HHS Public Access

Author manuscript

Vaccine. Author manuscript; available in PMC 2024 October 22.

Published in final edited form as:

Vaccine. 2022 September 29; 40(41): 5933–5941. doi:10.1016/j.vaccine.2022.08.041.

Epidemiology and pre-vaccine burden of rotavirus diarrhea in Democratic Republic of Congo (DRC): results of sentinel surveillance, 2009–2019

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Declaration of conflicts of interest

The authors of this article declare that they have no conflict of interest with the implementation of gastroenteritis surveillance in the DRC.

We can rather say that some authors have a direct link with the implementation of this surveillance. However, the entire process of producing this article was done while keeping all the qualities required of any researcher, including: honesty, integrity.

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the World Health Organization or US Centers for Disease Control and Prevention

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Abstract

Introduction—Since August 2009, the Democratic Republic of Congo (DRC) has implemented sentinel site surveillance for rotavirus gastroenteritis. Limited hospital studies have been carried out, in DRC, describing the epidemiology of rotavirus diarrhea before rotavirus vaccine introduction in October 2019. This analysis describes the epidemiology of rotavirus gastroenteritis and characteristics of circulating viral strains from 2009 to 2019.

Materials and methods—We analyzed demographic and clinic data collected from children < 5 years old enrolled at three rotavirus sentinel surveillance sites in DRC during 2009–2019, prior to rotavirus vaccine introduction in 2019. Data have been described and presented as mean ± standard deviation for quantitative variables with normal distribution, or as median with an interquartile range [Q1-Q3] for quantitative variables with non-normal distribution, or as absolute value with percentage for qualitative variables.

Results—Between August 2009 and December 2019, 4,928 children < 5 years old were admitted to sentinel surveillance sites for gastroenteritis in the DRC; the rotavirus positivity rate was 60%. There was a slight male gender predominance (56%), and the majority of children (79%) were 0–11 months of age. Every year, the incidence was highest between May and September corresponding to the dry and cool season. Genotyping was performed for 50% of confirmed rotavirus cases. The most common G genotypes were G1 (39%) and G2 (24%) and most common P genotypes were P[6] (49%) and P[8] (37%). The most common G-P genotype combinations were G1P[8] (22%), G2P[6] (16%) and G1P[6] (14%). Genotype distribution varied by site, age group, and year.

Conclusion—From 2009 to 2019, rotavirus-associated gastroenteritis represented a significant burden among DRC children under 5 who were admitted to sentinel sites. G1P[8] was the most commonly identified genotype. Continued monitoring after the introduction of rotavirus vaccine will be essential to monitor any changes in epidemiology.

Keywords

Surveillance; sentinel sites; epidemiology; rotavirus gastroenteritis; Democratic Republic of Congo

1. Introduction

Rotavirus gastroenteritis is one of the public health problems facing the world associated with increased morbidity and mortality, especially among children younger than 5 years old (1–11). In 2016, 258 million episodes of rotavirus-associated diarrhea and 128,500 rotavirus-associated deaths worldwide occurred among children under 5, more than 80%

of which occurred in the sub-Saharan African region (10). The Democratic Republic of Congo (DRC) along with Angola, India, Nigeria and Pakistan share more than half of rotavirus-associated deaths globally (12). In developed countries in general, the proportion of cases of acute gastroenteritis caused by rotavirus is estimated at 21% (16–26%) for outpatient consultations, 32% (25–38%) for emergency department visits and 41% (36–47%) for hospitalizations (2).

There are multiple genotypes of rotavirus and the most predominant strains associated with human gastroenteritis worldwide are G1, G2, G3, G4, G9 and G12 for G type and P[4], P[6] and P[8] for P type, with different geographical distribution. Among these genotypes, 90% are G1P[8], G2P[4], G3P[8], G4P[8], G9P[8] and G12P[8] (13,14). In Africa, a diversity of strains has been observed with an unusually high proportion of combinations of P and G genotypes suggesting viral reassortment due to zoonotic transmission of the virus; G9 and P[6] genotypes are observed with high frequency (15). Moreover, an Indian study found an association between rotavirus genotypes and the severity of gastroenteritis (16).

In August 2009, DRC implemented rotavirus gastroenteritis surveillance at three sentinel sites in Kinshasa and Lubumbashi (17) with the objectives of (i) determining the epidemiology of gastroenteritis attributable to rotavirus, (ii) identifying the rotavirus strains circulating in the country and (iii) collecting evidence to guide the introduction of the rotavirus vaccine (18). After this implementation, two studies that summarized partial data reported a positivity rate for rotavirus infection of 61% (19) and 54% (20) respectively among the cases of diarrhea recorded in children younger than 5 years old. In 2016, the process for the introduction of rotavirus vaccine in DRC's national vaccination program was initiated. This process culminated in October 2019 with the introduction of the Rotasiil vaccine (Serum Institute of India Ltd), 10 years after the establishment of rotavirus sentinel site surveillance. This study aims to describe the epidemiology of rotavirus gastroenteritis from August 2009 to December 2019, just before the introduction of vaccination.

2. Materials and methods

2.1. Rotavirus gastroenteritis surveillance in DRC

Surveillance of rotavirus gastroenteritis was conducted in three hospitals. Two sites are located in the city-province of Kinshasa, in the western part of the country: the pediatric hospital of Kalembelembe ("HPK") and the Hospital Center of Kingasani ("CHK"). The third site is located in the city of Lubumbashi, in the province of Haut-Katanga in the south-eastern part of the country: the General Provincial Hospital Sendwe ("HGS"). These three health facilities are representative provincial hospitals, caring for most of the pediatric patients in their province. This surveillance began in the DRC in 2009 (in August at HPK, in November at CHK and in December at HGS).

2.2. Framework and design

This is part of routine disease surveillance for vaccine preventable diseases (VPD) in DRC. The clinical definition of cases followed World Health Organization standard operating procedures. The enrollment criteria were as follows: "at least three loose or liquid stools in

a 24-hour period in a child younger than 5 years of age who is admitted for treatment of diarrhea in a hospital or in the emergency unit of a facility participating in the surveillance" (21). All cases corresponding to this definition were enrolled and admitted to the care sites and were recorded in the database for the entire period. Stool samples were collected within 48 hours of hospital admission to avoid detection of nosocomial pathogens. The detection of the viral antigen in the stools of the patients was carried out by means of the immunoenzymatic assay (EIA: ProSpecT Rotavirus Microplate Assay, Oxoid, Ltd., Basingstoke, Hampshire, United Kingdom) and the characterization of the strains of rotavirus was made using reverse transcription polymerase chain reaction (OneStep RT-PCR Kit, Qiagen, Inc.).(27, 28)

2. 3. Data management, processing and analysis

Data were collected using standardized case investigation forms with information in seven groups: general information (demographics), medical history, clinical condition on admission, information on parents or guardians, the final outcome of the hospitalization, and laboratory results. Data were entered into an EpiInfo database. These data were then collated in Microsoft Excel 2016 software, then analyzed with R version 4.1.2 software (R Foundation for Statistical Computing, Vienna, Austria).

Duplicate observations were identified and removed. We excluded 14 (0.22%) observations whose results were "undetermined" on the diagnostic test and 10 (0.16%) observations for which this diagnostic test was not done. All the variables which had complete information and those which had a proportion of less than 5% of missing data were retained for the analyses. Those with high proportions (>5%) of missing data were not analyzed. Data have been described and presented as mean ± standard deviation (s.d) for quantitative variables with normal distribution, or as median with an interquartile range [Q1-Q3] for quantitative variables with non-normal distribution, or as absolute value with percentage for qualitative variables.

2. 4. Ethical considerations

This activity was determined to be part of routine surveillance for vaccine preventable diseases and public health practice, and thus was granted exceptional approval by WHO Ethical Review committee (ERC) - surveillance was conducted in accordance with all applicable national guidelines. Due to the retrospective nature of the analyses, we did not need to obtain the written consent of the participants. We note, however, that the verbal consent of the parents was obtained after explanations provided by the sentinel site teams when filling out the investigation sheets for the enrollment. The protocol of this study has obtained the agreement and certified respecting the ethical aspects of health research by the national health ethics committee of the DRC: n ° 351 / CNES / BN / PMMF / 2022 of April 18, 2022. The final database was anonymized.

3. Results

3.1. Sociodemographic characteristics of children admitted to surveillance sites

Out of a total of 4952 children under 5 years old admitted for consultation in the sentinel sites from August 2009 to December 2019, 4928 children who had their laboratory results available were included in our analyses. Among which, 56% of them (n=2765) were males; and 60% (n=2943) tested positive for rotavirus by EIA (Table 1). The positivity rate was similar across all three facilities. Of all confirmed rotavirus positive cases, 1493 (50%) were genotyped.

The mean age of the admitted children was 8.7 ± 6.1 months. Overall, rotavirus positivity was inversely related to age with high positiviy (64%) in children 0–5 months of age and lower positivity (43%) in children 24–59 months of age. This pattern was observed at both Kingsani Hospital Center and Sendwe Pediatric Hospital but not at Kalembelembe Hospital with positivty rate does not vary by age group.

3.2. Clinical characteristics of children admitted to surveillance sites

Among all enrolled children, 60% were treated with fluids in the emergency department, with this proportion highest among children enrolled at Kalembelembe (Table 2). The median time to consultation after the onset of diarrhoea was 2 days with an interquartile range of 1 to 5 days. In addition, 100% of enrolled children had diarrhea as the main complaint and 92% had vomiting as a complaint associated with diarrhea. On admission, 60% of children had a general state altered by agitation and irritability. Among enrolled children, 58% had severe dehydration, 40% moderate dehydration, and only 1% had no obvious clinical signs of dehydration. Throughout hospital stay, more than half (54%) of the children had a high fever (38°C to 41°C). Recovery was high (93%) and did not differ substantially by rotavirus positivity status. The other 7% was either deceased (2%) or transferred (1%) or left against medical advice (4%). The median duration of hospitalization regardless of the underlying diagnosis was 3 [s.d.: 1.8] days.

3.3. Seasonality of rotavirus cases

Analysis of seasonality over the course of a year shows that cases of rotavirus gastroenteritis are more numerous between the month of May and the month of September corresponding to the dry and cool season in DRC (Figure 1).

3.4. Characterization of circulating viral strains

From 2010 to 2019, the predominant G genotypes were G1 (N=585; 39%), G2 (N=361; 24%) and G12 (N=144; 10%). The G1 and G2 genotypes were present in considerable proportions in all sites, while the G12 genotype had a significant share only in two sites (CHK and HGS), and the G3 genotype (N=50; 3%) had a considerable proportion only in the HGS site, which is in a different geographic area than the other two sites.

The predominant P genotypes were P6 (49%) and P8 (37%). Proportions were similar by site, though HGS had slightly higher proportions of P6 and lower proportions of P8 compared with the Kinshasa-based sites. The most frequently detected G and P

combinations were G1P[8] (22%), G1P[6] (14%), G2P[6] (16%), and G12P[8] (6%) (Table 3).

The distribution of G genotypes is similar across age groups among children <24 months of age and very few children >= 24 months of age were enrolled as reflected in (Figure 2).

The distribution of P genotypes by age group shows that the proportions of P4 and P8 genotypes increase while that of P6 genotype decreases slightly with age (Figure 3).

When analyzing genotypes by year, we found that G2 was present in significant proportions from 2010 to 2017 (Figure 4), later then gradually decreasing in favor of the increasing proportions of G3 and G12. G1 genotypes were prevalent across all the years analyzed. G12 was almost non-existent in the first years but began to have considerable proportions during the last three years (2017, 2018 and 2019) before the introduction of the vaccine. Non-typable (NT) genotypes had considerable proportions in 2013 and 2015.

With regard to the P genotypes, the analysis of the temporal evolution of the different genotypes found that the P6 and P8 genotypes were the majority P genotypes identified from 2010 to 2019 (Figure 5).

4. Discussion

In this analysis carried out in the DRC on data collected from 2009 to 2019, we found that the rotavirus positivity rate was 60%, with positivity decreasing with age. Rotavirus gastroenteritis cases were more numerous between May and September, corresponding to the dry and cool season in DRC. The predominant G genotypes were G1, G2 & G12 and the analysis of these G genotypes by age group showed that the G1 and G3 genotypes increased with age while the G2 and G12 genotypes had a somewhat lower prevalence in the oldest age group; the predominant P genotypes were P[6] and P[8], and the distribution of P genotypes by age group showed that the proportions of P[4] and P[8] genotypes increased while that of P[6] genotype decreased slightly with age.

The majority of chidren enrolled in rotavirus surveillance were aged 0 to 11 months as reported in several other studies (23–26). The slight male predominance we observed has also been reported in Bangui in the Central African Republic (27). In this study, we observed that the male predominance contrasted with the gender distribution in the 0 to 4 year old bracket in the overall DRC population, which showed rather a slight female predominance (28). The clinical presentation of gastroenteritis conformed to what was expected (24, 29) and the supported recovery rate (93%) was close to what has been found elsewhere (30).

The rotavirus positivity rate in our study (60%) is very high compared to previous publications on the prevaccinal rotavirus positivity rate in other African countries: 26% in Kenya (31), 22% in Gambia (32), 23% in Ethiopia (33), 39.8% in Benin (34), 24% in South Africa (35), 28.8% in Abidjan (in Ivory Coast) (36). The positivity rate we reported in DRC remains above regional values for sub-Saharan Africa, which range between 25% and 42% (2, 37, 41, 54, 55). However, our observed positivity still falls within the confidence interval observed by Aliabadi et al. describing an annual positivity rate of 38% (95% CI: 4.8–73.4)

among admissions for acute gastroenteritis in African countries that had not introduced rotavirus vaccine in their national immunization programs (data from 2008–2016) (1). This situation should be analyzed for factors that would explain DRC's higher rate compared to other countries, and may consider hypotheses derived from literature review: malnutrition, climatic conditions, socio-economic factors of households, a very low rate of breastfeeding (39–44) and possibly strict adherenace to the case definition of severe gastroenteritis. This high positivity may also be associated with the distribution by age because there are many very young children enrolled in the DRC (88% were less than one year old). Decreasing rotavirus positivity with increasing age has also been described by Tate et al (45).

Regarding the seasonality of cases, which found in Zimbabwe by Mwenda et al with a peak between May and September was similar to the seasonality in DRC (23). However, in Burkina Faso, rotavirus gastroenteritis cases have been observed to increase between December and February (24).

Genotyping results were similar to those found in many studies. The most detected genotypes in Africa during the period from 2006 to 2016 were G1, G2, G3, G9 and G12 and P[8], P[6] and P[4] and the following combinations were predominant: G1P[8], G2P[4], G9P[8] and G2P[6]; North Africa presented the highest prevalence of the P genotype [8] (46). A meta-analysis carried out on data collected in Africa from 1990 to 2009 showed that the most detected genotypes were G1, G2 and G3 as well as P[8] and P[6] (47), and the study conducted in eight African countries by Mwenda et al found (G1P[8], G2P[4] and P[8]) to be predominant (23). Compared to the results obtained by these studies carried out in Africa, we note that the genotypes G1, P[6] and P[8] were the most-detected during all the ten years of pre-vaccine rotavirus surveillance in DRC. Taken together, these findings suggest that G1, P[6], and P[8] genotypes are ubiquitous in Africa. On the other hand, the G2 genotype had significant proportions from 2010 to 2016 and then began to decline in the following years; the G12 and G3 genotypes which were almost absent started from 2017 to 2019. However, the G3 genotype did not take such a large proportion as to become predominant, as we reported in other countries. (33–36) Additional analyses are needed after the introduction of vaccination to understand possible impact of rotavirus vaccine on the predominant genotypes. We also found that the G12 genotype was almost non-existent in the first years and gradually began to have considerable proportions from 2017 onwards. Genetic characterization of G12 strains circulating in six African countries between 2010 and 2014 demonstrated that these strains were closely related regardless of the year or country of detection.(48) This shows that the G12 genotype is expanding across the continent, and the DRC has not been spared (34,49–52).

We were limited in the analyses due to missing data which were not well integrated into the investigation form from the start and by other variables which had many missing values not filled in and which would have helped us to deepen the analyses. Here are some other analyzes that we would have liked: to research the sociodemographic factors of parents associated with the consultation delay, calculate the Vesikari score and perhaps compare it by age group, look for the association between the clinical expression of the disease at admission and factors such as type of diet of the child, home use of rehydration serum before admission.

The strength of this surveillance in sentinel sites is that it refers to a system that continuously records cases, making it possible to provide useful information on the impact of vaccines, epidemiology and risk factors, as well as the disease-causing pathogens and circulating strains of causative agents; however, this type of surveillance also has weaknesses in that the denominator used is not the general population, which makes it difficult to calculate the incidence of diseases (53).

5. Conclusion

From 2009 to 2019, rotavirus-associated gastroenteritis represented a significant burden among children younger than 5 years old who were admitted for gastroenteritis in sentinel sites. The analysis of the results of the genotyping of viral strains made it possible to identify the predominant viral genotypes (G1P[8], G2P[6], G1P[6], and G12P[8]) during this period with some specific ones according to the age groups, the surveillance sites as well as their evolution over time. This information guided policy makers in the Democratic Republic of the Congo in developing a plan for the introduction of the new rotavirus vaccine into the Expanded Program on Immunization schedule. Analysis of data from the post-introduction follow-up period of the rotavirus vaccine will make it possible to observe any changes that may occur following introduction of rotavirus vaccine.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgements

We would like to sincerely thank the thesis supervision team and the research unit (CESP) who support us in carrying out our research. We also appreciate the contribution of all the stakeholders: the expanded vaccination program (PEV-RDC), the national biomedical research institute (INRB-RDC), the epidemiological surveillance department (DSE-RDC), the World Health Organization (WHO Country office - DRC and Regional Office, Brazzavile) and the Centers for Disease Control and Prevention (CDC) which support the surveillance of gastroenteritis in the DRC because without them we would not have had this data. We will be ungrateful if we do not express our gratitude to the sentinel teams (nurses, laboratories and data managers) who not only allow the implementation of this surveillance activities in the field and also regularly report to us the data. We also thank the patients as well as their parents or guardians who, even if because of the retrospective analysis, did not give us their written consent to participate in this study, but their passage in the care structures contributed to obtaining these data.

References

1. Aliabadi N, Antoni S, Mwenda JM, Weldegebriel G, Biey JNM, Cheikh D, et al. Global impact of rotavirus vaccine introduction on rotavirus hospitalisations among children under 5 years of age, 2008–16: findings from the Global Rotavirus Surveillance Network. Lancet Glob Health. july 2019;7(7):e893–903. [PubMed: 31200889]
2. Ardura-Garcia C, Kreis C, Rakic M, Jaboyedoff M, Mallet MC, Low N, et al. Rotavirus disease and health care utilisation among children under 5 years of age in highly developed countries: A systematic review and meta-analysis. Vaccine. 21 mai 2021;39(22):2917–28. [PubMed: 33934916]
3. Clark A, Black R, Tate J, Roose A, Kotloff K, Lam D, et al. Estimating global, regional and national rotavirus deaths in children aged <5 years: Current approaches, new analyses and proposed improvements. PLoS ONE. 11 sept 2017;12(9):e0183392. [PubMed: 28892480]

4. Fletcher SM, Stark D, Ellis J. Prevalence of gastrointestinal pathogens in Sub-Saharan Africa: systematic review and meta-analysis. J Public Health Afr. 5 sept 2011;2(2):e30. [PubMed: 28299071]
5. Kawai K, O'Brien MA, Goveia MG, Mast TC, El Khoury AC. Burden of rotavirus gastroenteritis and distribution of rotavirus strains in Asia: a systematic review. Vaccine. 8 févr 2012;30(7):1244–54. [PubMed: 22212128]
6. Lanata CF, Fischer-Walker CL, Olascoaga AC, Torres CX, Aryee MJ, Black RE, et al. Global causes of diarrheal disease mortality in children <5 years of age: a systematic review. PloS One. 2013;8(9):e72788. [PubMed: 24023773]
7. Malek MA, Teleb N, Abu-Elyazeed R, Riddle MS, Sherif ME, Steele AD, et al. The epidemiology of rotavirus diarrhea in countries in the Eastern Mediterranean Region. J Infect Dis. 1 sept 2010;202 Suppl:S12–22. [PubMed: 20684691]
8. Sanchez-Padilla E, Grais RF, Guerin PJ, Steele AD, Burny ME, Luquero FJ. Burden of disease and circulating serotypes of rotavirus infection in sub-Saharan Africa: systematic review and meta-analysis. Lancet Infect Dis. sept 2009;9(9):567–76. [PubMed: 19695493]
9. Tate JE, Burton AH, Boschi-Pinto C, Steele AD, Duque J, Parashar UD, et al. 2008 estimate of worldwide rotavirus-associated mortality in children younger than 5 years before the introduction of universal rotavirus vaccination programs: a systematic review and meta-analysis. Lancet Infect Dis. févr 2012;12(2):136–41. [PubMed: 22030330]
10. Troeger C, Khalil IA, Rao PC, Cao S, Blacker BF, Ahmed T, et al. Rotavirus Vaccination and the Global Burden of Rotavirus Diarrhea Among Children Younger Than 5 Years. JAMA Pediatr. 1 oct 2018;172(10):958–65. [PubMed: 30105384]
11. Zaraket H, Charide R, Kreidieh K, Dbaibo G, Melhem NM. Update on the epidemiology of rotavirus in the Middle East and North Africa. Vaccine. 27 oct 2017;35(45):6047–58. [PubMed: 28986034]
12. Tate JE, Burton AH, Boschi-Pinto C, Parashar UD, World Health Organization–Coordinated Global Rotavirus Surveillance Network. Global, Regional, and National Estimates of Rotavirus Mortality in Children <5 Years of Age, 2000–2013. Clin Infect Dis Off Publ Infect Dis Soc Am. 1 mai 2016;62 Suppl 2:S96–105.
13. Santos N, Hoshino Y. Global distribution of rotavirus serotypes/genotypes and its implication for the development and implementation of an effective rotavirus vaccine. Rev Med Virol. févr 2005;15(1):29–56. [PubMed: 15484186]
14. Gentsch JR, Laird AR, Bielfelt B, Griffin DD, Bányai K, Ramachandran M, et al. Serotype Diversity and Reassortment between Human and Animal Rotavirus Strains: Implications for Rotavirus Vaccine Programs. J Infect Dis. 1 sept 2005;192(Supplement_1):S146–59. [PubMed: 16088798]
15. Todd S, Page NA, Steele AD, Peenze I, Cunliffe NA. Rotavirus Strain Types Circulating in Africa: Review of Studies Published during 1997–2006. J Infect Dis. 1 sept 2010;202(Supplement_1):S34–42. [PubMed: 20684715]
16. Saluja T, Dhingra MS, Sharma SD, Gupta M, Kundu R, Kar S, et al. Association of rotavirus strains and severity of gastroenteritis in Indian children. Hum Vaccines Immunother. 29 sept 2016;13(3):711–6.
17. Pukuta ES, Esona MD, Nkongolo A, Seheri M, Makasi M, Nyembwe M, et al. Molecular surveillance of rotavirus infection in the Democratic Republic of the Congo August 2009 to June 2012. Pediatr Infect Dis J. avr 2014;33(4):355–9. [PubMed: 24637513]
18. Agócs MM, Serhan F, Yen C, Mwenda JM, de Oliveira LH, Teleb N, et al. WHO Global Rotavirus Surveillance Network: A Strategic Review of the First 5 Years, 2008–2012. MMWR Morb Mortal Wkly Rep. 25 juill 2014;63(29):634–7. [PubMed: 25055187]
19. Pukuta ES, Esona MD, Nkongolo A, Seheri M, Makasi M, Nyembwe M, et al. Molecular surveillance of rotavirus infection in the Democratic Republic of the Congo August 2009 to June 2012. Pediatr Infect Dis J. avr 2014;33(4):355–9. [PubMed: 24637513]
20. Sangaji M, Mukuku O, Mutombo A, Mawaw P, Swana E, Kabulo B, et al. Etude épidémio-clinique des diarrhées aiguës à rotavirus chez les nourrissons à l'hôpital Jason Sendwe de Lubumbashi, République Démocratique du Congo. Pan Afr Med J. 10 juin 2015;21.

21. WHO_SurveillanceVaccinePreventable_19_Rotavirus_FRENCH_R1.pdf [Internet]. [cited 27 déc 2021]. Disponible sur: https://www.who.int/immunization/monitoring_surveillance/burden/vpd/WHO_SurveillanceVaccinePreventable_19_Rotavirus_FRENCH_R1.pdf
22. Pickering LK, Bartlett AV, Reves RR, Morrow A. Asymptomatic excretion of rotavirus before and after rotavirus diarrhea in children in day care centers. J Pediatr. mars 1988;112(3):361–5. [PubMed: 2831326]
23. Mwenda JM, Ntoto KM, Abebe A, Enweronu-Laryea C, Amina I, Mchomvu J, et al. Burden and Epidemiology of Rotavirus Diarrhea in Selected African Countries: Preliminary Results from the African Rotavirus Surveillance Network. J Infect Dis. sept 2010;202(S1):S5–11. [PubMed: 20684718]
24. Nitiema LW, Nordgren J, Ouermi D, Dianou D, Traore AS, Svensson L, et al. Burden of rotavirus and other enteropathogens among children with diarrhea in Burkina Faso. Int J Infect Dis. 1 sept 2011;15(9):e646–52. [PubMed: 21763172]
25. Godfrey O, Zhang W, Amponsem-Boateng C, Bonney Oppong T, Zhao Q, Li D. Evidence of rotavirus vaccine impact in sub-Saharan Africa: Systematic review and meta-analysis. PloS One. 2020;15(4):e0232113. [PubMed: 32339187]
26. Athiyyah AF, Utsumi T, Wahyuni RM, Dinana Z, Yamani LN, Soetjipto, et al. Molecular Epidemiology and Clinical Features of Rotavirus Infection Among Pediatric Patients in East Java, Indonesia During 2015–2018: Dynamic Changes in Rotavirus Genotypes From Equine-Like G3 to Typical Human G1/G3. Front Microbiol [Internet]. 2019 [cité 4 févr 2022];10. Disponible sur: https://www.frontiersin.org/article/10.3389/fmicb.2019.00940
27. Gouandijka-Vasilache I, Manirakiza A, Gody JC, Banga-Mingo V, Kongombe OO, Esona MD, et al. Rotavirus Epidemiology in Bangui, Central African Republic, 20081. Emerg Infect Disease. july 2014;20(7):1254–5. [PubMed: 24959927]
28. DHS Survey DRC Preliminary results 2013.pdf [Internet]. [cited 9 mars 2022]. Disponible sur: https://files.givewell.org/files/DWDA%202009/DMI/DHS%20Survey%20DRC%20Preliminary%20results%202013.pdf
29. Uhnoo I, Olding-Stenkvist E, Kreuger A. Clinical features of acute gastroenteritis associated with rotavirus, enteric adenoviruses, and bacteria. Arch Disease Child. août 1986;61(8):732–8. [PubMed: 3017237]
30. Morris SK, Awasthi S, Khera A, Bassani DG, Kang G, Parashar UD, et al. Rotavirus mortality in India: estimates based on a nationally representative survey of diarrhoeal deaths. Bull World Health Organ. 1 oct 2012;90(10):720. [PubMed: 23109739]
31. Omore R, Khagayi S, Ogwel B, Onkoba R, Ochieng JB, Juma J, et al. Rates of hospitalization and death for all-cause and rotavirus acute gastroenteritis before rotavirus vaccine introduction in Kenya, 2010–2013. BMC Infect Disease. 11 janv 2019;19:47. [PubMed: 30634922]
32. Sanneh B, Sey AP, Shah M, Tate J, Sonko M, Jagne S, et al. Impact of pentavalent rotavirus vaccine against severe rotavirus diarrhoea in The Gambia. Vaccine. 12 nov 2018;36(47):7179–84. [PubMed: 29544688]
33. Damtie D, Melku M, Tessema B, Vlasova AN. Prevalence and Genetic Diversity of Rotaviruses among under-Five Children in Ethiopia: A Systematic Review and Meta-Analysis. Viruses. 3 janv 2020;12(1):E62.
34. Agbla JM, Esona MD, Agbankpe AJ, Capo-Chichi A, Gautam R, Dougnon TV, et al. Molecular characteristics of rotavirus genotypes circulating in the south of Benin, 2016–2018. BMC Res Notes. 19 oct 2020;13:485. [PubMed: 33076976]
35. Omatola CA, Ogunsakin RE, Olaniran AO. Prevalence, Pattern and Genetic Diversity of Rotaviruses among Children under 5 Years of Age with Acute Gastroenteritis in South Africa: A Systematic Review and Meta-Analysis. Viruses. 23 sept 2021;13(10):1905. [PubMed: 34696335]
36. Akran V, Peenze I, Akoua-Koffi C, Kette H, de Beer MC, Dosso M, et al. Molecular Characterization and Genotyping of Human Rotavirus Strains in Abidjan, Cote d'Ivoire. J Infect Dis. sept 2010;202(S1):S220–4. [PubMed: 20684706]
37. Oppong TB, Yang H, Amponsem-Boateng C, Kyere EKD, Abdulai T, Duan G, et al. Enteric pathogens associated with gastroenteritis among children under 5 years in sub-Saharan Africa:

a systematic review and meta-analysis. Epidemiol Infect. 2 mars 2020;148:e64. [PubMed: 32115003]

38. Waggie Z, Hawkridge A, Hussey GD. Review of Rotavirus Studies in Africa: 1976–2006. J Infect Dis. sept 2010;202(S1):S23–33. [PubMed: 20684708]
39. Strina A, Rodrigues LC, Cairncross S, Ferrer SR, Fialho AM, Leite JPG, et al. Factors associated with rotavirus diarrhoea in children living in a socially diverse urban centre in Brazil. Trans R Soc Trop Med Hyg. juill 2012;106(7):445–51. [PubMed: 22657535]
40. Bhavnani D, Goldstick JE, Cevallos W, Trueba G, Eisenberg JNS. Impact of rainfall on diarrheal disease risk associated with unimproved water and sanitation. Am J Trop Med Hyg. avr 2014;90(4):705–11. [PubMed: 24567318]
41. D'SOUZA RM, HALL G, BECKER NG. Climatic factors associated with hospitalizations for rotavirus diarrhoea in children under 5 years of age. Epidemiol Infect. janv 2008;136(1):56–64. [PubMed: 17352836]
42. Kismul H, Acharya P, Mapatano MA, Hatløy A. Determinants of childhood stunting in the Democratic Republic of Congo: further analysis of Demographic and Health Survey 2013–14. BMC Public Health. 1 août 2017;18(1):74. [PubMed: 28764669]
43. Nichols GL, Iacono GL. Examining the influence of weather on rotavirus infection. Lancet Planet Health. 1 juin 2019;3(6):e236–7. [PubMed: 31228993]
44. Babakazo P, Donnen P, Akilimali P, Ali NMM, Okitolonda E. Predictors of discontinuing exclusive breastfeeding before six months among mothers in Kinshasa: a prospective study. Int Breastfeed J. 27 mai 2015;10(1):19. [PubMed: 26075010]
45. Tate JE, Parashar UD. Rotavirus vaccines in routine use. Clin Infect Dis Off Publ Infect Dis Soc Am. 1 nov 2014;59(9):1291–301.
46. Ouermi D, Soubeiga D, Nadembega WMC, Sawadogo PM, Zohoncon TM, Obiri-Yeboah D, et al. Molecular Epidemiology of Rotavirus in Children under Five in Africa (2006–2016): A Systematic Review. Pak J Biol Sci PJBS. 2017;20(2):59–69. [PubMed: 29022996]
47. Sanchez-Padilla E, Grais RF, Guerin PJ, Steele AD, Burny ME, Luquero FJ. Burden of disease and circulating serotypes of rotavirus infection in sub-Saharan Africa: systematic review and meta-analysis. Lancet Infect Dis. 1 sept 2009;9(9):567–76. [PubMed: 19695493]
48. Rakau KG, Nyaga MM, Gededzha MP, Mwenda JM, Mphahlele MJ, Seheri LM, et al. Genetic characterization of G12P[6] and G12P[8] rotavirus strains collected in six African countries between 2010 and 2014. BMC Infect Disease. 22 janv 2021;21:107. [PubMed: 33482744]
49. Damtie D, Melku M, Tessema B, Vlasova AN. Prevalence and Genetic Diversity of Rotaviruses among under-Five Children in Ethiopia: A Systematic Review and Meta-Analysis. Viruses. 3 janv 2020;12(1):E62.
50. Moyo SJ, Blomberg B, Hanevik K, Kommedal O, Vainio K, Maselle SY, et al. Genetic Diversity of Circulating Rotavirus Strains in Tanzania Prior to the Introduction of Vaccination. PLoS ONE. 20 mai 2014;9(5):e97562. [PubMed: 24844631]
51. Manjate F, João ED, Chirinda P, Garrine M, Vubil D, Nobela N, et al. Molecular Epidemiology of Rotavirus Strains in Symptomatic and Asymptomatic Children in Manhiça District, Southern Mozambique 2008–2019. Viruses [Internet]. janv 2022 [cité 9 mars 2022];14(1). Disponible sur: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8781303/
52. João ED, Munlela B, Chissaque A, Chilaúle J, Langa J, Augusto O, et al. Molecular Epidemiology of Rotavirus A Strains Pre- and Post-Vaccine (Rotarix®) Introduction in Mozambique, 2012–2019: Emergence of Genotypes G3P[4] and G3P[8]. Pathogens. 19 août 2020;9(9):671. [PubMed: 32824938]
53. WHO_SurveillanceVaccinePreventable_01_Overview_French_R1.pdf [Internet]. [cited 11 mars 2022]. Disponible sur: https://www.who.int/immunization/monitoring_surveillance/burden/vpd/WHO_SurveillanceVaccinePreventable_01_Overview_French_R1.pdf

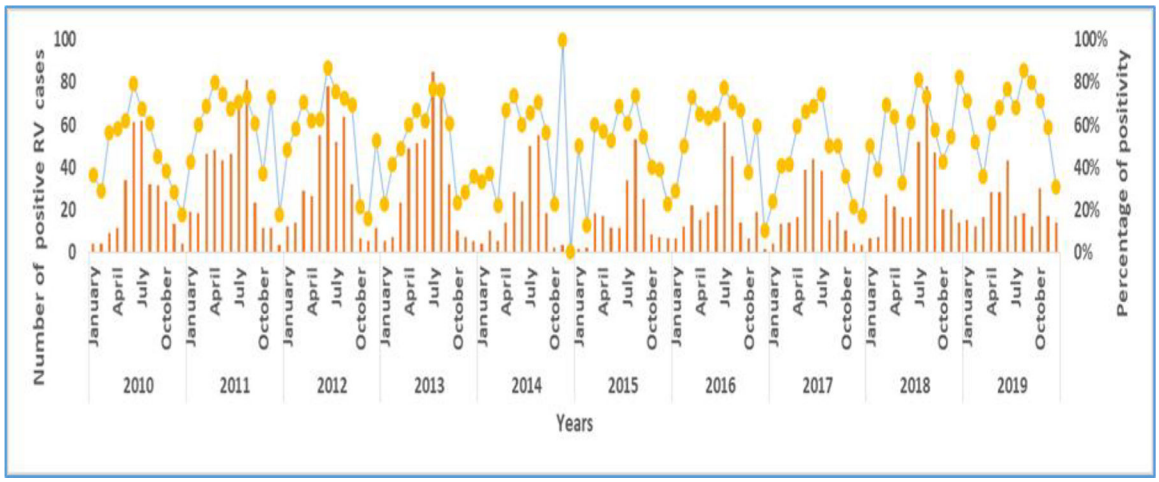

Figure 1:
Temporal distribution of rotavirus gastroenteritis cases from 2010 to 2019.

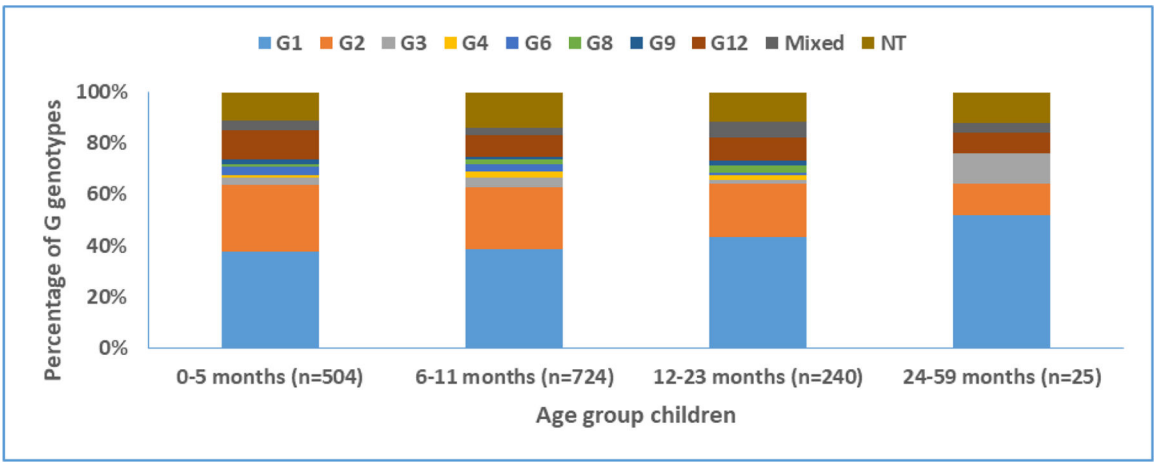

Figure 2:
Proportions of G genotypes by age group.

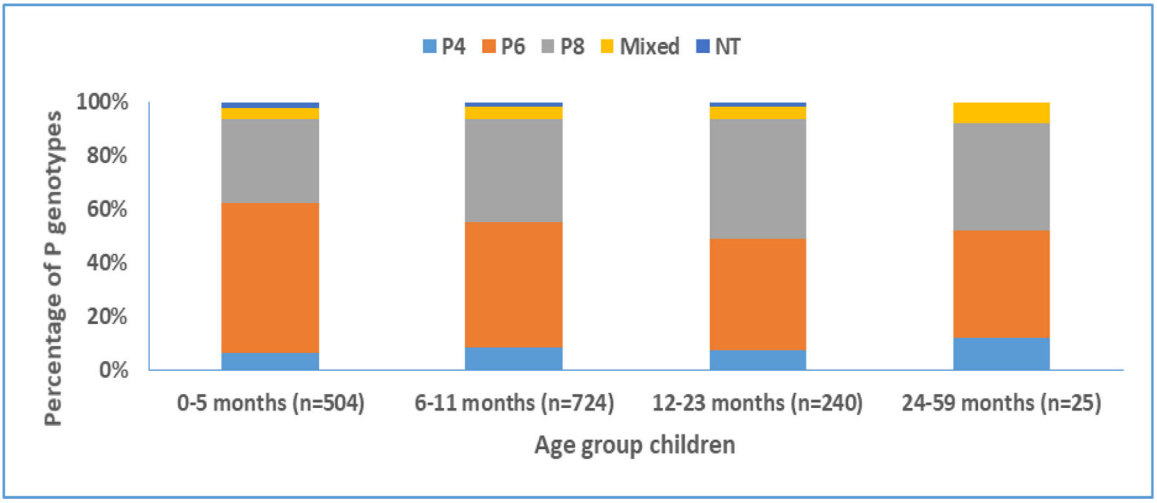

Figure 3:
Proportion of P genotypes by age group

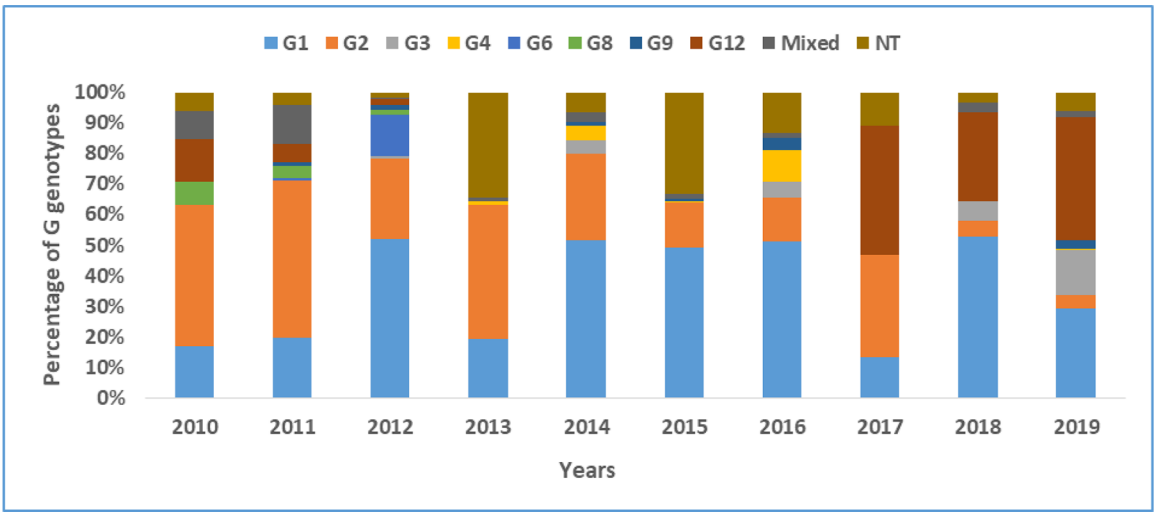

Figure 4:
Temporal evolution of the proportions of G genotypes from 2010 to 2019.

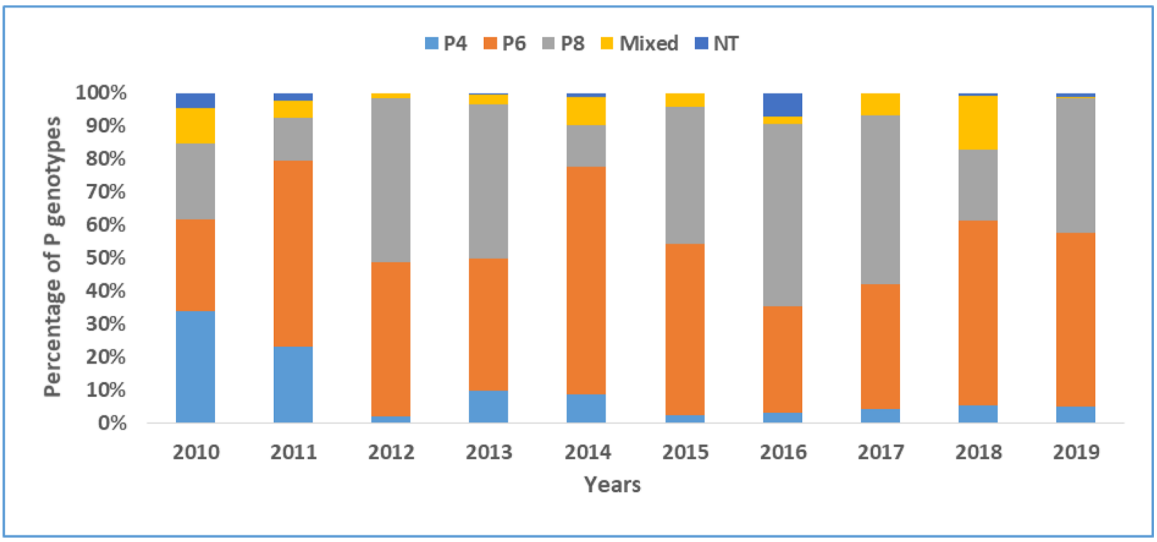

Figure 5:
Temporal evolution of the proportions of P genotypes from 2010 to 2019.

Table n° 1:

Sociodemographic characteristics of children admitted to rotavirus surveillance sites from August 2009 to December 2019.

	Sentinel sites							
	All sites		CHK*		HPK*		HGS*	
	RV−	RV+	RV−	RV+	RV−	RV+	RV−	RV+
Sex								
Female	888 (45%)	1275 (43%)	374 (45%)	432 (41%)	315 (45%)	597 (44%)	199 (46%)	246 (47%)
Male	1097 (55%)	1668 (57%)	452 (55%)	627 (59%)	391 (55%)	763 (56%)	254 (54%)	278 (53%)
Age								
0–5 months	543 (27%)	953 (32%)	180 (22%)	311 (29%)	202 (29%)	412 (30%)	161 (36%)	230 (44%)
6–11 months	987 (50%)	1428 (49%)	455 (55%)	529 (50%)	350 (50%)	676 (50%)	182 (40%)	223 (44%)
12–23 months	382 (19%)	508 (17%)	168 (20%)	202 (19%)	140 (20%)	243 (18%)	74 (16%)	63 (12%)
24–59 months	73 (4%)	54 (2%)	23 (3%)	17 (2%)	14 (1%)	29 (2%)	36 (8%)	8 (2%)
Total	1985	2943	826	1059	706	1360	453	524

*(CHK: centre hospitalier de Kingasani, HPK: Hôpital pédiatrique de Kalembelembe et HGS: Hôpital Général Sendwe), RV-: Rotavirus negative, and RV+: Rotavirus positive.

Table n°2:

Clinical characteristics of children admitted to Rotavirus surveillance sites from August 2009 to December 2019.

Variables	Elisa test results		Sentinel sites			
	RV negative	RV positive	CHK*	HPK*	HGS*	All sites
Treatment site						
Hospitalization	782 (39%)	1030 (35%)	867 (46%)	398 (19%)	547 (56%)	1812 (37%)
Emergency department	1203 (61%)	1913 (65%)	1018 (54%)	1668 (81%)	430 (44%)	3116 (63%)
Duration of diarrhea before admission (days)						
Mean ± standard deviation	2.52 ± 2.12	2.41 ± 1.76	2.71 ± 1.87	2.21 ± 1.53	2.48 ± 2.56	2.46 ± 1.91
Median [Q1, Q3]	2 [1,3]	2 [1,3]	3 [2,3]	2 [1,3]	2 [1,3]	2 [1,3]
Minimum	0	0	0	0	0	0
Maximum	28	26	28	12	28	28
Vomiting associated with diarrhea						
Yes	1765 (89%)	2773 (94%)	1881 (100%)	1912 (93%)	745 (77%)	4538 (92%)
No	216 (11%)	160 (5%)	3 (0%)	154 (7%)	219 (22%)	376 (8%)
Not specified	4 (0%)	10 (0%)	1 (0%)	0 (0%)	13 (1%)	14 (0%)
General condition on admission						
Awake, active	829 (42%)	1042 (35%)	1448 (77%)	267 (13%)	156 (16%)	1871 (38%)
Restless, irritable	1120 (56%)	1854 (63%)	427 (23%)	1791 (87%)	756 (77%)	2974 (60%)
Lethargic or unconscious	17 (1%)	23 (1%)	4 (0%)	7 (0%)	29 (3%)	40 (1%)
Not specified	19 (1%)	24 (1%)	6 (0%)	1 (0%)	36 (4%)	43 (1%)
State of thirst on admission						
Not thirsty, drinks normally	894 (45%)	1161 (39%)	1470 (78%)	387 (19%)	198 (20%)	2055 (42%)
Thirsty, drinks eagerly	1038 (52%)	1705 (58%)	406 (22%)	1637 (79%)	700 (72%)	2743 (56%)
Drinks with difficulty, unable to drink	26 (1%)	40 (1%)	3 (0%)	36 (2%)	27 (3%)	66 (1%)
Not specified	27 (1%)	37 (1%)	6 (0%)	6 (0%)	52 (5%)	64 (1%)
Level of dehydration on admission						
Severe	1136 (57%)	1703 (58%)	1841 (98%)	808 (39%)	190 (19%)	2839 (58%)
Moderate	799 (40%)	1196 (41%)	44 (2%)	1258 (61%)	693 (71%)	1995 (40%)
State of shock	7 (0%)	16 (1%)	0 (0%)	0 (0%)	23 (2%)	23 (0%)
No signs of dehydration	22 (1%)	14 (0%)	0 (0%)	0 (0%)	6 (4%)	36 (1%)

Variables	Elisa test results		Sentinel sites			
	RV negative	RV positive	CHK*	HPK*	HGS*	All sites
Not specified	21 (1%)	14 (0%)	0 (0%)	0 (0%)	35 (4%)	35 (1%)
Maximum temperature during hospitalization						
≤ 37°C	397 (20%)	558 (19%)	52 (3%)	593 (29%)	310 (32%)	955 (19%)
37.1°C – 37.9°C	460 (23%)	772 (26%)	673 (36%)	416 (20%)	143 (15%)	1232 (25%)
38°C - 41°C	1088 (55%)	1582 (54%)	1160 (62%)	1050 (51%)	460 (47%)	2670 (54%)
Not specified	40 (2%)	31 (1%)	0 (0%)	7 (0%)	64 (7%)	71 (1%)
Outcome at discharge						
Recovered	1809 (91%)	2797 (95%)	1838 (98%)	2017 (98%)	751 (77%)	4606 (93%)
Deceased	39 (2%)	43 (1%)	27 (1%)	48 (2%)	7 (0,5%)	82 (2%)
Transferred	8 (0,5%)	5 (0,4%)	11 (0,6%)	1 (0%)	1 (0%)	13 (0,5%)
Left against medical advice	6 (0,5%)	9 (0,6%)	9 (0,4%)	0 (0%)	6 (0,5%)	15 (0,5%)
Not specified	123 (6%)	89 (3%)	0 (0%)	0 (0%)	212 (22%)	212 (4%)
Duration of hospitalization						
Mean ± standard deviation	3.67 ± 4.25	3.56 ± 3.61	2.54 ± 3.45	4.13 ± 3.14	4.83 ± 5.65	3.61 ± 3.87
Median [Q1, Q3]	3 [1,5]	3 [1,5]	1 [1,4]	4 [2,5]	3 [2,6]	3 [1–5]
Minimum	0	0	0	0	0	0
Maximum	60	65	60	48	65	65
Total	**1985**	**2943**	**1885**	**2066**	**977**	**4928**

*(CHK= centre hospitalier de Kingasani, HPK= Hôpital pédiatrique de Kalembelembe, HGS= Hôpital Général Sendwe), Q1: 1st quartile, Q3: 3rd quartile.

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Table n°3:

Distribution of G and P genotype associations from 2009 to 2019.

Genotypes	Sentinel sites			
	CHK	HPK	HGS	All sites
P-types (VP4)				
P[4]	23 (6%)	59 (8%)	30 (8%)	112 (8%)
P[6]	179 (46%)	349 (47%)	201 (56%)	729 (49%)
P[8]	162 (42%)	293 (39%)	101 (28%)	556 (37%)
Mixed *1	17 (4%)	25 (3%)	26 (7%)	68 (5%)
NT **	5 (1%)	20 (3%)	3 (1%)	28 (2%)
G-types (VP7)				
G1	133 (34%)	331 (44%)	121 (34%)	585 (39%)
G2	87 (23%)	180 (24%)	94 (26%)	361 (24%)
G3	2 (1%)	15 (2%)	33 (9%)	50 (3%)
G12	60 (15%)	16 (2%)	68 (19%)	144 (10%)
Others	25 (6%)	74 (10%)	10 (3%)	109 (7%)
Mixed *2	15 (4%)	31 (4%)	9 (2%)	55 (4%)
NT **	64 (17%)	99 (14%)	26 (7%)	189 (13%)
Combined genotypes				
G1P[8]	83 (22%)	219 (29%)	29 (8%)	331 (22%)
G1P[6]	41 (11%)	94 (13%)	78 (22%)	213 (14%)
G2P[4]	20 (5%)	43 (6%)	14 (4%)	77 (5%)
G2P[6]	54 (14%)	116 (16%)	65 (18%)	235 (16%)
G3P[6]	0 (0%)	8 (1%)	25 (7%)	33 (2%)
G6P[6]	13 (3%)	24 (3%)	1 (0%)	38 (3%
G12P[6]	28 (7%)	5 (1%)	10 (3%)	43 (3%)
G12P[8]	30 (8%)	11 (1%)	45 (12%)	86 (6%)
Others	117 (30%)	226 (30%)	94 (26%)	437 (29%)

* Mixed: infections combining several genotypes;

** NT: Not typable

[1]There were also mixed P genotype infections in the following combinations: P[4]+P[6], P[4]+P[6]+P[8], P[4]+P[8] and P[6]+P[8].

[2]Regarding the forms of mixed infections identified, 11 different combinations of the following G genotypes were detected: G1+G2, G1+G4, G1+G8, G1+G9, G1+G12, G2+G12, G3+G8, G3+ G9, G3+G9+G12, G8+G12 and G8+G9.