Burden of respiratory viral infections among inmates of a Ghanaian prison

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Abstract

Respiratory viral infections are important causes of morbidity and mortality worldwide. Information on circulating respiratory viruses among prisoners is lacking, although this is of public health importance and knowledge would assist in putting in place preventive measures to forestall disease outbreaks. The aim of this study therefore was to get the footprint of such diseases that have epidemic potential to be described and quantified for control. Prisoners on remand numbering 203 in a prison in Kumasi, the Ashanti Regional capital, were interviewed using prevalidated questionnaire, nasopharyngeal samples taken and screened by real-time PCR for common respiratory viruses in February, 2018. Of the total number of 203 participants enrolled, majority were males (n = 198, 97.54%). The modal age unsurprisingly was in the active working class of 18 to 35 years (n = 155, 76.36%) with 48 (23.65%) of participants older than 35 years. Inmates reported nasal congestion (n = 83, 40.89%), cough with or without pharyngitis (n =108, 53.20%) and fever (n = 74, 39.48%). Viruses detected in throat samples were Influenza A (n = 1, 0.49%) and Rhinovirus (n = 8, 3.94%). There was no statistically significant association between respiratory virus positivity and age (p = 0.118), gender (p > 0.900), duration of incarceration (p = 0.239) and reported symptoms (p = 0.724). The prison population may have a lower prevalence of respiratory viruses circulating in them. This may be dominated by those with high antigenic diversity.

Introduction

Respiratory infections particularly involving the lower respiratory tract are a major cause of morbidity and mortality and are among the leading causes of death worldwide [1]. Acute respiratory infections have been found to be responsible for up to 4 million deaths every year and associated with low immunization rates, HIV infection, poor nutrition and overcrowding as major risk factors [2]. Viruses constitute the major causes of upper respiratory tract infections with influenza viruses, coronaviruses, respiratory syncytial viruses and adenoviruses serving as some of the major contributors [3, 4].

Transmission of respiratory viruses is enhanced in crowded environments like schools, offices, hospitals and prisons [5, 6]. Prisons worldwide often experience overcrowding and Ghana is not an exception to this phenomenon. This situation coupled with other factors such as delayed diagnosis often makes prisons a prime area for the spread of respiratory infections among inmates [7–9].

A high prevalence of viral respiratory infections maintained in the prison population could serve as a potential source of infection to the general population through prison officers and workers, visitors and released inmates [10]. Information on circulating respiratory viruses among prison inmates in Ghana is lacking. This is important for preventing the spread of such infections to the general population possibly through improvement of the healthcare delivery system in the penal system. This would ultimately also improve the general wellbeing of prison inmates. The purpose of this study was to assess the burden of respiratory viral infections among inmates of a prison in Ghana.

Materials And Methods

Study design and setting

The study was an exploratory one conducted at the Kumasi Central Prison (KCP) in February 2018. The KCP is one of the forty-five prisons in Ghana and happens to be the largest correctional facility in the Ashanti Region of Ghana (Figure 1). Originally built to accommodate 800 inmates, the facility, at the time of the study held 1838 inmates. Ethical approval for the study was obtained from the Committee on Human Research Publications and Ethics (CHRPE) of the School of Medicine and Dentistry of the Kwame Nkrumah University of Science and Technology (KNUST) and the Komfo Anokye Teaching Hospital (KATH), Kumasi (CHPRE No. CHRPE/AP/577/17). In addition, institutional approval was obtained from the Ghana Prisons Service Headquarters, Accra.

We contacted the Prison Officers on site and the prison inmates to explain the aims and objectives of the study to them especially the inmates. During this time, inmates were given the opportunity to ask questions to which the study team answered to the best of their abilities.

We organized a day's training for our research assistants on how to administer the questionnaire in capturing data. The original version of the questionnaire was pretested, with five individuals who were on detention at a different prison. These were similar in their characteristics to the prison inmates at the study prison but outside the area of jurisdiction and study to ensure validity and measurement bias. The questionnaire was revised based on the suggestions and comments (mainly on how the questions had been constructed). This was the final and validated data capturing tool used during the study.

Prior to the study, a sample size of at least 202 was determined taking into consideration a two- sided alpha level of 5%, a study power of 95%, design effect of 1 and precision of 0.058. The estimate was based on a respiratory virus prevalence of 23.24% among adults returning from a pilgrimage to Ghana [11].

The study was voluntary and involved inmates with or without signs and symptoms of respiratory tract infections. A written informed consent was obtained from all participants. A total of 203 remand inmates who agreed to willingly participate in the study were enrolled and interviewed with a semi-structured questionnaire. The questionnaire examined their socio-demographic characteristics, detention status and self-reported medical history.

Sample collection

We collected throat swabs from participants with flocked swabs (Copan Group, Brescia, Italy). Swabs were rotated three times to obtain epithelial cells and stored in 500 l RNAlater (Qiagen, Hilden, Germany). These were transported at ambient temperature to the Kumasi Centre for Collaborative Research in Tropical Medicine (KCCR) laboratory for viral RNA purification and downstream testing.

Viral RNA extraction and PCR testing

Extraction of viral RNA from the samples collected was done using the Qiagen viral RNA mini kit (Qiagen, Hilden, Germany) according to manufacturer's instruction. Samples were extracted in pools with an input volume of 140 µl and eluted in 60 µl of elution buffer.

Detection of viral nucleic acid was done by real-time Polymerase Chain Reaction (PCR) and performed on a CFX96 Bio-Rad real-time PCR platform (Bio-Rad, Singapore). RNA viruses were reverse transcribed before amplification using the Invitrogen SuperScript III OneStep buffer system (Invitrogen, CA, USA) for Parainfluenza 1 to 3 and Enterovirus detection. The Qiagen OneStep buffer and enzyme system (Qiagen, Hilden, Germany) were used for the detection of Coronaviruses, Rhinovirus, human metapneumovirus virus, Respiratory Syncytial virus and Influenza viruses. Further, we employed the Qiagen 10X PCR buffer with *Taq* polymerase for Adenovirus testing.

In vitro transcribed RNA and RNAase free water were used as positive and negative controls respectively. To include only study subjects with relevant viral loads for the targets, only samples with a threshold cycle (CT)-value below 38 were rated as positive and included in our analysis. All primers and probes as well as testing conditions were performed as previously described for the various viruses shown in Table 1.

Data management

Data were double-entered and aggregated into Microsoft Excel file, and cleaned. It was exported into R statistical software version 3.6.0 and analyzed [12]. We summarized the distribution of various variables into tables and figures by using descriptive statistics. Analysis involving 2X2 contingency tables and tests for statistical associations were performed by Fisher's exact test. All alpha values ≤ 0.05 were considered significant.

Results

Demographics and self-reported symptoms of inmates

A total of 203 participants were recruited for the study with majority of them being male (n = 198, 97.5%) and only 5 females (2.5%). A higher proportion of the participants were within the age range of 18 to 35 years (n = 155, 76.4%) with only 23.6% (n = 48) being older than 35 years. Most of the inmates had been incarcerated for less than 5 years (n = 182, 89.7%) with the remaining having been in the prison for 6 to 10 years (n = 9, 4.4%) and more than 10 years (n = 12, 5.9%). The most frequent symptom of respiratory virus infection that inmates reported having within the past week at the time of interview was cough with or without pharyngitis (n = 108, 53.20%) followed by nasal congestion (n = 83, 40.89%) and fever (n = 71, 34.98%) (Table 2).

Respiratory virus detection

A total of 9 inmates tested positive for respiratory viruses representing 4.43% of the samples tested in the study. Two viruses were detected among the inmates. These were Rhinovirus (n = 8, 3.94%) and Influenza A (n = 1, 0.49%). More inmates with reported symptoms of cough, pharyngitis, nasal congestion or fever tested positive for respiratory viruses (n = 7, 3.48%) compared to those that did not report any signs or symptoms (n = 2, 1%). There was however no statistically significant relationship between reporting symptoms and being positive for a respiratory virus as determined by Fisher's exact test (p = 0.724). A substantial number of inmates reported symptoms but were negative for respiratory viruses (n = 132, 65.7%). Similarly, there was no significant association between testing positive for a respiratory virus and age (p = 0.118) as well as gender (p = 0.900). Among the PCR-positive inmates, 3.48% (n = 7) had been incarcerated for less than 5 years and 1% (n = 2) had been in prison for more than 5 years. There was however no statistically significant association between duration of incarceration and being positive for a respiratory virus (p = 0.239) (Table 3).

Discussion

Knowledge of respiratory viruses circulating in the prison population is important due to the potential for rapid spread because of overcrowding. Prison overcrowding, as observed in this study was also previously reported in a lot of African prisons where healthcare delivery and monitoring of potential outbreaks is not so well established [7]. Additionally, the prevalence of other infectious diseases, mainly sexually transmitted diseases have been found to be higher than the general population [8].

Limited available data on the prevalence of respiratory viruses in the general adult Ghanaian population makes comparison with the prison population challenging. However, in one study, influenza viruses were found in 8% of patients presenting with severe acute respiratory infection and 6% presenting with acute febrile illness to a Ghanaian healthcare facility [13]. This was much higher than those that tested positive to influenza and self-reported nasal congestion, fever or other signs of respiratory infection in the present study indicating potentially higher prevalence of respiratory viruses in the general population compared to the prison population.

Given that most respiratory virus infections are more prevalent in children [14, 15], the prevalence in the adult prison inmates reporting symptoms of respiratory infections in the present study was unsurprisingly lower than in Ghanaian children also presenting with symptoms of respiratory infections [16]. Active respiratory infections have been found to be mostly associated with symptoms and hence have a higher likely contagion during the symptomatic phase [17]. Having a substantial number of inmates reporting symptoms with only a few testing positive for respiratory viruses was an unusual observation in this study. This may however be attributed to other conditions like viral hepatitis which may also exhibit some flu-like prodromal symptoms and is also highly prevalent in prisons in Ghana [18–20].

For respiratory viruses which are known to have the potential to cause outbreaks like Adenoviruses in crowded or contaminated environments, specific serotypes have been found to be responsible for these [21, 22] and wide spread infection may be absent in the population under study if the circulation of these specific strains is low or absent.

Most respiratory viruses have previously been found to circulate at a higher prevalence during the rainy season from April to early dry season (April to December) in Ghana [16, 23]. The seasonality of these viruses may therefore explain the general low detection rate observed in this study since the study participants were mainly recruited in the late dry season.

For common respiratory infections that are mainly asymptomatic and stable antigenically, their spread would be limited in a closed system like a prison where people have stayed long and been exposed to the same circulating viruses and developed long-lasting immunity to the circulating serotype [4]. The observation of lower positivity in the longer serving inmates in this study hints at this possibility, however, the association was not statistically significant. This phenomenon may likely be the case even in immunocompromised HIV-positive inmates as was demonstrated previously in a study which found that with the exception of human Rhinovirus, there was no difference between viral causative agents of acute respiratory infections among HIV-positive and -negative Africans [24]. For Rhinoviruses, for which there are over 100 different serotypes [25], and influenza A viruses which also exhibit variations in circulating strains from year to year due to antigenic drift [26], the situation may be different. For these two viruses, there would likely be a broad enough variety of circulating viruses for reintroduction of new strains even in a relatively closed system like the prison environment as was observed in the present study with the detection of only these two viruses.

Conclusions

This study had some inherent limitations. This was an exploratory study and our sample size was limited. As such, the low prevalence of respiratory viruses could be due to smaller numbers of symptomatic prisoners recruited into the study. Targeting high numbers of prisoners with respiratory tract infections could increase the chances of detecting more variable types of viruses. Additionally, since our study focused mainly on one prison, we are careful in extrapolating these to reflect other facilities. Despite these limitations, our study suggests that the prison population in Ghana may habour potentially lower prevalence of respiratory viruses. Rhinoviruses and Influenza A viruses are likely to be the dominant viruses in the prison environment due to their high diversity. It is possible that some element of seasonality may influence the circulation of common respiratory viruses with a lower occurrence in the dry season.

Abbreviations

PCR: Polymerase Chain Reaction; KNUST: Kwame Nkrumah University of Science and Technology; KCP: Kumasi Central Prisons; CHRPE: Committee for Human Research, Publications and Ethics; KATH: Komfo

Anokye Teaching Hospital; KCCR: Kumasi Centre for Collaborative Research in Tropical Medicine; CT; Threshold Cycle.

Declarations

Ethics approval and consent to participate: We obtained ethical approval from the Scientific and Ethical review Committee of the School of Medical Sciences, Kwame Nkrumah University of Science and Technology (KNUST) and the Komfo Anokye Teaching Hospital, Kumasi (CHRPE/AP/577/17). Written informed consent was also obtained from each participant at the time of recruitment through signatures and thumbprints

Consent for publication: Not applicable.

Availability of data and materials: The datasets obtained and analyzed during the current study available from the corresponding author on reasonable request.

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Authors' contributions: AAS, PED and MO conceived the study and drafted the manuscript. RY, AK, RG and LAO assisted in analyzing the and interpreting the data. AAS, MO and AK supervised data collection. KOD and EOD critically reviewed the manuscript. All authors have read and approved the final manuscript.

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Tables

Table 1:

Table 1. Oligonucleotides and their genome targets used for detection of respiratory viruses.

Virus	Target gene	Function	Oligonucleotide sequence
RSV (A/B)	Matrix gene [27]	Forward primer	5’-GGAAACATACGTGAACAAGCTTCA
		Reverse primer A	5’-CATCGTCTTTTTCTAAGACATTGTATTGA
		Reverse primer B	5’-TCATCATCTTTTTCTAGAACATTGTACTGA
		Probe	6FAM-TGTGTATGTGGAGCCTT- MGBNFQ
Adenovirus	Hexon gene [28]	Forward primer	5’-GCCACGGTGGGGTTTCTAAACTT
		Reverse primer	5’-GCCCCAGTGGTCTTACATGCACAT
		Probe	6FAM-TGCACCAGACCCGGGCTCAGGTACTCCGA-TAMRA
PIV I	Polymerase gene [29]	Forward primer	5’-ACAGATGAAATTTTCAAGTGCTACTTTAGT
		Reverse primer	5’-GCCTCTTTTAATGCCATATTATCATTAGA
		Probe	6FAM-ATGGTAATAAATCGACTCGCT-MGBNFQ
PIV II	Polymerase gene [29]	Forward primer	5’-TGCATGTTTTATAACTACTGATCTTGCTAA
		Reverse primer	5’-GTTCGAGCAAAATGGATTATGGT
		Probe	6FAM-ACTGTCTTCAATGGAGATAT- MGBNFQ
PIV III	Matrix gene [29]	Forward primer	5’-TGCTGTTCGATGCCAACAA
		Reverse primer	5’-ATTTTATGCTCCTATCTAGTGGAAGACA
		Probe	6FAM-TTGCTCTTGCTCCTCA- MGBNFQ
Influenza A	Matrix gene [30]	Forward primer	5'-GTGCTATAAACACCAGCCTYCCA-3'
		Reverse primer	5'-CGGGATATTCCTTAATCCTGTRGC-3'
		Probe	5'-CAGAATATACATCCGTCACAATTGGARA-3'
Influenza B	Hemagglutinin (HA)gene [31]	Forward primer	5’-AAATACGGTGGATTAAATAAAAGCAA-3'
		Reverse primer	5’-CCAGCAATAGCTCCGAAGAAA-3'
		Probe	6FAM-CACCCATATTGGGCAATTTCCTATGGC-MGBNFQ
hMPV	Nucleoprotein [32]	Sense	5’-CATCAGGTAATATCCCACAAAATCAG-3'
		Antisense	5’-GTGAATATTAAGGCACCTACACATAATAARA-3'
		Probe	6FAM-TCAGCACCAGACACAC-BBQ
HRV	Conserved regions of HRV [33]	Sense	5’-CYAGCCTGCGTGGC-3'
		Antisense	5’-GAAACACGGACACCCAAAGTA-3'
		Probe	5’-TCCTCCGGCCCCTGAATGYGGC-3'
HCoV-OC43	Nucleoprotein [34]	Forward	CGATGAGGCTATTCCGACTAGGT

		Reverse	CCTTCCTGAGCCTTCAATATAGTAACC
		Probe	6FAM-TCCGCCTGGCACGGTACTCCCT-BHQ1
HCoV-NL63	Nucleoprotein [34]	Forward	GACCAAAGCACTGAATAACATTTTCC
		Reverse	ACCTAATAAGCCTCTTTCTCAACCC
		Probe	6FAM-ATGTTATTCAGTGCTTTGGTCCTCGTGAT-BHQ1
HCoV-HKU1	Replicase gene [34]	Forward	CCTTGCGAATGAATGTGCT
		Reverse	TTGCATCACCACTGCTAGTACCAC
		Probe	6FAM-TGTGTGGCGGTTGCTATTATGTTAAGCCTG-BHQ1
HCoV-229E	Nucleoprotein [34]	Forward	CAGTCAAATGGGCTGATGCA
		Reverse	AAAGGGCTATAAAGAGAATAAGGTATTCT
		Probe	6FAM-CCCTGACGACCACGTTGTGGTTCA-aBHQ1
Enterovirus (ENTV)	Highly conserved internal ribosomal entry site [35]	EQ1	5'-ACA TGG TGT GAA GAG TCT ATT GAG CT-3'
		EQ2	5'-CCA AAG TAG TCG GTT CCG C-3'
		EP	FAM-5'-TCC GGC CCC TGA ATG CGG CTA AT-BHQ1-3

RSV: Respiratory syncytial virus, **PIVI**: Parainfluenza type 1, **PIVII**: Parainfluenza type 2, **PIVIII**: Parainfluenza virus type 3, **hMPV**: human metapneumovirus, **HRV**: Human rhinovirus, **HCoV-OC43**: Human coronavirus OC43, **HCoV-NL63**: Human coronavirus NL63, **HCoV-HKU1**: Human coronavirus HKU1, **HCoV-229E**: Human coronavirus 229E

Table 2:

Table 2. Demographic characteristics and self-reported symptoms of study participants

Demographics	Response	Frequency	Percentage
Gender	Male	198	97.54
	Female	5	2.46
Age range (years)	18-35	155	76.35
	>35	48	23.65
Duration of incarceration (years)	<5	182	89.66
	6-10	9	4.43
	>10	12	5.91
Signs of infection within past week	**Response**	**Frequency**	**Percentage**
Nasal congestion	Yes	83	40.89
	No	118	58.13
	Missing	2	0.99
Cough and/or pharyngitis	Yes	108	53.20
	No	94	46.31
	Missing	1	0.49
Fever	Yes	71	34.98
	No	132	65.02

Table 3:

Table 3. Associations between demographics and respiratory virus infections

Characteristic	Group	Respiratory virus PCR		Fisher's exact test
N = 201	n (%)	n (%)		*p* value
		Negative	Positive	
Age (years)	18-35 153 (76.12)	144 (71.64)	9 (4.48)	0.1181
	>35 48 (23.88)	48 (23.88)	0 (0)	
Gender	Male 197 (98.01)	188 (93.53)	9 (4.48)	>0.9
	Female 4 (1.99)	4 (1.99)	0 (0)	
Duration of Incarceration (years)	>5 21 (10.45)	19 (9.45)	2 (1.00)	0.2391
	<5 180 (89.55)	173 (86.07)	7 (3.48)	
Symptoms	Present 139 (69.15)	132 (65.67)	7 (3.48)	0.724
	Absent 62 (30.85)	60 (29.85)	2 (1)	

Figures

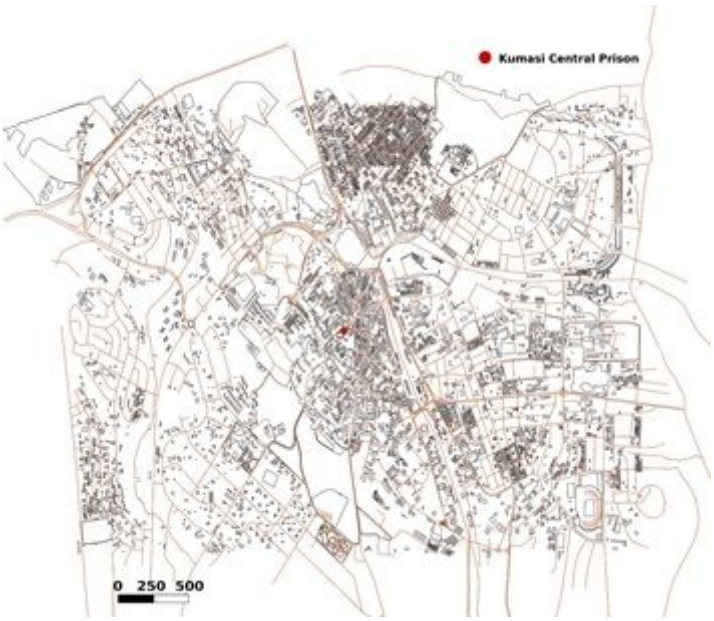

Figure 1

Map of Kumasi showing the location of the Kumasi Central Prison in the centre of the city. Map was generated using Quantum GIS with data freely available from openstreetmap.com