Human norovirus contamination in water sources: A systematic review and meta-analysis

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Abstract

The human norovirus (HNoV), on a global scale, is the prevailing cause of contagious viral gastroenteritis outbreaks, with more than 200 000 deaths annually. This study aimed at assessing specific prevalence of HNoV pollution in different water sources and their roles in the dissemination of HNoV, with a view to refocus water sources and sewage management options for policy making towards public health safety. In this regard, we conducted a systematic review and meta-analysis (SR/MA) of the prevalence of HNoV in water sources. We searched PubMed, Google Scholar, Scopus and Web of Science for studies on HNoV prevalence in water sources without temporal restriction, till January 30, 2021. We conducted a random-effects meta-analysis of the HNoV prevalence and stratified the study by water type, continent, gross national income (GNI) group and genogroup. Further, a mixed-effects meta-regression model was performed for sensitivity analysis. The literature search identified 61 studies on water source-based HNoV (WsHNoV) prevalence. The pooled WsHNoV prevalence was 31.7% (95%CI: 25.1–38.5) but varied according to water sources types; river water showing the highest estimate at 43.5% (95%CI: 33.9–53.4), followed by estuarine water (30.6%, 95%CI: 12.5–52.2), composite water (27.9%, 95%CI: 13.5–44.9), marine water (25.9%, 95%CI: 10.0–45.6), groundwater (19.7%, 95%CI: 9.4–32.3) and lake water (2.2%, 95%CI: 0–25.8). Further, the findings indicated the highest WsHNoV prevalence in Africa as 55.9% (95% CI: 28.2–81.9), followed by Asia (31.6%, 95% CI: 22.3–41.6), Europe (29.8%, 95% CI: 17.9–43.2), North America (27.7%, 95% CI: 11.2–47.6) and South America (27.1%, 95%CI: 0.09–49.4). The WsHNoV prevalence stratified by GNI group was 40.6% (95%CI: 27.9–53.9) in middle-income countries and 28.7% (95%CI: 21.7–36.1) in high-income countries respectively. The prevalence of GI, GII and GI & GII genogroup in natural water was 16.4% (95%CI: 12.0–21.3), 20.6% (95%CI: 15.7–25.8) and 12.8% (95%CI: 6.9–20.6) respectively. Evidently, prevalence of the HNoV genogroup in water sources mirrors the pattern of HNoV gastroenteritis and GII genogroup dominance worldwide. In conclusion, public health efforts against waterborne diseases should prioritize water resource/sewage management options and policies towards ardent water sources pollution prevention.

Keywords: Prevalence; Water quality; Public health; Sewage management; River; Estuary; Marine water; Groundwater; Lake; Pollution prevention

1. Introduction

The human norovirus (HNoV) is a positive-sense, non-enveloped ssRNA virus; and a low-infectious-dose causal agent of gastroenteritis worldwide, with more than 600 million cases annually (Pires et al., 2015; Alsved et al., 2020; Guo et al. 2020). HNoV is also known for its high environmental stability (Alsved et al., 2020). Both the low infectivity dose and high environmental stability characteristics of HNoV make the pathogen a leading cause of viral gastroenteritis with a global distribution (Alsved et al., 2020; Guo et al. 2020). Global community prevalence of HNoV gastroenteritis has been estimated as 24% with 17% prevalence associated with hospitalized cases (Ahmed et al., 2014).

HNoV has a wide spectrum of transmission pathways spanning through faecal-oral pathways by ingestions of contaminated foodstuffs and water such as groundwater supplies, fresh and marine waters, person-to-person vehicles, contacts with contaminated matrices and airborne pathways through inhalation and swallowing of aerosols during toilet flushing, aerosolized vomitus, and water splashes (Johnson et al., 2013; Alsved *et al.* 2019; Pouillot et al., 2015; Alsved et al., 2020). Generally, the substantial disparities in access to sanitation, safe water and hygiene among different regions of the world, especially between developed and developing countries (Thapar and Sanderson, 2004; WHO/UNICEF, 2012), have been correlated with differences in risk of HNoV gastroenteritis. Clinical manifestations of HNoV infection varies from asymptomatic infections, acute, severe, and life-threatening gastroenteritis to chronic infection in immune deficient patients (Bok and Green, 2012; Green et al., 2020).

Natural waters (sources) are generally the main sources of drinking water and water for other domestic purposes for >95% of the world populations. However, most natural waterbodies/water sources are discharge hubs for untreated sewage from municipal and industrial settings, contributing to increased physicochemical, microbial and faecal pollution of the aquatic milieu and eventually poise a great hazardous risk to human wellness (Gibney et al., 2017; Sekwadi et al., 2018). HNoVs have been found in drinking water (Victoria et al., 2010), surface water (Hernandez-Morga et al., 2009Hernandez-Morga et al., 2009), lakes (Horman et al. 2004), groundwater (Gabrieli et al. 2009), tap water (Tong et al., 2011), rivers (Fernández et al., 2011; Perez-Sautu et al. 2012; Kishida et al. 2012), seawater (Rosa et al. 2017; Boonchan et al., 2017), marine water (Laverick et al. 2004), and wastewater (Aw and Gin, 2010). Domestic use of water and contact remains a public health concern for the transmission of HNoV as it has been ascertained that HNoV is resistant to inactivation in wastewater treatment plants (Hewitt et al., 2011). Environmental dissemination through natural waters is likely to be significant and might frustrate control efforts of HNoV infections (Lopman et al., 2012).

The norovirus remains a leading cause of viral gastroenteritis associated morbidity and mortality, hence it is pressing to fill the gap of quantitative evidence of norovirus prevalence in water sources for directed interventions. Eventually this SR/MA pool current data-driven evidence of norovirus prevalence and pollution in water sources in order to pre-inform policy makers the need to prioritize watershed/water sources management options/implementation for preventing the spread of norovirus and considerably reduce the amount of associated human mortality and morbidity globally.

The aim of this study was to assess the pooled prevalence of the human norovirus pollution in water sources and determine the specific contribution of different water sources in its

dissemination, thereby refocusing watershed and sewage management options for policy making towards public health safety. It further sought to determine its regional prevalence/pollution in water sources in high income countries (HIC), upper middle-income countries (UMIC) and lower middle-income countries (LMIC). In other words, the study aimed at answering the research question: what is the prevalence of HNoV in water sources/watershed and does it vary with water source types, regionally as well as between HIC and MIC? This study therefore presents the first systematic and meta-analysis specific to prevalence of norovirus in natural waters (water sources) and it hopes to spur and reawaken researchers and policy makers into actions relevant to prevention of the spread of the pathogen through water sources.

2. Methods

2.1. Study strategy and databases

The study researched articles on prevalence of the human norovirus in natural waters in the Web of Science (WoS), PubMed, Google Scholar and Scopus. The selection of relevant studies for the SR/MA was pre-informed by the inclusion criteria set for the study. All electronic database searches were conducted following the "Preferred Reporting Items for Systematic Reviews and Meta-analyses (PRISMA) guidelines" (Moher et al., 2009).

2.2. Inclusion and exclusion criteria

2.2.1. Inclusion criteria

To be included in the SR/MA, studies had to satisfy the following criteria (at least 1–5):

1. The study must be an intentional primary investigation (original article) of the prevalence or its index variants (occurrence incidence, enumeration, isolation, characterization or distribution) of the human noroviruses in natural waters;
2. The definition of natural water or water sources in this study was restricted to stream/river water, estuarine water, ponds, groundwater, lake water, marine water, and seawater;
3. The method(s) (e.g., adsorption/elution/flocculation/ultrafiltration etc.) by which the norovirus was concentrated in the water sample must be adequately described;
4. The detection method(s) (e.g., PCR, RT-PCR, RT-nested PCR, qRT-PCR etc.) whereby noroviruses were assessed or quantified in the waters, must be described adequately;
5. The full text of the study or article must be available in the English language. A non-English language full–text article, whose abstract is available in English and satisfied inclusion conditions 1–4, was included in the analysis; and
6. In the case where wastewater/sewage was investigated co-concurrently with natural waters, the data specific to the natural water was extracted.

2.2.2. Exclusion criteria

To be excluded from the SR/MA, studies had to satisfy at least one of the following exclusion criteria:

1. The HNoV must have been studied in other samples not including natural water. For instance, HNoV in freshwater animals/aquatic animals with no water sampled; stool samples and questionnaire-based studies;
2. Surface water/natural waters must have been artificially seeded with HNoV or murine norovirus studies;
3. Development of human norovirus recovery/concentration or detection methodology at laboratory based on HNoV artificially seeded experiments with no corresponding/direct application on natural water;
4. Modelling/quantitative microbial risk assessment of HNoV without report of water sampling; and
5. Studies on human norovirus in natural waters with sample size less than five.

2.3. Data search and extraction

The literature search was performed using a subject-specific Boolean approach. The search Boolean varied according to specific database requirements. Generally, the subject-specific Boolean consisted in norovirus and inclusion criteria 1 and 2 (section 2.2.1). A second search was performed for validation of the document retrieval using "norovirus" and to retrieve document(s) probably lost due to the former search approach. Detailed information on the search strategy can be found in supplementary material.

Article records from two search strategies in all the databases were first downloaded in comma separated, tab-delimited or plaintext file formats. These were then combined for sequential computer-assisted deduplication using R Version 4.1.0 (R Core Team, 2021), with Bibliometrix R programme package (Aria and Cuccurullo, 2017), ScientoPy v.2.0.3 Python programme package (Ruiz-Rosero et al., 2019) and Microsoft Excel version 2016, using the authors' names and title fields. The download was done on December 28, 2020 followed up by email alert tracking of new articles until the day the final analysis was completed (January 30, 2021). Fig. 1 provides information on study selection and screening for pooled prevalence analysis of the human noroviruses in natural waters.

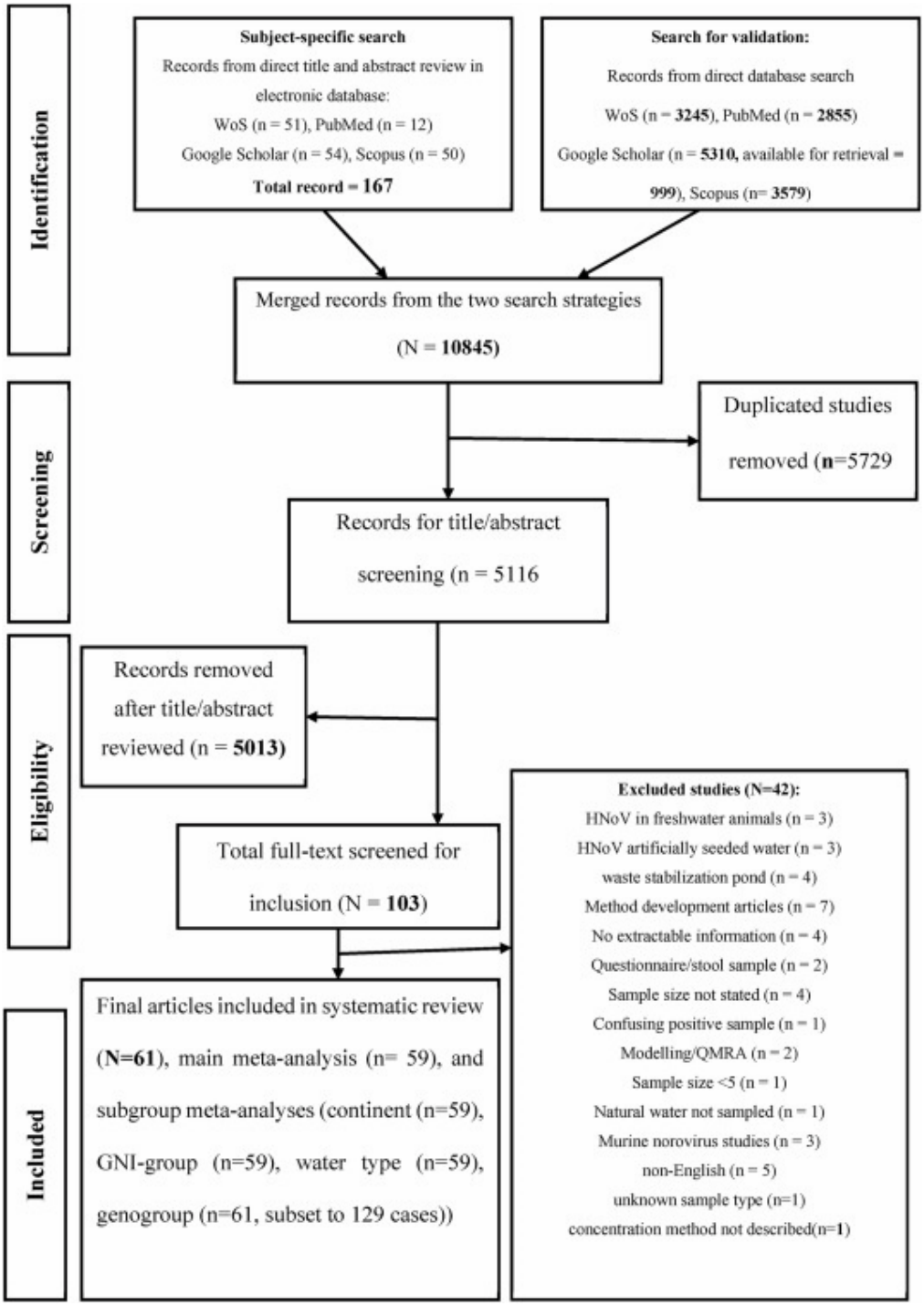

Fig. 1. Study selection and screening for pooled prevalence analysis of human noroviruses in natural waters.

After the deduplication process, titles/abstracts were reviewed. To be included at the title/abstract review step, studies had to satisfy inclusion criteria 1 and 2 (section 2.2.1) at least. Then, the full-text of the remaining unique articles were retrieved for a full-text review against the inclusion and exclusion criteria listed in Section 2.2.

During data extraction, reports of norovirus positive samples, sample sizes, concentration methods, detection methods, water types sampled, HNoV genogroups, and the country/continent where the studies were carried out, were recorded. Any study that failed the inclusion criteria 1–5 (section 2.2.1.) or satisfied the exclusion criteria (section 2.2.2) were further removed from the analysis at the full text review stage. Data were extracted by ETC and IBE.

Disagreements between ETC and IBE were resolved by discussion and/or intervention from OYD. When additional information was required about a study, ETC contacted the study's corresponding author via email with weekly reminder messages until the final analysis was conducted. For example, a study comprising samples from multiple countries to clarify country-specific sample allotment. However, there was no response from the authors contacted. Therefore, the study was designated under a country with the Alpha 2 country code of all involving countries (see Table 1). We further grouped the studies according to World Bank 2019) GNI per capita grouping of countries into HIC, UMIC and LMIC (https://data.worldbank.org/indicator/NY.GNP.PCAP.CD). Additionally, two articles were agreed upon to be included only in genogroup meta-analysis after a failed attempt to clarify the total number of positive cases of the norovirus in the studies by contacting their authors; which were only stated for the GI and GII genogroup (the studies were GI- and GII-targeted).

2.4. Data analysis

2.4.1. Main meta-analysis

An exploratory analysis was first conducted on the extracted data. The preliminary analysis revealed that some extreme proportions (≤ 0.2 and ≥ 0.8) exist in the data and that the data did not follow normal distribution. Therefore, we normalized the data using double arcsine transformation (Freeman and Tukey, 1950). Thereafter, we meta-analyzed the normalized data using a random-effects model (DerSimonian and Laird, 1986). The heterogeneity between studies was evaluated by using Cochran's *Q*-, H- and I^2-statistics, with an $I^2 > 75\%$ showing significant heterogeneity (Hedges and Olkin, 1985; Higgins et al. 2003; Cornell et al., 2014). We performed an influence analysis to determine potential influential studies among the included studies according to Viechtbauer and Cheung (2010). Further, we assessed publication bias in the study using Egger's regression test (Egger et al., 1997) with $p < 0{\cdot}05$ indicating significant publication bias.

2.4.2. Subgroup meta-analysis

Following an observed large degree of heterogeneity in the main meta-analysis, we further stratified the meta-analysis by continents where the studies were conducted (Asia, Africa, Europe, South America and North America); gross national income (GNI) per capita (HIC, UMIC and LMIC) based on 2019 GNI groups developed by the World Bank (https://data.worldbank.org/indicator/NY.GNP.PCAP.CD); norovirus genogroups (GI, GII, GI_II [co-occurrence of GI & GII]) and types of natural water – estuarine water, groundwater, lake water, marine water, river water, seawater, surface water, and composite water [river-estuarine water, river-groundwater, river-lake water and groundwater-brackish water], using a mixed effects model.

Table 1. Detailed information of the studies included in systematic review and meta-analysis of the human norovirus prevalence in water sources.

S/n	Author	Year	Positive sample	Sample size	GI	GII	GI &GII	Water type	Concentration method	Detection method	Country	GNI group	GNI per capita (US$)
1	Hörman et al.	2004	13	139	3	10		Surface water (lake/river)	Adsorption-elution/flocculation	Reverse transcriptase PCR	Finland	HIC	49580
	Hörman et al.	2004	1	35				Lake	Adsorption-elution/flocculation	Reverse transcriptase PCR	Finland	HIC	49580
	Hörman et al.	2004	12	104	3	10		River	Adsorption-elution/flocculation	Reverse transcriptase PCR	Finland	HIC	49580
2	Laverick et al.	2004	9	61				Marine/river water	Adsorption-elution/flocculation	Semi-nested RT-PCR	United Kingdom	HIC	42370
	Laverick et al.	2004	5	36				Marine water	Adsorption-elution/flocculation	RT-PCR	United Kingdom	HIC	42370
	Laverick et al.	2004	4	25				river water	Adsorption-elution/flocculation	RT-PCR	United Kingdom	HIC	42370
3	Haramoto et al.	2005	37	64	34	28	25	River water	Adsorption-elution (Cation(Al3+)-coated filter)	TaqMan PCR/real-time PCR	Japan	HIC	41690
4	Ueki et al.	2005	10	16	–	–		River water	Polyethylene glycol precipitation	RT-PCR	Japan	HIC	41690
5	Rutjes et al.	2006	15	16				Surface water	Adsorption-elution	RT-PCR	Netherlands	HIC	53200
6	Rosa et al.	2007	0	5				Estuarine water	PrepScale tangential flow filtration/polyethylene glycol	RT-PCR	Italy	HIC	34460
6	Rosa et al.	2007	3	26		3		Seawater	PrepScale tangential flow filtration/polyethylene glycol	RT-PCR	Italy	HIC	34460
7	Lee and Kim	2008	38	58	32	26	20	River water	Adsorption-elution/polyethylene glycol	RT-nested PCR	South Korea	HIC	33720
8	Jones et al.	2009	0	5	–	–		River water	Adsorption-elution/flocculation	RT-PCR	United States	HIC	65760
9	Hernandez-Morga et al.	2009	28	40	–	–		Estuarine water	Ultrafiltration	RT-PCR	Mexico	UMIC	9430
10	Kitajima et al.	2009	15	48				River water	Adsorption-elution (HA electronegative filter)	TaqMan-based real-time RT-PCR	Japan	HIC	41690

S/n	Author	Year	Positive sample	Sample size	GI	GII	GI &GII	Water type	Concentration method	Detection method	Country	GNI group	GNI per capita (US$)
11	Gabrieli et al.	2009	4	26	1	3		Groundwater (spring/well)	Adsorption-elution (positively charged cartridge filter)	RT-PCR	Italy	HIC	34460
	Gabrieli et al.	2009	0	12	0	0		Spring water	Adsorption-elution	RT-PCR	Italy	HIC	34460
	Gabrieli et al.	2009	4	14	1	3		Well water	Adsorption-elution	RT-PCR	Italy	HIC	34460
12	Gentry et al.	2009	6	72	5	1		Estuarine water	Adsorption-elution	RT-PCR	United States	HIC	65760
13	Aw et al.	2009	43	60	27	39	23	Urban catchment waters and an estuarine bay	Ultrafiltration techniques	Reverse transcription-seminested PCR	Singapore	HIC	59590
14	Félix et al.	2010	15	32	–	–		Marine recreational waters	Adsorption-elution	RT-PCR	Mexico	UMIC	9430
15	Kitajima et al.	2010	30	60	28	18	16	River water	Cation-coated filter method	RT-PCR	Japan	HIC	41690
16	Victoria et al.	2010	10	48	4	5	1	Seawater/brackish	Adsorption–elution/ultrafiltration	Semi-nested PCR	Brazil	UMIC	9130
17	Tong et al.	2011	13	16	5	10	3	Recreational water	Filtration-based method	RT-PCR	United States	HIC	65760
18	Lee h et al.	2011	8	10	6	1	1	Surface water/groundwater	Adsorption-elution (1MDS filter/NanoCeram filter)	RT-PCR	South Korea	HIC	33720
	Lee h et al.	2011	4	5	4	0		Surface water	Adsorption-elution (1MDS filter/NanoCeram filter)	RT-PCR	South Korea	HIC	33720
	Lee h et al.	2011	4	5	2	1	1	Groundwater	Adsorption-elution (1MDS filter/NanoCeram filter)	RT-PCR	South Korea	HIC	33720
19	Fernández et al.	2011	5	14	0	5		River water	Adsorption-elution-peg	RT-PCR, semi-nested PCR	Argentina	UMIC	11200
20	Lee H et alb	2011	46	109	26	16		Groundwater	Adsorption-elution (NanoCeram filters) ultrafiltration	RT-PCR	South Korea	HIC	33720
21	Lee et al.	2011	117	300	43	74	14	Groundwater	Adsorption-elution (NanoCeram filters)	RT-PCR	South Korea	HIC	33720

S/n	Author	Year	Positive sample	Sample size	GI	GII	GI &GII	Water type	Concentration method	Detection method	Country	GNI group	GNI per capita (US$)
22	Jung et al.	2011	7	39	5	2		Groundwater	Adsorption-elution (1MDS filters)	RT-PCR	South Korea	HIC	33720
23	Wyn-Jones et al.	2011	137	1410	49	88		Recreational waters (marine/freshwater)	Adsorption-elution (glass wool filtration	RT-PCR	CY, NL, UK, IT, DE, FR, ES, PL, PT	HIC	35258.9*
	Wyn-Jones et al.	2011	58	928	11	47		Recreational waters (freshwater)	Adsorption-elution (glass wool filtration)	RT-PCR	CY, NL,UK, IT, DE, FR, ES, PL, PT	HIC*	35258.9*
	Wyn-Jones et al.	2011	79	482	38	41		Recreational waters (marine)	Adsorption-elution (nitrocellulose membranes, elution and organic flocculation)	RT-PCR	CY, NL,UK, IT, DE, FR, ES, PL, PT	HIC*	35258.9*
24	Park et al.	2011	25	60	5	14	6	Groundwater (spring water)	Adsorption-elution (1MDS filter/NanoCeram filter)	RT-PCR	South Korea	HIC	33720
25	Kittigul et al.	2012	13	59	9	1	3	River water	Adsorption-elution	RT-nested PCR/qRT-PCR	Thailand	UMIC	7260
26	Lee et al.	2012	14	160	5	9		Groundwater	Adsorption–elution (NanoCeram cartridge filter)	RT-PCR	South Korea	HIC	33720
27	Fernández et al.	2012	53	209	–	–		River water	Adsorption–elution	RT-PCR, RT-seminested PCR	Argentina	UMIC	11200
28	Perez-Sautu et al.	2012	87	108	81	37		River water	Adsorption–elution (positively charged glass wool, PEG precipitation)	Real-time RT-PCR	Spain	HIC	30390
29[a]	Kishida et al.	2012	not stated	52	28	33		River water	Adsorption–elution	RT-PCR	Japan	HIC	41690
30	Maunula et al.	2012	20	65	3	17		River water	Adsorption-elution	RT-PCR	Finland	HIC	49580
31	Yang et al.	2012	6	6	4	6	4	Seawater	Ultra-filtration	RT-PCR	Hong Kong	HIC	50840
32	Mans et al.	2013	95	151	31	28	36	River water	Glass wool adsorption-elution	RT-PCR	South Africa	UMIC	6040
33	Lee et al.	2013	7	1090	–	7		Groundwater	Adsorption-elution (1-MDS filter)	RT-PCR	South Korea	HIC	33720

S/n	Author	Year	Positive sample	Sample size	GI	GII	GI &GII	Water type	Concentration method	Detection method	Country	GNI group	GNI per capita (US$)
34	Grøndahl-Rosado et al.	2014	34*	52	32	24		Surface water	Electropositive disc filter and polyethylene glycol precipitation	qPCR	Norway	HIC	82500
35	Kiulia et al.	2014	25	40	1	17	7	River water/borehole water	Glass wool adsorption-elution technique and/or PEG/NaCl precipitation	Real-time RT-PCR	Kenya	LMIC	1750
36	Lee et al.	2014	16	265	12	4		Groundwater/river/lake	Adsorption-elution/flocculation	RT-PCR	South Korea	HIC	33720
	Lee et al.	2014	13	166	9	4		River water	Adsorption-elution/flocculation	RT-PCR	South Korea	HIC	33720
	Lee et al.	2014	1	61	1	0		Lake water	Adsorption-elution/flocculation	RT-PCR	South Korea	HIC	33720
	Lee et al.	2014	2	34	2	0		Groundwater	Adsorption-elution/flocculation	RT-PCR	South Korea	HIC	33720
	Lee et al.	2014	0	4				Mixed water	Adsorption-elution/flocculation	RT-PCR	South Korea	HIC	33720
37	Giammanco et al.	2014	10	21	1	10	1	Groundwater	Ultra-filtration system	RT-PCR	Italy	HIC	34460
38	Kim et al.	2016	104	504	67	84		Estuaries/stream	QIAamp viral RNA mini kit	RT-PCR	South Korea	HIC	33720
	Kim et al.	2016	28	352	7	23		Estuary water	QIAamp viral RNA mini kit	RT-PCR	South Korea	HIC	33720
	Kim et al.	2016	76	152	60	61		Stream water	QIAamp viral RNA mini kit	RT-PCR	South Korea	HIC	33720
39	Inoue et al.	2016	13	15	3	13		River water	Tangential flow concentration system	PCR/RT-PCR	Thailand	UMIC	7260
40	Teixeira et al.	2016	4	28				Surface water (river, stream)	Adsorption-elution	RT-PCR	Brazil	UMIC	9130
41	Vergara et al.	2016	36	48	17	31		River water	Hollow fiber ultrafiltration/Polyethylene glycol	qPCR	Singapore	HIC	59590
42	Dienus et al.	2016	25	58	7	18		River water	Adsorption-elution	Real-time PCR	Sweden	HIC	55840
43	Maite	2016	0	8	0	0		River water	Adsorption-elution	RT-qPCR	United States	HIC	65760
44	Tian et al.	2017	221	860	173	102	54	Lakes, rivers, streams, and ponds	Adsorption-elution method	RT-PCR	United States	HIC	65760
45	Rosa et al.	2017	8	68	–	–		Seawater	Adsorption-elution method	RT-nested-PCR	Italy	HIC	34460
46	Boonchan et al.	2017	15	25	4	14	3	River water	Tangential flow concentration system	q-PCR	Thailand	UMIC	7260

S/n	Author	Year	Positive sample	Sample size	GI	GII	GI &GII	Water type	Concentration method	Detection method	Country	GNI group	GNI per capita (US$)
47	Kang et al.	2017	9	80	9	3	3	River water	Adsorption-elution	Semi-nested PCR, real-time RT-PCR	South Korea	HIC	33720
48	Teixeira et al.	2017	38	120	28	28	18	Surface water	Adsorption-elution	Semi-nested RT-PCR	Brazil	UMIC	9130
49	Van Abel et al.	2017	30	34	17	25		Surface water	Glass wool adsorption-elution/polyethylene glycol	RT-PCR	South Africa	UMIC	6040
50	LoFranco -	2017	0	12					Adsorption-elution	qPCR, PCR, RT-qPCR	Canada	HIC	46370
51	Koo et al.	2017	8	24	–	8		Stream/estuary water	Adsorption-elution/NanoCeram filters/PEG	RT-PCR	South Korea	HIC	33720
52	Choi et al.	2018	4	81	–	4		Rivers/beaches	Inorganic cation-coated filter method	RT-PCR	South Korea	HIC	33720
53[a]	Tian et al.	2018	Not stated	258	44	16		River water	Adsorption-elution	Real-time RT-PCR	United States	HIC	65760
54	Lee sj et al.	2018	8	1360	2	5	5	Treated groundwater	Adsorption-elution/NanoCeram filters/PEG	RT-PCR	South Korea	HIC	33720
55	Sedji et al.	2018	15	15	15	15		River water	Glass wool method	Digital droplet PCR (ddPCR)	France	HIC	42400
56	Lee sl et al.	2018	178	1486	57	129	9	Groundwater	Adsorption-elution (1-MDS filter)	RT-PCR	South Korea	HIC	33720
57	Shaheen and Elmahdy	2019	2	24	1	1		River water	PEG 6000 precipitation method	Semi-nested RT-PCR	Egypt	LMIC	2690
58	Rosiles-González et al.	2019	9	20	5	7	3	Groundwater/brackish water/karst aquifer	Hollow fibre ultrafiltration	qPCR, Nested PCR	Mexico	UMIC	9430
59	de Deus et al.	2019	39	104	27	10	2	Estuarine beaches	Adsorption-elution	Semi-nested RT-PCR	Brazil	UMIC	9130
60	Miura et al.	2019	13	15				River water/lake water	Adsorption-elution	qRT-PCR	Japan	HIC	41690
61	Khamrin et al.	2020	0	21				River water	Polyethylene glycol (PEG) precipitation method	RT-nested PCR/seminested PCR	Thailand	UMIC	7260

[a]Only considered for genogroup meta-analysis; GNI = gross national income per capita (US$ value for 2019 according to World Bank), HIC = high income countries; UMIC = upper middle income countries; LMIC = lower middle income countries; in a case of study involving water samples from multiple countries from Europe (Wyn-Jones et al., 2011) such as Cyprus, Netherlands, United Kingdom; Italy, Germany, France, Spain, Poland and Portugal (all HIC), under column for country, the study was denoted by the alpha 2 country code (CY, NL, UK, IT, DE, FR, ES, PL, PT, respectively) of all countries involved, also average GNI (35258.9) from associated nations were assigned to Wyn-Jones et al. (2011) for estimation sake; I_II = co-occurrence of genogroup I and genogroup II.

2.4.3. Meta-regression analysis

We explored publication year, sample size, water type, concentration method, detection method, country, GNI group (HIC, UMIC, LMIC), GNI value and continent as covariates (categorical or continuous variables as the case may be) in a mixed-effects meta-regression model to identify sources of heterogeneity using the Metafor Package. Heterogeneity in the effect size estimate was explained in terms of the significant regression coefficient and associated R^2.

2.4.4. Software

The meta-analyses were conducted in the R (version 4.1.0) programming environment using the Metafor Package (version 3.0–2) (Viechtbauer, 2010) and Meta Package (version 4.18–2) (Balduzzi et al., 2019). All outputs were presented with 95% confidence interval.

3. Results

The search for studies on the prevalence of norovirus in water sources yielded 5116 articles for title and abstract review (Fig. 1). Following title and abstract review, 5013 articles were removed leaving 103 articles for full text review. Forty-one articles were further excluded for different reasons stated in Fig. 1. Hence, 61 articles on natural waters were included in the SR/MA.

Detail information of the 61 studies systematically reviewed and meta-analyzed are provided in Table 1. The studies were published from 2004 to 2020. Out of the 61 articles systematically reviewed, Asia had the highest contributions (n = 28, 45.9%), followed by Europe (n = 13, 21.3%), North America (n = 10, 16.4%), South America (n = 6, 9.8%), and the least from Africa (n = 4, 6.6%) (Table S1). Nation-wise; South Korea (n = 15, 24.6%) contributed the highest number of eligible articles, followed by Japan and United States (n = 6, 9.8% each), Italy, Brazil and Thailand (n = 4, 6.6%), Mexico (n = 3, 4.9%), Argentina, Finland, Singapore and South Africa (n = 2, 3.3% each). Canada, Egypt, France, Hong Kong, Kenya, Netherlands, Norway, Spain, Sweden and United Kingdom contributed only one article (1.6%) each. Further, a multiple-country (CY, NL, UK, IT, DE, FR, ES, PL, PT) (n = 1, 1.6%) article was also found (Table S1).

The water sources/water types reported in the 61 articles had a total of 71 records, among which river water shared the highest (n = 32, 45.1%), followed by groundwater (n = 14, 19.7%), composite water (n = 10, 14.1%), estuarine water (n = 6, 8.5%), marine water (n = 4, 5.6%), seawater (n = 3, 4.2%) and lake water (n = 2, 2.8%) (Table S2). Furthermore, 53 (41.1%), 53 (41.1%) and 23(17.8%) of the studies recorded occurrence of the GI, GII and GI&II co-occurrence norovirus genogroup respectively, adding up to 129 norovirus genogroup records (Table S2).

Fig. 2 present pooled prevalence of the human noroviruses in natural waters as 31.7% (95%CI: 25.1–38.5) with an I^2 of 98% revealing substantial heterogeneity between studies. However, the study-specific prevalence of human norovirus ranged from 0% (95%CI: 0–20.4) – 100% (95%CI: 88.8–100.0). Attempts to identify influential study or studies returned lack of influential study among the studies (Figure S1).

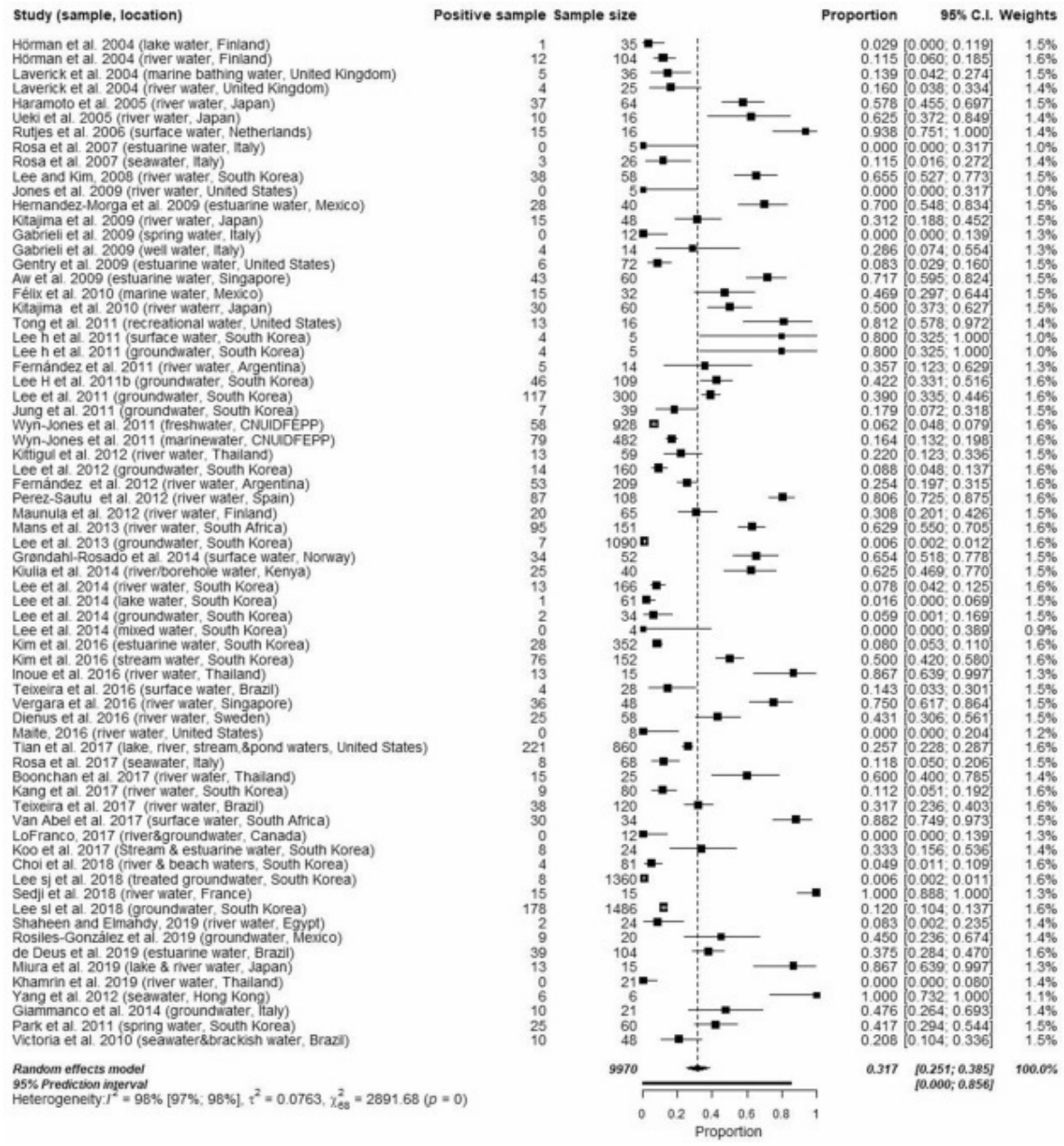

Fig. 2. Global pooled prevalence of human noroviruses in natural water sources.

The funnel plot for pooled prevalence of the HNoV in natural waters in Fig. 3 revealed dissociation (lack of precision) between estimate of effect size and its standard error as well as presence of publication bias; the Egger's regression test shows significant funnel plot asymmetry (z = 2.4558, p = 0.0141).

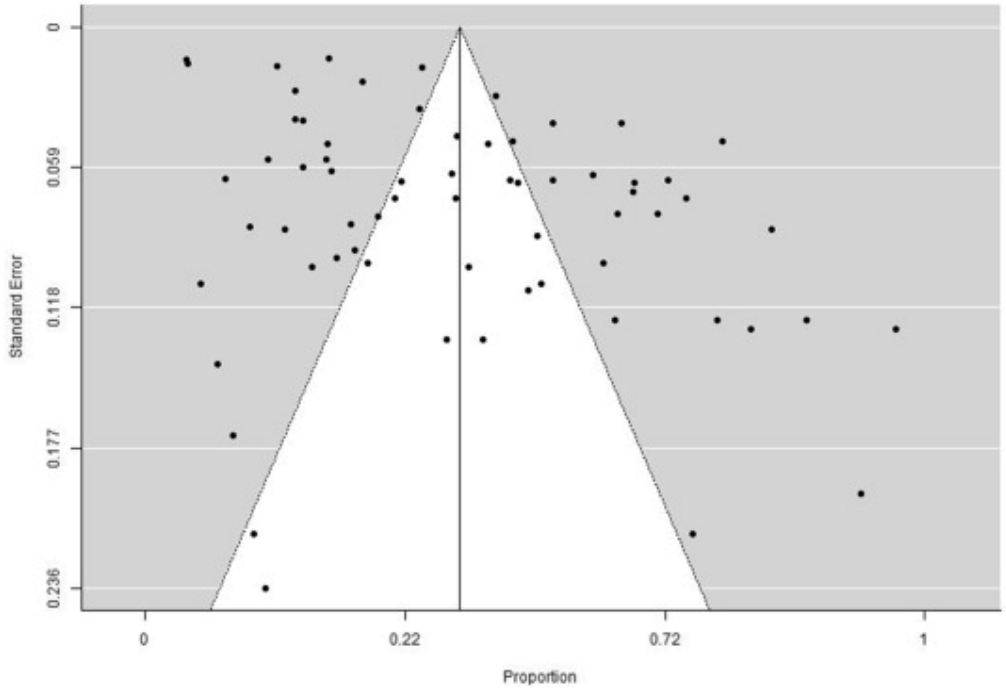

Fig. 3. Funnel plots for pooled prevalence of human noroviruses in natural water sources revealed dissociation (lack of precision) between estimate of effect size and its standard error. The Egger's Regression Test showed that the funnel plot was significantly asymmetry (z = 2.4558, p = 0.0141).

Figure S2 (Table 2) shows the pooled prevalence of HNoVs stratified by water source types. River water had highest pooled prevalence of the norovirus with 43.5% (95%CI: 33.9–53.4), followed by seawater with estuarine water with 30.6% (95%CI: 12.5–52.2), composite water with 27.9% (95%CI: 13.5–44.9), marine water with 25.9% (95%CI: 10.0–45.6), groundwater with 19.7% (95%CI: 9.3–32.3) and lake water with 2.2% (95%CI: 0–25.8).

Sub-group meta-analysis of HNoV prevalence in water sources by continent found that the pooled effect estimate of norovirus in Africa was 55.9 (95% CI: 28.2–81.9), in Asia 31.6 (95% CI: 22.3–41.6), in Europe 29.8 (95% CI: 17.9–43.2), in North America 27.7 (95% CI: 11.2–47.6) and 27.1 (95%CI: 0.09–49.4) in South America (Figure S3; Table 2).

The pooled prevalence of HNoVs in water sources stratified by GNI group was 40.6% (95%CI: 27.9–53.9) in MIC and 28.7% (95%CI: 21.7–36.1) in HIC (Figure S4; Table 2). Figure S5 (Table 2) presents the prevalence of different HNoV GI, GII. Their co-occurrence in natural waters was 16.4% (95%CI: 12.0–21.3), 20.6% (95%CI: 15.7–25.8), and 12.8% (95%CI: 6.9–20.6) respectively.

Table 2. Summary of subgroup meta-analyses of human norovirus contamination in water sources.

Subgroup	Prevalence (95% CI)	95% PI	I^2-statistic	Q-statistic	Q-pvalue
Pooled prevalence of HNoV stratified by water sources (Figure S2)					
Marine	25.9% (10.0%, 45.6%)	0.0–90.7%	85%(70%, 92%)	$^{2}_{6}= 39.28$	<0.0001
Lake	2.2% (0%, 25.5%)	–	0%	$^{2}_{1}= 0.21$	0
River	43.5% (33.9%, 53.4%)	2.5–91.0%	95%(94%, 96%)	$^{2}_{29}= 589.74$	<0.0001
Groundwater	19.7% (9.4%, 32.2%)	0–74.7%	98%(98%, 99%)	$^{2}_{13}= 774.45$	<0.0001
Composite	27.9% (13.5%, 44.8%)	0–86.8%	97%(95%, 98%)	$^{2}_{9}= 268.58$	<0.0001
Estuarine	30.6% (12.6%, 52.1%)	0–96.7%	97%(96%, 98%)	$^{2}_{5}= 183.79$	<0.0001
Pooled prevalence of HNoV stratified by continent (Figure S3)					
Asia	31.6% (22.3%, 41.6%)	0–86.3%	98% (98%, 98%)	$^{2}_{31}= 1629.66$	<0.0001
Europe	29.8% (17.9%, 43.6%)	0–87.0%	97% (96%, 98%)	$^{2}_{17}= 534.05$	<0.0001
North America	27.7% (11.2%, 47.6%)	0–92.7%	91% (86%, 95%)	$^{2}_{6}= 93.69$	<0.0001
Africa	55.9% (28.2%, 81.9%)	0–100%	93% (86%, 97%)	$^{2}_{3}= 45.89$	<0.0001
Pooled prevalence of HNoV stratified by gross national income grouping (Figure S4)					
HIC	28.7% (27.7%, 36.1%)	0–81.0%	97% (97%, 98%)	$^{2}_{51}= 2310.91$	0
MIC	40.6% (27.9%, 53.9%)	0.4–92.1%	92% (89%, 94%)	$^{2}_{16}= 2027.72$	<0.0001
Pooled prevalence of HNoV stratified by genogroup (Figure S5)					
GI	16.4% (12.0%, 21.3%)	0–56.8%	97% (97%, 98%)	$^{2}_{52}= 1906$	0
GII	20.6% (15.7%, 25.8%)	0–61.9%	97% (96%, 97%)	$^{2}_{52}= 1636.11$	<0.0001
GI and GII	12.8% (6.9%, 20%)	0–54.3%	96% (95%, 97%)	$^{2}_{22}= 526.19$	<0.0001

PI = prediction interval.

Table 3. Multivariate meta-regression model results on covariates in studies on norovirus prevalence in water sources.

S/n	Covariates	Coefficient (95% CI)	P value	R^2 (%)
1	**Country** (reference group: Argentina)			38.60
	Brazil	−0.04(-0.43–0.35)	0.8427	
	Canada	−0.44(-1.04–0.16)	0.1516	
	CY, NL, UK, IT, DE, FR, ES, PL, PT	−0.25(-0.69–0.20)	0.2776	
	Egypt	−0.26(-0.83–0.31)	0.37	
	Finland	−0.20(-0.61–0.22)	0.354	
	France	0.86(0.27–1.45)	0.0041**	
	Hong Kong	0.80(0.14–1.45)	0.0178*	
	Italy	−0.16(-0.55–0.22)	0.4004	
	Japan	0.27(-0.12–0.65)	0.17	
	Kenya	0.33(-0.23–0.88)	0.2481	
	Mexico	0.25(-0.17–0.67)	0.2452	
	Netherlands	0.69(0.11–1.28)	0.0207*	
	Norway	0.36(-0.19–0.91)	0.2033	
	Singapore	0.44(-0.01–0.90)	0.0552.	
	South Africa	0.47(0.02–0.92)	0.0409*	
	South Korea	−0.13(-0.47–0.22)	0.4735	
	Spain	0.53(-0.01–1.07)	0.0557.	
	Sweden	0.14(-0.41–0.69)	0.6265	
	Thailand	0.07(-0.33–0.47)	0.7371	
	United Kingdom	−0.17(-0.63–0.29)	0.4703	
	United States	−0.09(-0.49–0.30)	0.6393	
2	**Sample size**	−0.0004(-0.0005–−0.0002)	<.0001***	34.88

3	**Continent** (reference: Africa)			2.98
	Asia	–0.24(-0.53–0.06)	0.1136	
	Europe	–0.26(-0.57–0.05)	0.1023	
	North America	–0.27(-0.61–0.07)	0.1128	
	South America	–0.29(-0.65–0.07)	0.113	
	GNI (reference:HIC)			11.60
	LMIC	0.0468(-0.34–0.44)	0.8137	
	UMIC	0.13(-0.03–0.29)	0.1141	
4	**Year**	–0.002(-0.02–0.01)	0.7999	0.00
5	**Concentration** (reference: adsorption-elution)			41.80
	Adsorption-elution/ultrafiltration	0.08 (–0.28–0.44)	0.6645	
	Filtration/ultrafiltration	0.37 (0.18–0.55)	<.0001***	
	glass wool method	0.59(0.32–0.85)	<.0001***	
	QIAamp viral RNA mini kit	0.04(-0.33–0.37)	0.6004	
6	**Detection** (reference: ddPCR)			9.27
	nRT-PCR	–0.88(-1.49—0.27)	0.0050**	0.0050**
	nRT-PCR	–0.78(-1.56—0.01)	0.0479*	
	qRT-PCR	–0.81(-1.42—0.21)	0.0086**	
	RT-PCR	–0.85(-1.43—0.28)	0.0038**	0.0038**
	snPCR	–0.96(-1.75—0.18)	0.0160*	
	Multivariate metaregression	Test of coefficients		
7	~year + sample size + detection method	$QM_{(df=7)} = 25.74$	0.0006	32.49
8	~year + sample size	$QM_{(df=2)} = 16.04$	0.0003	33.62
9	~sample size + detection method	$QM_{(df=10)} = 28.04$	<.0001	28.88
10	~detection method + concentration method	$QM_{(df=24)} = 68.49$	<.0001	35.03
11	~sample size + country	$QM_{(df=22)} = 101.64$	<.0001	48.35
12	~sample size + detection method + concentration method	$QM_{(df=11)} = 53.55$	<.0001	40.87

***; **; * implies significant at $p \leq 0.001$, ≤ 0.01 and ≤ 0.05 respectively.

Regardless of sub-group meta-analyses performed on HNoV prevalence in natural water sources, significant presence of heterogeneity still existed in the result across the studies. The results of mixed-effects meta-regression models conducted thereafter to further assess sources of heterogeneity showed that most of the included variables significantly associated with the presence of heterogeneity across studies on HNoV prevalence in natural waters (Table 3). The amount of heterogeneity explained by the variables ranges from 2.98% to 42.6%. Specifically, the results showed that detection method, continent, GNI group, water resource type, sample size, country, and concentration method were significant sources of heterogeneity and in addition, accounted for 9.27%, 2.98%, 11.6%, 18.6%, 34.9%, 38.6%, and 41.8% of the true heterogeneity respectively, in the studies. Also, multivariate meta-regression of combination of some variables such as year + sample size + detection method, year + sample size, sample size + detection method, detection method + concentration method, sample size + detection method + concentration method, and sample size + country jointly accounted for 32.49%, 33.62%, 42.81%, 35.03%, 40.87%, and 48.35% of the true heterogeneity respectively, in the studies. Generally, sample size + country accounted for the highest amount of the true heterogeneity.

4. Discussion

Natural waters are the main sources of drinking water for the majority of the world populace and have been a major vehicle for the transmission of many waterborne pathogens including viral pathogens such as HNoV. The HNoV has been identified as a common cause of acute gastroenteritis and responsible for a considerable amount of mortality and morbidity globally (Qi et al., 2018). The prevalence of this virus in the aquatic milieu is influenced by human activities which therefore necessitates the need for regular monitoring of water sources and ardent management against sewage pollution (Kim et al., 2016). HNoV is the dominating aetiological agent of contagious viral gastroenteritis, sporadic and acute outbreaks across all ages with more than 200 000 deaths/year among c. a 700 million infections/year worldwide (Bartsch et al., 2016; Todd and Tripp, 2020). Therefore, we conducted a SR/MA of the prevalence of HNoVs in water sources.

The findings of this SR/MA indicated that the majority of reports on water source-based prevalence of HNoVs were from high income countries (HICs) in regions like Asia, Europe, North America and South America; while the least number of reports were from Africa (Table S1). A possible reason for the observed reports from HICs and MICs is that more HNoV tests in water sources might be conducted in HICs and thus more HNoV cases were reported in HICs. HNoV is not regularly monitored by water quality monitoring programs. HNoV contamination in water sources would not be reported in general if HNoV infections were not reported. Also, there might be no official HNoV surveillance systems or reporting mechanisms for HNoV contamination in water sources in many low income countries. There is an established HNoV surveillance systems in HICs compared to the lower income regions (Mans et al., 2016).

We found from country perspectives, that water source-based HNoV prevalence studies were only reported from South Korea, Japan, United States, Italy, Brazil, Thailand, Mexico, Argentina, Finland, Singapore, South Africa, Canada, Egypt, France, Hong Kong, Kenya, Netherlands, Norway, Spain, Sweden, United Kingdom, Cyprus, Germany, Poland and

Portugal. This might be due to different water resources management laws or regulations in different countries.

This study indicated that the majority of the studies were done on river water followed by groundwater, estuarine water, marine water, and lake water (Table S2). This is because rivers and groundwater are the commonest freshwater sources targeted for municipal and industrial purposes and in most cases, required less treatment complexity and resources compared to others that contain high concentrations of inorganic salts and compounds; and mostly used for recreational purposes. Also, most reported marine water sources contaminated with HNoV were associated with or motivated by contaminated seafood that are generally harvested from estuaries and coastal waters receiving sewage-contaminated river waters (Campos et al., 2015). Thus marine and river waters may play important role as reservoirs and vehicle for the dissemination of HNoVs (Boonchan et al., 2017).

The study found a high pooled water source-based prevalence (31.7%) of HNoV. Previous meta-analysis of HNoV in gastroenteritis report pooled prevalence of 15–18% (Ahmed et al., 2014; O'Ryan Gallardo et al., 2017; Phan et al., 2017), and pooled asymptomatic norovirus prevalence of 7% (Qi et al., 2018). The higher pooled prevalence of water source-based HNoV could suggests possible roles of natural waters in promoting asymptomatic and symptomatic norovirus infection via direct contact or drinking of untreated natural waters. Further, lack of access to safe water supply (World Health Organization and UNICEF, 2012) might promote HNoV infections through the route of natural waters.

We found evidence of publication bias in the studies on water source-based prevalence of HNoVs (Fig. 3). This bias is most probably caused by government policies of individual countries on water resources management.

Of the water sources studied, findings indicated that the pooled prevalence of HNoVs in the water sources followed the order of river water (43.5%), estuarine water (30.6%), composite water (27.9%), marine water (25.9%), groundwater (19.7%) and lake water (2.2%). These aquatic environments are majorly public resources which are open to diverse pollution sources, therefore becoming reservoirs for bacterial and enteric viral pathogens (Kiulia et al., 2010; Oliveira et al., 2011). The recorded high prevalence of HNoV in river and estuarine waters is probably due to sewage pollution or undertreated wastewaters. Most reports on water sources contaminated with HNoVs are usually motivated and associated with aquatic foods contaminated with HNoV that are generally harvested from estuaries and coastal waters receiving sewage-contaminated river waters. Sources of public water resources' contaminations with HNoVs include sewage effluents and agricultural runoffs (Gagliardi and Karns, 2000; Walters et al., 2011; Gorski et al., 2011; Jay et al., 2007; Kirk et al., 2002). The findings further suggest that prevalence of HNoVs in open aquatic environments (river, sea, estuaries and marines) were higher compared to the groundwater. Groundwater is a closed system that is less open to direct sewage pollution like non-groundwater water sources. Noteworthy, the observed differences in the water source-based HNoV prevalence might be dependent on local laws or regulations of individual countries on water resources management and water quality monitoring programs. Poor surveillance of HNoV in natural water in most parts of the world culminate into gross underestimation of HNoV in different natural water sources.

The findings from this study indicated that the highest pooled effect estimate of HNoVs was recorded in Africa at an estimate of 55.9%, followed by Asia at an estimate of 31.6% (Figure

S3; Table 2). The observed high prevalence of HNoV in Africa is because of few available records with high incidence of HNoV. It might be serving as pointer to the general trends of HNoV occurrence in African water sources but more studies are needed to validate this view.

Although HNoV has been shown to be the leading cause of acute gastroenteritis in children in the USA (Payne et al., 2013), the impact of diarrhoeal diseases caused by HNoVs are felt more in Africa and in Asia. This is linked to poor sanitation, poor hygiene practices and contaminated water supplies/water sources that are being used by community members (Boschi-Pinto et al., 2008). The observed water source-based prevalence of HNoV in Europe (29.8%), North America (27.7%) and South America (27.1%), suggest a good HNoV surveillance systems in water sources coupled with a substantial risk of HNoV from the natural water systems. Generally, there exist poor surveillance of HNoV in developing countries both in natural water and clinical settings, coupled with the proclivity of individuals who do not consult medical centres for mild gastroenteritis caused by HNoV leading to overall underestimation of its prevalence (Phan et al., 2017).

The prevalence of HNoVs in water sources was found to be higher in MIC (40.6%) than HIC (28.7%) (Figure S4). This could be linked to poor sanitation and poor sewage/water sources management, as well as policies/implementation (when they exist) in low resource countries in contrast to high income nations as aforementioned. Basically, the poor the sewage treatment, the higher risk of HNoV contamination in water sources. On average, 70%, 38%, 28% and 8% of sewage generated in HICs, upper MICs and lower MICs respectively, undergoes treatment (https://reliefweb.int/report/world/2017-un-world-water-development-report-wastewater-untapped-resource).

The patterns of the HNoV GI (16.4%) and HNoV GII (20.6%) prevalence in water sources found in this study mirrors their reports in surface waters (Lodder and Husman, 2004; La Rosa et al., 2007; Fernández et al., 2011; Fernández et al., 2012; Pérez-Sautu et al., 2012) and human gastroenteritis (Phan et al., 2017; O'Ryan Gallardo et al., 2017; Haddadin et al., 2020) in many previous studies. Higher prevalence of HNoV infections is commonly associated with GII genogroup Kabue et al., (2016); (Phan et al., 2017; O'Ryan Gallardo et al., 2017; Haddadin et al., 2020). However, a discordant of GII dominance over GI have been reported in groundwater (Jung et al., 2011), surface water (Ricardo et al. 2014), and estuarine beaches (de Deus et al., 2019). This study also found the prevalence of GI and GII co-occurrence in natural waters as 12.8%. Co-circulation of GI and GII might have implications for future outbreaks of HNoV infections and evolution of new genotypes/genogroups.

Another important finding from this SR/MA was the appreciable contributions of the studied covariates (GNI group, water resource type, sample size, country, concentration method and detection method) on the variation in HNoV prevalence in water sources. The amount of variations explained by the covariates ranges from 2.98% to 42.6%. Specifically, the results showed that continent, GNI group, water resource type, sample size, country, concentration method and detection method, were significant sources of variations in the HNoV prevalence in water sources in the studies. This supports the fundamental differences in the study settings (water resource type/country/continent) in terms of climate and socio-economic frameworks (country/GNI group i.e., MIC/HIC), local laws related to water resources management/water quality monitoring programs, concentration methods and detection method adopted across the included studies. Previous studies have shown that the performance/effectiveness of any viral concentration, DNA/RNA extraction and detection technique, varies crucially with the sample type, sample matrix characteristics as well as the targeted virus type (DNA/RNA

virus, enveloped or non-enveloped virus, etc.) (Hennechart-Collette et al., 2015; Haramoto et al., 2018).

Additionally, the execution of viral concentration protocols with/without pre-treatment and sample volume concentrated have been shown to affect the resultant efficacy/performance (Ahmed et al., 2020). The larger the volume of a sample concentrated by the ultracentrifugation/adsorption-extraction method, the resultant increase in the PCR inhibitors with viral particles and the decrease in the efficiency/performance of RNA/DNA extraction and PCR-based detection techniques (Haramoto et al., 2018; Ahmed et al., 2020). Further, the designs of centrifugal device promote variations in the efficiencies of ultracentrifugation methods' performances in viral recovery (Ahmed et al., 2020).

Limitations of the study

The limitations of this study consisted in the exclusion of articles written in the non-English Language aspect which may have limited and affected the study's findings. Additionally, the limited number of databases consulted for retrieval of the included studies might led to the loss of some few relevant articles hosted in other databases. The various shortcomings of the original included studies could also influence the interpretations of the findings of this study. The lack of sufficient information on seasonal prevalence of the HNoV such as clearly defined seasons and season-specific total number of samples collected in most of the included studies prevented meta-analysis for seasonal prevalence of HNoV known to affect HNoV distribution in water sources. Finally, the interpretation of the findings might be influenced by local laws or regulations of individual countries on water resources management and water quality monitoring programs.

5. Conclusion

This study found a high pooled prevalence of HNoV in water sources, with higher preponderance in Africa than other continents and in MICs compared to HICs. Further, the prevalence of HNoV in water sources mirrors the pattern of HNoV gastroenteritis and GII genogroup dominance globally. The study found lack of water sources-based studies on the prevalence of HNoV in lake water as well as substantial lack of studies on HNoV contaminatins in water sources in Africa. The study recommends that public health efforts against waterborne diseases should prioritize water resource/sewage management options and policies towards ardent pollution prevention. It recommends national surveillance of HNoV in sewage/water sources and associated contributions to HNoV infections as appropriate preventive models for potential outbreaks and a general campaign that could promote behavioural changes for protecting natural watersheds from pollution.

Author contributions

Conceptualization: ETC conceived and designed the research protocol. ETC and IBE conducted the literature review and data extraction. Formal analysis: ETC performed the data analysis tasks, led the interpretation and drafting of the manuscript. Data quality control and validation: ETC, IBE and OYD conducted the data quality control and validation. Writing - review & editing: ETC, IBE, ICD, OYD and OOO performed the data interpretation and manuscript preparation and language editing. All the authors (ETC, IBE, ICD, OYD and OOO) were involved in writing the original draft and reviewing, revising and editing the manuscript. All authors read and approved the final submission.

Data availability statement

All data and codes are available upon request from the corresponding author.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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