MACEDO, L., KHOURI, R., KOOLEN, H., LANDUCI, F., DE REZENDE, C., STROBEL, Í., DE MORAES, L., P. RAMOS, P. I., DE SOUZA, H., MOTTA, F., BARRAL-NETTO, M., AGUIAR-OLIVEIRA, M. D. L., DE SIQUEIRA, M., SASIKALA, C. & THOMPSON, F. 2025. Co-occurrence of SARS-CoV-2 variants in rivers and sewage in India and Brazil. *Science of The Total Environment,* 958**,** 178089.

TIWARI, S. & DHOLE, T. N. 2018. Assessment of enteroviruses from sewage water and clinical samples during eradication phase of polio in North India. *Virology Journal,* 15**,** 157.

UZZELL, C. B., ABRAHAM, D., RIGBY, J., TROMAN, C. M., NAIR, S., ELVISS, N., KATHIRESAN, L., SRINIVASAN, R., BALAJI, V., ZHOU, N. A., MESCHKE, J. S., JOHN, J., KANG, G., FEASEY, N., MOHAN, V. R. & GRASSLY, N. C. 2024. Environmental Surveillance for Salmonella Typhi and its Association With Typhoid Fever Incidence in India and Malawi. *The Journal of Infectious Diseases,* 229**,** 979-987.

WANI, H., MENON, S., DESAI, D., D'SOUZA, N., BHATHENA, Z., DESAI, N., ROSE, J. B. & SHRIVASTAVA, S. 2023. Wastewater-Based Epidemiology of SARS-CoV-2: Assessing Prevalence and Correlation with Clinical Cases. *Food and Environmental Virology,* 15**,** 131-143.

ZAMBRE, S., KATARMAL, P., PAWAR, S., DAWKHAR, S., IYER, P., RAJPUT, V., KADAM, P., BHALERAO, U., TUPEKAR, M., SHAH, P., KARMODIYA, K., DHARNE, M., ROY, B. & KORAKTAR, S. 2024. Wastewater surveillance of severe acute respiratory syndrome

coronavirus-2 in open drains of two Indian megacities captures evolutionary lineage transitions: a zonation approach. *Environmental Science and Pollution Research,* 31**,** 49670-49681.