



Gastrointestinal illness among attendees of the FIFA Football World Cup 2022 in Qatar

Sherin Shams¹, Thoraya Alyafei², Hanaa Nafady-Hego³, Emad Bashier Ibrahim Elmagboul^{2,4}, Aimon B. Malik¹, Anil G. Thomas¹, Samah Saleem¹, Zain Bhutta⁵, Atika Jabeen⁵, Muna Almaslamani⁶, Abdullatif Alkhal⁶, Aftab M. Azad^{5,7}, Abdul-Badi Abou-Samra¹, Adeel A. Butt^{1,8,9,*}

¹ Corporate Quality and Patient Safety Department, Hamad Medical Corporation, Doha, Qatar

² Department of Laboratory Medicine and Pathology, Hamad Medical Corporation, Doha, Qatar

³ Microbiology and Immunology department, faculty of Medicine, Assiut University, Assiut, Egypt

⁴ Biomedical Research Center, Qatar University, Doha, Qatar

⁵ Department of Emergency Medicine, Hamad Medical Corporation, Doha, Qatar

⁶ Communicable Diseases Center, Hamad Medical Corporation, Doha, Qatar

⁷ College of Medicine, Qatar University, Doha, Qatar

⁸ Departments of Medicine and Population Health Sciences, Weill Cornell Medicine New York, USA

⁹ Departments of Medicine and Population Health Sciences, Weill Cornell Medicine, Ar-Rayyan, Qatar

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ABSTRACT

Objectives: Mass gathering events may facilitate the transmission of foodborne diseases. We determined the presentations and causative organisms of gastrointestinal illness among the attendees of the Fédération Internationale de Football Association Football World Cup 2022 (FIFA 2022).

Methods: The study was conducted at Hamad Medical Corporation in Qatar, which served as the national reference laboratory for all microbiology testing. We retrieved all stool testing data from the attendees of FIFA 2022 from October 1 to December 31, 2022. Stool microscopy for ova and parasite and cultures were performed on all samples. Polymerase chain reaction testing was performed for cases of suspected foodborne outbreaks or when a rapid result was required for public health response.

Results: Among 2179 samples tested, one or more organisms were identified in 424 cases. The most common reasons for testing were acute diarrhea/gastroenteritis (51.4%), abdominal pain (11.5%), screening/surveillance of contacts (10.6%), and fever (7.6%). Bacteria were identified in 92.5% (*Salmonella* spp. 40%, *Escherichia coli* 25.7%, and *Shigella* spp. 8.8%), viruses in 7.8%, and parasites in 2.8% of the samples.

Conclusions: The number of individuals who underwent stool testing during the FIFA 2022 was low. The yield of stool testing was higher for those with acute diarrhea/gastroenteritis and fever but not for those with abdominal pain or for surveillance/screening.

Introduction

The World Health Organization defines a mass gathering event as “a planned or spontaneous event where the number of people attending could strain the planning and response resources of the community or country hosting the event [1].” Mass gathering events have the potential to facilitate the transmission of infectious diseases due to the large numbers and close proximity of the attendees. Due to the diverse geographical origin of the attendees, infectious diseases not endemic

in the hosting nation may be imported and may be challenging to detect. Respiratory and foodborne illnesses pose an especially high risk of transmission. The annual global burden of acute diarrheal illness is approximately 2.4 billion infections [2]. During the 2019 Hajj (the annual Muslim pilgrimage to Mecca in Saudi Arabia that routinely attracts over 2.5 million pilgrims and is among the largest annual mass gathering event worldwide) [3], 9.7% of the approximately 2.5 million pilgrims experienced gastrointestinal symptoms, with 5.1% of those reporting diarrhea [4]. A large outbreak of acute diarrheal/gastrointestinal illness

* Corresponding author.

E-mail address: aabutt@hamad.qa (A.A. Butt).

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at a mass gathering event can rapidly overwhelm health care resources, and, therefore, robust planning and resource allocation are required to effectively manage a potential outbreak.

Qatar hosted one of the largest global sporting events, the Fédération Internationale de Football Association Football World Cup (FIFA 2022) from November 20 through December 18, 2022. During this period, over 1.4 million visitors arrived in Qatar [5,6]. Qatar proactively developed a comprehensive surveillance, reporting, and management plan for providing health care services to all attendees requiring any such care. Our aim was to determine the number of persons who presented to any health care facility or unit with gastrointestinal illness and investigate the possible etiologic agents for acute diarrheal illnesses.

Methods

Study setting

The study was conducted at Hamad Medical Corporation (HMC) in Qatar, a public sector network of tertiary, secondary, and specialty hospitals throughout the country. HMC was designated as the provider and overseer of health care during the event to all visitors. In addition, HMC laboratories served as the centralized national reference laboratory for all microbiology testing, ensuring complete capture of microbiology data. All HMC facilities are accredited by the Joint Commission International (Chicago, IL, USA); the laboratories are accredited by the College of American Pathologists (Northfield, IL, USA) and use the same electronic medical records platform (Cerner, Kansas City, MO, USA) for clinical documentation and pharmacy management.

During FIFA 2022, HMC set up rapid medical evaluation units at each of the eight stadiums where matches were held. Additional units were set up at multiple “fan zones,” which were publicly accessible areas hosting multiple activities (e.g. concerts, live-match broadcast on large screens, etc.) throughout the duration of the tournament. Mobile health teams were stationed throughout the country where visitors and fans were housed. All services were linked to HMC and the national network of primary health care centers for any potential transfers or urgent or emergency care. These services were available and accessible to all visitors.

Study participants and data collection

We retrospectively retrieved all stool testing data sent to the HMC laboratories from October 1, 2022 to December 31, 2022. This included visitors who had entered the country for FIFA-2022 as well as long-term residents and Qatari nationals. Routine stool microscopy for ova and parasite and stool cultures were performed on all samples received. In addition, polymerase chain reaction (PCR) (BioFire Gastrointestinal Panel, BioFire Diagnostics, Salt Lake City, UT, USA) testing was performed on samples where foodborne illness outbreak was clinically suspected and/or a rapid result was required for immediate public health response. Data were retrieved from the microbiology laboratory database, including reason for testing (as listed by the requesting clinician), with additional demographic and clinical information retrieved from the individual electronic medical records. Results were tabulated by the reason for testing and type of organism(s) isolated.

Statistical analysis

The data were tested for normality using the Shapiro–Wilk test. Base-line summary statistics are presented as means with SDs for normally distributed data and medians with interquartile ranges for non-normally distributed data. For group comparisons, the Mann–Whitney U test was used to compare continuous variables and the chi-squared test for categorical variables. The odds ratios and 95% confidence intervals were computed using logistic regression to identify the variables linked to

PCR and/or culture positivity. Covariates having $P < 0.2$ in the univariable regression analysis were included in the stepwise multivariable model. In cases where P -values were produced, statistical significance was defined as a value < 0.05 . The data was analyzed using the Statistical Package of Social Sciences (IBM-SPSS 21 [IBM Corporation, Armonk, NY, USA]).

Ethical considerations

The study was reviewed by the institutional review board at HMC (MRC-01-23-004) and considered exempt due to its retrospective nature and anonymization of included individuals.

Results

A total of 2179 stool samples were tested in the HMC laboratories during the study period. Of the 2179 samples, PCR tests were conducted on 170 samples. The median age of the tested individuals was 31 years (interquartile range 5–45), 59% were males, and 74.2% were non-Qatari nationals (Table 1).

The most common reasons for testing were gastroenteritis or acute diarrhea (51.4%), abdominal pain (11.5%), screening/surveillance of potential contacts (10.6%), and fever (7.6%). A total of 424 (19.5%) samples tested positive for at least one organism by culture or PCR, with at least one bacterium identified in 393 (92.5%), virus in 33 (7.8%), and parasite in 12 (2.8%) of the individuals. Of the 463 bacterial isolates detected, the most common organisms were *Salmonella* spp. (185, 40%), *Escherichia coli* (119, 25.7%), *Shigella* spp. (41, 8.8%), gram-negative rods not further classified (32, 7%), and *Campylobacter* spp. (31, 6.7%) (Table 2). Among the 37 viruses detected, the most common were *Norovirus* (13, 35.1%), *Sapovirus* (eight, 21.6%), *Astrovirus* (seven, 19%), *Adenovirus* (five, 13.5%), and *Rotavirus* (four, 10.8%). Of the 12 parasites identified, seven were *Cryptosporidium* spp. and five were *Giardia* spp. (Table 2).

A list of bacterial, viral, and parasitic isolates detected by the reason for testing is provided in Supplementary Table 1. The most common reason for testing among those with a detectable organism was gastroenteritis/acute diarrhea. Other common reasons listed included fever, abdominal pain, and surveillance/screening (Supplementary Table 2). In a logistic regression model, factors associated with a lower risk of detecting an organism included testing in the pre-visitor phase (from October 1, 2022 to October 31, 2022) (odds ratio [OR] 0.73, 95% confidence interval [CI] 0.59–0.91) and increasing age (OR for each 10-year increase 0.95, 95% CI 0.91–1.00). Gastroenteritis or acute diarrhea as the reason for testing was associated with a higher risk of detecting an organism (OR 1.46, 95% CI 1.70–1.84) (Supplementary Table 2).

Discussion

We describe the spectrum of gastrointestinal symptoms and infections for which the attendees sought medical care during one of the world's largest mass gathering events. We also describe the putative causative organisms associated with those infections.

The most common reasons for stool testing were acute diarrhea/gastroenteritis, and more individuals with a putative organism detected on stool testing had acute diarrhea/gastroenteritis listed as the reason for testing. These are expected findings because individuals with clear acute gastrointestinal symptoms would be more likely to have a causative organism identified. This is partially borne out by the observation that abdominal pain was the second most common reason for testing and no difference was noted in the proportion of individuals with an organism detected on stool testing. The third most common reason for testing was surveillance/screening of potentially exposed individuals. In this group, there was no difference in proportion of individuals with an identified organism on stool testing. Fever was the

Table 1
Baseline characteristics of individuals who underwent stool testing.

	Overall N (%)	No organism identified N (%)	At least one organism identified N (%)	P-value
Median age (interquartile range)	2179 31.0 (5.0, 45.0)	1755 31.0 (5-46)	424 28.0 (5.0-41.0)	0.05
Sex, N (%)				0.63
Female	896 (41.1)	726 (41.4)	170 (40.1)	
Male	1283 (59.0)	1029 (58.6)	254 (60.0)	
Nationality N (%)				0.85
Qatari	563 (25.8)	455 (26.0)	108 (25.5)	
Non-Qatari	1616 (74.2)	1300 (74.1)	316 (74.5)	
Timeline				0.02
October 2022	888 (40.7)	690 (39.3)	198 (46.7)	
November 2022	691 (31.7)	572 (32.6)	119 (28.1)	
December 2022	600 (27.5)	493 (28.1)	107 (25.2)	
Time of testing^a				0.006
Pre-visitor phase	888 (40.8)	690 (39.3)	198 (46.7)	
Visitor phase	1291 (59.2)	1065 (60.7)	226 (53.3)	
Reason for testing^b				
Gastroenteritis/Acute diarrhea	1120 (51.4)	865 (49.3)	255 (60.1)	<0.0001
Abdominal pain	250 (11.5)	207 (11.8)	43 (10.1)	0.34
Surveillance/Screening	230 (10.6)	190 (10.8)	40 (9.4)	0.40
Fever	166 (7.6)	121 (6.8)	45 (10.6)	0.01
Bloody diarrhea	36 (1.7)	32 (1.8)	4 (0.9)	0.20
Cancer	27 (1.2)	24 (1.4)	3 (0.7)	0.27
Chronic diarrhea	19 (0.9)	15 (0.9)	4 (0.9)	0.86
Anemia	17 (0.8)	16 (0.9)	1 (0.2)	0.16
Liver disease	10 (0.5)	10 (0.6)	0	0.12
Pregnancy	8 (0.4)	6 (0.3)	2 (0.5)	0.69
Gastrointestinal bleeding	4 (0.2)	4 (0.2)	0	0.33
Inflammatory bowel disease	3 (0.1)	2 (0.1)	1 (0.2)	0.54
Not listed	447 (20.5)	374 (21.3)	73 (17.2)	0.06

^a Pre-visitor phase: starting from October 1, 2022 to October 31, 2022; visitor phase: starting from November 1, 2022 to December 31, 2022.

^b Some test requests listed more than one reason for testing.

Table 2

List of organisms detected by culture and/or PCR. (Note that the number of organisms is higher than that of the patients because some patients had more than one organism identified). At least one organism was detected in 424 individuals.

Bacteria	463
<i>Salmonella</i> spp. ^a	185 (40.0)
<i>E. coli</i>	119 (25.7)
<i>Shigella</i> spp. ^b	41 (8.8)
Gram Negative Rods ^c	32 (7.0)
<i>Campylobacter</i> ^d	31 (6.7)
<i>Citrobacter</i>	19 (4.1)
<i>Pseudomonas aeruginosa</i>	6 (1.3)
<i>Aeromonas</i>	5 (1.1)
Others ^e	25 (5.4)
Viruses	37
Norovirus	13 (35.1)
Sapovirus	8 (21.6)
Astrovirus	7 (19.0)
Adenovirus	5 (13.5)
Rotavirus	4 (10.8)
Parasites	12
<i>Cryptosporidium</i>	7 (58.3)
<i>Giardia</i>	5 (41.7)
Fungal	2
Yeast	2 (100)

^a Of these, five isolates were *S. typhi*. 14 were *S. paratyphi* B, and one was *S. paratyphi* C. The rest were non-typhoidal *Salmonella*.

^b Of these, 16 were *S. flexneri*, five were *S. sonnei*, three were *S. dysenteriae*, and one was *S. boydii*, and others were listed without species.

^c No further speciation provided.

^d *C. jejuni* (21); *C. coli* (four).

^e Others include *Vibrio* spp. (four), *Clostridium Difficile* (four), *Staphylococcus aureus* (three), *Klebsiella pneumoniae* (three), *Plesiomonas shigelloides* (two), *Enterobacter* (two), *Hafnia alvei* (two), *Morganella morganii* (one), *Proteus mirabilis* (one), *Burkholderia cepacia* (one), *Bacillus cereus* (one), and *Leclercia adecarboxylata* (one).

next most commonly listed reason for testing, and, again, more individuals in this category had an organism detected on stool testing. Collectively, these data suggest that stool testing may be more useful in identifying a putative causative organism in individuals who present with acute diarrhea/gastroenteritis or fever, whereas testing those with non-specific abdominal pain or for screening purposes may not be much useful.

The fewer parasites and *E. coli* were detected due to their detection solely through PCR, a procedure performed exclusively for the suspected population. Whether the lower number of cases of *Rotavirus* was due to the routine administration of *Rotavirus* vaccination in the individual's country of origin was not studied.

Previously published reports list Norovirus as the most common etiologic agent in acute gastroenteritis and foodborne illness outbreaks worldwide [7,8]. Among the bacteria, *Salmonella*, *E. coli*, and *Campylobacter* are the leading cause of acute gastroenteritis and foodborne illnesses. In our study, bacterial isolates were far more frequently observed in stool samples than viruses. Norovirus-associated acute gastroenteritis is often self-limited, which may have led those individuals to not seek medical care [9]. The route of transmission may have played a part in the pattern of spread of specific causative agents. For example, Norovirus is most commonly transmitted from person to person, whereas other agents may be more likely to be transmitted through contaminated food or water [9]. We did not investigate the routes of infection acquisition and, therefore, cannot determine whether this finding is due to specific eating behaviors or patterns of direct or indirect physical contact.

Although our study was not designed to calculate the incidence rate of gastroenteritis, our results indicate a low incidence of such infections during the duration of FIFA 2022. During the entire event, a total of 2179 individuals underwent stool testing of the 1.4 million visitors who entered Qatar during that period. It is possible that some individuals with mild or moderate symptoms may not have sought care and recovered without any formal medical intervention. It is also possible that

stool testing was not ordered for some individuals who presented with gastrointestinal symptoms. However, more serious cases would be expected to seek medical care, undergo testing, and require interventions. It is also noteworthy that three-quarters of the individuals who underwent stool testing were non-Qataris, comprising mostly or almost entirely of visitors who had entered the country for FIFA 2022.

The strengths of our study include an integrated health care system and a single reference laboratory where all individuals sought care and samples were tested. Several limitations also need to be considered while interpreting our results. Our data were collected during routine clinical care and not systematically and uniformly collected for all individuals who may have been infected with a foodborne or waterborne gastrointestinal illness. Our sample was limited to those individuals for whom a stool test was ordered by the clinical care provider. Individual care-seeking behavior and provider preference or biases in ordering stool tests may have biased our results. It should also be noted that mere detection of microorganisms in the stool samples does not necessarily imply the presence of disease or symptoms. Indeed, healthy individuals may have numerous bacteria and fungi, which may reside as commensals.

In summary, the number of individuals who sought care and underwent stool testing during FIFA 2022 was low. Bacteria were more frequently isolated than viruses. The yield of stool testing was higher for those presenting with acute diarrhea/gastroenteritis and fever but not for those with abdominal pain or for surveillance/screening.

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Ethical considerations

The study received an exemption from the institutional review board at Hamad Medical Corporation due to its conduct as a part of the national public health surveillance and testing program.

Author contributions

Concept and study design: AAB; drafting of the manuscript: AAB, SS (Shams); data collection: SS (Shams), TA, EBIE, ABM, AGT, SS (Saleem); data analysis and interpretation: AAB, HN; laboratory testing: TA, EBIE; critical appraisal and review: SS (Shams), TA, HN, EBIE, ABM, AGT, SS (Saleem), AMU, AA, AAB; final approval: SS (Shams), TA, HN, EBIE, ABM, AGT, SS (Saleem), AMU, AA, AAB.

Additional contributions

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Data access

Drs. Alyafei, Shams, and Butt had full access to all the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

Declarations of competing interest

Dr. Butt has received investigator-initiated grant funding from Gilead Sciences and Merck and Company (to the institution), which is unrelated to the work presented here. The remaining authors declare no financial conflict of interest regarding the content of this article.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.ijregi.2024.100493](https://doi.org/10.1016/j.ijregi.2024.100493).

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