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Pathogens associated with respiratory, gastrointestinal and febrile illness in patients consulting at Mbacke healthcare centre during the 2018 Grand Magal of Touba: A preliminary study

The annual Grand Magal of Touba (GMT) is the largest Muslim mass gathering in West Africa with about 4–5 million Mourides participating in the event [1]. During the 2015 GMT, of the 32,229 patients who consulted health services in Touba and the surrounding area, 22.0% reported gastrointestinal symptoms, 17.2% fever and 17.1% respiratory symptoms [2]. With the exception of rapid malaria tests, no microbiological investigations were conducted due to a lack of laboratory resources. In this preliminary study we investigated by polymerase chain reaction (PCR) (Supplementary document) the pathogens responsible for respiratory and gastrointestinal infection symptoms and for febrile syndrome in patients consulting at Mbacke healthcare centre close to Touba, during the GMT 2018. The centre operated 24 hours a day during the five days period of medical coverage of the GMT (26–October 30, 2018). Results were compared with those in asymptomatic matched control pilgrims (Supplementary Table 1). The protocol was approved by the National Ethics Committee for Health Research in Senegal (SEN17/62).

The study included 88 patients (51.1% female, median age 22 years, 46.6%) children < 15, 6.8% over 60). These patients were those presenting at the centre from 26 to October 28, 2018, between 9am and 5pm with the required symptoms. They accounted for 7.1% of all patients seen round the clock during this period. 56.7% patients came from other regions of Senegal to participate in the GMT. Out of 52 patients with a cough, 71.1% had rhinitis, 48.1% sore throat and 63.5% fever. 92.3% nasal and throat samples tested positive for at least one pathogen with influenza viruses A or B (42.3%), *H. influenzae* (63.5%), *S. pneumoniae* (46.1%) and *M. catarrhalis* (36.5%) the most frequent (Table 1). Asymptomatic controls also showed a high positive rate of bacterial carriage overall. Using multivariate analysis, coinfection with *H. influenzae* and virus was associated with a higher prevalence of respiratory tract infection symptoms (aOR = 16.9, 95%CI [3.71–77.78]). Of 23 patients with diarrhoea, 69.5% reported loss of appetite, 65.2% vomiting, 8.7% nausea, and 52.2% fever. 60.9% rectal samples were positive for at least one pathogen with bacterial carriage ranging from 8.6% for *T. wipplei* to 30.4% for EPEC. In controls, high rates of bacterial carriage were also observed, notably for EAEC in stool samples. Using multivariate analysis, EAEC carriage was negatively associated with the prevalence of gastrointestinal symptoms (aOR = 0.15, 95%CI [0.04–0.55]). Among 26 patients with systemic febrile illness, 19.2% were treated by antimalarial drugs and 19.2% received antibiotics. 50% blood samples tested positive for at least one pathogen. 26.9% tested positive for dengue virus, 19.2% for *P. falciparum,* and 3.8% for *Borrelia* sp.

In this preliminary study we were able to identify potential respiratory pathogens circulating at the GMT including influenza viruses, *H. influenzae, S. pneumoniae and M. Catarrhalis.* Very high rates of pathogens were detected among both patients suffering diarrhoea and asymptomatic controls, with none being significantly more prevalent among patients. This is likely to be because asymptomatic carriage of gastrointestinal pathogens is very frequent in Senegal, particularly when assessed using a very sensitive method such as PCR. This suggests that quantitative molecular methods should be used to better evaluate the etiological role of potential gastrointestinal pathogens in this setting [3]. Dengue and malaria were the most frequent pathogens responsible for fever in our study. During 2018, dengue outbreaks occurred in Senegal [4]. It should be noted that, according to national data, only one case was reported from Mbacké, as of December 9, 2018 [5]. We identified seven additional cases among the 26 febrile patients who were tested in Mbacké, which suggests that national surveillance data possibly underestimated the true burden of the epidemic. Because the results of PCR testing were available weeks after the survey was done, antibiotic treatments were prescribed empirically. A proportion of 32.7% patients suffering from respiratory symptoms were prescribed antibiotics at the centre, as well as 82.6% of those with diarrhoea. Among patients with a negative malaria rapid test result, 23.8% were prescribed an antibiotic at the centre. These results are in line with previous observations at the GMT [3].

Our study has some limitations. We have no information on the follow-up of the patients after they left the healthcare centre; the number of patients was small and the study and took place over only three days. Different intestinal samples were used in patients (rectal swabs) and controls (stool samples). We did not include afebrile control patients for the interpretation of blood pathogen testing. Nevertheless, we demonstrated that positivity rates of potential pathogens among patients suffering from respiratory or gastrointestinal symptoms or febrile systemic illness were high. Given the high rate of asymptomatic carriage of respiratory and gastrointestinal pathogens, when assessed using a highly sensitive PCR method, the results should be interpreted with caution. Further studies with larger numbers of patients and a full coverage of the GMT period are needed. The use of a quantitative PCR method may be needed in this context, notably for the detection of gastrointestinal pathogens. Such studies may help to design point-of-care laboratory methods that could be used in the context of the GMT for assessing the microbial etiology of respiratory or gastrointestinal symptoms or febrile systemic illness on which to base therapeutic management.

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Table 1
Prevalence of respiratory pathogens among patients with respiratory symptoms and matched controls (52 patients and 52 controls) and prevalence of gastrointestinal pathogens among patients with gastrointestinal symptoms and matched controls (23 patients and 23 controls).

	Patients n (%)	Controls n (%)	OR [95%CI]	P-value		Patients n (%)	Controls n (%)	OR [95%CI]	P-value
At least one respiratory pathogen	48 (92.3)	50 (96.1)	0.48 [0.08–2.74]	0.40	**At least one gastrointestinal pathogen**	14 (60.9)	20 (87.0)	0.15 [0.03–0.79]	0.04
At least one virus	27 (51.9)	3 (5.8)	17.64 [4.87–63.85]	<0.0001	**At least one virus**	2 (8.7)	2 (8.7)	1.00 [0.13–7.78]	0.70
Influenza A	7 (13.5)	0 (0)	NA	0.006	Adenovirus	2 (8.6)	1 (4.3)	2.10 [0.17–24.87]	0.35
Influenza B	15 (28.8)	0 (0)	NA	<0.0001	Hepatitis E	0 (0)	1 (4.3)	NA	0.50
Human rhinovirus	3 (5.8)	1 (1.9)	3.12 [0.31–31.04]	0.31	At least one bacterium	13 (56.5)	19 (82.6)	0.28 [0.07–1.06]	0.06
Respiratory syncytial virus	2 (3.8)	0 (0)	NA	0.15	Enteropathogenic *Escherichia coli* (EPEC)	7 (30.4)	10 (43.5)	0.57 [0.17–1.91]	0.36
Metapneumovirus	1 (1.9)	0 (0)	NA	0.31	Shigella/Enteroinvasive *Escherichia coli* (EIEC)	6 (26.1)	4 (17.4)	1.67 [0.40–6.97]	0.47
Adenovirus	0 (0)	0 (0)	NA	NA	Enteroaggregative *Escherichia coli* (EAEC)	5 (21.7)	15 (65.2)	0.15 [0.04–0.55]	0.003
Coronaviruses	0 (0)	2 (3.8)	NA	0.15	Enterohaemorrhagic *Escherichia coli* (EHEC)	0 (0)	3 (13.0)	NA	0.07
Human para-influenza virus	0 (0)	0 (0)	NA	NA	*Tropheryma whipplei*	2 (8.6)	2 (8.6)	1.00 [0.13–7.78]	1.00
At least one bacterium	46 (88.8)	50 (96.1)	0.31 [0.06–1.60]	0.14	*Salmonella* sp.	0 (0)	1 (4.3)	NA	0.31
Haemophilus influenzae	33 (63.5)	14 (26.9)	4.71 [2.05–10.85]	<0.001	**At least one parasite**	4 (17.4)	3 (13.0)	1.04 [0.28–7.12]	0.68
Streptococcus pneumoniae	24 (46.1)	15 (28.8)	2.11 [0.94–4.76]	0.06	*Giardia lamblia*	2 (8.6)	3 (13.0)	0.63 [0.10–4.21]	0.65
Moraxella catarrhalis	19 (36.5)	11 (21.1)	2.15 [0.90–5.14]	0.08	*Entamoeba histolytica*	1 (4.3)	0 (0)	NA	0.31
Staphylococcus aureus	15 (28.8)	27 (51.9)	0.38 [0.17–0.84]	0.02	*Cryptosporidium parvum/ hominis*	1 (4.3)	0 (0)	NA	0.31
Klebsiella pneumoniae	2 (3.8)	35 (67.3)	0.02 [0.01–0.09]	<0.0001	**More than one pathogen**	6 (26.1)	15 (65.2)	0.19 [0.05–0.67]	0.02
Mycoplasma pneumoniae	0 (0)	0 (0)	NA	NA					
Bordetella pertussis	0 (0)	0 (0)	NA	NA					
More than one pathogen	33 (63.4)	33 (63.4)	1.00 [0.45–2.22]	1.0					
H. influenzae – virus	21 (40.4)	2 (3.8)	16.94 [3.71–77.28]	<0.0001					
S. aureus - virus	9 (17.3)	2 (3.8)	5.24 [1.07–25.54]	<0.0001					
Virus - Bacteria	25 (48.1)	4 (7.7)	11.11 [3.50–35.30]	<0.0001					

Hepatitis virus A, astrovirus, norovirus, rotavirus and *Campylobacter jejuni* were tested but there were no positive results.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.tmaid.2020.101820.

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