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Transmission of *Cryptosporidium* Species Among Human and Animal Local Contact Networks in Sub-Saharan Africa: A Multicountry Study

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Background. Cryptosporidiosis has been identified as one of the major causes of diarrhea and diarrhea-associated deaths in young children in sub-Saharan Africa. This study traces back *Cryptosporidium*-positive children to their human and animal contacts to identify transmission networks.

Methods. Stool samples were collected from children < 5 years of age with diarrhea in Gabon, Ghana, Madagascar, and Tanzania. *Cryptosporidium*-positive and -negative initial cases (ICs) were followed to the community, where stool samples from households, neighbors, and animal contacts were obtained. Samples were screened for *Cryptosporidium* species by immunochromatographic tests and by sequencing the 18S ribosomal RNA gene and further subtyped at the 60 kDa glycoprotein gene (*gp60*). Transmission clusters were identified and risk ratios (RRs) calculated.

Results. Among 1363 pediatric ICs, 184 (13%) were diagnosed with *Cryptosporidium* species. One hundred eight contact networks were sampled from *Cryptosporidium*-positive and 68 from negative ICs. Identical *gp60* subtypes were detected among 2 or more contacts in 39 (36%) of the networks from positive ICs and in 1 contact (1%) from negative ICs. In comparison to *Cryptosporidium*-negative ICs, positive ICs had an increased risk of having *Cryptosporidium*-positive household members (RR, 3.6 [95% confidence interval {CI}, 1.7–7.5]) or positive neighboring children (RR, 2.9 [95% CI, 1.6–5.1]), but no increased risk of having positive animals (RR, 1.2 [95% CI, .8–1.9]) in their contact network.

Conclusions. Cryptosporidiosis in rural sub-Saharan Africa is characterized by infection clusters among human contacts, to which zoonotic transmission appears to contribute only marginally.

Keywords. cryptosporidium; transmission; molecular epidemiology; Africa.

The apicomplexan parasite *Cryptosporidium* is the causative agent of cryptosporidiosis in a wide range of vertebrate hosts [1]. Infections can remain asymptomatic but may lead to malnutrition, persistent growth retardation, and cognitive deficits [2, 3]. *Cryptosporidium* species are responsible for large waterborne outbreaks, especially in industrialized countries [4, 5], and have been identified as a major cause of diarrhea and diarrhea-associated deaths in young children in sub-Saharan Africa [6, 7]. In this region, an estimated 2.9 million cases occur annually in children < 2 years of age. Despite this tremendous public health burden, there is only suboptimal treatment, and no vaccine is currently available [8].

So far, 38 *Cryptosporidium* species have been recognized, with *Cryptosporidium hominis* and *Cryptosporidium parvum* being the main human pathogens. Data from genotyping studies have supported human-to-human (anthroponotic) transmission as the major route for pediatric infection in endemic regions, despite close human–animal contact in these settings [9–11]. However, studies have been restricted to single-site locations and specific study populations, such as people living with human immunodeficiency virus or immunocompromised hosts, patients in tertiary care hospitals, or symptomatic patients with diarrhea [11]. Furthermore,

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although the One Health approach has been widely promoted in recent years, the majority of studies on cryptosporidiosis thus far have focused on either animals or humans, limiting our understanding of *Cryptosporidium* transmission and epidemiology.

The present study aims to identify *Cryptosporidium* transmission networks and reservoirs in Gabon, Ghana, Madagascar, and Tanzania by tracing back infected children to their closest human and animal contacts.

METHODS

Study Sites

The study took place at 4 study sites in sub-Saharan Africa, namely the Albert Schweitzer Hospital and Georges Rawiri Hospital in Lambaréné, Gabon, the Agogo Presbyterian Hospital in the Ashanti Region of Ghana, the Korogwe District Hospital in the Tanga Region of Tanzania, and the Imerintsiatosika Health Post in the rural outskirts of Antananarivo, Madagascar. Ethical approval for the study was obtained from the respective ethics committees (see Supplementary Methods for country details).

Sampling Procedure

Between November 2016 and April 2018, stool samples were collected from all children < 5 years of age presenting to outpatient departments with diarrhea or a history of diarrhea, defined as at least 3 loose stools in 24 hours within the past 3 days. Stool samples from all children were screened for *Cryptosporidium* species with an immunochromatographic rapid test (Certest Biotech, Zaragoza, Spain). In case of a positive test result, 1 stool sample per contact of the initial case (IC) was collected as follows: (1) household contact (HC), defined as somebody who lives on the same compound sharing food on a regular basis with the IC; (2) neighboring children (NC) < 5 years of age living in the proximity of the IC with regular contact to the IC's family; and (3) animal contacts (ACs), defined as ruminants (ie, goats, sheep, cows) and dogs belonging to the family or kept within a 100-m radius around the respective household. Chickens, although common, were not considered due to difficulties in obtaining fresh fecal specimens. Samples from contacts were only considered for further analysis when collected within 1 week after an IC was identified.

A subset of children with a negative rapid diagnostic test for *Cryptosporidium* species (later confirmed by polymerase chain reaction [PCR] as described below) were followed to their homes and contact samples were collected as described above. Data from these children and their contacts were included in the analysis as negative control data. Contact networks from positive ICs are hereinafter referred to as positive IC networks and those from negative ICs as negative IC networks.

Molecular Characterization

The molecular analyses are described in detail in the Supplementary Methods. In brief, all study stool samples arrived within 24 hours in the laboratory and DNA was extracted using the Qiagen DNeasy PowerSoil Kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions. *Cryptosporidium* species were identified using a nested PCR protocol for the amplification of the 18S ribosomal RNA gene as published previously [12]. All samples positive for *C. hominis* or *C. parvum* were further subtyped by sequencing a 850-bp fragment of the *gp60* gene using a nested PCR as previously described [13, 14]. For a sample subset, 4 loci containing short sequence repeats (TP14, MS9, MM18, and MM19) were amplified by PCR as previously described [15] to confirm identified *gp60* subtype clusters.

Data Analysis

Transmission clusters were defined as at least 2 *Cryptosporidium* cases with the same *gp60* subtype diagnosed among contacts (HCs, NCs, or ACs) of an individual IC—that is, occurring within the same contact network. This cluster analysis was also applied to the negative IC networks, and the number of clusters within negative IC networks was compared to the number of clusters within positive IC networks. The statistical analysis is described in detail in the Supplementary Methods.

RESULTS

Between May 2016 and April 2018, 1363 ICs with diarrhea were recruited. Of these, 184 (13%) tested positive for *Cryptosporidium* species. The highest proportion of positive ICs was identified in Gabon (n = 44 [21%]), while the prevalence at the other study sites ranged between 11% and 15% (Table 1). Contacts of positive ICs were sampled, resulting in a total of 350 HCs, 258 NCs, and 338 ACs, of which 47 (13%), 60 (23%), and 45 (13%), respectively, were positive for *Cryptosporidium* species. The fraction of positive samples was therefore highest among NCs, even higher than in ICs. In Gabon, no samples from NCs or ACs were available.

In addition to the contacts of positive ICs, contacts from 68 negative patients were investigated to construct negative control contact networks. Characteristics of the positive ICs contacts from the 4 study countries and the pooled negative IC contacts are summarized in Table 1.

The proportion of *Cryptosporidium* infections in all study individuals was highest in participants aged 1–2 years and decreased with increasing age (Figure 1). Comparable age-stratified infection rates were observed in ICs with diarrhea and their human contacts.

Distribution of *Cryptosporidium* Species and *gp60* Subtypes

The distribution of *Cryptosporidium* species differed among humans and animals. Apart from Madagascar, where no

Table 1. Characteristics of the Study Participants and Identified *Cryptosporidium* Species, by Study Site and Sampling Group

Characteristic	Initial Cases	Household Contacts	Neighboring Children	Animal Contacts
Gabon				
Observations, No.	214	79	0	0
Age, y, median (IQR)	0 (0–1)	15 (6–25)	…	…
Female sex	93 (43)	48 (62)	…	…
Cryptosporidium spp	44 (21)	16 (20)	…	…
C. hominis	35 (80)	13 (81)	…	…
C. parvum	8 (18)	2 (13)	…	…
C. meleagridis	1 (2)		…	…
C. felis		1 (6)	…	…
Ghana				
Observations, No.	410	105	97	133
Age, y, median (IQR)	1 (0–1)	15 (6–31)	3 (0–5)	ND
Female sex	183 (45)	75 (71)	43 (44)	ND
Cryptosporidium spp	47 (11)	11 (10)	18 (19)	20 (15)
C. hominis	26 (55)	4 (36)	8 (44)	
C. parvum	15 (32)	6 (55)	7 (39)	2 (10)
C. meleagridis	3 (6)	…	…	…
C. felis	2 (4)	1 (9)	3 (17)	
C. xiaovi/bovis	1 (2)	…	…	17 (85)
C. ubiquitum	…	…	…	1 (5)
Madagascar				
Observations, No.	209	52	50	80
Age, y, median (IQR)	1 (0–1)	21 (18–36)	3 (1–3)	ND
Female sex	106 (51)	35 (67)	23 (46)	ND
Cryptosporidium spp	25 (12)	4 (8)	18 (36)	6 (8)
C. hominis	20 (80)	4 (100)	16 (89)	3 (50)
C. meleagridis	5 (20)	…	2 (11)	…
C. xiaoi/bovis	…	…	…	1 (17)
C. canis	…	…	…	1 (17)
C. avian genotype III	…	…	…	1 (17)
Tanzania				
Observations, No.	462	114	111	125
Age, y, median (IQR)	1 (0–1)	18 (7–30)	3 (1–3)	ND
Female sex	216 (47)	67 (59)	61 (55)	ND
Cryptosporidium spp	68 (15)	16 (14)	24 (22)	19 (15)
C. hominis	63 (94)	15 (94)	19 (79)	10 (53)
C. parvum	3 (4)	1 (6)	2 (8)	…
C. meleagridis	1 (1)	…	1 (4)	…
C. felis	…	…	2 (8)	…
C. xiaoi/bovis	…	…	…	6 (32)
C. ubiquitum	…	…	…	2 (11)
C. ryanae	…	…	…	1 (5)
Negative initial cases and contacts (all countries)				
Observations, No.	68	215	162	244
Age, y, median (IQR)	1 (0–1)	20 (8–32)	2 (1–3)	ND
Female sex	22 (32)	122 (57)	92 (57)	ND
Cryptosporidium spp	0 (0)	8 (4)	13 (8)	27 (11)
C. hominis	…	4 (50)	10 (77)	8 (30)
C. parvum	…	2 (25)	1 (8)	…
C. meleagridis	…	1 (13)	…	…
C. felis	…	1 (13)	1 (8)	…
C. suis	…	…	1 (8)	1 (4)
C. xiaoi/bovis	…	…	…	11 (41)
C. canis	…	…	…	2 (7)
C. ubiquitum	…	…	…	2 (7)
C. ryanae	…	…	…	2 (7)
C. baileyi	…	…	…	1 (4)

Data are presented as no. (%) unless otherwise indicated.
Abbreviations: IQR, interquartile range; ND, not determined.

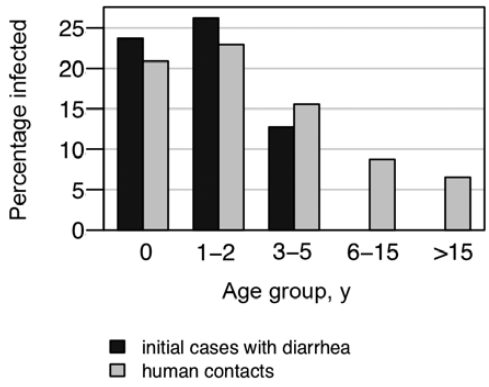

Figure 1. Proportion of *Cryptosporidium* species cases for initial patients and human contacts (household contacts and neighboring children), stratified by age.

C. parvum was detected, *C. hominis* (n = 237 [76%]) and *C. parvum* (n = 47 [15%]) were the most frequently detected species among humans, followed by *Cryptosporidium maleagridis* (n = 14 [5%]) and *Cryptosporidium felis* (n = 11 [4%]). Among animals, *C. hominis* was the most frequently detected species in Madagascar (n = 4 [57%]) and Tanzania (n = 17 [57%]), whereas *Cryptosporidium xiaoi/bovis* (n = 24 [89%]) was the most frequently detected species in Ghana (Table 1). Ghana was the only country where *C. parvum* was detected in animals (n = 2 [7%]). The distribution of *Cryptosporidium* species in the different animal hosts is described in Supplementary Table 1.

Subtyping for *gp60* was applied to *C. hominis* and *C. parvum* species to identify closely related strains, and data were available for 242 of 307 (79%) specimens; *gp60* subtyping revealed 25 *C. hominis* and 8 *C. parvum* subtypes, which were heterogeneously distributed over the study sites (Figure 2). Among the 8 *C. parvum* subtypes, 5 belonged to the IIc subtype family, likely to be of anthroponotic origin. Only 4 *C. hominis* and 1 *C. parvum* subtype were detected at > 1 study site, and no single *gp60* subtype was detected at all study locations.

Six *gp60* subtypes were responsible for > 50% of infections in humans and animals, namely *C. hominis* IeA11G3T3 (n = 42 [17%]), *C. hominis* IbA9G3 (n = 22 [9%]), *C. hominis* IaA15 (n = 21 [9%]), *C. hominis* IfA14G1 (n = 20 [8%]), *C. hominis* IdA22 (n = 13 [5%]), and *C. hominis* IaA24 (n = 13 [5%]). *gp60* diversity was highest in Gabon and Ghana, where the ratio of observed *gp60* subtypes over infected subjects was 0.24 (95% confidence interval [CI], .11–.40) and 0.21 (95% CI, .11–.33), respectively, compared to 0.13 (95% CI, .07–.21) in Tanzania and 0.11 (95% CI, .03–.25) in Madagascar.

Seasonal Distribution and Temporal Clustering

The seasonal occurrence of *gp60* subtypes in human and animal samples along with the monthly precipitation within the study regions are displayed in Figure 3. Seasonal patterns were visible in Ghana and Madagascar, where rising case numbers followed

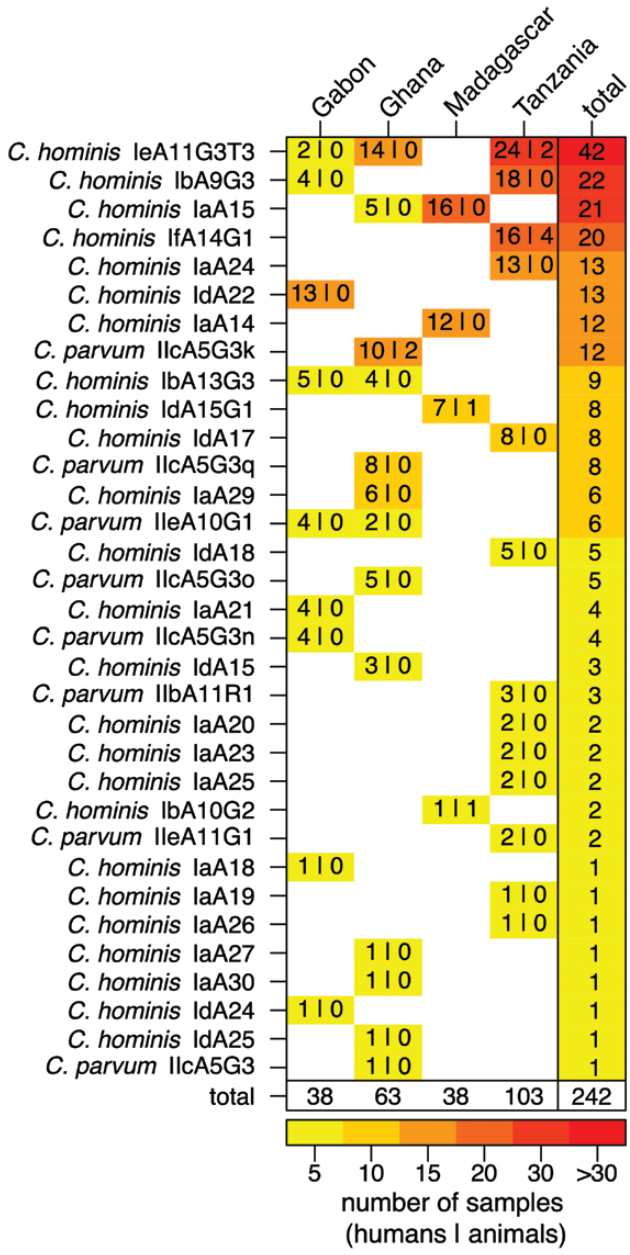

Figure 2. Frequency of *Cryptosporidium gp60* subtypes at the 4 study sites. Frequencies of *gp60* subtypes at the 4 study sites are presented for humans (first number) and animals (second number) along with strain and study site totals. The heatmap displays the lowest frequencies in yellow and the highest frequencies in red.

increasing precipitation. In all countries, particular *gp60* subtypes were detected repeatedly during the study period while other subtypes were only detected sporadically at distinct time points. In Ghana, for example, *C. hominis* IeA11G3T3 (n = 14) occurred within 8 months over a period of 15 months, while *C. parvum* IIeA10G1 (n = 2) was detected during 1 month only.

Overall, 112 of 177 (63%) infections belonged to a temporal cluster, defined as the occurrence of at least 2 isolates with the same *gp60* subtype occurring within a 2-week period at a study site. The proportion of subjects belonging to temporal clusters

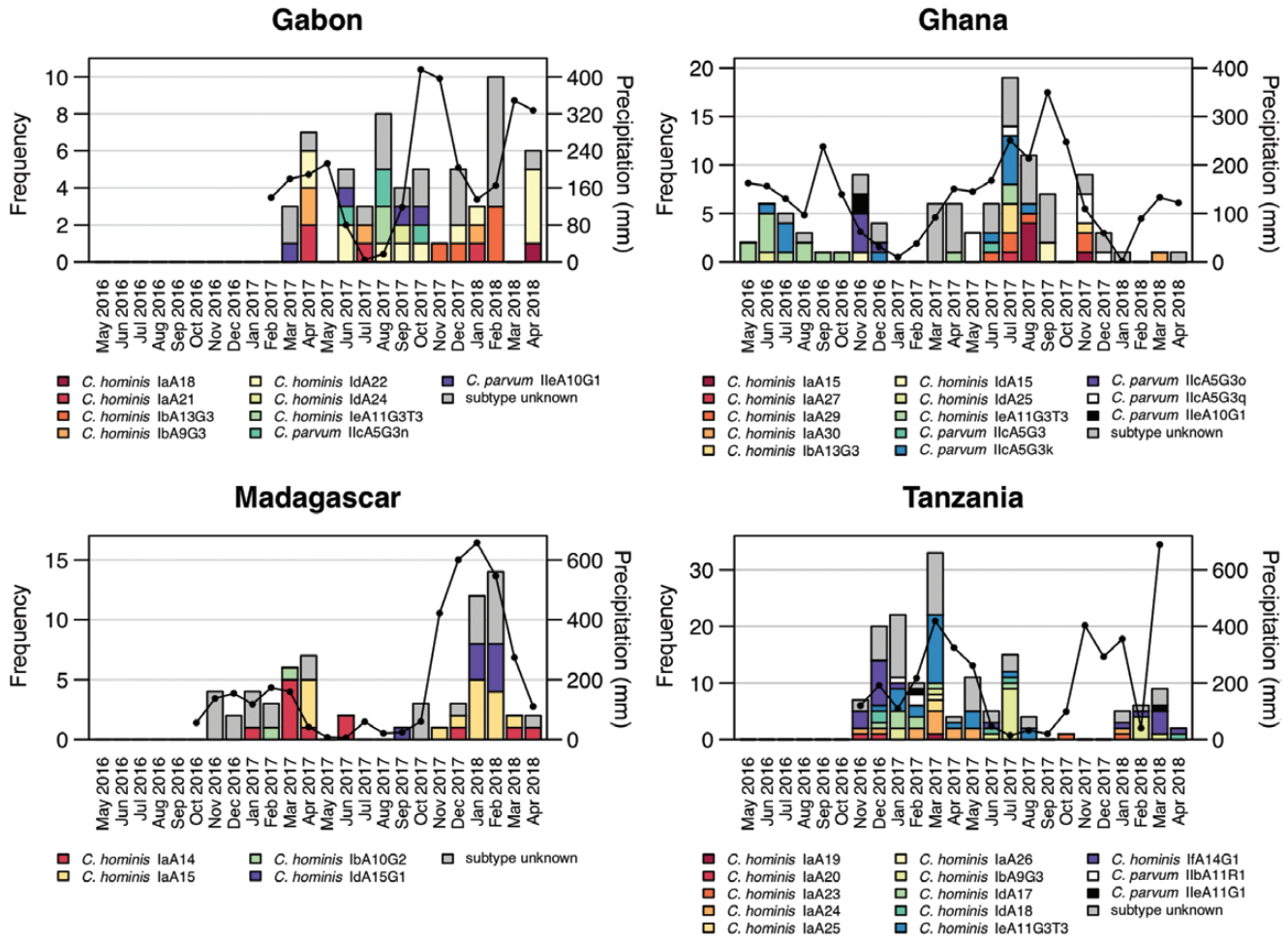

Figure 3. Occurrence of *gp60* subtypes over time at the 4 study sites. Gray bars represent *Cryptosporidium* species infections of unknown subtype. Black lines represent monthly precipitation (in millimeters, z-axis).

was considerably lower in Gabon (n = 4/21 [19%]). However, the overall contact network size was smaller in Gabon, containing ICs and HCs only, and therefore decreasing the likelihood of detecting identical *Cryptosporidium* subtypes. In total, among all countries, 55 temporal clusters were detected, which were composed of a median number of 3 (interquartile [IQR], 2–4) subjects and which persisted over a median time of 5 days (IQR, 2–12 days). The largest temporal cluster contained 11 humans and 2 animals infected with *C. hominis* IeA11G3T3 and occurred in Tanzania over a period of 32 days. However, nearly half of the temporal clusters (n = 27/55 [49%]) contained only 2 infected subjects.

Contact Networks and Transmission Clusters

In total, 108 positive IC contact networks were sampled: 17 in Gabon, 33 in Ghana, 19 in Madagascar, and 39 in Tanzania. As a comparison, contact networks from 68 *Cryptosporidium*-negative ICs were sampled (5 from Gabon, 11 from Ghana, 26 from Madagascar, and 26 from Tanzania). The composition of all contact networks, including proportions of HCs, NCs, and ACs within each network, is presented in Supplementary Figure 1.

The proportion of positive HCs (risk ratio [RR], 3.6 [95% CI, 1.7–7.5]) and positive NCs (RR, 2.9 [95% CI, 1.6–5.1]) was higher in positive IC networks compared to negative IC networks. However, the proportion of positive ACs was comparable between both groups (RR, 1.2 [95% CI, .8–1.9]). Thus, positive ICs were more likely to have *Cryptosporidium*-positive individuals than *Cryptosporidium*-positive animals in their households and neighborhood networks.

Transmission clusters were defined as at least 2 *Cryptosporidium* cases with the same *gp60* subtype diagnosed within the contact network of an individual IC. Among the 108 positive IC networks, 39 contained transmission clusters: 5 of 17 (29%) in Gabon, 15 of 33 (45%) in Ghana, 7 of 19 (37%) in Madagascar, and 12 of 39 (31%) in Tanzania, while only a single transmission cluster was identified among the negative IC networks (1/68 [1%]) (Figure 4). There was an 8.9 (95% CI, 1.2–65.7) times higher risk of transmission clusters occurring within positive compared to negative IC networks.

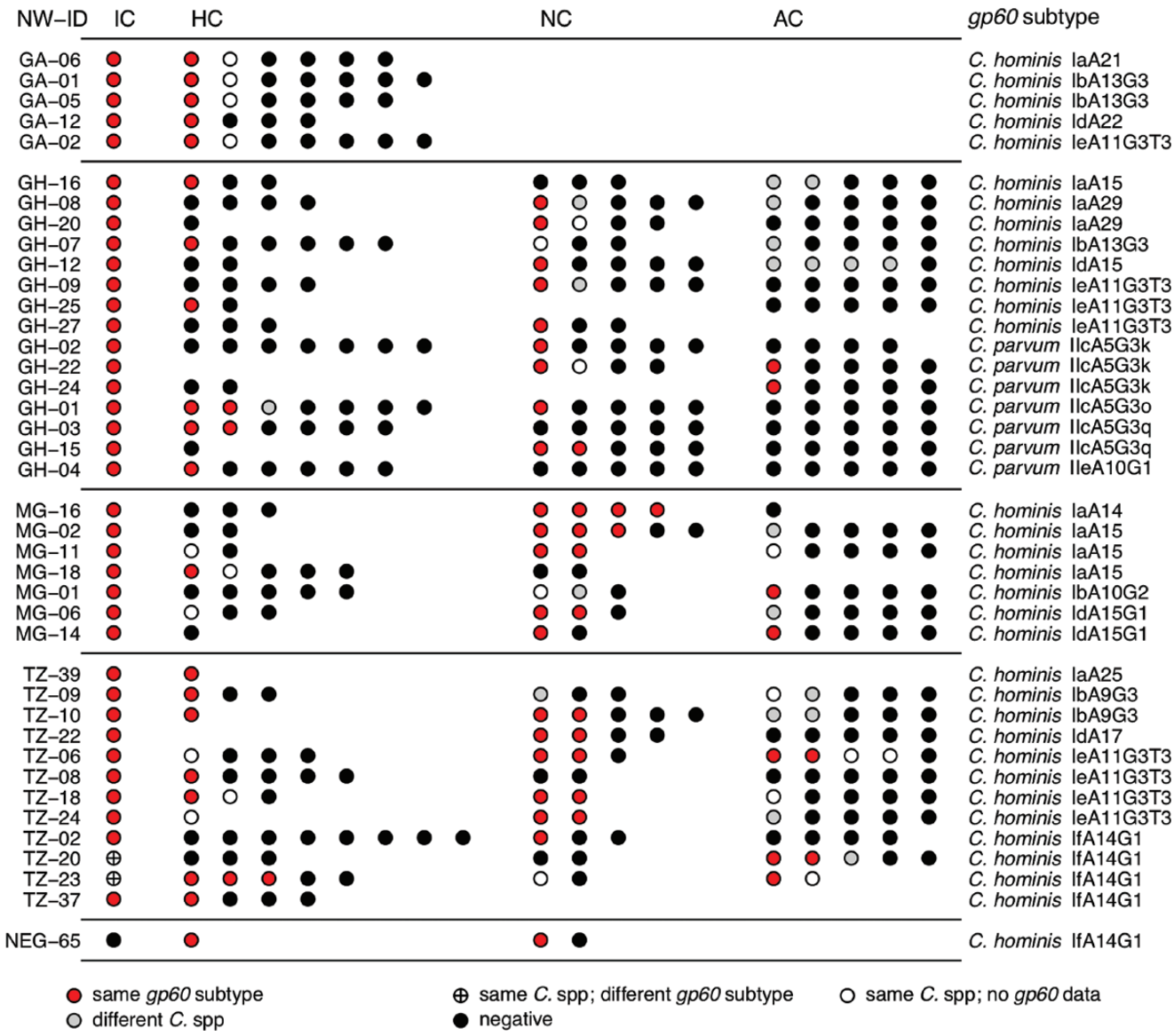

Figure 4. Transmission clusters of individual study subjects (circles) with identical *gp60* subtypes among contact networks at the different study sites. Cluster structures are displayed, including study subjects infected with the same *Cryptosporidium* species but lacking *gp60* data, which could potentially be related to the detected cases. The occurrence of differing, non-cluster-defining *Cryptosporidium* species within networks is also shown. Abbreviations: AC, animal contact; *C., Cryptosporidium*; GA, Gabon; GH, Ghana; HC, household contact; IC, initial case; MG, Madagascar; NC, neighboring child; NW-ID, network identifier as defined in Supplementary Figure 1; TZ, Tanzania.

Of the 433 study subjects (ICs, HCs, NCs, and ACs) who belonged to contact networks with transmission clusters, 147 (34%) tested positive for *Cryptosporidium* species, and of those, 104 (71%) were infected with the *gp60* subtype defining the cluster. Within these networks, 17% (24/144) of HCs and 31% (34/108) of NCs were positive for the cluster-defining *gp60* subtype (Figure 4). Animals were less likely to be positive for the respective *gp60* cluster subtype (9/141 [6%]).

The 40 contact networks with transmission clusters could be allocated to 36 temporal clusters (occurrence of at least 2 identical *gp60* strains within a time window of 2 weeks). Temporal clusters containing multiple transmission clusters of the same *gp60* subtype were only identified in Tanzania. The transmission clusters within networks TZ-06 and TZ-18, with 9 infected subjects, were nested within a *C. hominis* IeA11G3T3 temporal cluster, which lasted over 32 days with 13 infected subjects in total. The transmission clusters within networks TZ-20, TZ-23, TZ-37, and NEG-65, with 10 infected subjects, occurred within a *C. hominis* IfA14G1 temporal cluster, which lasted over 18 days with 11 infected subjects in total. GPS-coordinates indicate that TZ-06 and TZ-18 as well as TZ-20 and TZ-37 are neighboring families living within a distance of < 50 m.

Multilocus Variable Number of Tandem Repeats Analysis

To corroborate *gp60* clusters, 6 clusters with 23 *Cryptosporidium* species samples, for which sufficient genetic material remained

available, were selected for further variable number of tandem repeats (VNTR) analysis (Supplementary Table 2). Amplification of fragments encompassing tandem repeats was successful for 20 isolates (87%) at the TP14 locus, 19 isolates (83%) at the MM19 locus, 18 isolates (78%) at the MS9 locus, and 14 isolates (61%) at the MM18 locus. Notably, most animal samples positive for *C. hominis* could not be amplified at any of these loci. The combined analysis identified 4 different multilocus types, 1 of which was shared by 3 clusters of *C. parvum* IIc subtype in Ghana, while the remaining 3 were each found in 1 of the 3 *C. hominis* clusters from Tanzania (IeA11G3T3 and IdA17) and Madagascar (IaA14) (Supplementary Table 2). The VNTR analysis therefore supported the previously defined *gp60* clusters.

DISCUSSION

Across all study sites, 13% of hospital-attending children with diarrhea (in Gabon, up to 21%) were positive for *Cryptosporidium*, in agreement with the high prevalence in sub-Saharan Africa described by the Global Enteric Multicenter Study in 2013 [6]. Prevalence from other African studies varies widely, and comparisons are difficult to draw due to differences in age groups and detection methods [11]. Interestingly, our study detected a similarly high prevalence of *Cryptosporidium* species (18%) in the community, which suggests a high number of asymptomatic or mild diarrheal cases, which are missed by hospital-based studies. The clinical relevance of such cases has been demonstrated in Peru, where even asymptomatic infections were associated with growth retardation in children [16].

The high infection rate among household contacts and neighbors points toward the existence of *Cryptosporidium* transmission clusters. Indeed, *gp60* subtyping more frequently detected transmission clusters in neighborhoods with a positive initial child when compared to negative controls. While household members and neighboring children were significantly more likely to be part of transmission clusters, animals do seem to play a minor role for *Cryptosporidium* transmission.

Subtyping data from animals and humans in this study suggest a predominant anthroponotic transmission of *Cryptosporidium* species in sub-Saharan Africa. Previous studies from sub-Saharan Africa have similarly hypothesized a predominantly anthroponotic transmission in the region, but are based on either animal or human data [9, 11, 17]. Surveys including both human and animal samples combined with geospatial data collection for the identification of transmission clusters are lacking in sub-Saharan Africa [11]. A few existing One Health studies from Ghana and Nigeria do not allow any final conclusions on the extent of zoonotic transmission [18, 19]. A recent meta-regression analysis of *C. parvum* IIc prevalence data suggests that anthroponotic transmission prevails in lower-income countries due to limited access to sanitation facilities [10]. The high subtype diversity, which is commonly seen in sub-Saharan Africa [20] and also in the current study, is thought to reflect this intensive and stable anthroponotic transmission.

A distinct geographic distribution was observed in the present study, with only 5 of 33 *C. parvum* and *C. hominis gp60* subtypes detected in >1 country. For instance, subtype IdA22 was the most frequently detected subtype in Gabon, but was not detected at any other study site. However, this *C. hominis* subtype has previously been described in Kenya [17]. Similarly, the most commonly detected human *C. parvum* subtypes in Ghana (IIcA5G3k, IIcA5G3q, and IIcA5G3o) were exclusively found at this site. Such geographic segregation of *C. parvum* subpopulations has been observed before in European countries, Israel, and New Zealand [21, 22]. Interestingly, no *C. parvum* was identified in either humans or animals in Madagascar. *Cryptosporidium parvum* may not be a clinically relevant species in Madagascar; 2 previous studies from this region found only 1 child infected with *C. parvum*, while *C. hominis* and *Cryptosporidium suis* were the predominant human species [23, 24].

Although anthroponotic transmission appears to predominate in the study areas, there is evidence for the occurrence of zoonotic transmission. *Cryptosporidium hominis* was detected in 11 cows, 5 goats, and 1 sheep in Tanzania, and from 1 cow and 3 dogs in Madagascar. There is indeed increasing evidence that *C. hominis* not only infects humans, but can also be observed in symptomatic and asymptomatic animals [25]. The detection of *C. hominis* in animals, however, does not infer direct transmission from humans, as it may simply reflect circulation of *C. hominis* in the animal reservoir of the study region. Nevertheless, the present data suggest potential zoonotic transmission of the *C. hominis* subtypes IeA11G3T3 and IfA14G1 within Tanzanian clusters (detected in humans, cows, and goats) and IbA15G1 and IbA10G2 within Malagasy clusters (detected in humans and dogs). Furthermore, *C. parvum* IIcA5G3k was found in humans and goats in a Ghanaian transmission cluster. IIcA5G3k has so far only been described in humans from Nigeria [26, 27]. Formerly considered an anthroponotic subtype, other IIcA5G3 variants have since been detected in a goat (IIcA5G3q) from Ghana and from hedgehogs (IIcA5G3j) in the United Kingdom and Germany [19, 28, 29]. Zoonotic IIa subtypes, prevalent in some European countries, Australia, Canada, and the United States [20], were not observed in this study and indeed are rarely seen in sub-Saharan Africa [11].

The high proportion of HCs (17%) and NCs (31%) positive for cluster-defining *gp60* subtypes supports the hypothesis of predominantly anthroponotic transmission within households and neighborhoods. The higher proportion among neighboring children can be explained by the fact that cryptosporidiosis primarily affects young children <2 years of age, whereas adults were included among household contacts. This transmission pattern points to a common neighborhood source, such as shared sanitation facilities or water sources.

In agreement with our results, a study from Bangladesh identified person-to-person transmission of *Cryptosporidium* species among urban households characterized by crowded living conditions and shared sanitation facilities [30]. The present study design did not allow further risk factor analysis due to very similar household characteristics, such as sanitation facilities or housing conditions. Furthermore, the geographical extent of the identified neighborhood clusters could not be estimated, as samples from no more than 5 neighboring families were collected.

The VNTR analysis data supported the *gp60* subtype-defined transmission clusters identified in this study. Within spatiotemporally confined clusters, *gp60* subtyping may therefore represent a useful marker for epidemiological analysis, providing a good proxy for genome-wide variability. However, in high-transmission settings, discriminatory power may be limited due to extensive genetic recombination.

CONCLUSIONS

Cryptosporidiosis in rural sub-Saharan Africa is characterized by high subtype diversity, distinct geographic subtype distributions, and high prevalence, not only among children with diarrhea, but also among their household and neighborhood contacts. Animal infections contributed only marginally to the epidemiologically linked transmission clusters observed within neighborhoods. The data from all study sites provide evidence for the central role of anthroponotic transmission within neighborhoods and suggest common infection sources within the community. Water sources or shared sanitation facilities likely represent suitable targets for cryptosporidiosis prevention measures and integrated public health interventions.

Supplementary Data

Supplementary materials are available at *Clinical Infectious Diseases* online. Consisting of data provided by the authors to benefit the reader, the posted materials are not copyedited and are the sole responsibility of the authors, so questions or comments should be addressed to the corresponding author.

Notes

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