http://www.pjbs.org

PJBS

ISSN 1028-8880

Pakistan Journal of Biological Sciences

ANSInet
Asian Network for Scientific Information
308 Lasani Town, Sargodha Road, Faisalabad - Pakistan

OPEN ACCESS Pakistan Journal of Biological Sciences

ISSN 1028-8880
DOI: 10.3923/pjbs.2017.59.69

Review Article
Molecular Epidemiology of Rotavirus in Children under Five in Africa (2006-2016): A Systematic Review

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Abstract

Group A human rotaviruses (RVA) are the most common causes of severe viral gastroenteritis in infants and young children worldwide. The available vaccines, while effective in Europe and North America have shown a reduced efficacy in Africa. One issue raised is the genetic variability of RVA. The objective of this study was to perform a literature review of molecular epidemiology to determine the prevalence of RVA genotypes circulating in Africa so as to establish a mapping of reliable data on these various genotypes. The search for articles was done from the National Institutes of Health (PUBMED) using three set of keywords. Articles were selected with inclusion criteria such as the date of publication, the age of the children, the sample size and the diagnostic techniques (standardized laboratory techniques). The data were imported into STATA SE version 11 software. Specific prevalence was estimated with Confidence Intervals (CI) of 95%. A total of 326 published studies were initially retrieved, out of which 27 studies were finally selected for the systematic review. The selected studies cover 20 African countries. The most encountered genotypes in Africa during this period were G1 (32.72%), followed by G2 (17.17%), G3 (9.88%), G9 (8.61%) and G12 (7.56%) among the G-types. The most common P-types were P[8] (48.71%) followed by P[6] (22.60%) and P[4] (11.58%) and the G1P[8] combination (22.64%) was the most encountered followed by G2P[4] (8.29%), G9P[8] (6.95%) and G2P[6] (5.00%). North Africa presented the highest prevalence of the P[8] genotype (65.70%). This review provides a comprehensive view of the current circulating rotavirus strains in Africa, which can be important in light of the new rotavirus vaccinations. Indeed, in Africa, the pursuit of national and continental studies for epidemiological surveillance of circulating rotavirus strains is vital for the promotion of future successful vaccines.

Key words: Rotavirus, molecular epidemiology, genotypes, children, AGE

Received: October 21, 2016 **Accepted:** December 01, 2016 **Published:** January 15, 2017

Citation: D. Ouermi, D. Soubeiga, W.M.C. Nadembèga, P.M. Sawadogo, T.M. Zohoncon, D. Obiri-Yeboah, F.W. Djigma, J. Nordgren and J. Simpore, 2017. Molecular epidemiology of rotavirus in children under five in Africa (2006-2016): A systematic review. Pak. J. Biol. Sci., 20: 59-69.

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Competing Interest: The authors have declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Acute gastroenteritis (AGE) is one of the leading causes of morbidity and mortality among children[1]. Each year, AGE causes two million deaths among children under 5 in the world[2,3]. Rotavirus (RV) is the pathogen responsible for most of these severe pediatric diarrhea diseases[4,5]. Each year: 114 million episodic diarrhea, 24 million day hospital consultations, 2.4 million hospitalizations and more than 453,000 deaths are reported[2,6-12]. This high rotavirus-dependent mortality occurs mainly in South Asia and sub-Saharan Africa[1,4,13,14]. In Burkina Faso, a study conducted from 2009-2010 revealed a prevalence of 32.4% of rotavirus infections with 63.8% of cases occurring during the cold dry season[15]. In countries with limited resources, where there is a lack of healthy lifestyle, the median age of first infection with RV is between 6 and 9 months while in the high-income countries where hygiene rules are strictly observed, the first episode frequently occurs between 2-5 years[16-18]. Therefore, rotaviruses are a real public health issue, not only for developing countries with inadequate sanitation where the majority of children under 5 are infected but also for developed countries where hygiene conditions are quite satisfactory.

Structurally, RVs are non-enveloped viruses of the *Rotavirus* genus within the Reoviridae family. The mature infectious particle of rotavirus is icosahedral with 100 nm in diameter (including spikes) of which the capsid is composed of three layers[19]. The genome is a double stranded RNA composed of eleven segments. These sequences formed of RNA encode six structural proteins (VP1-VP4, VP6 and VP7) and six non-structural proteins (NSP1-NSP6). The inner and intermediate layers of the capsid are formed respectively of VP2 and VP6 viral protein, while the outer layer is formed of VP4 and VP7 proteins that contain neutralizing antigens which are classified into G and P serotypes, respectively through neutralization tests. Apart from these serotypes, genotypes G and P, based on the genetic diversity of VP7 and VP4 genes have been classified to at least 27 G-types and 37 P-types, respectively. Currently, in many parts of the world, five combinations G1P[8], G2P[4], G3P[8], G4P[8] and G9P[8]) are the source of approximately 90% of all human rotavirus infections, where the G1P[8] genotype has the highest prevalence[10,18,20-23].

Despite the observed global genotype distribution, there is a heterogeneous global distribution of the genotypes of group A human rotavirus (RVA). The G-P combinations encountered in Africa often differ markedly from those circulating in other parts of the world[20]. Today, there are two types of rotavirus vaccine that are used worldwide: Rotarix® and RotaTeq®, which have shown a reduced efficacy in African countries of which one factor is speculated to be related to differences of RV genotypes present in the sub-continent[24].

The objective of this study was two fold: Conduct a literature review on molecular epidemiology to determine the prevalence of group A human RV genotypes circulating in Africa and establish a mapping of reliable data on these different genotypes that could be used to make a new vaccines covering all the different RV genotypes.

MATERIALS AND METHODS

Research strategy: The study review was conducted from the National Institutes of Health (PUBMED) using the following three set of keywords. The first set consisted of the following words "Rotavirus, genotypes, Africa". The second set consisted of: "Rotavirus, molecular epidemilogy, Africa". And finally the third set included the words "Diarrhea, rotavirus, pédiatric children, Africa". After examining each study, the studies were selected if meeting the following inclusion criteria: The date of publication (from 1 January, 2006 to 30 June, 2016), the age of children (X<5 years), the sample size (30<X), diagnostic techniques (using standardized laboratory techniques such as ELISA for RV positive detection, multiplex RT-PCR, qRT-PCR and sequencing for genotyping and/or RV sequencing), the language of study (English or French), the quality of the journal (Journal indexed in PUBMED), the health facilities where samples of pediatric patients were selected: University hospitals (CHU), regional hospitals (CHR), Medical Centers (CM) and Health and Social Promotion Centers (CSPS). The selected studies have conducted prevalence calculations based on confidence intervals.

Excluded from the study were: Data from article analysis, articles written in languages other than English or French and studies related to RV infecting animals.

Data extraction: For each selected study where available, we extracted the following data: Name of the first author, time and duration of the study, the country, the study population, the age group, the genotyping methods used, the number of samples tested, absolute numbers and percentages of positive subjects for the relevant genotypes.

Data were extracted by two investigators (SD and MS) and verified by a third investigator (OD). All disagreements were resolved by consensus.

Estimates of specific prevalence of rotavirus genotypes: Data on the different genotypes found in the studies were extracted. Then, the specific prevalence of rotavirus genotypes was calculated by dividing the number of positive cases for a particular genotype by the number of samples tested.

Data analysis: The data were imported into the STATA SE version 11 software. Specific prevalences are estimated at 95% Confidence Intervals (CI).

RESULTS

From 1 January, 2006 to 30 June, 2016 we obtained a total of 326 published studies of which 27 studies were finally selected for the systematic review according to the inclusion criteria (Fig. 1). The selected studies cover 20 countries in four regions of Africa: West (6 studies), Center (7 studies), East (8 studies), North (3 studies) and South (3 studies) (Fig. 2).

The samples analyzed were collected from different categories of health facilities (University or regional hospitals, medical centers or health centers). However, many articles do not specify the type of facilities or the type of patients (inpatients or outpatients).

The genotyping methods used were multiplex RT-PCR (n = 17 studies), multiplex RT-real time-PCR (n = 1), multiplex semi-nested RT-PCR (n = 5), multiplex semi-nested RT-PCR combined with sequencing (n = 1) and multiplex RT-PCR combined with sequencing (n = 3). Most studies have tested the most common P and G-types only. Table 1 shows the complete list of uncombined and combined genotypes identified by the 27 articles.

The most encountered genotypes in Africa during this period (Table 2-4) are P[8] (48.71% IC: 47.54-49.89), G1 (32.72% IC: 31.62-33.83) and the G1P[8] combination (22.64% IC : 21.67-23.64). It is also worth noting that there were non-typed cases in some studies. Depending on the different parts of Africa whose studies had been taken into account, the most encountered G-types are distributed as follows (Table 5): G1 is the most encountered in all parts of Africa with the highest prevalence in North Africa (39.71% IC: 36.71-42.77) and the lowest in Southern Africa (20.44% IC: 18.09-22.94).

In West Africa, G1 is followed by G2 (22.75% IC: 20.91-24.67) and G12 (13.64%, IC: 12.15-15.24) while in East Africa it is followed by G9 (14.77% IC: 12.79-16.94) and G8 (10.59% IC: 8.88-12.49). In Central Africa, G1 is followed by G2 (23.47% IC: 21.55-25.47) as in West Africa.

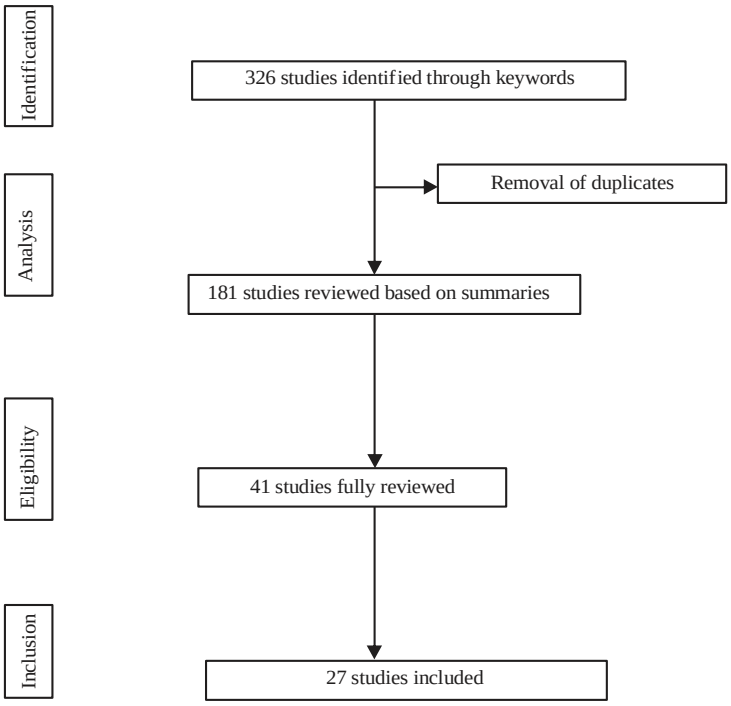

Fig. 1: Flowchart for study selection

Fig. 2: Spatial distribution of the studies included in the study

In North Africa, G9 comes second after G1 with 18.07% (IC: 15.77-20.55) as in East Africa and G2 is third with 17.58% (IC: 15.31-20.04). Unlike Central Africa, in Southern Africa, G3 is the most prevalent after G1 with 20.07% (IC: 18.09-22.94) and it is followed by G2 (9.99% IC: 8.28-11.92).

Regarding the P-types, P[8] (38.72%, IC: 36.51-40.97) followed by P[6] (26.88%, IC: 24.88-28.95) and P[4] (14.29% IC 12.74-15.96) were the most prevalent in West Africa. In East Africa, these 3 P-types are also the most found, respectively in 52.35% (IC: 49.44-55.24), 20.41% (IC: 18.14-22.83) and 11.10% (IC: 9.36-13.04) of cases. Similar results from Central Africa where their prevalences were 46.33% (IC: 44.04-48.64), 35.85% (IC: 33.66-38.09) and 9.72% (IC: 8.41-11.17). In South Africa they were found with the following prevalences: 49.86% (IC: 46.87-52.86), 13.08% (IC: 11.14-15.21) and 10.17% (IC: 8.45-12.11). However, in North Africa, these 3 P-types are found but with a much higher prevalence of P[8] (65.70% IC: 62.72-68.59) compared to its prevalence in other African regions. In North Africa, the second most prevalent is P[4], 11.98% (IC: 10.06-14.12) and P[6] 3.86% (IC: 2.78-5.23) which is much lower compared to other regions.

The G1P[8] combination is the most common in all regions but with a higher prevalence in North Africa (37.10% IC: 34.15-40.13). In West Africa, with a prevalence of 14.35% (12.79-16.02), it is followed by G12P[8] 12.32% (IC: 10.87-13.89) and G2P[4] 11.41% (IC: 10.01-12.94). However, in East Africa, G1P[8] 29.46% is followed by G9P[8] which is second prevalent (14.52% IC: 12.55-16.67). In Central Africa, G1P[8] is first with 22.32% (IC: 20.44-24.30) followed by G2P[6] 10.54% (IC: 9.17-12.03). In North Africa, G1P[8] is followed by

Table 1: Genotypes identified by each study and method used

References	Region of Africa	Country	No. of genotyped samples	List of genotypes found in the study	Genotyping method used
Banga-Mingo *et al.*[33]	Center	Central African Republic	160	G1P[6] G1P[8] G2P[4] G2P[6] G2P[8] G9P[8] G12P[6] G12P[8]	Multiplex RT-PCR
Boula *et al.*[34]	Center	Cameroon	898	G1P[4] G1P[6] G1P[8] G2P[4] G2P[6] G2P[8] G3P[4] G3P[6] G3P[8] G4P[6] G4P[8] G6P[6] G6P[8] G8P[4] G8P[6] G8P[8] G9P[4] G9P[6] G9P[8] G12P[4] G12P[6] G12P[8] GMIX PMIX	Semi-nested multiplex RT-PCR
Esteves *et al.*[23]	Center	Angola	117	G1P[8], G1P[6], G2P[4] G8P[6] G9P[6] G12P[6]	Multiplex RT-PCR
Lekana-Douki *et al.*[35]	Center	Gabon	86	G6 G1 G12 G3 G6 P[6] P[8] P[4] G6P[6], G1P[8], G2P[4], G12P[8], G3P[6]	Multiplex RT-real time PCR
Mayindou *et al.*[36]	Center	Democratic Republic of Congo	219	G1, G2, G1G2, P[8], P[6], P[6]/P[8] G12P[6]	Semi-nested multiplex RT-PCR
Ndze *et al.*[37]	Center	Cameroon	31	G2P[4] G2P[6], G3P[6], G9P[6], G6P[6]	Multiplex RT-PCR
Pukuta *et al.*[38]	Center	Democratic Republic of Congo	330	G1P[4] G1P[6] G1P[8] G2P[4] G2P[6] G2P[8] G3P[6] G4P[6] G4P[4] G6P[6] G6P[8] G8P[4] G8P[6] G8P[8] G9P[8] G12P[4] G12P[6] G12P[8] GMIX PMIX	Multiplex RT-PCR
Hokororo *et al.*[39]	East	Tanzania	100	G1, G8, G2 G9 P8, G1P[8], G1P[6], G8P[4] G8P[6] G2P[4] G8P[8] GMIX/P G/PMIX	Multiplex RT-PCR
Kiulia *et al.*[40]	East	Kenya	189	G2P[6], G1P[8], G9P[8], G2P[4], G8P[4], G8P[8], G9P[6], G9P[4], G12P[6]	Semi-nested multiplex RT-PCR
Moyo *et al.*[41]	East	Tanzania	211	G1P[4] G1P[6] G1P[8] G4P[4] G4P[6] G4P[8] G8P[4] G8P[6] G9P[8] G12P[6]	Semi-nested multiplex RT-PCR, sequencing
Mukaratirwa *et al.*[42]	East	Zimbabwe	127	G1P[8] G9P[8] G2P[4] G2P[6] G12P[6] G8P[4] G9P[6] G1P[6], G9P[4] G8P[6] G12P[8] G12P[4]	Multiplex RT-PCR
Odiit *et al.*[43]	East	Uganda	354	G1P[8], G9P[8], G2P[4], G8P[6], G12P[6], G1P[6], G8P[4], G8P[8], G3P[6]	Semi-nested multiplex RT-PCR
Raini *et al.*[44]	East	Kenya	30	G9P[8], G1P[8], G3P[8] G9P[6], G1P[4]	Multiplex RT-PCR
Yassin *et al.*[45]	East	Ethiopia	44	G3P[6], G1P[8], G2P[4] G8P[6], G12P[8] G9P[8] G12P[6]	Multiplex RT-PCR
Pursem *et al.*[46]	East	Mauritius	116	G9P[8], G6P[6], G1P[6], G3P[8] G3P[6], G1P[8], G4P[8] G8P[14] G4P[6]	Multiplex RT-PCR
Abugalia *et al.*[47]	North	Libya	164	G19P[8] G1P[8], G3P[9]	Multiplex RT-PCR
Benhafid *et al.*[9]	North	Morocco	548	G1P[8] G9P[8],G2P[4],G4P[8], G3P[8] G1P[4] G1P[6] G2P[6] G2P[8] G3P[6] G3P[4]	Multiplex RT-PCR, sequencing
Chouikha *et al.*[48]	North	Tunisia	323	G1P[4] G1P[6] G1P[8] G1P[11] G2P[4] G2P[6] G2P[8] G2P[11] G3P[4] G3P[6] G3P[8] G3P[11] G4P[6] G4P[8] G4P[11] G9P[11] G9P[6] G9P[8] GMIX PMIX	Multiplex RT-PCR, sequencing
Bonkoungou *et al.*[49]	West	Burkina Faso	140	G1, G9 P[6] P[8] G1P[8], G9P[8] G2P[6] G1P[9] G12P[6] G10P[6] G2P[8]	Multiplex RT-PCR
Enweronu-Laryea *et al.*[50]	West	Ghana	876	G1P[4] G1P[6] G1P[8] G2P[4] G2P[6] G2P[8] G3P[4] G3P[6] G3P[8] G4P[6] G4P[4] G8P[4] G9P[8] G10P[6] G10P[4] G12P[8] G12P[6] GMIX PMIX	Multiplex RT-PCR
Kwambana *et al.*[51]	West	Gambia	204	G1P[4], G2P[4], G1P[6], G2P[6], G1P[8], G2P[8], G1P[10], G4P[10], G2P14]	Multiplex RT-PCR
Ndze *et al.*[52]	West	Cameroon	135	G1P[6] G2P[4] G2P[6] G3P[6] G3P[8]G8P[6] G9P[8] G12P[6] G12P[8] GMIX PMIX	Multiplex RT-PCR
Nordgren *et al.*[20]	West	Burkina Faso	100	G1P[6] G1P[8] G2P[4] G3P[6] G6P[6] G9P[6] G9P[8] GMIX PMIX	Semi-nested multiplex RT-PCR
Page *et al.*[53]	West	Niger	420	G1P[8] G9P[8], G2P[4], G12P[8], G6P[6], G2P[6]	Multiplex RT-PCR, sequencing
Seheri *et al.*[54]	South	South Africa	729	G1P[8] G2P[4], G3P[8], G9P[8], G1P[6], G1P[4], G2P[6], G3P[6], G3P[4], G8P[6], G8P[8], G8P[4], G9P[6], G9P[4], G12P[6]	Multiplex RT-PCR
Ramudingana[55]	South	South Africa	319	G8P[8], G3P[8], G9P[8]	Multiplex RT-PCR
Langa *et al.*[56]	South	Mozambique	53	G1P[8] G1P[6], G2P[6], G4P[6], G9P[8], G12P[8], G12P[6]	Multiplex RT-PCR
Total No. of genotyped samples			7,023		

G9P[8] and G2P[4] with 17.78%, (IC: 15.49-20.25) and 11.40% (IC: 9.53-13.50), respectively. With 13.26% (IC: 11.31-15.41), G3P[8] is the most common in Southern Africa after G1P[8] which has a prevalence of 16.44% (IC: 14.30-18.76).

DISCUSSION

This systematic review of RVA genotypes in children under 5 in Africa focused on studies over a period of 11 years. The results showed a high prevalence of G1 (32.72%) followed

Table 2: Specific prevalence of G genotypes circulating in Africa from 2006-2016

				IC (95%)	
Genotypes	No. of genotyped samples	Positive cases for this genotype	Prevalence (%)	Minimum	Maximum
G1	7,023	2,298	32.72	31.62	33.83
G2	7,023	1,206	17.17	16.30	18.07
G3	7,023	694	9.88	9.19	10.60
G9	7,023	605	8.61	7.97	9.30
G12	7,023	531	7.56	6.95	8.20
G8	7,023	273	3.89	3.45	4.37
G6	7,023	95	1.35	1.10	1.65
G4	7,023	87	1.24	0.99	1.53
G10	7,023	34	0.48	0.34	0.68

Table 3: Specific prevalence of the P genotype circulating in Africa from 2006-2016

				IC (95%)	
Genotypes	No. of tested cases	Positive cases for this genotype	Prevalence (%)	Minimum	Maximum
P[8]	7,023	3,421	48.71	47.54	49.89
P[6]	7,023	1,587	22.60	21.62	23.59
P[4]	7,023	813	11.58	10.84	12.35
P[9]	7,023	51	0.73	0.54	0.95
P[11]	7,023	32	0.46	0.31	0.64
P[10]	7,023	22	0.31	0.20	0.47
P[14]	7,023	1	0.01	0.00	0.08

Table 4: Specific prevalence of combined G-P genotypes circulating in Africa from 2006-2016

				IC (95%)	
Genotypes	No. of tested cases	Positive cases for this genotype	Prevalence (%)	Minimum	Maximum
G1P[8]	7,023	1,590	22.64	21.67	23.64
G2P[4]	7,023	582	8.29	7.65	8.96
G9P[8]	7,023	488	6.95	6.36	7.57
G2P[6]	7,023	351	5.00	4.50	5.53
G12P[8]	7,023	337	4.80	4.31	5.32
G3P[8]	7,023	316	4.50	4.03	5.01
G3P[6]	7,023	270	3.84	3.41	4.32
G1P[6]	7,023	229	3.26	2.86	3.70
G12P[6]	7,023	123	1.75	1.46	2.09
G9P[6]	7,023	83	1.18	0.94	1.46
G6P[6]	7,023	79	1.12	0.89	1.40
G8P[4]	7,023	77	1.10	0.87	1.37
G8P[6]	7,023	75	1.07	0.84	1.34
G8P[8]	7,023	62	0.88	0.68	1.13
G1P[4]	7,023	60	0.85	0.65	1.10
G2P[8]	7,023	55	0.78	0.59	1.02
G4P[8]	7,023	55	0.78	0.59	1.02
G12P[6]	7,023	54	0.77	0.58	1.00
G10P[6]	7,023	24	0.34	0.22	0.51
G4P[6]	7,023	22	0.31	0.20	0.47
G1P[10]	7,023	21	0.30	0.19	0.46
G3P[11]	7,023	10	0.14	0.07	0.26
G3P[14]	7,023	9	0.13	0.06	0.24
G3P[4]	7,023	8	0.11	0.05	0.22
G2P[11]	7,023	7	0.10	0.04	0.21
G4P[4]	7,023	7	0.10	0.04	0.21
G9P[4]	7,023	7	0.10	0.04	0.21
G10P[8]	7,023	7	0.10	0.00	0.21
G12P[4]	7,023	6	0.09	0.03	0.19

Table 4: Continue

Genotypes	No. of tested cases	Positive cases for this genotype	Prevalence (%)	IC (95%)	
				Minimum	Maximum
G1P[11]	7,023	5	0.07	0.02	0.17
G1P[9]	7,023	2	0.03	0.00	0.10
G6P[8]	7,023	2	0.03	0.00	0.10
G2P[14]	7,023	1	0.01	0.00	0.08
G4P[10]	7,023	1	0.01	0.00	0.08
G4P[11]	7,023	1	0.01	0.00	0.08
G6P[9]	7,023	1	0.01	0.00	0.08
G9P[11]	7,023	1	0.01	0.00	0.08
G9P[14]	7,023	1	0.01	0.00	0.08

Table 5: Most encountered genotypes in the various regions of Africa from 2006-2016

Region of Africa	Most prevalent genotypes in the region	No. of genotyped samples	Positive cases for this genotype	Prevalence (%)	IC (95%)	
					Maximum	Minimum
North	P[8]	1,035	680	65.70	62.72	68.59
	G1	1,035	411	39.71	36.71	42.77
	G1P[8]	1,035	384	37.10	34.15	40.13
	G9	1,035	187	18.07	15.77	20.55
	G9P[8]	1,035	184	17.78	15.49	20.25
	G2	1,035	182	17.58	15.31	20.04
	P[4]	1,035	124	11.98	10.06	14.12
	G2P[4]	1,035	118	11.40	9.530	13.50
	P[6]	1,035	40	3.86	2.780	5.23
Center	P[8]	1,841	853	46.33	44.04	48.64
	G1	1,841	668	36.28	34.08	38.53
	P[6]	1,841	660	35.85	33.66	38.09
	G2	1,841	432	23.47	21.55	25.47
	G1P[8]	1,841	411	22.32	20.44	24.30
	G2P[6]	1,841	194	10.54	9.170	12.03
	G3	1,841	187	10.16	8.810	11.63
	P[4]	1,841	179	9.72	8.410	11.17
	G2P[4]	1,841	137	7.44	6.280	8.74
East	P[8]	1,171	613	52.35	49.44	55.24
	G1	1,171	424	36.21	33.45	39.04
	G1P[8]	1,171	345	29.46	26.86	32.17
	P[6]	1,171	239	20.41	18.14	22.83
	G9	1,171	173	14.77	12.79	16.94
	G9P[8]	1,171	170	14.52	12.55	16.67
	P[4]	1,171	130	11.10	9.360	13.04
	G8	1,171	124	10.59	8.880	12.49
	G8P[4]	1,171	57	4.87	3.710	6.26
West	P[8]	1,875	726	38.72	36.51	40.97
	G1	1,875	619	31.50	29.45	33.61
	P[6]	1,875	504	26.88	24.88	28.95
	G2	1,965	447	22.75	20.91	24.67
	G1P[8]	1,875	269	14.35	12.79	16.02
	P[4]	1,875	268	14.29	12.74	15.96
	G12	1,965	268	13.64	12.15	15.24
	G12P[8]	1,875	231	12.32	10.87	13.89
	G2P[4]	1,875	214	11.41	10.01	12.94
South	P[8]	1,101	549	49.86	46.87	52.86
	G1	1,101	225	20.44	18.09	22.94
	G3	1,101	221	20.07	17.74	22.56
	G1P[8]	1,101	181	16.44	14.30	18.76
	G3P[8]	1,101	146	13.26	11.31	15.41
	P[6]	1,101	144	13.08	11.14	15.21
	P[4]	1,101	112	10.17	8.450	12.11
	G2	1,101	110	9.99	8.280	11.92
	G2P[4]	1,101	70	6.36	4.990	7.96

by G2 (17.17%), G3 (9.88%), G9 (8.61%) and G12 (7.56%) among the G-types. The most common P-types were P[8] (48.71%) followed by P[6] (22.60%) and P[4] (11.58%) and the most encountered combinations were G1P[8] (22.64%) followed by G2P[4] (8.29%), G9P[8] (6.95%) and G2P[6] (5.00%). Todd *et al.*[25] in their 1997-2006 review in Africa had also found that G1P[8] was the most frequent (17.4%), followed by G2P[6], G8P[6] and G3P[8]. On the other hand, they found that G2 was the most common (15.8%) in that period among the G-types. Other systematic reviews in other regions of the world showed data that are similar to the findings in this review. Liu *et al.*[26] review found that P[8] (50.2%), P[4] (18.2%) and P[6] (7.2%) are the most common in China, but among G-types, the most common was G3 (39.3%), followed by G1 (30.3%), G2 (7.2%) and G9 (3.3%). They also showed that the most prevalent G-P combinations were G3P[8] (32.1%), G1P[8] (23.0%) and G2P[4] (7.9%)[26]. In Colombia, Ospino *et al.*[27] that G1 was also the most common but with a higher prevalence (57.9%), followed by G3, G9 and G2 among the G-types. However, among the P-types, the most frequent were P[4] (49.1) followed by P[6] and P[8]. But the most common combinations they found were G3P[8] (32.7%) followed by G1P[8] and G2P[4][27]. Ogilvie *et al.*[28] review in the Eastern and Central European regions showed that combinations such as G1P[8], G4P[8] and G2P[4] were the most common in these parts of Europe. In Latin America in 2004, Castello *et al.*[29] found that G1P[8] was also the most common with 40%, followed by G2P[4] (30%), G3P[8] (6%) and G4P[8] (7%). Note that in large parts of the world, the following five combinations (G1P[8], G2P[4], G3P[8] G4P[8] and G9P[8]) are currently the source of about 90% of all human rotavirus infections, with G1P[8] having the highest prevalence[20]. This review has shown that all those combinations are actually common in Africa

Almost all the African regions where the studies were conducted showed the same predominant genotypes with some variations in prevalence. Genotypes G1, G2, G9, G12 and G3 accounted for 75.94% of all G-types circulating in Africa, whereas genotypes P[8], P[6] and P[4] were predominant during the period and accounted for 82.89% of the P-types encountered. It is worth noting that fluctuation mostly relates to G2, G3, G4, G6, G8, G9 and G12, P [6] and P[4]. Indeed, after G1, the following are predominant: G2 and G12 in West Africa, G9 and G8 in East Africa, G2 and G3 in Central Africa and G9 and G2 in North Africa. The P[6] is the most prevalent after P[8] in central, West, East and South of Africa. However, P[4] is the second after P[8] in North Arica. This difference in circulating strains is not surprising given that genotypes vary much from one year to another, from one region to another, from one country to another and from one season to another. There are currently two second generation vaccines, RotaTeq® and Rotarix®, that have been authorized in more than 100 countries[14,30,31]. Rotarix® is a human rotavirus strain with a live attenuated P1A [8] G1 and RotaTeq® is a pentavalent human-bovine reassortment containing G-types 1-4 and P[8]. Both vaccines show good efficacy in preventing rotavirus diarrhea (85-98%)[32] in Europe and North America. However, the efficacy is lower in developing countries[13] and one factor could be related to the present of unusual strains. Therefore, with the unusual strains such as G12, G9, G8 and P[6] which predominate in Africa, it is essential to develop vaccines covering a wide range of genotypes.

This systematic review has some limitations. First, all studies are not designed to identify the full range of the G and P-types. Most studies use techniques that only detect common G and P-types since sequencing was not used in all the studies, this is a probable reason why some strains were not characterized. Furthermore, although the studies included in this review provide an indication of genotypes circulating across the African continent, they are not representative of all countries.

CONCLUSION

This review has provided a view of the current rotavirus strains circulating in Africa. The common rotavirus genotypes should remain the primary targets for vaccine development. However, due to the emergence of unusual strains and the reassortment between animal and human rotavirus especially in most African countries where animals are very close to humans, pursuing national and continental studies for epidemiological surveillance of circulating rotavirus strains will be vital for the promotion of future successful vaccines and the interpretation of any vaccine failure. Efforts to establish rotavirus surveillance are needed in Africa as to continuously update the information of circulating RV strains in each country and region.

ACKNOWLEDGMENTS

The authors are thankful to the Pietro ANNIGONI Association and the WAEMU Commission through the PACER-II program for their financial support.

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