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Geographical distribution of enteric pathogenic viruses in Burkina Faso: a systematic review and meta-analysis

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Abstract

Background Viruses, which are transmitted mainly via the digestive tract, are responsible for the high morbidity and mortality of diseases, particularly in low-income countries. Although several studies have established the prevalence and characterization of various enteric viruses in Burkina Faso, to date, no aggregate data have been released.

Objective Our objective was to describe the available data on the prevalence and circulating genotypes of enteric pathogen viruses responsible for human infections in Burkina Faso by carrying out a systematic review and meta-analysis.

Methods Potentially relevant studies were identified by a search of PubMed, ScienceDirect, Google Scholar, university libraries and by a manual search of the reference lists of identified studies. The search with no restrictions on language or age was limited to studies conducted only in Burkina. Study selection, data extraction, and methodological quality of the included studies were performed independently by two investigators. Heterogeneity between studies was assessed using the Cochrane Q test and I2 test statistics based on the random effects model. Comprehensive meta-analysis (CMA 3.7) was employed to compute the pooled prevalence of pathogens identified in the studies.

Results Forty-three (43) studies reporting 4,214 diagnosed cases in all aged human populations were selected. Overall, 72.6% of the pathogens diagnosed were gastroenteritis, and 27.2% were entero-transmissible hepatitis viruses. Rotavirus was the most common cause of human viral gastroenteritis, accounting for 27.7% (95% CI: 20.9 - 35.8) of the cases, followed by norovirus (16% (95% CI: 12.25 - 20.6)) and sapovirus (11.2% (95% CI: 6.2 - 19.4)). In terms of human entero-transmissible infections, hepatitis A virus (HAV) was the most prevalent (52% [95% CI: 14.2–87.7] of total antibodies), followed by hepatitis E virus (HEV) (28.3% [95% CI: 17.7–42]).

Conclusions This study highlights the substantial burden of viral enteric infections and highlights the need for more molecular epidemiological studies to improve preventive measures against these viruses.

Keywords Gastroenteric viruses, Enteric hepatitis viruses, Systematic review and meta-analysis, Burkina Faso

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Introduction

Enteric diseases caused by infectious agents represent a major burden among all infectious diseases. They cause approximately 1.7 million deaths and 4.5 billion episodes per year worldwide, making them a major global public health problem [1]. In developing countries, the endemicity of these infections is associated with poor hygiene, particularly inadequate supplies of drinking water, nutrition, ignorance of transmission mode, socioeconomic level and lack of adequate sanitation. It is estimated that 50-70% of enteric infections are viral in origin [2]. They are transmitted to humans mainly via the feco-oral route, by direct person-to-person contact or by ingestion of contaminated water or undercooked food, particularly shellfish, fruit and vegetables [3]. The main diseases associated with enteric viruses are acute gastroenteritis and hepatitis. However, some of these viruses can cause other diseases, such as poliomyelitis, and in some cases, these diseases could even lead to certain types of cancers.

In Africa, the human health hazard posed by enteric viruses is particularly serious, where rapid urbanization in a relatively short period of time has led to the expansion of informal settlements with poor sanitation and failing or non-existent wastewater treatment infrastructure and where rural communities with limited or no access to municipal water are dependent on nearby open water sources for subsistence[4]. These difficulties are compounded by major epidemics due to enteric viruses [5–8], which cause many deaths [9].

In Burkina Faso, populations are exposed to these viruses due to poor hygienic conditions. Indeed, several prevalence and characterization studies have been carried out on these feco-oral viruses. These studies focused on the prevalence ranging from 14% to 64.54%, and a variety of viruses responsible for gastroenteritis in pediatric patients with seasonal peaks were observed [10, 11], with prevalences reaching 63.3% of cases [12] during the coldest months of the year in Burkina Faso. High genetic variability resulting in cocirculation of gastroenteritis virus strains such as rotavirus in the burkinabe population has also been reported [13]. However, the introduction of *RotaTeq*® a pentavalent rotavirus vaccine in children in 2013 led to a decrease in the rate of hospitalizations, particularly in infants, and in the efficacy of the vaccine in older children [14, 15]. On the other hand, other studies focused on the epidemiology of enterotransmissible hepatitis virus and indicated a silent circulation of these viruses in the asymptomatic population at low but significant levels [16–18].

The aim of this study was to establish a state-of-the-art study on feco-orally transmitted viruses that are mainly responsible for enteric infections circulating in Burkina Faso, with data on the prevalence, age group, gender, geographical settings, diagnostics methods, incidence and species, and genotypes, to guide both decision-makers and future research.

Methods

Study design

A systematic review and meta-analysis were conducted to document the epidemiology of feco-oral viruses infecting and causing human infections in Burkina Faso. This study was performed according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines [19].

Databases and search strategy

PubMed, ScienceDirect, Research Gate and Google Scholar were searched for original studies written in English or French that included studies on enteric viruses responsible for human infections in Burkina Faso. To include unpublished studies, university libraries were searched, and reference lists of eligible studies were screened to maximize the inclusion of relevant studies. The following terms with MeSH (Medical Subject Headings) and Boolean operators were used to search PubMed, Google Scholar and Science Direct: Gastroenteritis OR Enteric viruses OR Rotavirus OR Norovirus OR Astrovirus OR Adenovirus OR Sapovirus OR Torovirus OR Reovirus OR Enterovirus OR Hepatitis A OR Hepatitis E and Burkina Faso. This search strategy used for each database is included in Supplementary Table S1. The search was performed independently by each reviewer to minimize bias and missing studies. The search results were combined into an EndNote X9 file (Clarivate Analytics, USA), and duplicates were removed. All articles published up to March 2022 were included in the review if they fulfilled the eligibility criteria.

Study eligibility criteria

All available studies and data were incorporated based on the predefined eligibility criteria and were derived from the following research question: "What is the etiology and burden of fecal peril-associated infections, and what factors may influence them?" Studies conducted in Burkina, published articles, cross-sectional studies, and reported articles with sample sizes ≥50 were used as inclusion criteria. The population of interest was all persons residing in Burkina Faso (regardless of age or sex), animals and the environment. The primary outcome of interest was the number of laboratory-confirmed infections (positive serology or molecular characterization). Studies containing mixed populations were included unless they did not clearly and explicitly report the prevalence for each group. The exclusion criteria were articles

with duplicate or overlapping data and articles without full text available.

The eligibility criteria

This review included primary studies reporting seroprevalence data for feco-oral viruses responsible for human infections. Eligibility criteria were derived from the following research question: "What is the etiology and burden of infections associated with fecal peril, and what factors may influence them?". We considered observational studies (cross-sectional and cohort) with sample sizes ≥50. In the event of duplicate publications, the most complete study was retained. The population of interest was all people residing in Burkina Faso (regardless of age and sex), animals and the environment. The primary outcome sought was the number of laboratory-confirmed infections (positive serology or molecular characterization). Studies containing mixed populations were included unless they did not clearly and explicitly report the prevalence for each group. Articles were further excluded if quantitative data were absent, could not be extracted, or lacked an explicit description of the methods employed.

Data extraction

Data were extracted from full-text articles and were reviewed by two independent authors after their titles and abstracts had been screened for relevance. During the screening process, an additional author was appointed to resolve any discrepancies that may arise with study selection. The following data were extracted from a customized Microsoft Excel spreadsheet under multiple headings from each study: authors' names, year of publication, study period, locality, infected population, sample size, number of confirmed cases, proportion of infections, detection method used, prevalence, diagnostic test used, virus types, serotypes, genogroups, genotypes and virus variants.

Assessment of study quality

Two authors independently assessed the risk of bias for each original study. The quality of the studies was evaluated using an adaptation of a critical appraisal tool specifically designed for prevalence studies by the Joanna Briggs Institute (JBI) [20] and on criteria relevant to the designs of studies included in the systematic review to assess study quality/risk of bias in individual studies. The checklist included nine main criteria (representativeness and sample size, response rate and participant recruitment, data analysis, testing method and other sources of bias) that could be answered 'yes', 'no' or 'cannot tell/not applicable'. Each study was given an overall quality assessment score based on answers to the nine questions; 9 points were assigned if all nine responses were positive. Overall study quality was categorized as 'high' (scores ≥8 points), 'moderate' (scores >5 to <8 points) or 'low' (scores ≤5 points).

Data processing and analysis

Studies providing data on the crude prevalence of viral pathogens associated with fecal peril infections or numbers of cases and study participants were included in the meta-analysis. The virus prevalence for individual studies was determined by multiplying the ratio of cases to sample size by 100. The estimation of the pooled prevalence and summary odds ratios of enteric viral pathogen infection was performed using Comprehensive Meta-Analysis (CMA) 3.0 software, which is based on a random-effects meta-regression model that takes into account variation between studies. The estimated pooled prevalence with a 95% confidence interval according to the forest plot and publication bias according to the funnel plot are presented. Subgroup analysis was performed based on publication year, laboratory tests used (types and numbers) and study period. Heterogeneity among reported prevalences was assessed by computing p values from the Cochrane Q test and I2 statistics [21]. The Cochrane Q test was used to evaluate the existence of heterogeneity, and $p < 0.05$ was considered to indicate statistical significance [22]. The I2 statistics provide an estimate of the percentage of the variability in effect estimates that is due to heterogeneity rather than sampling error or chance differences. I2 values of 25–50%, 51–75%, and > 75% were considered to represent low, medium and high heterogeneity, respectively [23]. Low I2 values suggest that variability between estimates is consistent with random variation. Interstudy heterogeneity was considered significant if the P value of Cochran's Q test was less than 0.05.

Publication *bias* and sensitivity analysis

Funnel plots were drawn to assess the possibility of publication bias. We plotted the studies' logit event rate and the standard error to detect asymmetry in the distribution. A gap in the funnel plot indicates the potential for publication bias. In addition, Begg's adjusted rank Correlation and Egger's regression asymmetry tests were used to assess publication bias, with p-value < 0.05 considered to indicate potential publication bias [24].

Results

Published data

The distribution of the 143 articles found in our initial research was as follows: 114 publications came from Google Scholar, PubMed, Science Direct and Research Gate, and 29 from other sources. Of the 143 citations initially identified, 58 (40.55%) were retained after removing

duplicates. Examination of the titles and abstracts revealed that 56 (39.16%) citations were retained for full-text evaluation. At the end of this final stage, 48 (33.56%) articles were retained for analysis. The reasons for exclusion are detailed in Fig. 1. This number breaks down into 27 (56.25%) eligible studies, 6 (12.5%) studies resulting from reference mining and 15 (31.25%) from the literature searches at university libraries.

Descriptive characteristics of the included studies

The included studies were conducted between 1983 and 2020, of which 31 were published and 15 were unpublished. Thirty-four studies were conducted in Ouagadougou; two in Bobo-Dioulasso; two in Bobo and Ouagadougou; one in the northern, central and southern regions; one in the Sahelian region;; one in Nanoro; one in Boromo and Gourcy; one in Kadiogo, Gourma and Houet; one in Garango and Satiri; one in Ouagadougou and Gaoua; and one in Ouagadougou, Fada N'Gourma, Koudougou, Pô and Ziniaré (Fig. 2).

Thirty-one studies (31) involved children, and more specifically, children aged 0 to 5 years (26), while the remaining studies (15) involved pregnant women (4), animals (3), adults and children (3), patients with acute febrile jaundice (1), blood donors and pregnant women (1), blood donors (1), blood donors and butchers (1), and the environment (1) (Fig. 3).

The majority of the studies received a high-quality assessment (36/46). Ten studies received a "moderate" or "low" assessment score because of inadequate response rate and the lack of sample data and/or the subjects and study setting, in addition to the lack of representativeness of some study populations. A detailed description of the study characteristics is presented in Table 1. A total of 4214 cases of human viral enteric infections were recorded in all 42 studies reviewed. Viral gastroenteritis accounted for 72.59% of the patients whose infection

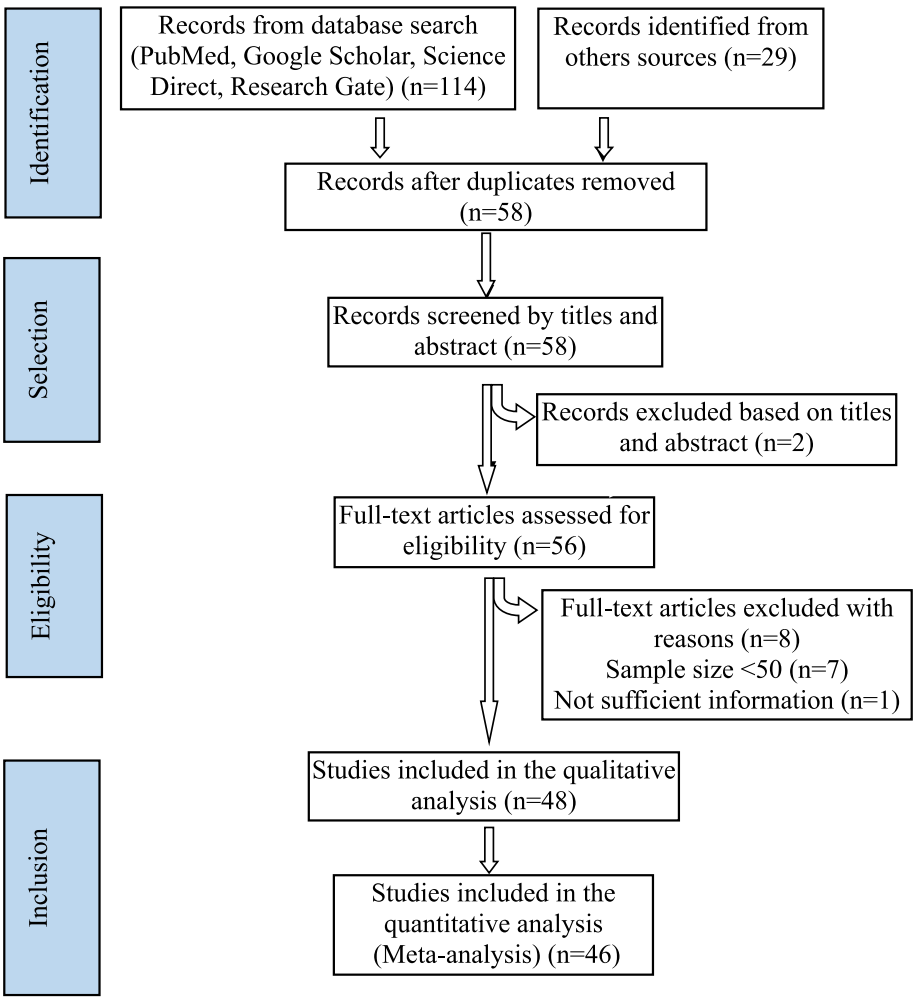

Fig. 1 Flow chart of study selection and criteria

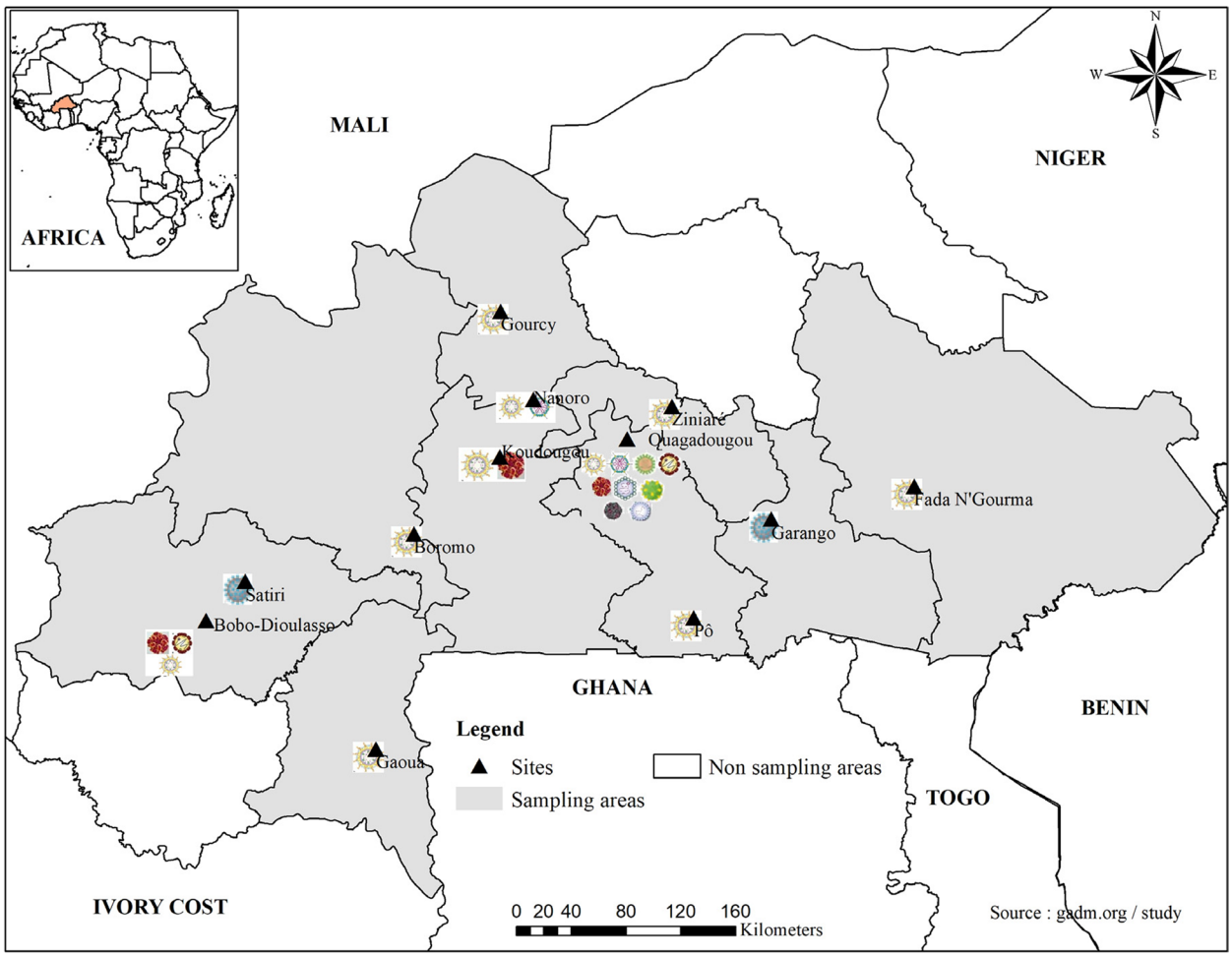

Fig. 2 Map of Burkina Faso showing the study area. Legend: RV: Rotavirus; NoV: Norovirus; AdV: Adenovirus; SaV: Sapovirus; AstV: Astrovirus; PoV: Poliovirus; PaV: Parvovirus; HAV: Hepatitis A virus; HEV: Hepatitis E virus; AiV: Aichi virus

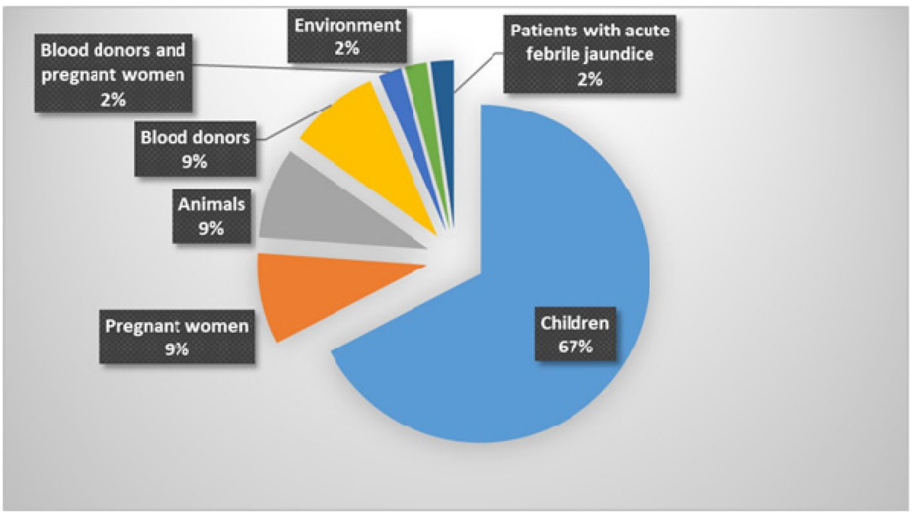

Fig. 3 Cheese diagram showing study shares

Table 1 Descriptive characteristics of the included studies

Author, year	Study period	Locality	Study subjects	Lab test used	Sample size	diagnosis cases	Virus	Quality score
(Steele *et al.* 2010) [9]	1999	Bobo – Ouaga	Children 0 to 5 years	ELISA RT- PCR	166	37	RV	4 (Low)
(Kaboré et al. 2017) [25]	2013 - 2014	Ouagadougou	Children 0 to 5 years	ICG	332	213	RV	9 (High)
(Matussek *et al.* 2015) [26]	2009-2010	Ouagadougou	Children 0 to 5 years	RT–PCR	309	56	SaV	6 (Moderate)
(Dimeglio *et al.* 2019) [27]	2013-2016	Burkina Faso	Patients with acute febrile jaundice	RT–PCR	900	187	HEV	7 (Moderate)
(Baudon, 1986) [28]	1983- 1984	Bobo-Dioulasso	adults and children	ELISA	635	93	RV	9 (High)
(Kouéta *et al.* 2014) [29]	2009	Ouagadougou	Children 0 to 5 years	ICG	103	34	RV, AdV	9 (High)
(Bonkoungou *et al.* 2010b) [10]	2008- 2010	Ouagadougou	Children 0 to 5 years	ICG	447	157	RV, Adv	9 (High)
(Bonkoungou *et al.* 2013) [30]	2009-2010	Ouagadougou	Children 0 to 5 years	ICG	283	96	RV, AdV	9 (High)
(Bonkoungou *et al.* 2018) [14]	2012 - 2013	Ouagadougou	Children 0 to 5 years	EIA -RT–PCR	154	93	RV, NoV	9 (High)
(Nordgren, *et al.* 2012) [31]	2010	Boromo-Gourcy	Children 0 to 5 years	ICG	80	56	RV	8 (High)
(Nordgren *et al.* 2013) [32]	2009-2010	Ouagadougou	Children with diarrhea	RT–PCR	309	37	NoV	8 (High)
(Simpore *et al.* 2009) [33]	2006 -2008	Ouagadougou	Children	PCR	648	149	RV, AdV	8 (High)
(Kafando *et al.* 2016) [34]	2014	Ouagadougou	Pregnant women	ELISA	179	19	HEV	9 (High)
(Traoré *et al.* 2012) [16]	2010-2012	Ouagadougou	Blood donors - Pregnant women	ICG- ELISA	369	97	HEV, HAV	8 (High)
(Traoré *et al.* 2016) [35]	2014	Ouagadougou	Blood donors	ELISA	1 497	597	HEV	9 (High)
(Nitiema *et al.* 2011) [11]	2009-2010	Ouagadougou	Children 0 to 5 years	ELISA	309	100	RV	9 (High)
(Ouedraogo *et al.* 2017) [12]	2011- 2012	Ouagadougou	adults and children	PCR	170	114	RV, NoV, SaV, AstV ,AdV, AiV	9 (High)
(Ouedraogo *et al*, 2016) [13]	2011 - 2012	Ouagadougou	Children 0 to 5 years	PCR	263	225	Rv, NoV, SaV, AstV ,AdV, AiV	7 (Moderate)
(Ouermi *et al.* 2007) [36]	2006	Ouagadougou	HIV (-) and HIV (+) children 0 to 5 years	ICG	66	16	RV, AdV	9 (High)
(Lompo *et al.* 2021) [37]	2012 - 2014	Nanoro	Children 0 to 5 years	ICG	191	35	RV, AdV	9 (High)
(Huynen *et al.* 2013) [38]	2011	Bobo-Dioulasso	Children	RT–PCR	418	93	NoV	7 (Moderate)
(Somda *et al.* 2019) [17]	2017	Ouagadougou	Pregnant women 16 to 49 years	ICG-ELISA	180	41	HAV	9 (High)
(Somda *et al.* 2019) [18]	2017	Ouagadougou	Pregnant women 16 to 49 years	ELISA	90	50	HEV	9 (High)
(Rönnelid, 2020) [15]	2015	Ouagadougou	Children 0 to 5 years	RT–PCR	146	49	Rv, NoV	9 (High)
(Gamsonré *et al.* 2019) [39]	2009 - 2010	Ouagadougou	Children 0 to 5 years	RT–PCR	213	31	AstV	9 (High)

Table 1 (continued)

Author, year	Study period	Locality	Study subjects	Lab test used	Sample size	diagnosis cases	Virus	Quality score
(Ouédraogo *et al.* 2016) [40]	2009-2015	Ouagadougou	Various animal species	ICG ELISA RT–PCR	756	132	RV, AdV	9 (High)
(Ouoba *et al.* 2019a) [41]	2015	Burkina	Dromedaries	ELISA	133	11	HEV	9 (High)
(Ouoba *et al.* 2019b) [42]	2015-2017	Kadiogo, N'Gourma, Houet,	Pets and hunting hares	ELISA	347	121	HEV	9 (High)
(Traoré *et al.* 2015) [43]	2012-2013	Ouagadougou	Pork, Blood donors Butchers	ELISA RT-PCR	447	282	HEV	9 (High)
(Phan *et al.* 2012) [44]	2008/2010	Ouagadougou	Children 0 to 5 years	PCR	98	4	PaV	6 (High)
(Tonde *et al.* 2018) [45]	2014 -2017	Ouagadougou	Children 0 to 5 years	ELISA	739	477	RV	7 (Moderate)
(Dahourou, 1998) [46]	1994-1995	Garango, Satiri	Children 0 to 5 years	PCR	123	7	PoV	7 (Moderate)
(Bonkoungou, 2007) [47]	2007	Ouagadougou	Children 0 to 5 years	ICG-PCR	150	21	RV	9 (High)
(Bambara, 2013) [48]	2003	Ouagadougou	Children	ICG	323	54	RV	6 (Moderate)
(Sama, 2017) [49]	2016 -2017	Ouagadougou-Gaoua	Children	ICG-ELISA	236	92	RV	8 (High)
(Dakouo, 2020) [50]	2019 -2020	Ouagadougou	Children 0 to 5 years	PCR	200	37	RV, AdV NoV, AstV	8 (High)
(Soubeiga, 2020) [51]	2015	Ouagadougou	Children 0 to 5 years	PCR	146	29	NoV	8 (High)
(Tiendrébéogo, 2016) [52]	2014 -2015	Ouagadougou	Children 0 to 5 years	ICG-PCR ELISA	152	21	RV	8 (High)
(Ouedraogo, 2011) [53]	2010 -2011	Ouagadougou, Fada N'Gourma, Koudougou, Pô, Ziniaré	Children 0 to 5 years	ICG	100	56	RV	9 (High)
(Traore, 2015) [43]	2013 -2014	Ouagadougou	Children 0 to 5 years	ICG	438	277	RV, AdV	9 (High)
(Fody, 2010) [54]	2010	Ouagadougou	Children 0 to 5 years	ICG	97	55	RV, AdV	6 (Moderate)
(Tahita, 2015) [55]	2004 - 2005	Ouagadougou	Children 0 to 5 years	ICG	250	113	RV	8 (High)
(Cisse, 2016) [56]	2014	Ouagadougou	adults and children	ICG	196	6	RV, AdV	8 (High)
(Setondji, 2019) [57]	2017 - 2018	Ouagadougou Bobo	Waste water	PCR	318	12	HEV	6 (Moderate)
(Somda, 2010) [58]	2009	Ouagadougou	Pregnant women	ICG	125	43	HAV	8 (High)
(Kabre, 2010) [59]	2009	Ouagadougou	Children 0 to 5 years	ICG	51	8	RV, AdV	8 (High)

Legend: *RV* Rotavirus, *NoV* Norovirus, *AdV* Adenovirus, *SaV* Sapovirus, *AstV* Astrovirus, *PoV* Poliovirus, *PaV* Parvovirus, *HAV* Hepatitis A Virus, *HEV* Hepatitis E Virus, *ICG* Immunochromatography, *EIA* Enzyme immunoassay, *PCR* Polymerase chain reaction, *ELISA* Enzyme-linked immunosorbent assay

prevalence ranged from 4.1% to 85.6%, with sample sizes ranging from 51 to 1497 participants. Rotaviruses accounted for 60.86% (28/46) of enteric virus studies (Norovirus, Adenovirus, Astrovirus, Sapovirus, Parvovirus Aichivirus, Poliovirus, Hepatitis A virus and Hepatitis E virus) in Burkina Faso.

Twenty-six studies used serological methods (enzyme-linked immunosorbent assay [ELISA] or immunochromatographic [IC]) to detect enteric viruses, fourteen studies employed only molecular methods, and six studies used molecular methods combined with serology (Table 1).

Etiology of viral gastroenteritis

A meta-analysis of the 32 studies showed that the most prevalent virus associated with gastroenteritis in Burkina was rotavirus (pooled estimates from 4.1% to 70.0%), with an overall estimated pooled prevalence of 27.7% (95% CI: 20.9 - 35.8), followed by norovirus (estimated pooled prevalence between 3.0% and 22.2%), with an overall estimated pooled prevalence of 16% (95% CI: 12.25 - 20.6), and sapovirus (pooled estimates between 6.5% and 18.1%), with an overall estimate of 11.2% (95% CI: 6.2 -19.4) (Fig. 4).

Etiology of entero-transmissible viral hepatitis

A meta-analysis of the six studies showed that the most prevalent entero-transmissible viral hepatitis was HAV (pooled estimates between 21.7% and 90.0%), with an overall estimate of 52.0% (95% CI 14.2–87.7), while HEV (pooled estimates between 10.6% and 64.7%) had an overall estimate of 28.3% (95% CI 17.8–42.6) (Fig. 5).

Prevalence of enteric viruses in animals and the environment

A meta-analysis of the five studies showed that the most prevalent type of entero-transmissible viral hepatitis was HEV (pooled estimates between 3.8% and 80.2%), with an overall estimate of 23.1% (95% CI: 4.9-63.7) (Fig. 6).

Assessment of publication *bias*

Symmetrical funnel plot visual inspection (Fig. 7) revealed the absence of publication bias, which was statistically confirmed by Egger's test (p =0.06197) and Begg's correlation (p= 0.12393). High heterogeneity was found among the included studies (I2=97.83%). The heterogeneity could partly be attributed to the large variation in sampling. Some studies investigated large samples, while others investigated small samples. Last, heterogeneity could also be attributed to the diagnostic methods used to detect enteric viral pathogens since different methods may have different sensitivities, specificities, and positive predictive and negative predictive values.

Genetic diversity of enteric viruses detected in Burkina Faso

Distribution of rotavirus strains in the Burkina Faso population

In the 27 studies included, 6925 samples were analysed for molecular characterization out of 2368 rotavirus antigen-positive samples, and 425 rotavirus strains were detected.

Among the G/P combinations, G9P [8] (28%) was the most predominant, followed by G1P [8] (14.58%), G6P [6] (14.11%), G12P [8] (9.88%), and G2P [6] (9.64%) (Fig. 8). Only the G9 genotype was detected in farm animals in Burkina Faso

Distribution of norovirus strains in the Burkina-Faso population

In the eight studies included, 1806 samples were analysed for norovirus. A total of 303 samples were positive, of which 58 (19.14%) were genogroup I (GGI) and 204 (67.32%) were genogroup II (GGII) (Fig. 9). GII.4 was the most common GII genotype (29.41%), followed by GI.3, the most common GI genotype.

Distribution of Sapovirus strains in the Burkina Faso population

Sapovirus strains catalogued from two molecular characterization studies of sapoviruses in Burkina Faso identified the following four main genogroups: GI, n=22; GII, n=14; GIV, n=3; and GV, n=2. The 18 strains in the GI genogroup were classified into three (3) distinct genotypes as follows: GI.1 (n=13); GI.2 (n=1); and GI.4 (n=4). For genogroup GII, the genotypes were GII.1 (n=4), GII.2 (n=2), GII.3 (n=1), GII.4 (n=1), and GII.6 (n=1) (Fig. 10).

Distribution of Astrovirus strains in the Burkina Faso population

In this qualitative analysis of the four studies included, five Astrovirus strains were characterized as type 1 (AstV-1), three strains as type 2 (AstV-2), one strain as type 5 (AstV-5) and three strains as type 8 (AstV-8). All type 1 astroviruses showed 78 to 91% nucleotide identity with the Oxford/Type 1 reference strain (L23513), but two type 1 astrovirus strains were strongly related to the ITA/2012/PR1365 reference strain (KF668570). Astrovirus type 2 showed 94% nucleotide identity with the Oxford/type 2 reference strain (L13745). The new astrovirus (human astrovirus-BF34) was closely related to mamastrovirus species 8 and 9.

Distribution of Aichi virus A strains in the population

The four strains of Aïchivirus A detected in two studies included were classified into genotype A (n = 1), genotype B (n = 1) and genotype C (n = 2). Aïchivirus A genotype A showed 95% nucleotide identity with the J-4397/02/Japan reference strain (EF079149), and Aïchivirus A genotype B showed 95% nucleotide identity with the 139/96 (IND)/Japan reference strain (AB092830). Finally, Aïchivirus A genotype C showed 83-97% nt (87-94% aa) identity with the sequence of the reference strain RN48/France (DQ145759).

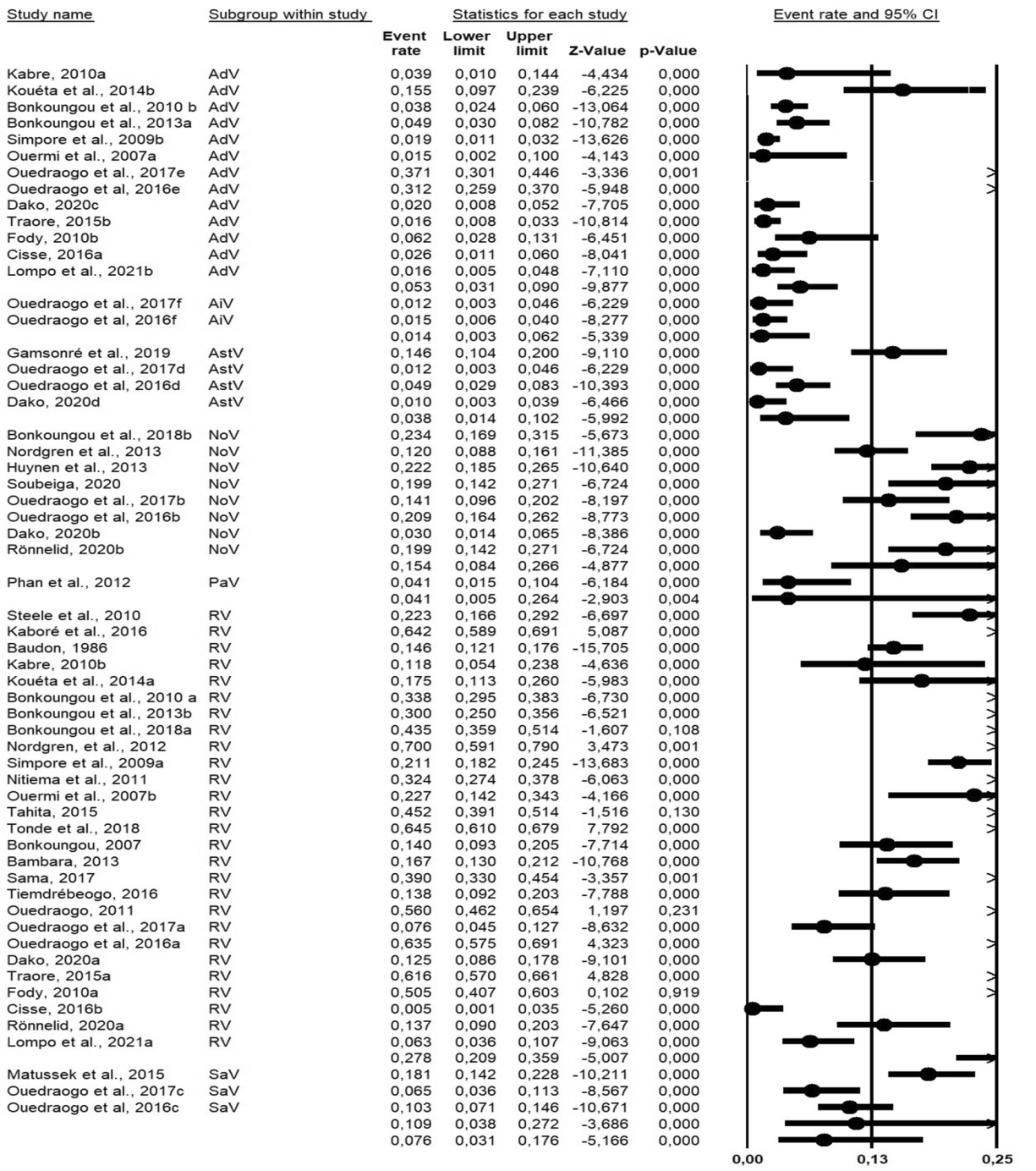

Fig. 4 Forest plot of the pooled prevalence of viral gastroenteritis in Burkina. Legend: RV: Rotavirus; NoV: Norovirus; AdV: Adenovirus; SapV: Sapovirus; AstV: Astrovirus; PaV: Parvovirus; AiV: Aichi Virus

Potential circulating hepatitis E virus (HEV) genotypes

Two of the six studies included reported potential circulating HEV genotypes. Thus, 14 HEV strains detected in patients with a febrile form of jaundice were of genotype 2 and showed a homology of 86.4-94.8% with the HEV subtype 2b recently identified in Nigeria. The HEV genotype 3

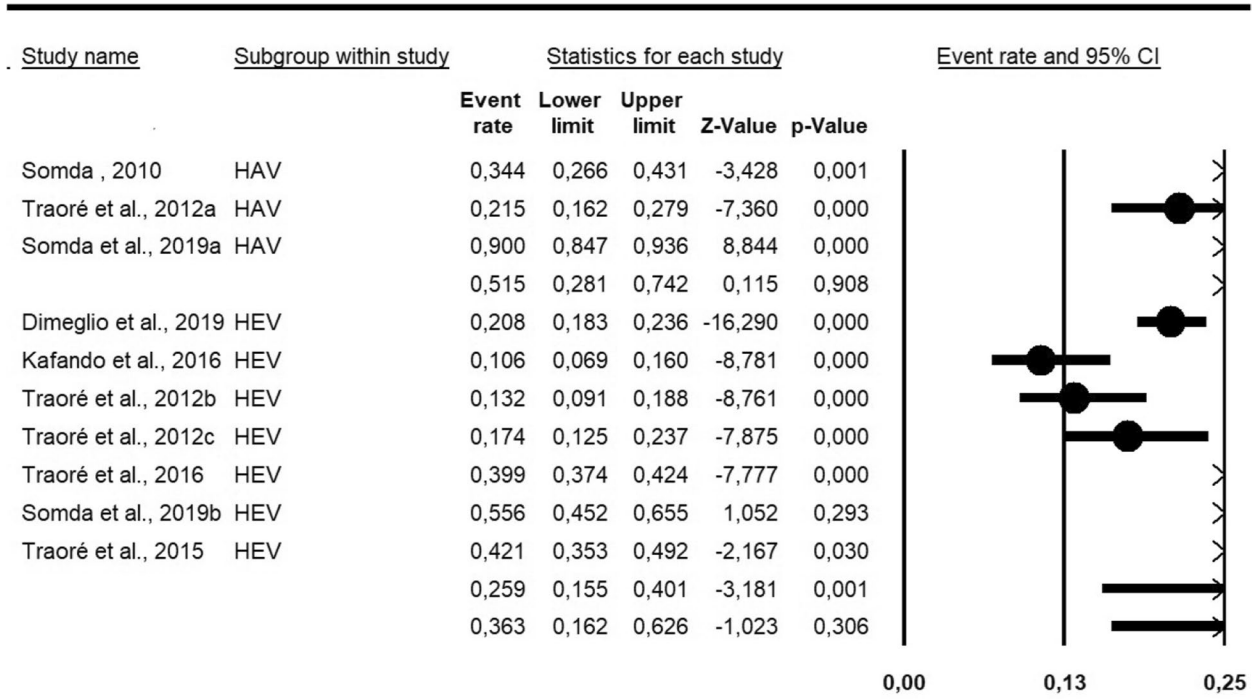

Fig. 5 Forest plot of the pooled prevalence of enterovirus-transmissible viral hepatitis. Legend: HAV: hepatitis A virus, HEV: hepatitis E virus

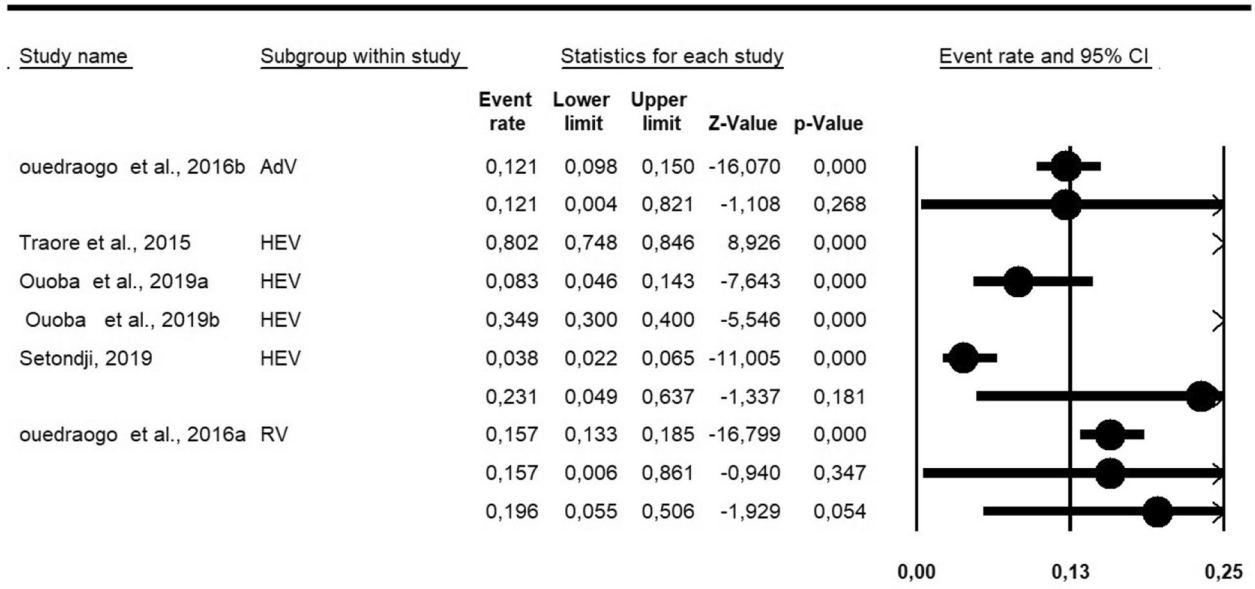

Fig. 6 Forest plot of the pooled prevalence of enteric viruses in animals and the environment. Legend: RV: Rotavirus; AdV: Adenovirus; HEV: Hepatitis E Virus

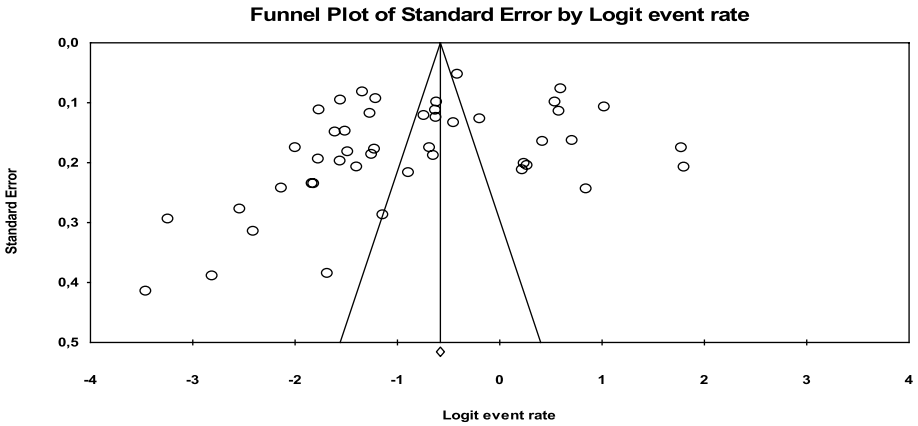

Fig. 7 Publication bias assessment funnel plot of Egger's regression test ($p = 0.062$) and Begg's rank correlation ($p = 0.123$)

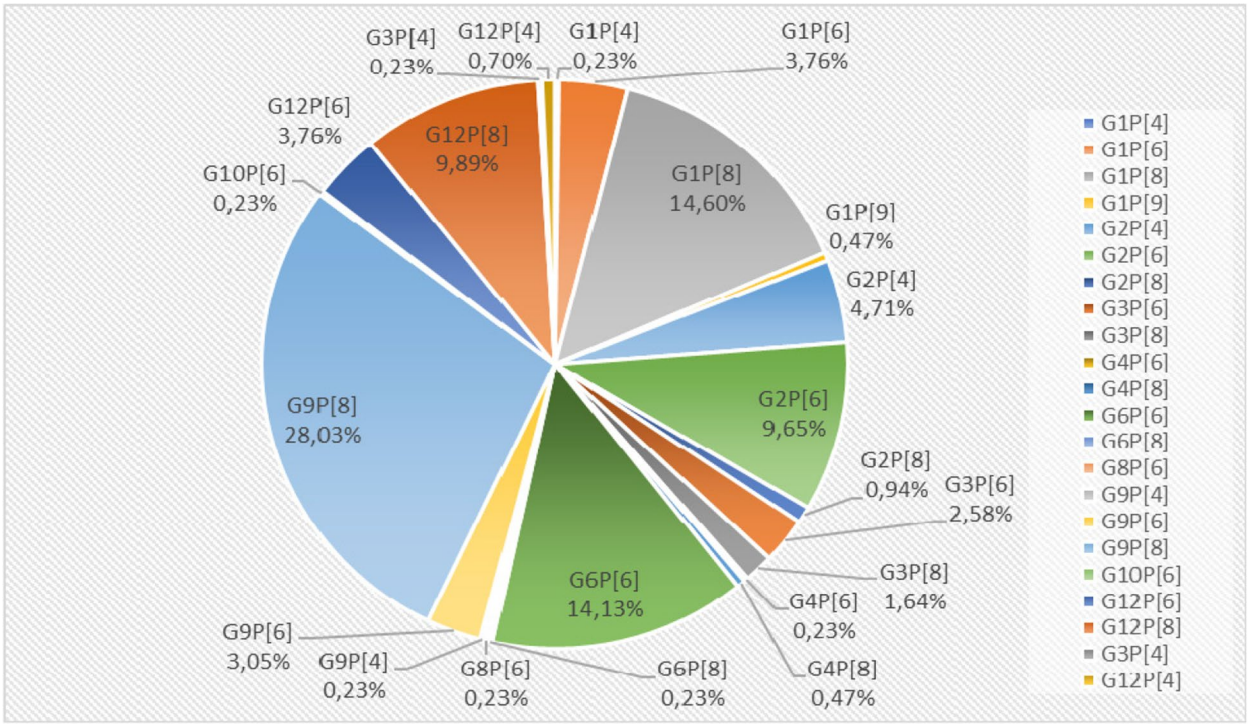

Fig. 8 Distribution of rotavirus genotypes in the population

detected in pig liver from Burkina Faso had a similarity of more than 98% with an African HEV genotype 3 sequence from Yaoundé (Cameroon) and Madagascar.

Subgroup analysis based on diagnostic methods

Analysis of the distribution of enteric viruses according to detection technique and population type yielded the results shown in Table 2.

In studies in which RT–PCR was used for primary detection, the prevalence of rotavirus was 19.7% (95% CI 7.9–40.9%), while in studies in which EIA, ELISA, and IGG were used for detection, the prevalence rates were 43.5% (95% CI 8.9–85.8%), 29% (95% CI 15–48.6%), and 28.5% (95% CI 19–40.3%), respectively (Fig. 11).

Discussion

In Burkina Faso, enteropathogenic viruses are among the most common pathogens, causing both sporadic illness and outbreaks, as reported by several studies. However, information has been scattered, and this raises questions about the current global burden of

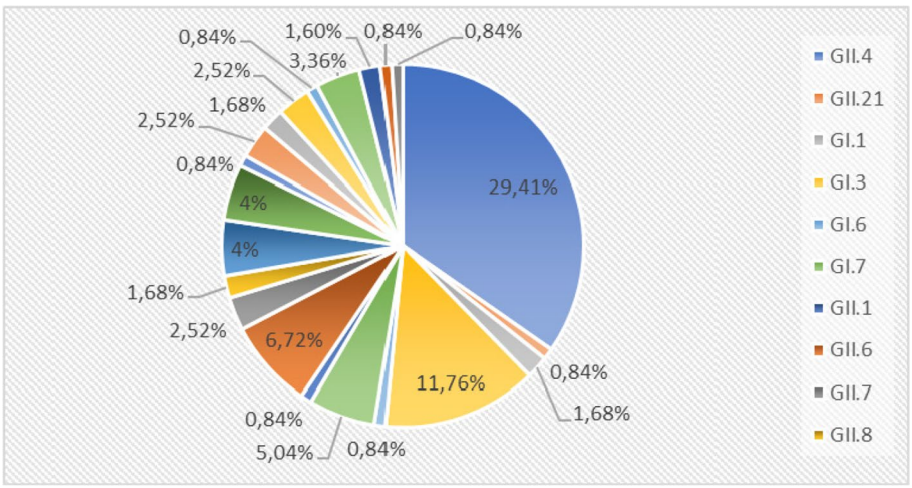

Fig. 9 Genotype distribution of the norovirus strains in the population

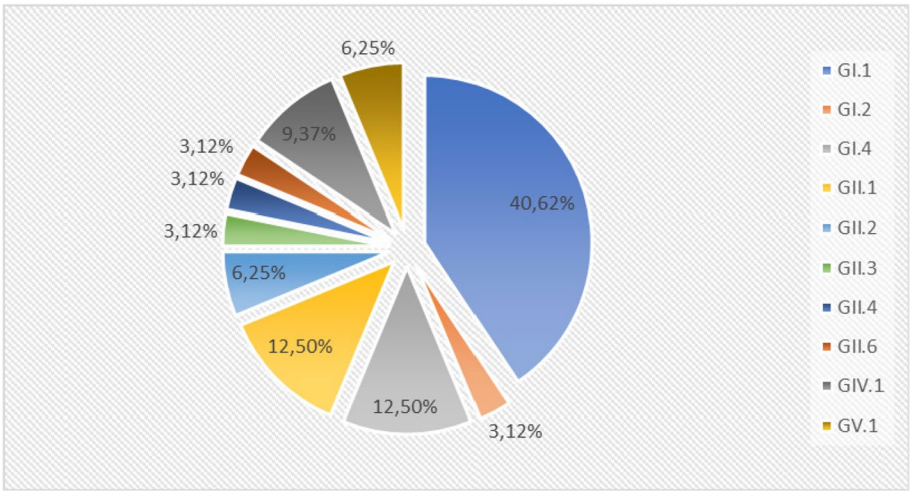

Fig. 10 Distribution of sapovirus genotypes in the population

these viral infections. The present systematic review and meta-analysis included 46 studies. Of the 43/46 studies on the human population (4214 patients), we showed that pathogenic viruses associated with gastroenteritis accounted for more than 72.6%, and entero-transmissible hepatitis viruses accounted for 27.2%. This may be explained by the fact that the majority of studies (31/46) included in this review focused on the diagnosis of viruses responsible for gastroenteritis. In fact, 67.39% of the estimates came from studies carried out on cohorts of children, more specifically, children under the age of five, which is the group most vulnerable to infection and at risk of severe disease. It is largely recognized that the vulnerability of this population might be related either to a higher dehydration risk or a less developed immune system [60]. Indeed, the incidence and severity of diarrheal diseases were found to be much lower in human breast-fed infants, which may provide protection from the mother's antibodies and microbiota, than in sterilized cow's milk–fed infants [61].

In this review, the pooled rotavirus prevalence among under-five children accounted for 27.7% of the cases, which confirms that rotavirus is and remain common cause of acute diarrhea in sub-Saharan Africa [62], even though some studies assert that the introduction of rotavirus vaccines has changed this trend [9, 63]. The current rate is slightly higher than the overall pooled estimate of rotavirus incidence of 24% reported from a meta-analysis of under-five children with acute gastroenteritis in South Africa [64], Ethiopia [65], the

Table 2 Pooled prevalence of enteric viruses by method

Virus	Method	Population	Pooled prevalence
Rotavirus	IGG	Child	28,5%
	EIA	Child	43,5%
	ELISA	Child	29,0%
	PCR	Child	19,7%
Norovirus	PCR	Child/Adult	15.4%
	EIA	Child	26.4%
Adenovirus	IGG	Child/Any age	3,5%
	PCR	Child/Adult	17,7%
Sapovirus	PCR	Child/Adult	11,2%
Parvovirus	PCR	Child	4,1%
Astrovirus	PCR	Child/Adult	3,6%
Aichivirus A	PCR	Child/Adult	1,4%
Hepatitis A Virus	ICG	Pregnant women/Blood donor	27,4%
	ELISA	Pregnant women	90%
Hepatitis E Virus	ELISA	Patients with acute febrile jaundice/Pregnant women/Any age/Blood donor	26,0%

Legend: *ICG* Immunochromatography, *EIA* Enzyme immunoassay, *PCR* Polymerase chain reaction, *ELISA* Enzyme-linked immunosorbent assay

Caribbean region and Latin America [66]. This disparity could be attributed to differences in the burden of disease across study settings, the sensitivity of the diagnostic assays used, and the choice and characteristics of the study subjects [64]. The majority of these studies used the IGG method, and only a few studies used RT–PCR for primary detection of viruses, which is more sensitive than the IGG, ELISA, and EIA methods [13, 14, 31, 45]. These factors may have contributed to the significant heterogeneity within the studies. Our qualitative analysis findings indicate an overall decline in the proportion of diarrhea episodes due to viral gastroenteritis in Burkina between 2012 and 2020 following the introduction of the rotavirus vaccine to the National Childhood Immune Program, as corroborated by other studies [9, 63]. These observations are consistent with meta-analysis findings in sub-Saharan Africa [67] and provide further evidence that rotavirus vaccinations are associated with a reduction in rotavirus-diarrhea morbidity, emergency visits, and hospitalizations [64].

In this review, the globally common G (G1–G4, G9, G12) and P (P[4], P[6], and P[8]) rotavirus (RV) genotypes were also observed, although G3 and G4 were reported at low prevalence. The rotavirus genotypes circulating in Burkina Faso showed a diverse pattern, with G9P[8] strains (28%) being the dominant strain. G9P[8], the predominant genotype combination, has been reported elsewhere in the West African subregion (Ghana and Kenya) [63, 68]. However, previous rotavirus surveillance studies in Burkina Faso revealed that G1P[8] was the predominant strain in the pre-vaccine era [69]. These results suggest that the predominant genotype of RV in Burkina Faso can change rapidly within a short period of time. Other studies in Europe and Asia have shown that large fluctuations in the genotype distribution of human rotaviruses occur continuously from one place to another [70, 71].

The unusual types G6P[6] (14.11%) and G12P[8] (9.88%) were also found. The emergence of G6P[6] has been reported in Burkina Faso [14, 31] and elsewhere in Africa, including Gabon and the Democratic Republic of the Congo, in children with diarrhea [72, 73]. Given that G6 viruses of bovine origin are capable of rapid adaptation to human populations, it is possible that the VP7 genes found in these studies could provide a mechanism for the generation of more genetic diversity through the reassortment of genomes. G12 strains began to emerge worldwide, mainly in association with P[8] or P[6] in several countries [74], and are rare when today's vaccines are formulated and therefore not included in vaccine formulations, including G6P[6] strains. It is therefore not possible to rule out the possibility that the circulation of the G6, G9 and G12 strains affects the effect of the vaccine, and this possibility needs to be studied further. The emergence of rotavirus G12P[8] confirmed that these strains have the potential to become the sixth most common genotype worldwide [75].

Norovirus (NoV) is a causative virus of gastroenteritis in all age groups and is known to contaminate food, causing viral epidemics [76]. According to this review,

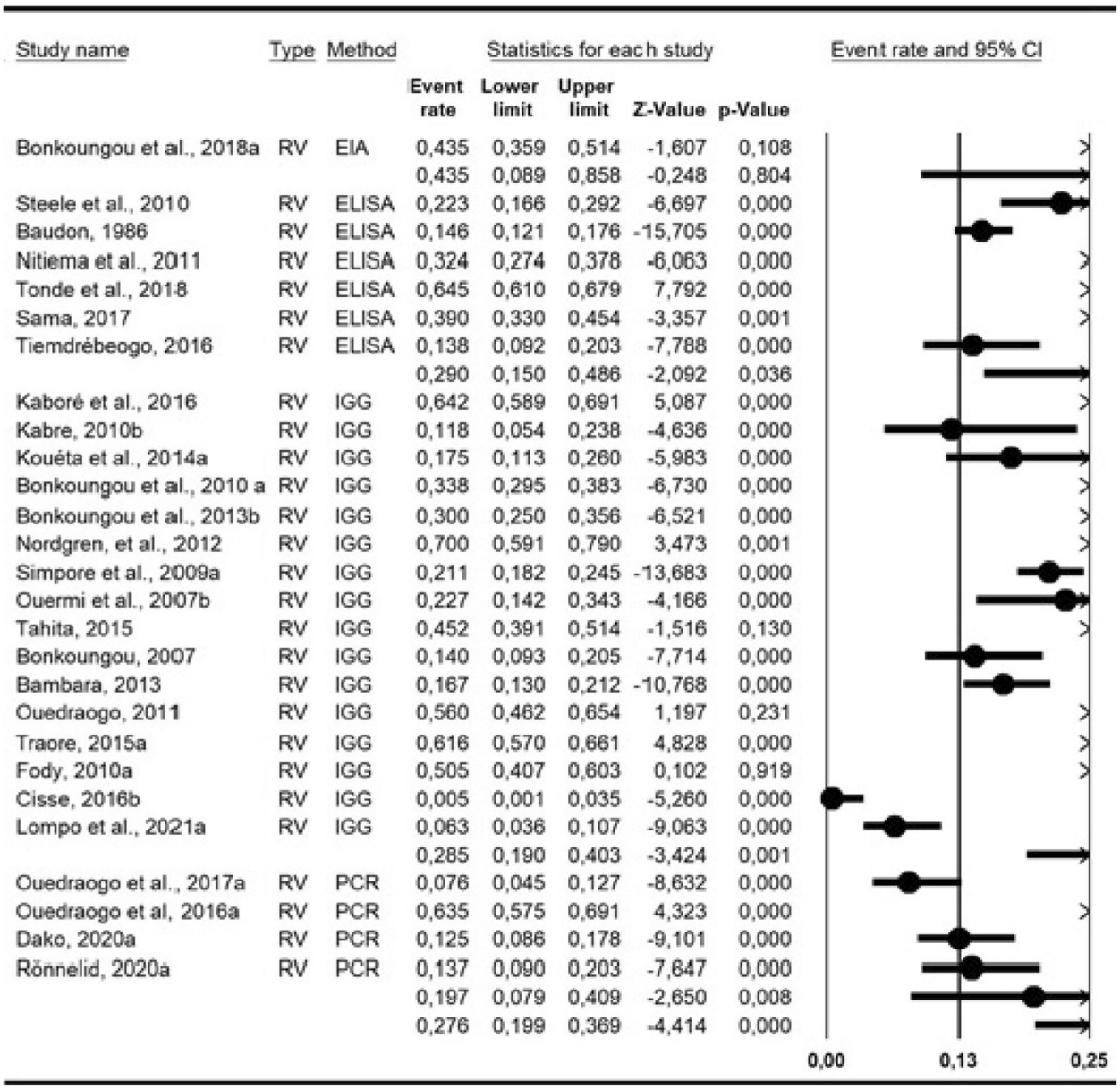

Fig. 11 Pooled estimates of rotavirus stratified by diagnostic methods. Legend: ICG: Immunochromatography; EIA: Enzyme immunoassay; PCR: Polymerase chain reaction; ELISA: Enzyme-linked immunosorbent assay; RV: Rotavirus

the pooled prevalence of NoV among the 8 included studies was 16% (95% CI: 12.25, 20.6), which was in agreement with a recent global analysis conducted worldwide (17.7% (95% CI: 16.3%-19.2%)) [77]. This high frequency underlines the importance of noroviruses in the etiology of gastroenteritis, given that the role and contribution of these viruses have long been underestimated in human pathology [78]. In contrast, our finding was higher than that of a previous review conducted in Africa (13.5%, 95% CI 12.7–14.3) [79]. The source of this variation could be the difference in the study participants, the study period, the study setting, and the mode of transmission, which is via food contamination and asymptomatic infected individuals favoring the spread of the disease [80, 81]. Another reason could be the introduction of the rotavirus vaccine. Indeed, Ronnelid *et al* revealed that norovirus was more frequently detected and associated with more severe symptoms than rotavirus in children in Burkina Faso after the introduction of the rotavirus vaccine [15].

In this study, the most common NoV genogroup detected was NoV GII (67.32%), with a small proportion of NoV GI (19.14%). Our findings were in agreement with those of a previous review conducted in sub-Saharan countries, where GII strains represented 76.4% of all detected NoVs, and GI strains 21.7% [82]. This study supports the growing recognition that genogroup II is generally responsible for sporadic cases of gastroenteritis in children [83]. NoV-GII.4 was the predominant genotype (29.41%) identified in most studies presenting genotyping data. Our finding was in agreement with previous studies performed in Sub-Saharan Africa that also reported the dominance of NoV-GII.4, which was 65.2% [82]. This genotype is considered to be the predominant genotype responsible for the majority of acute gastroenteritis outbreaks worldwide [77, 84].

Sapovirus was found in 11.2% (95% CI: 6.2%-19.4%) of the gastroenteritis patients in this study. This result was consistent with published reports showing that its prevalence is generally much lower than that of norovirus [85, 86]. Indeed, sapoviruses of genogroup I were found to be the most common, with GI.1 being the most predominant strain. This finding is consistent with a study carried out in northwest Ethiopia [87, 88]. These results contradict those reported in other regions of Malawi and Tunisia, South Africa [89–91]. This could be explained by the fact that in Burkina Faso, there are very few studies on the epidemiology of sapoviruses.

Although limited, 52% (95% CI: 14.2%-87.7%) of the HAV seroprevalence data in this review met the WHO's definition of an intermediate HAV endemic setting of ≥ 50% IgG seroprevalence by 15 years of age [92]. This very high detection rate may be explained by the low socioeconomic status of the Burkinabe population. Moreover, we estimated that 28.3% (95% CI: 17.7%-42%) of the general population had experienced recent or past HEV infection based on their seropositivity for total anti-HEV antibodies. These findings indicate that entero-transmissible hepatitis circulates at low but significant levels in the Burkinabè population [16]. Genotype 2 b has been detected in samples from patients with acute febrile jaundice in Burkina Faso [27]. This genotype has been identified in several African countries, such as the Central African Republic [93] and Namibia [94]; in a refugee camp in Chad [95]; and during recent epidemics in Nigeria [96]. In this study, HEV was ubiquitously detected in animals and in the environment (23.1%), particularly in pigs in which HEV genotype 3 was detected [43]. This also suggests that there are several sources of contamination in Burkina.

These data were obtained from credible studies conducted by national and international peers. The authorship of the publications also includes international teams from Europe, America and Africa, demonstrating collaboration with the availability of a technical platform for scientific confirmation of the identity of the viruses described.

The main limitation we encountered with this review is that the majority of the included studies focused on rotaviruses; this limits the possibility of accessing the real impact of other enteric viruses. In addition, most of the studies included were from the capital Ouagadougou.

Conclusion

This systematic review and meta-analysis highlight the substantial burden of viral enteric infections in Burkina Faso. In this study, rotavirus and norovirus were the two predominant viruses associated with cases of viral gastroenteritis, and among the hepatic viruses associated with human entero-transmissible infections, HAV was the most prevalent. The relatively high incidence of infection reported here suggests a possible hygiene problem, such as water contamination or the sociodemographic level of the population.

On the other hand, the scarcity of data on certain enteric viruses limits the strength of the results of this systematic review. However, more molecular epidemiological studies are needed to improve preventive measures.

Supplementary Information

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Supplementary Material 1.

Authors' contributions

KAT, MMA, PR and NB conceived this study. KAT developed the study protocol with the help of MMA and NO. KAT implemented the review under the supervision of PR and NB. KAT and MMA performed the search, screening, and data extraction under the guidance of NB. NO., JBO and PR provided content expertise for this review. All authors have provided comments on the final manuscript before publication. KAT is the guarantor of this review. All the authors have read and approved the final manuscript.

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Availability of data and materials

The findings of this study were generated from publication data collected from the Google Scholar database, PubMed database, Research Gate database, and Science direct database and analysed. All generated data are included in the manuscript.

Declarations

Ethics approval and consent to participate

No ethics approval was required for this study, as it is a systematic review using preexisting, publicly published data.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

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