



AFRICAN JOURNAL OF CLINICAL AND EXPERIMENTAL MICROBIOLOGY (AJCEM) ISSN 1595-689X

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AFRICAN JOURNAL OF CLINICAL AND EXPERIMENTAL MICROBIOLOGY JANUARY 2018 ISBN 1595-689X VOL19 No.1 AJCEM/1901 COPYRIGHT 2018 https://dx.doi.org/10.4314/ajcem.v19i1.1 AFR. J. CLN. EXPER. MICROBIOL. 19 (1): 1-9

MOLECULAR CHARACTERIZATION OF EXTENDED SPECTRUM BETA-LACTAMASE AMONG CLINICAL MULTIDRUG RESISTANT ESCHERICHIA COLI IN TWO HOSPITALS OF NIAMEY, NIGER

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ABSTRACT

Objective: The aim of this study was to identify the multiple ESBL genes in Multidrug-resistant (MDR) *Escherichia coli* isolated in various biological samples in two hospitals of Niamey.

Methodology: A total of 195 multidrug-resistant *Escherichia coli* were included in the study. These isolates were tested using polymerase chain reaction (PCR) for detection of the presence of *bla* CTX-M, *bla* TEM, *bla* SHV and *bla* OXA-1 beta-lactamase genes.

Results: A total of 27.7% of *Escherichia coli* isolates were ESBL producing strains. Globaly, the *bla* TEM gene was the most prevalent (70.3%) followed by *bla* CTX-M (43.1%), *bla* OXA-1 (31.8%) and *bla* SHV (4.1%) genes. The four genes type of ESBL were founded simultaneously only in stool samples. Furthermore, none *bla* SHV gene was found in other samples type.

Conclusion: This study showed the presence of various ESBL genes among clinical MDR *Escherichia coli*. That is why a rational use of antibiotic and appropriate methods of screening ESBL genes in routine laboratories in Niger is needed to control the ESBL genes dissemination.

Keywords: MDR Escherichia coli, ESBL, bla genes, PCR, Niamey, Niger.

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CARACTERISATION MOLECULAIRE DES BETALACTAMASES A SPECTRE ETENDU CHEZ LES SOUCHES DE ESCHERICHIA COLI MULTI RESISTANTES DANS DEUX HOPITAUX DE NIAMEY, AU NIGER

Fody^{1,2*}, A. M., Bagré^{1,3}, T. S., Traoré¹, A. K., Yacouba ⁴, A., Dembelé¹, R., Boubou², L., Inoussa², A., Sidikou,⁵ R., Traoré,¹ A. S., Gassama-Sow,³ A. and Barro,¹ N.

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RESUME

Objectifs: Le but de cette étude était d'identifier les multiples gènes de BLSE chez les souches de *Escherichia coli* multi résistantes isolées de différents types d'échantillons biologiques dans deux hôpitaux de Niamey.

Méthodologie : Un total de 195 *Escherichia coli* multi résistants a été inclus dans l'étude. Ces isolats ont été testés par la réaction de polymérase en chaîne (PCR) pour détecter la présence des gènes *bla* CTX-M, *bla* TEM, *bla* SHV et *bla* OXA-1.

Résultats : Au total, 27,7% des isolats de *Escherichia coli* multi-résistants étaient des souches productrices de BLSE. Globalement le gène *bla* TEM (70,3%) était le plus détecté suivi des autres gènes *bla* CTX-M (43,1%), *bla* OXA-1 (31,8%) et *bla* SHV (4,1%). Notons que seul dans les échantillons de selles quatre types de gènes de BLSE ont été trouvés simultanément. Par ailleurs notons qu'aucun gène de type *bla* SHV n'a été trouvé dans les autres types d'échantillons.

Conclusion : Cette étude avait montré la présence de divers gènes de BLSE chez les souches cliniques de *Escherichia coli*. C'est pourquoi une utilisation rationnelle des antibiotiques et des méthodes appropriées de dépistage des gènes de BLSE dans les laboratoires sont nécessaires afin de contrôler la diffusion des gènes de BLSE.

Mots clés : Escherichia coli multi résistantes, BLSE, gènes bla, PCR, Niamey, Niger

INTRODUCTION

Resistance to beta-lactam antibiotics is an increasing problem and beta-lactamase production in Gramnegative bacteria, is one of the most common mechanisms of drug resistance. Beta-Lactamases, very diversified due to their continuous mutation, belong to the Ambler classes A (1) and are usually plasmidencoded that also harbor resistant genes to other antimicrobial classes with resulting multidrugresistant isolates (2, 3). These multidrug resistant (MDR) Gram negative bacilli belonging to the Enterobacteriaceae family are increasingly responsible for hospital infections (bacteremia urinary tract and intra-abdominal infection) in many countries (4, 5). The MDR extended-spectrum beta-lactamase (ESBL) producing Enterobacteriaceae have become a concern in bacteriology medical regarding antimicrobial treatment and infection control in hospitals (6). Indeed, these enzymes (ESBL) have the capacity to hydrolyze extended-spectrum cephalosporins and monobactam antibiotics, but are inhibited by clavulanic acid (7, 8). The emergence of ESBLproducing isolates has important clinical and therapeutic implications. High prevalence of ESBLproducing Enterobacteriaceae has been reported in the literature for clinical samples from a variety of infection sites (9). In the past decade, there has been a significant increase in the prevalence of resistance to extended spectrum cephalosporin in Escherichia coli (10). From the clinical and epidemiological side, the ESBL-producing Escherichia coli represent a significant therapeutic challenge as they are resistant to all betalactam antibiotics currently available and other antibiotic families alternative (fluoroquinolones, cotrimoxazole, aminosides or tetracyclines), to except cephamycins (cefoxitin and cefotetan) and carbapenems (imipenem and ertapenem) (11, 12). Different types of ESBLs have been found in different

countries. There are currently three main ESBL (TEM, SHV and CTX-M) types, which are the most widespread and clinically relevant (13). The TEM and SHV types were first reported from Klebsiella pneumoniae in Western Europe. In the late 1990s, the prevalence of TEM and SHV had decreased, while that of CTX-M, especially associated to species Escherichia coli increased (10). The CTX-M type betalactamases represent a rapidly emerging group which worldwide, have been found in Enterobacteriaceae, particularly in Escherichia coli, Klebsiella pneumoniae, Proteus mirabilis and Salmonella typhimurium (14). Genotypic tests have the potential to accurately identify different genes encoding the ESBLs (15). Several reports have described the prevalence of ESBLs genes in the Middle East North Africa region and most of the Gulf Cooperation Countries (16). So the detection of specific genes by PCR and sequencing are commonly used for final confirmation of ESBL producers. The association of ESBLs and the presence of TEM, SHV, OXA and CTX-M-type enzymes have been investigated in many studies (17). However, there are insufficient scientific data on the ESBLs gene characterization available from Niger.

To our knowledge, no data are so far available on ESBL-producing *Escherichia coli* clinical isolates in Niger. The aim of this study was to screen the presence of *bla* _{TEM}, *bla* _{SHV}, *bla* _{OXA-1} and *bla* _{CTX-M} genes among clinical MDR *Escherichia coli* isolated from various biological samples in Niamey.

MATERIALS AND METHODS Samples collection

The present prospective study was conducted from March 2014 to June 2016 in the medical biology laboratory of "hôpital national de Niamey" and "hôpital national Lamordé" in Niamey, Niger. The isolates were obtained from various samples. Multidrug resistant *Escherichia coli* isolates, were isolated from stool (n=49), urinary tract infection (n=134), pus (n=7), blood (n=4), and vaginal swabs (n=1) samples.

Bacterial identification and antibiotic susceptibility testing

Isolation, identification, antimicrobial susceptibility testing of isolates and phenotypic characterization of ESBL were described in our previous study (18). All isolates included in this study were multidrug resistant.

Preparation of DNA

Total DNA was extracted as previously described by Steward (19) using boiling process. Samples were cultured onto Bromo-Cresol Pourpre (BCP) agar and incubated at 37°C for 24 hours. For DNA extraction, two loopful of each strain were homogenized into 250 µl of sterile water. The mixture was boiled for 10 min and centrifuged for 10 min. After 5 min at room temperature, the supernatant was collected and used for the PCR reactions.

Detection of *bla* _{TEM}, *bla* _{SHV}, *bla* _{OXA-1} and *bla* CTX-M genes.

The beta-lactamase genes bla TEM, bla SHV, bla OXA-1, and bla CIX-M were detected by PCR using specific primers (Table 1). PCR mixtures were prepared by using 2.5 µl of template DNA, 4.0 µl of Master Mix PCR (Solis BioDyne, Estonia), 0.5 µl of Forward primer, 0.5 µl of Reverse primer in a final volume of 20 µl. Amplification conditions were 94°C for 5 min following 35 cycles of 94°C for 30 Sec, 55°C for 60 Sec, and 72°C for 60 Sec with a final extension at 72°C for 10 min. PCR amplified fragments were separated by agarose gel (1% w/v) electrophoresis in 1 x TAE visualized under buffer and UV light.

TABLE 1: BETA-LACTAMASE GENES PRIMERS

Genes	Primers	Sequences (5'-3')	Amplicon size (bp)
bla _{TEM}	TEM-F	ATAAAATTCTTGAAGACGAAA	1080
	TEM-R	GACAGTTACCAATGCTTAATCA	
bla _{SHV}	SHV-F	TTATCTCCCTGTTAGCCACC	650
	SHV-R	GATTTGCTGATTTCGCTCGG	
bla _{OXA-1}	OXA-1-F	ATGAAAAACACAATACATATC	890
	OXA-1-R	AATTTAGTGTGTTTAGAATGG	
bla _{CTX-M}	CTX-M-F	GTTACAATGTGTGAGAAGCAG	593
	CTX-M-R	CCGTTTCCGCTATTACAAAC	

Ethical considerations

All biological specimens were collected as part of the routine clinical management of patients. The study was approved by the medical establishment committee of hôpital national de Niamey" and "hôpital national Lamordé" in Niamey and permission to conduct the study was obtained from the hospital authorities of Niger.

Statistical analysis

Data analysis was carried out using Microsoft Excel 2013 and Med Cal version 11.0.1.0. P < 0.05 was considered to be statistically significant.

RESULTS

A total of 195 MDR *Escherichia coli* were included in this study. Among these isolates, 27.7% (54/195) were positive for the phenotypic character of extended spectrum beta-lactamases. Molecular analysis had shown the presence of various beta-lactamase genes. The genes identified by PCR method using specific primers i.e TEM, SHV CTX-M and OXA-1 on agarose gel were shown in Figures 1 and 2.



FIGURE 1: PCR AMPLIFICATION OF E. COLI bla TEM GENES



FIGURE 2: PCR AMPLIFICATION OF E. COLI bla CTX-M GENES

Forty nine (49) *MDR Escherichia coli* isolates from stool samples were tested for ESBL resistant genes. Overall, *bla* _{TEM} gene was the most prevalent (93.9%) followed by *bla* _{OXA-1} (71.4%), *bla* _{CTX-M} (65.3%) and *bla* _{SHV} (16.3%) (P < 0.0001) (Table 2). All the fourteen (14) ESBL isolates positive by phenotypic method, were

positive for the *bla* _{TEM} gene (100%), 85.7% for the *bla* _{CTX-M} gene, 85.7% for the *bla* _{OXA-1} gene and 21.4% for *bla* _{SHV} gene (P < 0. 0001) as indicated in Table 3. Globally, *bla* _{SHV} gene was only detected in stool samples.

	Clinical source								
	Stools	Urine	Pus	Blood	Vaginal swabs				
ESBL genes	N=49	N=134	N=7	N=4	N=1				
<i>bla</i> _{тем} n (%)	46 (93.9)	82 (61.2)	4 (57.1)	4 (100)	1 (100)				
bla _{SHV} n (%)	8 (16.3)	0 (0)	0 (0)	0 (0)	0 (0)				
<i>bla</i> _{OXA-1} n (%)	35 (71.4)	20 (14.9)	5 (71.4)	2 (50)	0 (0)				
hla = (0/a)	32 (65 3)	15 (33.6)	5(714)	2(50)	0 (0)				

TABLE 2: DISTRIBUTION OF BETA-LACTAMASE GENES FROM MDR E. COLI

About the 134 MDR *Escherichia coli* isolated from urine samples, *bla* _{TEM} gene was the most prevalent (61.2%), followed by *bla* _{CTX-M} (33.6%) and *bla* _{OXA-1} (14.9%) respectively (Table 2). Out of the thirty-seven (37) ESBL isolates positive by phenotypic method, 27 (73.0%) were positive for *bla* _{TEM} gene, 13 (35.1%) for *bla* _{CTX-M} gene, and 3 (8.1%) for *bla* _{OXA-1} gene (P < 0.0001) (Table 3). None of the isolates was positive for *bla* _{SHV} genes.

The study of seven (7) MDR *Escherichia coli* isolated from pus samples, showed the presence of *bla* $_{CTX-M}$ gene, *bla* $_{OXA-1}$ gene and *bla* $_{TEM}$ gene with a prevalence of 71.4%, 71.4% and 57.1% respectively. The *bla* $_{SHV}$ gene was not found in any of the isolates (Table 2). There was no significant difference between the expressing of these genes in pus samples (P = 0.3735).

Only the *bla* $_{CTX-M}$ gene (50%) and *bla* $_{OXA-1}$ gene (50%) were found in *Escherichia coli* isolates positive for ESBL by phenotypic method (Table 3).

In the four (4) MDR *Escherichia coli* isolated from blood culture samples, *bla* $_{\text{TEM}}$, *bla* $_{\text{OXA-1}}$ and *bla* $_{\text{CTX-M}}$ genes were found in 100%, 50%, and 50% respectively (Table 2). However, *bla* $_{\text{TEM}}$ (100%), *bla* $_{\text{OXA-1}}$ (100%) and *bla* $_{\text{CTX-M}}$ (100%) were found in *Escherichia coli* isolates producing ESBL by phenotypic method (Table 3).

Concerning vaginal swabs, only *bla* _{TEM} gene was found in *Escherichia coli* isolates as indicated in Table 2 and Table 3.

					Clinical	source				
	Stool		U	Urine Pus			Blood		Vaginal swabs	
ESBL genes	ESBL + N=14	ESBL - N=35	ESBL + N=37	ESBL- N=97	ESBL+ N=2	ESBL - N=5	ESBL+ N=1	ESBL - N=3	ESBL+ N=0	ESBL - N=1
bla тем n (%)	14 (100)	32 (91.4)	27 (73.0)	55 (56.7)	0 (0)	4 (80)	1 (100)	3 (100)	0 (0)	1 (100)
bla sнv n (%)	3 (21.4)	5 (14.3)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
bla 0XA-1 n (%)	12 (85.7)	23 (65.7)	3 (8.1)	17 (17.5)	1 (50)	4 (80)	1 (100)	1 (33.3)	0 (0)	0 (0)
bla _{стх-м} п (%)	12 (85.7)	20 (57.1)	13 (35.1)	32 (33.0)	1 (50)	4 (80)	1 (100)	1 (33.3)	0 (0)	0 (0)

TABLE 3: DISTRIBUTION OF ESBL GENES FROM MDR E COLI POSITIVE TO ESBL

In this study, there was co-existence of ESBL genes in some *Escherichia coli* isolates. The co-existence of *bla* TEM and *bla* CTX-M genes was found in stool, blood, pus and urine samples in 63.3%, 50%, 42.9%, 22.4% (P = 0. 0002) respectively, while *bla* CTX-M gene and *bla* OXA-1 gene were detected in 57.1%, 50.0%, 71.4%, and 4.5% respectively. The co-existence of three ESBL genes belonging to group *bla* CTX-M + *bla* TEM + *bla* OXA-1 genes was observed in 57.1%, 50%, 28.6% and 3%

respectively from stool, blood, pus and urine samples (P < 0. 0001). However, other multiple co-detection of ESBL genes belonging to different groups: *bla* _{CTX-M} + *bla* _{SHV} (14.3%), *bla* _{CTX-M} + *bla* _{TEM} + *bla* _{SHV} (12.2%), *bla* _{CTX-M} + *bla* _{SHV} + *bla* _{OXA-1} (14.3%) were observed in stool samples. A combination of four genes (12.2%), *bla* _{CTX-M} + *bla* _{TEM} + *bla* _{SHV} + *bla* _{OXA-1} genes was found only in *Escherichia coli* isolated from stool samples (Table 4).

	Clinical sources							
ESBL genes combination	Stool N=49	Urine N=134	Pus N= 7	Blood N=4	Vaginal swabs N=1			
bla _{CTX-M} + bla _{TEM} n (%)	31 (63.3)	30 (22.4)	3 (42.9)	2 (50.0)	0 (0)			
bla _{CTX-M} + bla _{SHV} n (%)	7 (14.3)	0 (0)	0 (0)	0 (0)	0 (0)			
bla _{CTX-M} + bla _{OXA-1} n (%)	28 (57.1)	6 (4.5)	5 (71.4)	2 (50.0)	0 (0)			
bla _{CTX-M} + bla _{TEM} + bla _{SHV} n (%)	6 (12.2)	0 (0)	0 (0)	0 (0)	0 (0)			
$bla_{\text{CTX-M}} + bla_{\text{TEM}} + bla_{\text{OXA-1}} n (\%)$	28 (57.1)	4 (3.0)	2 (28.6)	2 (50.0)	0 (0)			
$bla_{\text{CTX-M}} + bla_{\text{SHV}} + bla_{\text{OXA-1}} n (\%)$	7 (14.3)	0 (0)	0 (0)	0 (0)	0 (0)			
$bla_{\text{CTX-M}} + bla_{\text{TEM}} + bla_{\text{SHV}} + bla_{\text{OXA-1}} n (\%)$	6 (12.2)	0 (0)	0 (0)	0 (0)	0 (0)			

DISCUSSION

Over the last decades, many studies have demonstrated the presence of ESBL resistance genes in bacteria isolated from patients during various infections (20 -22). This study reported the results of molecular characterization of ESBL resistance genes in MDR *Escherichia coli* strains isolated in two hospitals of Niamey, Niger.

The study of *Escherichia coli* producing ESBL (14 isolates) isolated from stool samples, had shown that the most frequent ESBL gene was *bla* _{TEM} followed by *bla* _{CTX-M}, *bla* _{OXA-1} and *bla* _{SHV} genes. However, previous studies from Qatar reported a higher prevalence of *bla* _{CTX-M} gene (66.1%), *bla* _{SHV} (53.2%) and *bla* _{TEM} (40.4%) (9). In another study, the predominant ESBL genes, were *bla* _{CTX-M}, *bla* _{TEM} and

 bla_{SHV} (23). Other studies in clinical isolates showed that *E. coli* harbored bla_{SHV} gene (88.9%), bla_{OXA} (44.4%) and bla_{CTX-M} genes (44,4), and bla_{TEM} gene (22.2%) (24). These results were contradictory to our results. The difference would be due to the sampling from different hospitals and from different geographic locations, whereas in our study, samples were collected only from two hospital setting.

This study revealed that, out of the 37 *E* coli producing ESBL isolated from urine samples, the percentage of *bla* TEM was 73.0% followed by *bla* CTX-M (35.1%) and *bla* OXA-1 (8.1%). Karimian et al. in Iran, reported similar data: *bla* TEM and *bla* CTX-M genes were observed in 71.2% and 37.3% of *E. coli* isolates, respectively (25). In our study, none of the isolate harbored *bla* SHV gene. A similar finding was reported

from Thai studies. (26). But our results contradicted those reported in some studies conducted by Egyptian and Indian authors, in which *bla* _{SHV} gene was detected among urinary *E. coli* isolates (27, 28). Also, in East Africa, ESBL genes, *bla* _{CTX-M}, *bla* _{TEM}, *bla* _{SHV} and *bla* _{OXA} were found frequently (23). Thus, this required a better understanding of the ESBL genes in order to give useful data about their epidemiology.

In this study, only 4 MDR *Escherichia coli* isolated from blood culture were tested for ESBL genes. Thus, the co-existence of *bla* TEM, *bla* OXA-1 and *bla* CTX-M was only seen in one strain producing EBSL. Our results correlated with other results reported in some African's countries which showed a significantly lower proportion of ESBL in blood cultures than in other specimens (29). The previous finding was contradicted with the finding of a Burkina Faso study which had shown the highest proportion of ESBL genes in blood samples (30). Whereas, none of ESBL producing isolates carried *bla* SHV or *bla* CTX-M genes as reported in Ghana (31). This discrepancy can be explained by differences in the antimicrobials use between countries.

The present study reported the multiple co-existence of ESBL genes. Thus, 63.3% of isolates from stool samples harbored two ESBL genes belonging to groups of *bla* $_{CTX-M}$ + *bla* $_{TEM}$, followed by blood samples (50%), pus samples (42.9%) and urine samples (22.4%). The greatest frequency of beta lactamase gene in *E. coli* samples was related to TEM/CTX-M in previous study as reported in Iran (32). The co-existence of *bla* $_{TEM}$ + *bla* $_{CTX-M}$ genes and *bla* $_{SHV}$ + *bla* $_{CTX-M}$ genes in two strains were reported in India (33).

This study revealed that the co-existence of three (3) ESBL genes ($bla_{CTX-M} + bla_{TEM} + bla_{OXA-1}$) was observed in 57.1%, 50%, 28.6% and 3% of the *Escherichia coli* isolates respectively in stool, blood,

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pus and urine samples. This result was also found in another study conducted in Bangladesh (24). These results indicated that ESBL-producing *Escherichia coli* frequently harbored more than one beta-lactamase genes.

Overall, only isolates from stool samples harbored simultaneously four (4) ESBL genes ($bla_{\text{CTX-M}} + bla_{\text{TEM}} + bla_{\text{SHV}} + bla_{\text{OXA-1}}$). According to a previous study in Lebanon, 15.9% of *Escherichia coli* harbored the four ESBL genes (34). The genetic diversity of *bla* genes in isolates, suggested that resistance genes can easily move from one specie to another with the possibility of easy interspecies transfer.

This study was conducted in two hospitals of Niamey; it may reflect the local antibiotic resistance patterns and this may be a limitation.

CONCLUSION

This first study in Niger showed a high incidence of ESBL resistance genes among clinical *Escherichia coli* isolates from two laboratories in two hospitals (Hôpital National de Niamey and Hôpital National Lamordé) of Niamey. Many isolates harboring more than one ESBL resistance genes, were also detected. Therefore, immediate implementation and recommendations for antimicrobial management and infection control measures were necessary to prevent the spread of these genes across the whole country.

ACKNOWLEDGEMENTS

This study was supported by CAMPUS France. The authors thank the "Institut Pasteur de Dakar" for the characterization of ESBL genes. They also thank the laboratories LABESTA of Ouagadougou University, "hôpital national de Niamey" and "hôpital national Lamordé" of Niamey, Niger.

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ORIGINAL ARTICLE

AFRICAN JOURNAL OF CLINICAL AND EXPERIMENTAL MICROBIOLOGY JANUARY 2018 ISBN 1595-689X VOL19 No.1 AJCEM/1902 COPYRIGHT 2018 https://dx.doi.org/10.4314/ajcem.v19i1.2 AFR. J. CLN. EXPER. MICROBIOL 19 (1): 9-17

IN VITRO ANTIMICROBIAL ACTIVITY OF FERMENTED SPICES AND CAPSICUM FRUTESCENSAGAINST MULTI DRUG RESISTANCE CLINICAL ISOLATE AND STANDARD REFERENCE BACTERIA

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ABSTRACT

Introduction: Food preservation is required to maintain for a long period of time. Traditional organic food preservative, "Datta" is spice mainly made up of Chili Peppers which frequently used in southern and western part of Ethiopia. Datta can be consumed almost with every kind of foods and it is believed as appetizer and antimicrobial agent against food borne pathogen. This study aimed to assess *in vitro* antimicrobial activity of fermented condiment and Capsicum *frutescens*against multi drug resistance clinical isolate and standard reference bacteria.

Method: Datta samples collected from different level hotels and *Capsicum frutescens* (Chili peppers) were extracted in different solvents. Agar well diffusion assay was used to determine antimicrobial activity and minimum inhibitory concentration (MIC) and minimum bactericidal concentration was determined by tube dilution method. One way analysis of variant was used in comparison of the finding.

Results: Extracted fermented condiment (Datta) sample and Chili Pepper showed antimicrobial activities against multidrug resistant clinical isolate and standard reference bacteria in well diffusion assay. Datta extract showed MIC ranged from 25 mg/L to 66.7 mg/L and MBC ranged from 25 mg/L to 100 mg/L. The Datta and Chili pepper extracts showed high antimicrobial activities against standard *Staphylococcus aureus*. The water based extract of Datta sample were exhibited significantly low antimicrobial activities (P=0.000) as compared to the other extraction solvents.

Conclusion: Water was weak extractor of active compounds having antimicrobial activities. Reference *S. aureus*wasmore susceptible organism while ATCC *Salmonella enteritidis*and clinical isolated multi-drug resistant *E. coli* less susceptible. The traditional use of fermented condiment for food preservation by the local people is supported by this study.

Key words: Antimicrobial activity; Chili Pepper extract; Fermented condiment; Minimum bactericidal concentration; Minimum inhibition contraction

ACTIVITÉ ANTIMICROBIENNE EN VITRO D'ÉPICES FERMENTÉES ET DE FRUITS DE CAPSICUME POUR LA RÉSISTANCE AUX MÉDICAMENTS ISOLATE CLINIQUE ET BACTÉRIES DE RÉFÉRENCE STANDARD

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ABSTRAIT

Introduction: La conservation des aliments est nécessaire pour maintenir pendant une longue période de temps. Conservateur de nourriture organiqu et raditionnel, "Datta" est l'épicé compose principalement de Chili Peppers qui fréquemment utilize dans le sud et l'ouest de l'Ethiopie. Datta peu têtre consommé presque avec toutes sortes d'aliments et on le croit comme un apéritif et un agent antimicrobien contre l'agent pathogène alimentaire. Cette etude visait à évaluer l'activité antimicrobienne *in vitro* du condiment fermenté et *Capsicum frutescens* contre l'isolement clinique de résistance aux médicaments multiples et les bactéries de référence standard.

Méthode: Les échantillons de Datta prélevés dans des hôtels de différents niveaux et *Capsicum frutescens* (Chili Peppers) ont été extraits dans différents solvants. Un dosage de diffusion de puits a été utilisé pour determiner l'activité antimicrobienne et la concentration inhibitrice minimale (MIC) et la concentration bactericide minimale a été determine par la méthode de dilution du tube. Une analyse à sens unique de la variante a été utilisée en comparaison de la découverte.

Résultats: L'échantillon extrait de condiments fermentés (Datta) et Chili Pepper ont montré des activités antimicrobiennes contre l'isolement Clinique résistant aux médicaments multiples et les bactéries de référence standard dans le dosage par diffusion de puits. L'extrait de Datta a montréque le MIC variait de 25 mg/L à 66,7 mg/L et le MBC variait de 25 mg/L à 100 mg / L. Les extraits de poisson de Datta et de Chili ont montré des activités antimicrobiennes élevées contre *Staphylococcus aureus* standard. L'extrait à base d'eau de l'échantillon de Datta a montré des activités antimicrobiennes significativement faibles (P = 0,000) par rapport aux autres solvants d'extraction.

Conclusion: L'eauétaitun extracteur faible de composes actifs ayant des activités antimicrobiennes. Référence *S. aureus* était un organisme plus susceptible tandisque ATCC *Salmonella enteritidis* et *E. coli*. *E. coli* résistant aux médicaments multiples isolés était moins susceptible. L'utilisation traditionnelle du condiment fermenté pour la conservation des aliments par les populations locales est soutenue par cette étude.

Mots clés: Activitéantimicrobienne; Extrait de poivre de piment; Condiment fermenté; Concentration bactéricide minimum; Contraction minimaled'inhibition

INTRODUCTION

Since ancient time, peoples have been using spices to prevent off-odor, off-flavors and spoilage of foods [1]. Besides flavoring food, currently spices have become an integral part of daily requirements such as for food preservation, cosmetics, medicinal preparation, bakery goods, perfumery, and various other products [2]. The preparation of this spices vary from place to place. One of well now and the most common spice that is used in most type of food in Ethiopia is known as "Datta" in southern part of the country and "Kotchkocha" in western part in Afan Oromo language. Datta is not heat processed and the main ingredient of this spice is pasted Chili Pepper whereas other ingredient such as Garlic, Ginger, Coriander, and Basil are added in limited amount. All these ingredients crushed together by simple grinding stone until it become semisolid. The Datta acquires original precursor chili pepper color, it became green if it is made of fresh green chili pepper or become red in color if red chili peppers are used [3, 4].

Some foods are not easily contaminated with microorganisms. This may be due to food intrinsic antimicrobial agent of raw materials that have inhibitory effect on growth of microorganisms. Many secondary metabolites of plants are antibiotic, protecting the plants against different microorganisms [5, 6]. Therefore, herbs are now more focused than ever because they have the capability of producing important metabolites which used as medicine or as precursor for many pharmacological products. Without specific knowledge of their cellular action or mechanisms phytochemicals have been considered possible drugs for times.

Chili peppers are also used worldwide in foods for their pungent flavor, aroma, and to prolong food spoilage. It is one of spice which considered as preservative as well as appetizer by the users. Every country in the world has its own way in making different types of foods and spice. Ethiopia is a country with different ethnic groups with different culture, preparation of spices varies in different part of the country. This study is conducted on Datta which is the most dominant and widely used spice product of pepper known in southern and western part of Ethiopia [3, 4].

Different study showed as Chili Pepper which is the major precursor of Datta has antimicrobial activities on different microorganisms [7, 8, 9]. The Capsaicin present in Chili Pepper is has

antimicrobial activities in addition to other secondary metabolites. Little is known about antimicrobial activities of Datta and scientific evidence is required to confirm its food preservative characteristic of the spice. Searching of effective and safe food preservatives has non debatable benefits now day. There are new concerns about food safety and preservatives due to increasing occurrences of new food-borne disease outbreaks caused by drug resistant pathogenic microorganisms. This advances considerable challenges, mainly since there is increasing unease regarding the use of chemical preservatives and artificial antimicrobials to inhibit growth of spoilage microorganisms [10]. These chemical preservatives may have so many side effects as compared to organic preservatives that has a little effect on food flavors are always needed. Spices Chili Peppers may be used as organic food preservative because people are using this condiment during eating delayed food. Currently, there is growing interest in using natural preservatives compounds as alternatives to synthetic compounds for food preservation [11]. In this study, the antimicrobial activity of Chili Pepper spices is going to be investigated as an alternative to antibiotics and food preservative option. The aim of this study is to assess in vitro antimicrobial activity of fermented condiment and chili pepper against multi drug resistance clinical isolate and standard reference bacteria.

MATERIALS AND METHODS

Study design, setting and period

Experimental study deign was carried out to asses antimicrobial activity Chili Pepper extract and Arba Minch town Datta collected from high, medium and low level Hotels. The study was conducted in Arba Minch town. The source of Datta's Chili Peppers for Arba Minch town is agriculture land of highland areas surrounding the town and the source of Datta samples were Hotels in the town with different level. Arba Minch town is located 500 kms south of Addis Ababa in southern nation nationality region of Ethiopia situated in the great African rift valley in elevation of 1285 meters above sea level with average temperature of about 29.7°C and the average annual rain fall of 900mm.

Sample collection

To obtain representative sample, Datta samples for assessing antimicrobial activities against ATCC and MDR clinical bacteria isolates were collected from hotels having different level. The Datta samples were collected using sterile and leak proof containers and transported to the microbiology laboratory using icebox, and kept in refrigerator during analysis periods. During collection, semi-structured questionnaire and observation check list were used to characterize the Datta samples.

Fresh chili peppers (*Capsicum frutescens*) which used as ingredient for Datta preparation were collected and characterized by local experts. Then the collected peppers were transported to laboratory in aseptic manner. The species name of collected the chili pepper is determined by the help of Taxonomist. Finally collected sample were extracted according to method discussed below.

Experimental organisms

The screening for antibacterial activities of Datta and Chili pepper crude extracts were carried out by using three bacterial pure cultures: Staphylococcus aureus (ATCC® 25923™), *Salmonella enterica subsp. enterica*(ATCC[®] 13311[™]) and Klebsiellapneumoniae (ATCC[®] 700603[™]) and three multi drug resistance clinical bacteria isolates particularly Methicillin resistant Staphylococcus aureus(MRSA), Pseudomonas aeruginosa, and Escherichia coli. The organisms were regularly sub-cultures on Nutrient agar slant until screening for antimicrobial activity.

Datta and Chili Pepper extraction

The collected Datta sample in each hotel was separated into two sterile containers. The first container was used for microbiological characterization of the sample while the second container was for antimicrobial activities. For antimicrobial analysis, 10% w/v proportion was used to extract in four different extraction solvents (Distilled water, Acetone, Ethanol, and Methanol). Then dissolved solution of each sample was kept in orbital shaker for 24 hrs at room temperature. Finally the solution was filtered by Whatman No. 1 filter paper and stored in deep freeze at negative 20°C for further use of antimicrobial analysis [6].

Chili Pepper extraction was performed in six different solvents: Distilled water, Acetone, Ethanol, Methanol, Ethyl acetate, and Chloroform. The collected fresh chili pepper was washed twice in running water and once in distilled. Then it was crushed in disinfected Morton and pestle. Then 7.5gm of crushed chili pepper will be dissolved in 75ml each solvents to obtain 10% w/v. Then the dissolved solutions were kept on orbital shaker for 24hr. Then the extract was filtered with sterile Whatman No. 1 filter paper and stored in deep freeze at -20°C for further use of antimicrobial analysis.

Agar well diffusion assay of Datta sample and chili pepper extracts

Datta sample and Chili pepper crude extract was obtained aforementioned methods was evaluated for antimicrobial activity by agar well diffusion assay. Muller Hilton agar (Oxoid Limited, CM0337) is used to perform antimicrobial activity of the extracts. Then agar well diffusion assay was carried out according to method described in clinical and laboratory standards institute [12]. Diffusion well of approximately 6mm diameter was prepared by a sterile micro pipette tip. A 0.5 McFarland standards diluted suspension of each test microorganisms was evenly inoculated on Muller Hilton agar. Then 50µl of the extracts from each sample of Datta and Chili Pepper extract was carefully filled in the well. Additional wells were prepared and filled with each solvent used as negative control. Then the inoculated agar plates were incubated at 37°C for 24 hours. All the tests were conducted in triplicate and the average of the three measurements was used to present the results.

Determination of minimum inhibitory concentration of Datta sample and chili pepper extracts

Minimum inhibitory concentration (MIC) of Datta sample and chili pepper extract was determined by tube dilution method. The extracted Datta and Chili Pepper were diluted from 100mg/L to 12.5mg/L in nutrient broth (Oxoid). To each test tube with extract, a loop full of 106 bacteria suspension per ml fresh nutrient broth inoculated in each tube. Then the culture tubes will be incubated at 37°C for 24 hours. After the period of incubation the tubes are checked for turbidity that indicates the growth of bacteria. Then the lowest concentration of Datta sample and pepper extract inhibits growth of the test organisms was considered as the MIC for the respective organisms. To confirm the inhibition, then a loop full of the incubated inoculum was sub-cultured on nutrient agar [5].

Determinationofminimumbactericidalconcentration ofDatta sampleand chili pepperextracts

Minimum bactericidal concentration (MBC) of Datta samples and Chili Pepper extract was determined by tube dilution method followed by confirmation on agar plates. The MIC and the two consecutive preceding concentrations were used to determine MBC. The three concentrations of Datta and Chili Pepper extract were adjusted in Nutrient broth and inoculated with loop full of test organisms. Then the inoculam was incubated at 37°C for 24 hours. After the period of incubation the loop full of the well mixed inoculam from nutrient broth was transferred to nutrient agar and incubated at 37°C for 24 hours. Then the plates were examined for visible colony and the MBC is the lowest concentration that demonstrates no growth of colony.

Statistical Analysis

Collected data was entered to excel and exported to SPSS version 20.0 for further analysis. Descriptive statistics such as means and standard deviations were calculated. One way ANOVA followed by Tukey's test was used to compare extracts and the difference in the susceptibility of the test microorganisms. The 95% level of confidence (P-value ≤ 0.05) was considered as statistically significant.

RESULTS

Characteristic of collected Datta sample

A total of nine Datta samples were collected in different level hotels of Arba Minch town. Among collected Datta samples, three of them have red color; the other three of them have green color while the others have gray and brown color. According to information collected from the Datta owners of each hotels, the Datta sample were prepared mainly from Chile pepper while some other spices such as garlic, ginger, coriander, and other locally available plant spices were added. The average storage time after preparation of the Datta samples were 2 weeks with a range of 3 days to the 30 days. About one third of the Datta samples collected from low profile hotel were stored at room temperature while the rests were stored in Refrigerator.

Antimicrobial activity of Datta extract by well diffusion assay

The collected Datta samples were subjected to four solvent extractions particularly with Acetone, Ethanol, Methanol and distilled water. Stock concentration of 100mg/L Datta extract was used for antimicrobial analysis by agar well diffusion assay against two set of bacteria. The test organisms were both multi drug resistant clinical isolates and standard (ATCC) bacteria. There is no significance difference in antimicrobial activities among the three profile hotels (P=0.93).

TABLE 1: ZONE OF INHIBITION OF DATTA SAMPLE AGAINST ATCC AND MULTI-DRUG RESISTANT CLINICAL BACTERIAL ISOLATES (100 MG/L).

		Zone of inhibition (mm) (Mean ± SD).							
Datta	Extract		ATCC Bacteria		MDR Clinical isolates Bacteria				
Source	solvent	S. aureus	K. pneumoniae	S. enteritidis	P. aeruginosa	E .coli	S. aureus		
HLH	Water	14.3±3.5	-	-	-	-	-		
	Acetone	23.7±1.5	12.7±0.8	13*	18.3±3.6	9±5.8	19.3±1.8		
	Ethanol	22±3	15.2±1	7±4.3	15.7±1.5	8.3±5.1	16.7±1		
	Methanol	20.7±2.3	15.3±1.1	11.3±1	13±1.8	8±4.9	16.3±2.3		
	Water	-	-	-	-	12*	-		
MLH	Acetone	18.7±2.2	14.3±2	13.5**	19.3±2.7	11*	15±2.1		
	Ethanol	21.3±3.9	16.3±1.6	12*	18.7±3.5	10±6.1	14±0		
	Methanol	20.7±3	14.3±1	15.7±04	18.3±2.2	11.7±0.8	15±1.1		
	Water	9.3±2.4	-	-	-	-	11*		
LLH	Acetone	26.3±0.4	14.3±0.8	12±1.2	16.3±3.6	12.5**	14.3±0.8		
	Ethanol	21.3±1.4	12±0.7	12.0**	16.7±0.8	8±4.9	16.7±1		
	Methanol	21.3±2.4	12.7±1	12.7±1	15±1.4	11*	16.7±4.2		

HLH= high level hotel MLH=medium level hotel LLH=low level hotel

*antimicrobial activity was observed only in one sample, **antimicrobial activity was observed only in two samples

The water based extract of Datta sample were exhibited significantly low antimicrobial activities (P=0.000) as compared to the other extraction solvents. The highest (14.3±3.5) zone of inhibition of water based extract was observed in high level hotel (HLH) Datta sample followed by medium profile hotel (MLH) against ATCC® 25923[™] S. aureus. Only one sample of the medium, and low profile hotels showed antimicrobial activity against clinical isolates E. coli andS. aureus respectively (Table 1). The alcohol based (ethanol and methanol) Datta extract showed no difference in antimicrobial activities (P=0.49) in agar well diffusion assay. The highest 26.3±0.3 zone of inhibition of Acetone based extract was observed in LLH against ATCC[®] 25923[™] S. aureus whereas the minimum was exhibited against Salmonella enteritidis (ATCC-1331). Methanol based extract showed overall average of 21, 16, and 15.4mm zone of inhibition against ATCC-25923 S. aureus, Methicillin-resistant S. aureus (MRSA), and clinical isolate Pseudomonas specious respectively. Acetone based extract exhibited 23, 18, and 16.2mm average inhibition zone against ATCC S. aureus, clinical isolate Pseudomonas spp., and

MRSA respectively (**Table 1**). Pair wise comparison of ANOVA this study showed that the test organisms' susceptibility against Datta samples extract varies. As a whole ATCC *S. aureus*was more susceptible than the other test organisms (P<0.05). Similarly there is significant difference between ATCC *Salmonella enteritidis* and clinical isolate *Pseudomonas* spp. (p=0.028), and ATCC *Salmonella enteritidis* and MRSA (P=0.037). On the other hand clinical isolate *Pseudomonas* spp. showed significant difference with ATCC *S. enteritidis*and clinical isolate *E.* coli whereas *E. coli* susceptibility varies with MRSA as well (P=0.036).

Antimicrobial activity of Chili Pepper extract by well diffusion assay

Similar to Datta samples, fresh chili pepper (*Capsicum frutescens*) family name of Solanaceaewas extracted in six different extraction solvents (acetone, ethyl acetate, chloroform, ethanol, methanol and distilled water) and evaluated for antimicrobial activity by agar well diffusion assay. No zone of inhibition was observed for water based chili extract against

all test organisms at 100mg/L. All other extracts showed different zone of inhibition on test bacteria. The largest average zone of inhibition (28mm) was observed by acetone based extract against ATCC *S. aureus* while the smallest (11mm) zone of inhibition was obtained in methanol based extract against clinical isolate

MDR *P. aeruginosa*. Like in the case of Datta extract overall result showed that ATCC *S. aureus* was the most susceptible followed by clinical isolate MDR *P. aeruginosa* whereas ATCC *S. enteritidis* and MRSA were the most resistant bacteria for chili extracts (**Table 2**).

TABLE 2: ZONE OF INHIBITION OF CHILLI EXTRACTS AGAINST ATCC AND MULTI-DRUG RESISTANT CLINICAL BACTERIAL ISOLATES (100 MG/L)

	Zone of inhibition (mm)							
Extract solvent		ATCC Bacteri	a	MDR Clinical isolates Bacteria				
	S. aureus	K. pneumonia	S. enteritidis	P. aeruginosa	E .coli	S. aureus		
Water	-	-	-	-	-	-		
Acetone	28	19	15	21	17	17		
Ethanol	27	18	12	19	18	12		
Methanol	24	12	13	11	16	13		
Ethyl Acetate	26	12	12	15	17	15		
Chloroform	23	13	17	22	13	12		

Antimicrobial activities of chili extract differ based on extraction solvent. Chili Pepper water based extract showed week antimicrobial activity than the other solvents (p=0.000) similar to Datta extract. ANOVA pair wise comparison also indicated significance difference between acetone and methanol. Acetone is better extraction solvent than distilled water and methanol while there was no significant difference with other solvents. As a whole there was no significant difference (P=0.12) in susceptibility of test bacteria for chili extracts.

Minimum inhibitory and minimum bactericidal concentration of Datta extract

Minimum inhibitory concentration (MIC) and minimum bactericidal concentrations (MBC) for ethanol and acetone based extract were performed by four serially diluted of Datta extracts. The result of MIC of Datta extract in both extractions solvent ranges from 25 mg/L to 66.7 mg/L. Similarly, the MBC of the extracts indicates the range from 25mg/L to 100m/L. The overview of the finding showed relatively minimum concentration was required to inhibit or kill ATCC *S. aureus* than the other test bacteria.

Datta	MIC/	Extract	MIC and MBC (mg/L)							
Source	MBC	solvent		ATCC Bacteria		MDR Clinical isolates Bacteria				
			S. aureus	K. pneumonia	S. enteritidis	P. aeruginosa	E .coli	S. aureus		
HLH	MIC	Ethanol	25±0	33.3±10.2	66.7±20.4	41.7±10.2	41.7±10.2	58.3±16.6		
	1 (2) (2)	Acetone	33.3±10.2	41.7±10.2	25±0	25±0	25±0	33.3±10.2		
	МВС	Ethanol	33.3±10.2	33.3±10.2	83.3±20.4	33.3±10.2	50±0	66.7±20.4		
		Acetone	58.3±27	75±10.3	25±0	41.7±10.2	41.7±10.2	50±0		
MLH	MIC	Ethanol	33.3±10.2	33.3±10.2	50±0	50±0	41.7±10.2	25±0		
	МВС	Acetone Ethanol Acetone	41.7±10.2 58.3±27 50±0	33.3±10.2 33.3±10.2 58.3±27	41.7±10.2 100±0 75±103.8	33.3±10.2 66.7±20.4 58.3±27	25±0 58.3±27 33.3±10.2	50±0 33.3±10.2 83.3±10.2		
LLH	MIC MBC	Ethanol Acetone Ethanol Acetone	50±0 33.3±10.2 83.3±20.4 50±0	41.7±10.2 33.3±10.2 58.3±27 58.3±27	25±0 33.3±10.2 66.7±20.4 50±0	58.3±27 25±0 66.7±20.4 33.3±10.2	25±0 25±0 33.3±10.2 33.3±10.2	66.7±20.4 25±0 83.3±20.4 25±0		

There was no major difference between the three profile hotels. The result shows MIC of ethanol extract range from 25mg/L to 66.7mg/L for tasted organisms and acetone extract had MIC that ranges from 25mg/L to 50mg/L test bacteria specious. The overall MBC for ethanol extract has value range from 33.3 mg/L to 100mg/L whereas acetone extract had MBC that range from 25mg/L to 83.3 mg/L (**Table 3**).

Minimum inhibitory and minimum bactericidal concentration of Chili pepper extract

For Chili Pepper extracts the minimum inhibitory and minimum bactericidal concentration was determined for five solvents. In general, ATCC *S*. aureus was inhibited by minimum concentration as compared to the other test organisms. Similar to MIC, the least concentration was required to kill ATCC S. aureus as compared to other test bacteria specious. The overview of the result showed the chloroform based extract kill test organisms at minimum concentration than the others. The least (12.5mg/L) minimum bactericidal concentration was observed in acetone based extract against ATCC S. aures and in chloroform based extract against ATCC K. pneumonia and S. enteritidis, and MDR clinical isolate *P. aeruginosa* while the highest (100mg/L) was observed in all extracts for most of test bacteria specious (Table 4).

TABLE 4: MINIMUM INHIBITORY AND MINIMUM BACTERICIDAL CONCENTRATION OF CHILLI PEPPER	EXTRACT

		MIC/MBC (mg/L)							
MIC/MB C	Extract		ATCC Bacteria		MDR Clinical isolates Bacteria				
	solvent	S. aureus	K. pneumoniae	S. enteritidis	P. aeruginosa	E .coli	S. aureus		
	Acetone	12.5	25	25	25	50	25		
	Ethanol	12.5	12.5	25	50	50	25		
MIC	Methanol	25	50	25	50	50	25		
	Ethyl Acetate	25	50	12.5	12.5	50	12.5		
	Chloroform	12.5	12.5	12.5	12.5	100	50		
	Acetone	12.5	50	50	50	100	50		
MBC	Ethanol	25	25	50	100	50	25		
	Methanol	50	100	50	100	100	50		
	Ethyl Acetate	50	100	25	50	50	25		
	Chloroform	25	12.5	12.5	12.5	100	100		

DISCUSSION

Collected Datta samples were characterized physically and microbiologically. The samples had three different colors: red, green, and grey. The difference in color may due to the color of precursor chili pepper which associated with harvesting time. The late harvested chili pepper has red color while the early harvested has green color [4]. In microbial assessment of collected Datta sample, only gram positive rods were observed and these bacteria may be lactobacilli which involved in fermentation of Datta [3, 4]. Lactobacilli had ability to resistant to different food preservatives and diverse intrinsic antimicrobial contents of food.

Datta extracts showed antibacterial activity against all test clinical isolates and standard culture (ATCC) bacteria with zone of inhibition that ranged from 11-27mm. Also along with determination of antimicrobial activities of Datta, antimicrobial activities of chili extract was performed in order to observe if there is significant differences. As information obtained from the Datta collected Hotels, different ingredients such as garlic and ginger were added during preparation and these have also have antimicrobial effect by themselves [13]. From this point of view more antimicrobial activities can expect from Datta as compared to sole Chili Pepper extract. However, our finding showed that there is no significant difference between Datta extract and Chili Pepper extract (P=0.069). This may be due to variation in storage time of both extracts that may be compensated by synergetic effect of ingredients in Datta because the mean storage time of Datta sample was two weeks whereas antimicrobial activities of Chili extract were performed from fresh extracted.

Antimicrobial activities of the Datta and Chili pepper water based extract showed significantly week antimicrobial activities as compared to in cell walls degradation which can extract polar and non-polar phytochemicals. Enzyme polyphenol oxidase is also active in water based extract and this inhibits phenol activities in the extract [14]. Furthermore, alcohols, acetone, ethyl acetate and chloroform are more volatile than water. This property helps them to penetrate the cellular membrane plant materials and extract the intracellular ingredients [15]. Some of phytochemicals that soluble in these solvents include tannins, polyphenols, polyacetylenes, flavone, sterols and alkaloids [16]. In other study methanol extracts of Capsicum frutescens were found to be more effective against *S*. aureus, and Salmonella typhimurium[7]. Other study also showed ethanol extract has better antimicrobial activities against E. coli and Pseudomonas specious than Chloroform and water extracts [9]. In study conducted by Tsegaye et al, Datta showed antimicrobial activities and eliminates the growth of E. coli in the period of fermentation [4]. The other study also showed Datta inhibits Salmonella specious during fermentation period [3]. In another study, on antimicrobial activity of Australian native herb extracts, the aqueous extracts displayed weak antimicrobial activities [17]. Similarly, Weerakkody et al. finding shows that water extracts of black and red pepper had weak antimicrobial activity as compared to ethanol extracts [18].

In this study multi-drug resistant (MDR) clinical bacteria isolate, and ATCC bacteria were used to assess antimicrobial effect of the extracts. Among experimental bacterial species, ATCC[®] 25923[™] S. aureus was highly susceptible to extraction solvents while gram negative bacteria E. coli of clinical isolate was resistant. This difference may be observed due to the difference in cell wall and cell membrane composition of both groups of bacteria. Study conducted in Iran showed similar finding on Capsicum annuum L ethanol extract against clinical isolated microorganisms included of K. pneumonia, P. aeruginosa, E. coli and S. aureus [8]. In current study the minimum inhibitory concentration and minimum bactericidal concentration supports the finding of agar well

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diffusion assay. In conducted in Brazil, lower minimum inhibitory concentration was observed against *E. coli, K. pneumoniae*, and *P. aeruginosa*as compared to our study [19]. The observed difference may be due to difference in the amount of active ingredient in a plant can vary with factors like the variety of plant, weather condition of the area, the geographic location, the season and time of harvest, soil conditions, storage conditions, and the method of preparation.

Capsaicin is the main compound in the *Capsicum frutescens* which is responsible for pungency. Chili Peppers contain phenolic compounds, flavonoids and carotenoids [20] which have antimicrobial activity, antibiotic synergism and bacterial virulence removal [21]. In study that isolated phytochemical compound of this specious of Chili Pepper, chrysoeriol was the most active compound that shows high antimicrobial activities [22].

Conclusion: Antimicrobial activities of collected Datta samples have no significant difference among different preparation methods. Significant difference in antimicrobial activity was observed in chili pepper and Datta sample extracted with water from the other solvents. Water was week extractor of active compounds having antimicrobial activities. As a whole standard culture of S. aureuswas more susceptible organism while standard S. enteritidisand clinical isolated MDR E. coli were less susceptible for the extracts. There was no significant difference in antimicrobial activity of chili pepper and Datta samples extracts. The traditional use of Datta for food preservation by the local people in various part of Ethiopia is supported by this study.

Acknowledgement: The authors are very grateful to Arba Minch University Department of Medical laboratory science technical assistances. We also thank Arba Minch town hotels for allowing and giving information about Datta during data collection.

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ORIGINAL ARTICLE

AFRICAN JOURNAL OF CLINICAL AND EXPERIMENTAL MICROBIOLOGY JANUARY 2018 ISBN 1595-689X VOL19 No.1 AJCEM/1903 COPYRIGHT2018 <u>https://dx.doi.org/10.4314/ajcem.v19i1.3</u> AFR. J. CLN. EXPER. MICROBIOL. 19 (1): 18-23

BACTERIAL CONTAMINATION OF WHITE COATS AND HANDS OF HEALTHCARE WORKERS AT MANSOURA UNIVERSITY CHILDREN'S HOSPITAL, MANSOURA-EGYPT

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Running Title: WHITE COATS AND HANDS CONTAMINATION OF HCWS AT MANSOURA UNIVERSITY

ABSTRACT

Background: Transmission of hospital acquired infections (HAIs) may be associated with contamination of healthcare workers' (HCWs) hands and white coats.

Objective: The purpose of this study was to clarify the role of HCWs' white coats in transmitting HAIs and to determine the association between bacterial contamination of HCWs' hands and white coats.

Methods: A total of 154 HCWs were enrolled in the study; different samples were taken from their hands and white coats. Samples were processed and both microbiological and biochemical characterization of the isolates were done using standard microbiological protocols.

Results: Up to 65.6% of hands and 61% of coats of HCWs were contaminated by microorganisms. *Staphylococcus aureus* was the most commonly isolated organisms from both hands and coats of HCWs (29.2%, 27.3% respectively) followed by MRSA (22.1%, 24.7% respectively).

Conclusions: The risk for contamination of hands and coats of HCWs is high in different clinical settings. In order to reduce the rate of HAIs, a strict dress protocol should be set into play to prevent cross contamination between HCWs and patients. **Keywords:** contamination, HCWs, coat, hand, *Staphylococcus aureus*, MRSA.

CONTAMINATION BACTÉRIENNE DE MANTEAUX BLANCS ET DE MAINS DE SOINS DE SANTÉ À L'HÔPITAL POUR ENFANTS DE L'UNIVERSITÉ MANSOURA, MANSOURA-ÉGYPTE

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Titre en cours: MANTEAUX BLANCS ET CONTAMINATION DES MAINS DE LA HCWS À L'UNIVERSITÉ MANSOURA

ABSTRAIT nosocomiales (IASS) peut être associée à la contamination des mains des travailleurs de la santé et des blouses blanches.

Contexte: La transmission des infections

Objectif: Le but de cette étude était de déterminer l'étendue, le type et l'association entre la contamination bactérienne des mains des travailleurs de la santé et les blouses blanches.

Méthodes: Au total, 154 travailleurs de la santé ont été inclus dans l'étude; différents échantillons ont été pris de leurs mains et des manteaux blancs. Les échantillons ont été traités et la caractérisation microbiologique et biochimique des isolats a été effectuée en utilisant des protocoles microbiologiques standard.

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Résultats: Jusqu'à 65,6% des mains et 61% des couches de TS ont été contaminées par des micro-organismes. Le Staphylococcus aureus était le plus souvent isolé des deux mains et des deux sexes (29,2%, 27,3%), suivi par le SARM (22,1%, 24,7% respectivement).

Conclusions: Le risque de contamination des mains et des couches de TS est élevé dans différents contextes cliniques. Afin de réduire le taux d'IASS, un protocole vestimentaire strict devrait être mis en place pour prévenir la contamination croisée entre les travailleurs de la santé et les patients.

Mots clés: contamination, agents de santé, manteau, main, Staphylococcus aureus, SARM

INTRODUCTION

Hospital acquired infections (HAIs), previously known as nosocomial infections, are those which are not present or incubated before admission of patient to the hospital but obtained during the patient's stay in hospital. The prevalence of these infections is estimated to be 5 to 10% in developed countries and 25% in developing countries.¹ Although the main form of transmission of HAIs is through health care workers' (HCWs) contaminated hands, HCWs' garments as coats and uniforms may play an important part in transmitting pathogenic bacteria within healthcare settings.² Within healthcare facilities, pathogenic bacteria may be transferred from patient to patient or from patient to the HCWs or the reverse.3 Classically, standard infection control precautions have emphasized on hand hygiene and personal protective equipment to disrupt the chain of infection in healthcare settings.

The HCWs' coats can get contaminated by microorganisms due to improper handling practices. They get easily contaminated from infectious microorganisms that are continuously dispersed by patients in the hospital environment.⁴ However, the role of bacterial contamination of uniforms of HCWs in the horizontal transmission of bacteria remains poorly understood.

There are accumulating data about incriminating HCWs' uniforms as a possible source of pathogenic microorganisms. These contaminated uniforms play a role in transmitting bacteria from patients to HCWs and the other way around.⁵ Furthermore, white coats are currently implicated in transmitting the potentially pathogenic multi-drug resistant type microorganisms.⁶

In recent years, there was an increasing attention to prevent HAIs to reduce costs, morbidity and mortality as well as to control the problem of antibiotic resistance.⁷ Our aim was to clarify the role of HCWs' white coats in transmitting HAIs and to determine the association between bacterial contamination of HCWs' hands and white coats.

MATERIAL AND METHODS

We have conducted a prospective cross sectional study during the period between August 2016 and June 2017 in Mansoura University Children Hospital. The study was a conjoined effort between Microbiology and Medical Immunology Department and the Infection Control Committee at Mansoura University Children Hospital. All the participating HCWs were informed about the study and informed consent was taken. The study protocol has been approved by Faculty of Medicine - Mansoura University ethical committee.

Samples Collection

Samples were collected from the participating HCWs' hands and white coats across intensive care units (ICUs), internal wards and outpatients' clinics in Mansoura University Children Hospital. In addition to obtaining samples, data were collected including date, unit and profession of the HCWs. None of the approached HCWs refused to participate in this study.

We obtained swabs from the hands of the HCWs as well as from their white coats. Four predetermined sites of the white coats were sampled: the sleeve ends, the front panel at the level of the chest, the upper part of pocket and the collar. The collection of microbiological samples from coats was performed by rolling a sterile swab moistened in sterile saline on the target site.

Culture and Identification

All swabs were cultured immediately using blood agar plates. All plates were aerobically incubated at 37 °C for 24 hours. Gram staining was used to examine the morphology and staining reaction of the organisms. Gram-negative organisms were then subcultured on MacConkey agar plates. Biochemical evaluation included testing for catalase, coagulase, oxidase, triple sugar iron, indole and citrate using protocols standard for identification and characterization of microorganisms. Methicillin resistant Staphylococcus aureus (MRSA) species were identified by using cefoxitin and oxacillin disks on Mueller Hinton agar.8 Kirby Bauer's disc diffusion method was used to determine the antibiotic sensitivity of bacterial isolates.8

We classified isolated bacteria into pathogens (including *Staphylococcus aureus* (*S. aureus*), any Gramnegative bacilli and Candida) and skin flora (including coagulase-negative Staphylococci, Bacillus species and Diphteroids).

Statistical Analysis

Statistical analysis was performed using the SPSS statistical package software for windows version 22 (SSPS Inc, Pennsylvania, USA). Differences between two categorical variables were evaluated using Chisquare test while the one-way analysis of variance (ANOVA) was used to determine any statistically significant differences between three variables. P value < 0.05 was considered significant difference.

RESULTS

Of the study participants, 31 (20.1%) were doctors, 105 (68.2%) were nurses, and 18 (11.7%) were other professions (e.g., technicians, therapists). A total of 154 HCWs hands were swabbed in different ICUs, ward and outpatients' clinics (Table 1).

Bacterial growth was detected on 100 (64.9%) HCWs' hands; 45 (29.2%) grew *S. aureus*, 34 (22.1%) grew MRSA, 4 (2.6%) grew Gram-negative bacilli and 6 (3.9%) grew normal skin flora. While bacterial growth was detected on 92 (59.7%) HCWs' white coats; 42 (27.3%) grew *S. aureus*, 38 (24.7%) grew MRSA and 1 (0.6) grew Gram-negative bacilli. Hand cultures revealed Gram-positive cocci in 79 samples (51.3%) while 80 (52%) coat samples recovered Gram-positive cocci. Negative cultures were revealed from 54 (35.1%) hand swabs and 62 (40.3%) coat samples (Table 2).

TABLE (1): DISTRIBUTION OF SAMPLES IN DIFFERENT CLINICAL SETTING AND AMONG DIFFERENT

		IICW3		
Place	ICU	Wards	Outpatients' clinic	Total
	No (%)	No (%)	No (%)	No (%)
Doctor	11 (7.1)	9 (5.8)	11(7.1)	31 (20.1)
Nurse	46 (29.9)	46 (29.9)	13 (8.4)	105 (68.2)
Other HCWs	1 (0.6)	14 (9.1)	3 (1.9)	18 (11.7)
Total	58 (37.7)	69 (44.8)	27 (17.5)	154 (100)

TABLE (2): BACTERIA ISOLATED FROM HCWS' HANDS AND WHITE COATS					
Isolated Bacteria	Hand No=154 (%)	Coat No=154 (%)			
No growth	54 (35.1)	62 (40.3)			
S. aureus	45 (29.2)	42 (27.3)			
MRSA	34 (22.1)	38 (24.7)			
Bacillus	5 (3.2)	6 (3.9)			
Diphteroids	1 (0.6)	0			
Klebsiella	4 (2.6)	0			
Pseudomonas	0	1 (0.6)			
MRSA + Bacillus	3 (1.9)	2 (1.3)			
S. aureus + Bacillus	5 (3.2)	1 (0.6)			
Klebsiella + Enterococci	1 (0.6)	0			
S. aureus + Candida	1 (0.6)	1 (0.6)			
MRSA + Candida	1 (0.6)	0			
MRSA + Pseudomonas	0	1 (0.6)			
Total	154 (100)	154 (100)			

Variable	Doctors (n=31)	Nurses N=(105)	Others N=(18)	Р
Hands	8 (25.8)	27 (25.7)	2(11.1)	0.23
Coats	6(19.4)	21(20.0)	2(11.1)	0.12
Hands & Coats	12(38.7)	44(41.9)	7 (38.9)	0.74
Neither	5(16.1)	13 (12.4)	7 (38.9)	0.02

TABLE (3): CONTAMINATION RATES OF SAMPLES AMONG DIFFERENT HCWS

In our study, 63 (40.9%) HCWs had microorganisms on their hands and white coats at the same time; and only 25 (16.2%) HCWs were negative for both their hands and coats. Bacterial contamination was found on the hands of doctors and nurses more than those of other HCWs but the difference did not reach a statistical significance, (25.8, 27.7 and 11.1 percent respectively, P=0.23). Similarly, the coats of doctors and uniforms of nurses were found to be contaminated with bacteria more than coats of other HCWs and the difference did not reach a statistical significance (19.4, 20.0 and 11.1 percent respectively, P=0.12). The combination of both hands and coats of all the HCWs were almost contaminated equally, P=0.74. Nevertheless, the percentage of other HCWs who found to be negative for bacterial contamination was significantly higher than those of doctors and nurses, p=0.02 as shown in Table 3.

TABLE (4): CONTAMINATION RATES OF SAMPLES IN DIFFERENT CLINICAL SETTING

Variable	Inpatients (n=127)	Outpatients (n=27)	Р		
Hands	26 (20.5)	11 (40.7)	0.02		
Coats	24 (18.9)	5(18.5)	0.89		
Hands &	53 (34.4)	10 (37.0)	0.68		
Coats					
Neither	24(18.9)	1 (0.6)	0.001		

Inpatients includes ICU and word

The hands of the HCWs in the outpatients' clinics were significantly contaminated with bacteria more than hands of HCWs in the inpatient wards and ICU, 40.7 vs 20.5, P=0.02. However, the percentage of contaminated coats and contaminated both hands and coats did not show any statistical significance P=0.89 and P=0.68 respectively. Health care workers hands and coats in the inpatient wards and ICU that did not show any bacterial contamination were significantly higher than those of outpatients, 18.9 vs 0.6, P=0.001 as shown in Table 4.

DISCUSSION

White coat is a symbol of identification for HCWs and is considered to be a sign of protection for our patients. However, they may act as a potential source in the transmission of pathogenic bacteria, including multidrug resistant types, in different hospital settings.⁹

In our study, the hands of the HCWs in the outpatients' clinics were significantly contaminated with bacteria more than hands of those in the inpatient wards and ICU, that may be explained with busy working environment in the outpatients set up and insufficient time for proper implementation of infection control measures between examined patients who continuously detach off infectious bacteria compared to inpatient wards and ICU. As the HCWs attend to patients without proper hand washing carries a great possibility of bacterial contamination and subsequently cross-contamination to other patients.

Lack of white coats and hands contamination among HCWS in the wards and ICU compared to outpatients' HCWs enforces our previous finding and suggests a solid relation between coats and hands contamination and lack of patient after care management that could carry a risk of HAIs in susceptible individuals.

We have shown that both doctors and nurses, who are more knowledgeable and medically experienced in implementing infection control measure, had more contaminated coats and hands than other HCWs such as technicians which might be due to nature of their work that is lacking direct contact with patients.

The majority of the isolated organisms in our study were *S. aureus* and MRSA while normal skin flora was not detected on a large scale. The rate of contamination of HCWs' hands was up to 64.9%, while their white coats were contaminated in a rate of 59.7%. Similarly, *Surase et al.*, found that the rate of contamination was 79% for hands of the HCWs and 75% for their coats.¹⁰ Other studies showed contamination of white coats ranging from 23% to 95%.¹¹ Therefore, white coats possess a risk of cross contamination in different healthcare settings.

Gram-positive cocci were the dominant isolated organisms, followed by Gram-negative organisms with the difference being statistically significant (p< 0.05). Gram-positive cocci have been recovered from (51.3%) and (52%) of hand and coat samples respectively making it the predominant bacterial group contaminating the hands and coats of the

HCWs. Other studies reported a similar predominance of Gram-positive cocci which might be potentially pathogenic particularly if the host is immune compromised. ^{6,12,13}

Among the Gram-positive cocci, *S. aureus* was recovered from 87 samples (hand: 45; 29.2%, coat: 42; 27.3%), while MRSA was detected in 72 samples (hand: 34; 22.1%, coat: 38; 24.7%). Fifty-four (35.1%) of the hand samples were negative, and 6 (3.9%) had skin flora only. High level of contamination of white coats with MRSA has been previously reported.^{11,14} In a study conducted by *Surase et al*, MRSA accounted for 12% of the potential pathogens.¹⁰

Potentially infectious Gram-negative bacilli were also isolated in this study, but they were significantly lesser in number, as was reported by previous studies.^{15, 16}

Despite of multiple infection control measures implementation, the horizontal transmission of nosocomial pathogens, including multidrug-resistant types, persists which suggest the presence of an overlooked reservoir for these pathogens. Previously, contamination of HCWs' uniforms with potentially pathogenic bacteria and skin flora has been reported.¹⁷ Similarly, those studies found pathogenic bacteria such as *S. aureus*, MRSA, Enterococci and Gram-negative bacilli.

A prohibition of wearing of white coats and any other long-sleeved garment while providing patient care

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was recommended by the British Government in a uniform and dress code for physicians that was published in 2007. This prohibition is not applied in other developed countries such as the United States and developing countries such as Egypt. Despite the emerging evidence indicating bacterial contamination of uniforms and the lack of frequent washing of white coats, white coats banning during patient care remains a controversial issue.¹⁸ However, we recommend, due to our findings, that a strict dress protocol should be implemented in order to prevent cross contamination between HCWs and patients and to guard against transmission of infection in different healthcare settings. Furthermore, HCWs should be encouraged to keep their white coats clean, to wash their hands frequently and to avoid touching their coats in particular after hand washing.

CONCLUSION

The risk for contamination of hands and coats of HCWs is high in different clinical settings. A large proportion of HCWs' white coats and hands might be contaminated with potentially pathogenic *S. aureus* and MRSA. HCWs ' coats may be an important vector for transmission of nosocomial pathogens. In order to reduce the rate of HAIs, a strict dress protocol should be set into play to prevent cross contamination between HCWs and patients.

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ORIGINAL ARTICLE

AFRICAN JOURNAL OF CLINICAL AND EXPERIMENTAL MICROBIOLOGY JANUARY 2018 ISBN 1595-689X VOL19 No.1 AJCEM/1904 COPYRIGHT 2018 https://dx.doi.org/10.4314/ajcem.v19i1.4 AFR. J. CLN. EXPER. MICROBIOL. 19 (1): 24-29

EVALUATING THE USE OF DEDICATED SWAB FOR RAPID ANTIGEN DETECTION TESTING IN GROUP A STREPTOCOCCAL PHARYNGITIS IN CHILDREN

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RUNNING TITLE: RAPID ANTIGEN DETECTION TESTING IN GAS PHARYNGITIS IN CHILDREN

ABSTRACT

Background: Group A streptococcus (GAS) is the most common and fearful bacterial cause in pediatric acute pharyngitis due to its serious complications. Several generations of rapid antigen detection tests (RADTs) have been developed to facilitate rapid detection of GAS pharyngitis. We assessed the value of using a dedicated swab for RADT rather than using the same swab for throat culture and RADT.

Methods: We conducted a prospective, single-center study that included children with suspected GAS pharyngitis. Paired throat swabs were taken simultaneously from each child. We dedicated one swab for RADT (RADT#1) and used the other swab to inoculate blood agar plate surface, and then immediately to process the RADT (RADT#2).

Results: The prevalence of GAS pharyngitis among the participants was 28% based on throat culture positive results. The RADT#1 and RADT#2 had sensitivity results of 92.9% and 84.3% respectively. Both RADT#1 and RADT#2 had 96.1% specificity.

Conclusion: We found that RADT resulted in a better sensitivity when one swab was dedicated for the test. Therefore, physicians are encouraged to use separate swabs for each diagnostic test when both RADT and throat culture are performed.

Key words: GAS, pharyngitis, rapid antigen detection test

ÉVALUATION DE L'UTILISATION D'UN SWAB DEDICÉ POUR DES ESSAIS RAPIDES DE DÉTECTION D'ANTIGÈNE DANS LE GROUPE A PHARYNGITE STREPTOCOCALE EN ENFANTS

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TITRE FONCTIONNEL: TEST DE DETECTION ANTIGENNE RAPIDE DANS LA PHARYNGITE DE GAZ DANS LES ENFANTS

ABSTRAIT

Contexte: Le streptocoque du groupe A (GAS) est la cause bactérienne la plus fréquente et la plus effrayante de la pharyngite aiguë pédiatrique due à ses graves complications. Plusieurs générations de tests de détection d'antigène rapide (RADT) ont été développés pour faciliter la détection rapide de la pharyngite GAS. Nous avons évalué la valeur de l'utilisation d'un tampon dédié pour RADT plutôt que d'utiliser le même écouvillon pour la culture de la gorge et la RAD

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Méthodes: Nous avons mené une étude prospective et à centre unique comprenant des enfants atteints de pharyngite soupçonnée de GAS. Des écouvillons de gorge appariés ont été pris simultanément par chaque enfant. Nous avons dédié un écouvillon pour RADT (RADT # 1) et utilisé l'autre écouvillon pour inoculer la surface de la plaque d'agar de sang, puis immédiatement pour traiter le RADT (RADT # 2).

Résultats: La prévalence de la pharyngite GAS chez les participants était de 28% selon les résultats positifs de la culture de la gorge. Le RADT # 1 et le RADT # 2 ont des résultats de sensibilité de 92,9% et 84,3% respectivement. Les deux RADT # 1 et RADT # 2 avaient une spécificité de 96,1%.

Conclusion: Nous avons constaté que RADT a permis une meilleure sensibilité lorsqu'un tampon a été dédié au test. Par conséquent, les médecins sont encouragés à utiliser des écouvillons séparés pour chaque test de diagnostic lorsque la RADT et la culture de la gorge sont effectuées.

Mots clés: GAS, pharyngite, test rapide de détection d'antigène

INTRODUCTION

Group A streptococcus [GAS] is considered the most prevalent and important bacteria that causes pediatric acute pharyngitis due to its serious complications (1, 2). It causes a considerable economic burden to the community due to the cost of medical care. Moreover, delay in school progress of children due to the disease is also a matter of concern. In the United States of America, GAS in children costs millions of US dollars per year (3)

The rapid and accurate diagnosis of GAS pharyngitis in children enables an early treatment with proper antibiotics reducing organism transmission in the community along with its complications (4). Furthermore, an accurate diagnosis of GAS pharyngitis allows proper use of antibacterial drugs with subsequent reduction in the potential risk of drug resistance (5,6). The clinical diagnosis of GAS pharyngitis is a challenging task as the symptoms are non-specific, and similar manifestations are also observed in other types of pharyngitis (7). Therefore, clinical scoring systems such as Centor and McIsaac scores were developed to identify the patients with GAS pharyngitis prior to prescribing antibiotics (8) .Unfortunately, these clinical diagnostic tools have vielded inaccurate results, therefore performing laboratory tests is a necessity in these cases (9).

The bacterial culture of collected throat swabs using blood agar plates continues to be the gold standard laboratory test for GAS pharyngitis (10). Although throat swab culture allows further investigations such as subtyping and antimicrobial susceptibility testing, it has many limitations for example laboratory infrastructure, costs, and the lag period to obtain the result (24–48 hours) which can delay an effective management (10,11). These limitations could be a problem with low resources, as most of the patients cannot come back for another visit and management (12).

RADTs have been used for detection of GAS pharyngitis since the 1980s (13). Their quick turnaround time enables the diagnosis of GAS

pharyngitis within few minutes and thus helps clinicians decide appropriate management at their healthcare facility. In addition, it is easy to perform in both outpatient clinics and professional laboratory settings (14).

Rapid antigen detection tests have a specificity ranging from 90- 99% which is considered high, however, the sensitivity is variable, ranging from 75% to 95%, compared to the throat culture technique (15). Although RADTs have been used in many societies in America and Europe as clinical practice guidelines, (16,17). their widespread use is limited by their variable sensitivities. Owing to the reported variable sensitivity of RADTs, the international protocols emphasize utilizing throat culture as a supporting method in the case of negative RADTs to avoid missing any positive instance of GAS pharyngitis (10,17,18).

Regardless of the test method, careful sampling from the posterior pharynx and tonsils is essential for the accurate results as per the recommendations of Infectious Diseases Society of America (11). Most of the studies comparing the performance of RADT with throat culture used either a single swab to perform culture and RADT or separate swabs for each diagnostic test. However, none of the previous studies, up to the best of our knowledge, presented a parallel comparison of these two approaches from a single patient.

In the current study, we evaluated the performance of using a dedicated swab for RADTs rather than using the same swab for a throat culture and RADTs.

MATERIALS AND METHODS

Study Participants

We included eligible patients from the outpatient clinics of Mansoura University Children Hospital during the period from October 2014 till June 2015. The inclusion criteria were based on the Modified Centor score as clinical manifestations of GAS pharyngitis, including the absence of cough, temperature > 38°C, anterior cervical lymphadenitis and the presence of pharyngeal or tonsillar exudates (19). We included the participants with Modified Centor score of ≥ 2 in our study. The patients who had a tonsillectomy or received antibiotics during the preceding week were excluded. An informed consent was obtained from at least one of the parents or legal guardians before enrollment in the study. Demographic and clinical data were also collected from the participants.

Study Design

We conducted a prospective, single-center study. Paired swabs, using the sterile swabs provided in RADT kit, were collected simultaneously from each child by rubbing the two swabs together against the back of the throat and tonsillar area (especially the areas of inflammation, ulceration or exudation), while avoiding contact with teeth, tongue, gums, and cheek surfaces. The swabs were placed in dry test tubes and immediately transported to the microbiology laboratory for further processing. We dedicated one swab for RADT (RADT#1) and used the other swab to inoculate blood agar plate surface, and then immediately to process the RADT (RADT#2).

BinaxNOW® Strep A Card RADT

We used a BinaxNOW® Strep A Card immunochromatographic test (Alere Scarborough, Inc. USA). The sample line in the card is a strip of antibody (anti-strep A), which is coated on a nitrocellulose membrane. The internal control line is formed by the anti-species antibody, which is coated on the same membrane forming the second stripe. The test was executed according to the manufacturer guidelines. The results were read within five minutes and interpreted by the presence or absence of pink to purple colored lines. A positive result indicated the detection of both sample and control lines, while a negative result showed only the control line. BinaxNOW® Strep A Card RADT is readily available in Egypt and it costs as low as 3 US dollars per patient that may be suitable for low and middle-income countries.

Culture and Identification

Incubation of blood agar plates (Oxoid, UK) was done at 37° C for 24 hrs. If there was no growth visible, reincubation of the plates for further 24 hrs was done. We identified potential GAS by beta-hemolytic colonial morphology, Gram staining, catalase test and bacitracin test. The SLIDEX® Strepto Plus A latex agglutination test (bioMérieux SA, France) was used for grouping to confirm GAS identification.

Statistical Analysis

Both sensitivity and specificity together with predictive values were calculated based on Greenhalgh's formulas (20). The data were presented as numbers and percentages. Categorical variables were compared using the Chi-squared test and are presented as percentages (%). Statistical values were considered significant at a P-value is less than 0.05. All statistical data were analyzed by using version 15.0 of SPSS software package (Chicago, IL, USA).

RESULTS

We included 250 patients into our study. All the demographic data of the participating subjects are illustrated in Table-1. The prevalence of GAS among participating subjects with pharyngitis was 28% (70/250) based on throat culture which was considered as the gold standard in our study. Cervical lymphadenitis and the presence of pharyngeal or tonsillar exudates were significantly associated with GAS pharyngitis as shown in Table 2.

TABLE 1: DEMOGRAPHIC FACTORS OF THE STUDY PARTICIPANTS

Demographic factors	Total patients n = 250 (%)
Gender	
Male	130 (52)
Female	120 (48)
Age	
Age <5 years	109 (43.6)
Age > 5 years	141 (56.4)

Clinical finding	Children with GAS pharyngitis n = 70 (%)	Children without GAS pharyngitis n = 180 (%)	P value*
Absence of cough	55 (78.6)	150 (83.3)	0.81
Fever (temperature > 38°C)	60 (85.7)	151 (83.9)	0.87
Cervical lymphadenitis	47 (67.1)	34 (18.9)	0.02
Pharyngeal or tonsillar exudates	50 (71.4)	40 (22.2)	0.01

TABLE 2: ASSOCIATION OF CLINICAL FINDINGS WITH CONFIRMED GAS PHARYNGITIS

*P value of the association of clinical findings with confirmed GAS pharyngitis

TABLE 3: PERFORMANCE CHARACTERISTICS OF RADT#1 AND RADT#2 COMPARED WITH THROAT CULTURE

	Culture- positive, assay- positive (n)	Culture- negative, assay- positive (n)	Culture- positive, assay-negative (n)	Culture- negative, assay- negative (n)	Sensitivity (%)	Specificity (%)	PPV (%)	NPV (%)
RADT#1	65	7	5	173	92.9	96.1	90.3	97.2
RADT#2	59	7	11	173	84.3	96.1	89.4	94

PPV: positive predictive value; NPV: negative predictive value

The performance of RADT#1 and RADT#2, compared with the throat culture, are shown in Table-3. Out of the 70 patients with culture confirmed GAS pharyngitis, RADT#1 and RADT#2 were truly positive in 65 and 59 patients, respectively. The RADT#1 and RADT#2 resulted in 5 and 11 false negative results, respectively. The RADT#1 sensitivity (92.9%) was considerably higher than that of RADT#2 (84.3%) however the difference was found to be statistically not significant. Both RADT#1 and RADT#2 assays had 96.1% specificity. The RADT#1 and RADT#2 had positive predictive values (PPV) of 90.3% and 89.4%, respectively, and negative predictive values (NPV) of 97.2% and 94%, respectively.

DISCUSSION

Streptococcal pharyngitis has drawn medical attention over the years, particularly because of its potential serious problems such as post-streptococcal autoimmune sequelae. The prevalence of GAS among the study participants with pharyngitis was found to be 28%, which is almost similar to an earlier reported prevalence in Egypt (12). Earlier studies reported that the prevalence of GAS pharyngitis varies from one region to another, reaching up to 41% in some regions. This may be due to the influence of several

regional factors such as the school crowdedness level, basic sanitation, and the efficiency of healthcare systems (12,21-23). Among the clinical manifestations of the disease, tender anterior cervical lymphadenitis and the presence of pharyngeal or tonsillar exudates were significantly associated with GAS pharyngitis, which is consistent with other reports (23,24).

Although the sensitivity difference between the RADT#1 and RADT#2 did not reach a statistical significance, the RADT#1 had a considerable better sensitivity than RADT#2 (92.9% versus 84.3%). The false negative results in the case of RADT#2 were more than two-fold higher than those obtained in RADT#1. This lower sensitivity of RADT#2 could be accounted for by an insufficient antigen extraction from the swab after plate inoculation, particularly if the collected swab has a low bacterial load. Such findings were also supported by low colony counts of GAS noticed with the samples that gave false negative results by RADT#2, although truly identified by RADT#1. Previous studies have also reported that the performance of RADTs is directly proportional to the bacterial load present on the collected swab (25,26). Furthermore, a law number of GAS colonies was previously noticed in the patients with false negative RADT results reflecting low bacterial load in the collected swabs (15). The sensitivity difference

between the RADT#1 and RADT#2 could also be attributed to a faulty technique and the interpretation of the RADT results. However, in this study, the processing of swabs from each patient was done by the same trained person to eliminate any user bias in the method. Both RADT#1 and RADT#2 assays had the same specificity of 96.1% that was close to previously reported data (23,27,28).

In some cases, a GAS asymptomatic carrier can be mistakenly identified for the illness that is caused by other organisms; this might be considered a study limitation. However, the discrimination between acute GAS pharyngitis and GAS carriers with acute viral pharyngitis cannot be achieved by either conventional throat culture or RADTs. Therefore, it is acceptable to treat GAS infection based on positive result of either throat culture or RADTs (15).

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CONCLUSION: BinaxNOW Strep-A Card is a simple and quick test that can be used clinically to reduce the unnecessary use of antibiotics in children with pharyngitis. We found that RADT resulted in a better sensitivity when one swab was dedicated for the test. Therefore, physicians are encouraged to use separate swabs for each diagnostic test when both RADT and throat culture are performed.

ACKNOLOGMENT: We appreciate the constant help of the doctors and nursing staff of Mansoura University hospital in providing professional care and proper implementation of research protocol to our candidates.

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ORIGINAL ARTICLE

AFRICAN JOURNAL OF CLINICAL AND EXPERIMENTAL MICROBIOLOGY JANUARY 2018 ISBN 1595-689X VOL19 No.1 AJCEM/1905 COPYRIGHT 2018 https://dx.doi.org/10.4314/ajcem.v19i1.5

AFR. J. CLN. EXPER. MICROBIOL. 19 (1): 30-37

ANTIFUNGAL SUSCEPTIBILITY AND TEST FOR CURE OF CANDIDA SPECIES AMONG VULVOVAGINAL CANDIDIASIS PATIENTS IN A SECONDARY CARE HOSPITAL, NIGERIA

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ABSTRACT

Background: Antimicrobial resistance among *Candida species* is an intense public health concern. The aim of the study was to determine the antifungal susceptibility pattern and test for cure of *Candida species* among women of child bearing age who visited the General Hospital Onitsha, Nigeria with symptoms suggestive of Vulvovaginal Candidiasis (VVC).

Materials and Methods: Eight hundred and seventy six female patients participated in the study of which high vaginal swabs were collected and evaluated mycological by standard microbiological methods: microscopic examination and culture using sabouraud dextrose agar (SDA). Susceptibility of isolates to 4 antifungal agents was tested using agar dilution method. Clinico-mycological evaluation was also performed among the patients.

Result: Higher minimum inhibitory concentration (MIC) to azole antifungals was observed predominantly among non-albicans *Candida species* increasingly involved in VVC. The rate of mycological resolution was higher than symptomatic relief at 2 weeks after treatment with antifungal drug.

Conclusion: Efficacious treatment of VVC requires an adequate knowledge of the causative agents and more importantly the antimicrobial to which they exhibit high susceptibility.

Keywords: Vulvovaginal Candidiasis, Clinico- mycology, Antimicrobial resistance, Candida species

SUSCEPTIBILITÉ ANTIFONIQUE ET TEST POUR LA CURE D'ESPÈCES DE CANDIDA ENTRE LES PATIENTS DE CANDIDASES VULVOVAGINALES DANS UN HÔPITAL DE SOINS SECONDAIRES, NIGERIA

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ABSTRAIT

Contexte: La résistance aux antimicrobiens chez les espèces de Candida est un problème de santé publique intense. L'objectif de l'étude était de déterminer le schéma de susceptibilité aux antifongiques et le test de guérison des espèces de Candida parmi les femmes en âge de procréer qui ont visité l'hôpital général de Onitsha, au Nigeria, avec des symptômes suggérant une candidose vulvovaginale (VVC).

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Matériaux et méthodes: huit cent soixante-seize six patientes ont participé à l'étude des prélèvements vaginaux élevés collectés et évalués par mycologie par méthodes microbiologiques standard: examen microscopique et culture à l'aide de la gélose sabouraud dextrose (SDA). La susceptibilité des isolats à 4 agents antifongiques a été testée en utilisant une méthode de dilution en agar. Une évaluation clinico-mycologique a également été réalisée chez les patients.

Résultat: une concentration minimale minimale d'inhibition (MIC) en anatoxines azoliques a été observée principalement chez les espèces non-albicans Candida de plus en plus impliquées dans VVC. Le taux de résolution mycologique était plus élevé que le soulagement symptomatique à 2 semaines après le traitement par un médicament antifongique.

Conclusion: Un traitement efficace de la VVC nécessite une connaissance adéquate des agents causaux et, plus important encore, des antimicrobiens auxquels ils présentent une forte susceptibilité.

Mots-clés: Candidiase Vulvovaginale, Clinico-mycologie, Résistance Antimicrobienne, Espèces Candida

INTRODUCTION

Antimicrobial resistance among *Candida species* involved in Vulvovaginal candidiasis (VVC) continues to thrive as a serious public health concern. Vulvovaginal candidiasis is a conventional gynecological opportunistic mycological infection caused by *Candida* species in the lower genital tract among females globally [1,2]. It has been ascertained that approximately 75 % of sexually active females have a minimum of one-time experienced symptomatic VVC [3].

The rise in incidence of fungal infection has resulted in an extensive use of antifungals [4] and the treatment is often carried out entirely on pragmatic basis, because vaginal cultures are not routinely taken, and susceptibility testing is scarcely done. Successful treatment of infections requires adequate information of the specific causative agent(s) and the drugs to which they are susceptible. Information available in the literature suggests that data on etiologic pattern in VVC and susceptibility to antifungal are lacking in Anambra State of Nigeria, particularly Onitsha, which is the commercial mainstay of the state.

Antifungal susceptibility testing provides an evaluation of antifungal efficacy, guaranteeing good treatment outcome, limiting the development of drug resistance and therapeutic ability of unendorsed composites [5-7].

MATERIALS AND METHODS

Study

Population

The present study took place between 2008 and 2009 at an Obstetrics and Gynecology Department at General Hospital Onitsha, Nigeria. A total of 876 women of different age groups were included in this study.

Ethical Consideration

Ethical approval of the study was sought from the Nnamdi Azikiwe University Teaching Hospital Institutional Review and Ethics Committee in Nnewi, Nigeria. Written consent was sought from the study subjects before inclusion into the study.

Collection of Clinical Samples

The sample: high vaginal swab was obtained for the study. The samples were collected by the clinician from the posterior fornix of the vagina with sterile Dacron cotton swab stick after dilation using a sterile speculum. Two swab samples were collected per subject.

Microscopic Examination

The first vaginal swab was rolled in drop of potassium hydroxide (KOH) then covered with cover slip. The slide was mounted on a microscope and examined using 10x and 40x objective.

Isolation and Identification

The second vaginal swab was inoculated onto Sabouraud dextrose agar (SDA) and incubated at 37°C and examined for growth daily for 4 days.

Clinico-mycological Evaluation

The patients with *Candida* positive cultures were asked to come back to the hospital after two weeks of treatment with antifungal drugs recommended to them. At the follow-up visit, the same questionnaire was administered and another vaginal swab was collected and processed as done previously. Clinico-mycological evaluation was then carried out using the following rating scale:

A. Symptom absent, culture negative = very good = 3 point score

B. Symptom present, culture negative = Good = 2 point score

C. Symptom absent, culture positive = fair = 1 point score
D. Symptom present, culture positive = poor = 0 point score

Antifungal Susceptibility Testing

Susceptibility of the isolates to antifungal drugs was carried out by agar dilution technique [8] using the following antifungal drugs: Fluconazole powder (Medich Plc, England); Itraconazole powder (Hanmi Pherm, Kore); Miconazole powder (Janssen Pharmaceutical Beerse Belgium); Clotrimazole powder (Symnedic Laboratories) as follows:

i. Preparation of stock solution of antifungal drugs:

Stock solution of each of the drugs was prepared by dissolving 25.6mg of the powder in

100ml of sterile 1: 9 dilution (in distilled water) of Dimethyl sulphoxide, to give 100ml of 256 μ g/ml. All the stock solutions were sterilized by tyndalization.

ii Agar Dilution Technique:

Double strength SDA was prepared and dispensed into McCartney bottles in 10ml amounts and sterilized by autoclaving at 121°C for 15 min, and allowed to cool to about 45°C. Two fold serial dilution of each of the drugs was subsequently made, in the molten agar, according to the protocol in table 1. The dilutions were up to 15th dilution (i.e. $0.008 - 128\mu g/ml$). The content of each McCartney bottle was thoroughly mixed and poured into plate and was allowed to set.

Table 3: PROTOCOL FOR THE DILUTION OF ANTIFUNGAL DRUGS IN CULTURAL MEDIA

—	Tube	Vol. of Medium	Vol. of Drug Soln*	Vol. of Water	Final Conc.
	No				
	1.	10 ml	10 ml	0.000ml	128 µg/ml
-	2.	10ml	5ml	5.00m1	64 µg/ml
-	3.	10 ml	2.5ml	7.500ml	32 µg/ml
Α	4.	10 ml	1.25ml	8.750ml	16 µg/ml
Τ-	5.	10 ml	0.625ml	9.375 ml	8 μg/ml
↓ -	6.	10 ml	0.3125ml	9.688ml	4 μg/ml
1	7.	10ml	10ml	0.00ml	2 µg/ml
-	8.	10ml	5ml	5.00ml	1 μg/ml
B	9.	10ml	2.5ml	7.500m1	0.5 μg/ml
ĽŬ-	10.	10ml	1.25ml	8.750ml	0.25 µg/ml
-	11.	10ml	0.62ml	9.375ml	0.125 μg/ml
	12.	10ml	0.3125ml	9.688ml	0.0625 μg/ml
↑ -	13.	10ml	10ml	0.00ml	0.032 μg/ml
	14.	10ml	5ml	5.00ml	0.016 µg/ml
Ľ-	15.	10ml	2.5ml	7.500ml	0.008 μg/ml

* Stock solutions used were: Stock solution A(Conc = 256 μg/ml) – for dilution 1-6; Stock solution B (Conc = 4 μg/ml) – for dilution 7-12; Stock solution C (Conc = 0.0625) – for dilution 13-15

Iii: Preparation and Standardization of Inoculums:

A total of 60 Candida isolates representing all the species identified were used for the test, as follows:

Candida albicans	n=39
Candida glabrata	n=8
Candida tropicalis	n=4
Candida krusei	n=5
Candida dubliniensis	n=4

Candida albicans ATCC 10231 (control organism).

Prior to testing, all isolates were sub-cultured on SDA plates and incubated overnight at 37^oC to ensure purity and viability. Approximately five isolated colonies were picked and then suspended in sterile saline and homogenized; the turbidity of the suspension was adjusted to match that of a Mac Farland 0.5 turbidity standard using a spectrophotometer.

iv. Inoculation of Plates:

The surface of the prepared SDA plates were dried at 37°C in the oven and each plate was divided into four segments. Each of the segments was inoculated with a loopful (0.01ml) of the standardized suspension of the organism. The organism was also inoculated into control plates (drug free).

v. Determination of MIC:

After 24hrs incubation at 37°C, the amount of growth in the plates containing the different concentrations of antifungal agents was compared with the amount of growth in the drug- free growth control plates. The MIC was read as the lowest concentration of antifungal that totally inhibited the growth of the organism.

INTERPRETATIVE CRITERIA

The interpretation of the results was based on the break points [9] established by the National Committee for Clinical Laboratory Standards (NCCLS) for different antifungal drugs against *Candida* species [Table 2].

TABLE 2: MIC BREAKPOINTS FOR SUSCEPTIBILITY OF CANDIDA TO ANTIFUNGAL DRUGS

interpre	cution of three values	
Susceptible	Intermediate(SDD)	Resistant
≤8µg/ml	16-32µg/ml	>64µg/ml
≤ 0.5µg/ml	1-4 µg/ml	>8µg/ml
≤ 0.125µg/ml	0.25-0.5 μg/ml	> 1µg/ml
	Susceptible ≤ 8µg/ml ≤ 0.5µg/ml ≤ 0.125µg/ml	Susceptible Intermediate(SDD) ≤ 8µg/ml 16-32µg/ml ≤ 0.5µg/ml 1-4 µg/ml ≤ 0.125µg/ml 0.25-0.5 µg/ml

Key: S - D D = Dose dependent susceptibility

STATISTICAL ANALYSIS

Statistical analysis: Chi square test, One way Analysis of Variance(ANOVA) and t- test conclude and validate the results at 0.05 level of significance.

RESULT

Yeasts cells were seen as a small, oval cell, measuring 2-4 in diameter that were budding or single. Following clinico-mycological evaluation of the

patients, 73%, 67%, 50% and 50% of patients on Clotrimazole Fluconazole, Miconazole, and Itraconazole respectively were symptomatically relieved while 91%, 89%, 88% and 17% of patients on Clotrimazole Fluconazole, Miconazole, and Itraconazole respectively were mycologically relieved at 2 weeks after treatment [Table 3]. The rate of mycological resolution was higher than symptomatic relief at 2 weeks after treatment with antifungal drug [Table 4].

		Α	В	С	D		
Drug	Number	Very Good	Good	Fair	Poor	Score	
A	dmitted						
Fluconazole	11	7	3	1	0	28	
Miconazole	9	5	3	1	0	22	
Clotrimazole	8	3	4	1	1	18	
Itraconazole	14	6	4	1	3	17	

TABLE 3: CLINICO -MYCOLOGICALLY EVALUATION AT 2 WEEKS AFTER TREATMENT WITH ANTIFUNGAL DRUGS.

The following rating scales were used: A. Symptom absent, culture negative = Very good =3 point score; B. Symptom present, culture negative = Good = 2 point score; C. Symptom absent, culture positive = Fair = 1 point score; D. Symptom present, culture positive = Poor= Zero point score

TABLE 4: SYMPTOMATIC RELIEF AND MYCOLOGICAL CURE RATES AT 2WEEKAFTER TREATMENT WITH ANTIFUNGAL DRUGS

Drug	Symptomatic relief	Mycological cure	
Fluconazole	8 (73%)	10 (91%)	
Miconazole	6 (67%)	8 (89%)	
Clotrimazole	4 (50%)	7 (88%)	
Itraconazole	7 (50%)	10 (71%)	

Mycological vs symptomatic relief at 2 weeks (t = 6.91 ;< 0.05)

The minimum inhibitory concentration (MIC) of Antifungal agents against *Candida species* isolated from women with vulvovaginal candidiasis was done using the interpretative criteria on Table 1. The susceptibility testing of 60 Candida isolates (representing different species) to fluconazole (*C. albicans, C. tropicalis, C. dubliniensis, C. krusei* and *C. glabrata*) showed varied degree of susceptibility. Of the 60 isolates, 52 (86.7%) were susceptible (MIC< 8 mg/ml) to fluconazole whereas, 8 (13.3%) isolates were intermediate with MIC 16-32 mg/ml. There was no record of resistance with fluconazole in this study [Table 5]. Of the 8 isolates with elevated MIC, 4 isolates were *Candida glabrata*, 1 isolate was *Candida tropicalis*, 2 isolates were *Candida krusei* and 1isolate *Candida albicans*. All the 60 *Candida* isolates (100%) had very low MIC to Miconazole and Cotrimazole (< 0.5 μ g/m1) [Table 6]. On the contrary, only 26 (43%) of the isolates were susceptible to Itraconazole (MIC <0.125 μ g/m1), whereas 21 (35%) were resistant (MIC>1 μ g/m1), while 13 (22%) showed dose dependent susceptibility to the drug. Among all the species, the most resistant was the *C. tropicalis* which recorded 100% resistance to Itraconazole, followed by *C. krusei* which has about 40% resistance. [Table 7].

TABLE 5: MINIMUM INHIBITORY CONCENTRATION OF FLUCONAZOLE ON CANDIDA SPECIES ISOLATED FROM VULVOVAGINAL CANDIDIASIS PATIENTS IN ANAMBRA STATE

	MIC (µg/ml)					
Candida species	≤ 8 μg /ml 16-32 μg/ml		≥ 64µg/ml			
	(Susceptible)	(Intermediate)	(Resistance)			
Candida albicans	38/39	1/39	0/39			
Candida tropicalis	3/4	1/4	0/4			
Candida dubliniensis	4/4	0/4	0/4			
Candida krusei	3/5	2/5	0/4			
Candida glabrata	4/8	4/8	0/4			
Total (%)	52/60 (86.7%)	8/60 (13.3%)	0/60 (0%)			

TABLE 6: MIC OF MICRONAZOLE / CLOTRIMAZOLE AMONG CANDIDA SPECIES

	MIC (μg/r	nl)
Candida species	≤ 0.5 µg /ml	≥ 8µg/ml
	(Susceptible)	(Resistance)
Candida albicans	39/39	0/39
Candida tropicalis	4/4	0/4
Candida dubliniensis	4/4	0/4
Candida krusei	5/5	0/5
Candida glabrata	8/8	0/8
Total (%)	60/60 (100%)	0/60 (0%)

TABLE 7: MINIMUM INHIBITORY CONCENTRATION OF ITRACONAZOLE ON CANDIDA SPECIES ISOLATED FROM VULVOVAGINAL CANDIDASIS PATIENTS IN ONITSHA, ANAMBRA STATE

		MIC (µg/ml)		
Candida species	≤0.125 µg/ml	0.25-0.5 μg/ml	≥1µg/ml	
	(Susceptible)	(Intermediate)	(Resistance)	
Candida albicans	19/39	8/39	12/39	
Candida tropicalis	0/4	0/4	4/4	
Candida dubliniensis	0/4	1/4	1/4	
Candida krusei	2/5	1/5	2/5	
Candida glabrata	2/8	3/8	2/8	
Total (%)	26/60 (43%)	13/60 (22%)	21/60(35%)	

DISCUSSION

The study compares the antifungal susceptibility patterns of 4 antifungal drugs against isolated Candida species. The antimicrobial susceptibility testing in this study revealed that most non albicans were resistant to Itraconazole. None of the candida isolates tested were resistant to Miconazole, Clotrimazole and Fluconazole, although susceptibility of 14% of the isolates to fluconazole was dose dependent (S-DD), and majority 7/8 (88%) of these (S-DD) were nonalbicans Candida (Candida glabrata and Candida krusei). The extensive use of Fluconazole leads to a shift in the causative agents of Candida infections to non-albicans species such as C.glabrata, C.krusei and C.tropicalis [10]. Although the efficacy of the drugs could not be established on the basis of the invitro susceptibility report since there was a degree of variability in the MIC values within the class of antifungals. Fluconazole, Miconazole and Clotrimazole appears to be the best choice, while Itraconazole due to its lower efficacy against nonalbicans candida would be a poor choice in the blind treatment of vulvovaginal candidiasis in this locality as non-albicans are increasingly important participant in vulvovaginal candidiasis in this locality.

A recent study by Kiguli et al., [11] described C. krusei with a high resistance of 71.43% to fluconazole whereas C. glabrata, and C. krusei exhibited 100% resistance and C. albicans exhibiting 20.59% to itraconazole. Resistance to clotrimazole was observed in 36.67% and 0.61% of C. glabrata and C. albicans respectively. Resistance to clotrimazole and fluconazole does not correlate with our study that revealed 0% resistance respectively by all Candida species. While, resistance to itraconazole by C.glabrata, C.krusei and C.albicans partially agrees with reports from our study which revealed 20%, 40% and 30.8%

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resistance to itraconazole by *C.glabrata*, *C.krusei* and *C.albicans* respectively.

Dharmik *et al.*, [12] revealed that fluconazole was highly effective against *Candida Species* (97.2 %) while, the highest resistance was observed in the case of miconazole (63 %). This is contrary to our study that observed highest resistance to itraconazole (35%).

Resistance to itraconazole was observed in 16.2% (MIC \geq 1 µg/ml). Among different species, elevated fluconazole MICs ($\geq 16 \mu g/ml$) were only observed in C. glabrata (15.2% resistant [R], 51.8% susceptible-dose dependent [S-DD]), and C. krusei (50% S-DD, 41.7% R, considered intrinsically fluconazole resistant). Resistance to itraconazole was observed among C. glabrata (74.1%) and C. krusei (58.3%). These results by Richter et al., [13] support that of this study which showed resistance to itraconazole ((MIC $\ge 1 \mu g/ml$) among C. glabrata (20%) and C. krusei (40%). Furthermore, supports elevated fluconazole MICs (16-32 µg/ml) observed more frequently among C.glabrata, C.krusei, C.tropicalis and C.albicans. Thus, fluconazole resistance among vaginal Candida albicans isolates is emerging.

Comparison of symptomatic relief and mycological cure rate at second week after treatment with Fluconazole, Miconazole, Clotrimazole and Itraconazole shows that the rate of mycological cure was significantly more than the symptomatic relief (t=6.91; p < 0.05). The time required by the body to recover after the annihilation of the infecting organism could be a contributing factor. Hence, the use of azoles for empirical therapy of uncomplicated Vulvovaginal candidiasis is recommended.

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ORIGINAL ARTICLE

AFRICAN JOURNAL OF CLINICAL AND EXPERIMENTAL MICROBIOLOGY JANUARY 2018 ISBN 1595-689X VOL19 No.1 AJCEM/1906 https://www.ajol.info/journals/ajcem COPYRIGHT2018 https://dx.doi.org/10.4314/ajcem.v19i1.6

AFR. J. CLN. EXPER. MICROBIOL. 19 (1): 38-46

VULVO-VAGINAL CANDIDOSIS IN A COHORT OF HORMONAL CONTRACEPTIVE USERS IN IBADAN, NIGERIA

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ABSTRACT

Introduction: Most women who acquire HIV and other sexually transmitted infections (STIs) are in their child bearing years and are current or potential users of contraceptive methods. The study was undertaken to provide information on the association between the hormonal contraceptive methods and vulvo vaginal candidiasis among women attending Family Planning clinics, University College Hospital, Ibadan, Nigeria.

Methods: It was a cross-sectional study in a population of women using hormonal contraceptive methods attending Family Planning clinics. Detailed medical history, endocervical and high vaginal swabs were collected from the women to establish diagnosis after clinical examination and informed consent. Aliquots of sera from venous blood samples of the women were tested for antibodies to HIV-1/2. Data was analysed using SPSS for windows' version 17.0.

Results: There were 116 women using hormonal contraceptive methods who participated in the study with mean age of 28.70 years (SD = 6.72, range = 19 -54). The mean age of sexual debut of the women was 19.2 years (SD = 2.96). The prevalence of vulvo-vaginal candidosis was 23.3%. Other associated sexually transmitted infections were bacterial vaginosis (24.1%), HIV (12.1%), trichomoniasis (10.3%), chlamydia cervicitis (7.8%), syphilis (5.2%), genital warts (6.0%) and gonorrhoea (2.6%). Younger age of sexual debut influenced the decision of selecting various forms of hormonal contraceptives especially the emergence of oral contraceptive forms (P = 0.043). Majority of the women on hormonal contraceptives had multiple sexual partners. Vulvovaginal candidosis is strongly associated with vaginal discharge and pruritus in women utilizing hormonal contraceptive methods (P = 0.001, 4.2 (1.0–13.2).

Conclusions: Women seeking contraception to prevent unintended pregnancy are as much in need of education about prevention of STIs. The study found that younger age, numbers sexual partners, and use of hormonal contraceptives could increase the risk of acquiring vulvovaginal candidosis.

CANDIDOSE VULVO-VAGINALE DANS UNE COHORTE D'UTILISATEURS CONTRACEPTIFS HORMONAUX A IBADAN, NIGERIA

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ABSTRAIT

Introduction: La plupart des femmes qui contractent le VIH et d'autres infections sexuellement transmissibles (IST) sont en âge de procréer et sont des utilisatrices actuelles ou potentielles de méthodes contraceptives. L'étude a été entreprise pour fournir des informations sur l'association entre les méthodes contraceptives hormonales et la candidose vulvo vagin chez les femmes fréquentant les cliniques de planification familiale, University College Hospital, Ibadan, Nigeria.

Méthodes: Il s'agissait d'une étude transversale menée auprès d'une population de femmes utilisant des méthodes contraceptives hormonales dans des cliniques de planification familiale.

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Des antécédents médicaux détaillés, des prélèvements endocervicaux et des prélèvements vaginaux élevés ont été effectués auprès des femmes pour établir un diagnostic après un examen clinique et un consentement éclairé. Des aliquotes de sérums d'échantillons de sang veineux des femmes ont été testées pour rechercher des anticorps anti-VIH-1/2. Les données ont été analysées à l'aide de SPSS pour la version 17.0 des veuves.

Résultats: 116 femmes utilisant des méthodes contraceptives hormonales ont participé à l'étude avec un âge moyen de 28,70 ans (ET = 6,72, intervalle = 19-54). L'âge moyen des débuts sexuels des femmes était de 19,2 ans (ET = 2,96). La prévalence de la candidose vulvo-vaginale était de 23,3%. Les autres infections sexuellement transmissibles étaient la vaginose bactérienne (24,1%), le VIH (12,1%), la trichomonase (10,3%), la chlamydia cervicite (7,8%), la syphilis (5,2%), les verrues génitales et la gonorrhée. L'âge plus jeune des débuts sexuels a influencé la décision de choisir différentes formes de contraceptifs hormonaux, en particulier l'émergence de formes contraceptives orales (p = 0,043). La majorité des femmes sur les contraceptifs hormonaux avaient plusieurs partenaires sexuels. La candidose vulvovaginale est fortement associée aux pertes vaginales et au prurit chez les femmes utilisant des méthodes contraceptives hormonales (p = 0,001, 4, 2 (1,0-13,2).

Conclusions: Les femmes qui recherchent une contraception pour prévenir les grossesses non désirées ont autant besoin d'éducation sur la prévention des IST. L'étude a révélé que le plus jeune âge, le nombre de partenaires sexuels et l'utilisation de contraceptifs hormonaux pourraient augmenter le risque d'acquisition de la candidose vulvo-vaginale.

INTRODUCTION

Contraception has been recognized as an important part of national efforts in many countries of the world to reduce adolescent pregnancies (1). Avoidance of unintended pregnancies requires access to, and appropriate use of effective and safe methods of fertility control (2), This invariably leads to the improvement of reproductive health of sexually active young women (2). Unhindered access to effective and safe contraceptive methods could be the key to individual and public health safety.(3) A number of safe and effective contraceptive methods are available, and these include abstinence, barrier methods, oral contraceptives, Depo-Provera, Norplant implant, Intra-uterine devices, and sterilization methods (1).

The current or potential users of different methods of contraceptives who acquire sexually transmitted infections and Human Immunodeficiency virus infections are in their child bearing years. There is a controversy over the extent to which specific contraceptive methods increase or perhaps reduce the risk of HIV infection(4). Hormonal contraception has been proven as one of the biological factors being linked to the acquisition of Human Immunodeficiency Virus (HIV) and other sexually transmitted infections (STIs).(5, 6) In a study conducted among a cohort of female sex workers in Kenya, compared with those who don't practice contraception; those who rely on oral contraceptives (OCPs) are more likely to acquire chlamydia infection or vaginal candidiasis, but are less likely to acquire bacterial vaginosis. (6, 7) The assumptions are that the cervical ectopy produced by oral contraceptives (OCPs) results in affected cervical -zone being more vulnerable to trauma and thus perhaps to HIV infection.(8). Injectable hormonal contraceptives may increase the risk by increasing bleedings and thinning of the vaginal epithelium.(4) Most hormonal contraceptives contain either or both progesterone and oestrogen.(9)

Hormonal contraceptives usually include combination of estrogen and progestin; and progestin only. Estrogen effects include inhibition of ovulation and prevention of follicular maturation through suppression of ovarian steroid production and possibly decreased responsiveness to gonadotropin-releasing hormone (9). Conversely, progestin leads to changes in the endometrium that make implantation less likely, increased thickness of cervical mucus that makes sperm penetration difficult, and impairment of normal tubal mobility.(10)

In spite of recent therapeutic advances, vulvovaginal candidiasis remains a common global problem of public health importance.(11) The prevalence of vulvo-vaginal candidiasis varies worldwide, and in community- based survey conducted among female commercial sex workers in Ibadan, Nigeria, VVC was the commonest sexually transmitted infections reported (12) in women. It has been estimated that more than 70% of women develop at least one episode in their life time, (11) 50% experience a second episode, (11, 13, 14) while 5-8% encounter recurrences.(15) Oestrogen dominance usually enhances overgrowth of Candida spp in the vaginal milieu; and it has also been established in previous studies that oral contraceptives may determine the possibility of recurrent vulvo-vaginal candidiasis (14, 16, 17). Other predisposing factors linked to vaginal candidiasis include HIV infection, pregnancy, diabetes and undue prolonged use of antibiotics. (14, 18) Sexual behaviour could play an important role in the acquisition of VVC since some of the risk factors have been linked to the level of sexual activities with these women. Sexual behaviour has been linked to influence both primary VVC infections and relapses.(19)

Presently there is a dearth of information of the prevalence of vulvo-vaginal candidiasis and its associated risk behaviours among hormonal contraceptive users in south western Nigeria. This study was aimed at evaluating the pattern of vulvo-vaginal candidiasis among the cohorts of hormonal contraceptive users attending the family planning clinic, University College Hospital, Ibadan.

MATERIALS AND METHODS

This was a cross-sectional study carried out in a population of child-bearing age women using different types of hormonal contraceptive methods and attending family planning clinic, University College Hospital between March – December 2006.

Sampling Procedure

Women were recruited into the study as they presented to the clinic consecutively and freely gave informed consents. The women that were enrolled into the study completed structured questionnaires to obtain baseline information on their socio-demographic characteristics, reproductive health history including sexual behaviours; and different types of hormonal contraceptives being used. Pre- test counselling was done for all clients recruited into the study which emphasized on client confidentiality; reasons for screening for candidiasis and HIV testing; information about their current and previous risk behaviours and also implication of positive test results. Women were excluded from being enrolled into the study if they were menstruating or have used antifungals especially the azoles in the preceding two weeks or within six weeks post-abortion.

Physical Examination and Specimen Collection

All women who freely gave informed consent and met the inclusion criteria had a complete pelvic examination under aseptic conditions for signs and symptoms suggestive of vulvovaginal candidiasis and other signs of sexually transmitted infections (STIs). High vaginal swabs and Endocervical swabs were collected from all the participants by the attending physicians following standard procedures. These samples were transported in Amies transport medium to the Special Treatment Clinic Laboratory, University College Hospital, Ibadan for microscopy, culture and sensitivity. The colour, character and the smell of the vaginal discharge were also noted.

Laboratory Procedures

Vaginal secretions collected were subjected to wet preparation and potassium hydroxide microscopy for the identification of round to oval budding yeast cells, trichomonads and clue cells. High vaginal secretions were also cultured on Sabouraud's dextrose agar (SDA) at 37°C for 24 to 48hrs. Saline wet preparation of the creamy-greyish colonies revealed the presence of multiple budding yeast cells and pseudohyphae suggestive of Candida species. Species identification was confirmed based on the results obtained from germ tube tests, sugar assimilation and fermentation tests based on standard methods. Germ tubes positive isolates were confirmed as *Candida albicans*.

Endocervical secretions were cultured for *N. gonorrhoeae* on modified Thayer Martins Agar. The media plates were incubated at 37°C in 5% CO₂ humidified extinction jar. Endocervical secretions were also Gram-stained for the presence of intracellular diplococci which were later confirmed as *Neisseria gonorrhoeae* by standard laboratory methods. Endocervical secretions were also tested for *Chlamydia trachomatis* by QuickView Chlamydia test kits following standard procedures (20). Diagnosis of genital warts was based on the clinical findings of typical lesions as previously described various researchers on the external genitalia, vaginal, cervix and perianal region. (21-23)

HIV-serology testing was done by rapid immunochromatographic test strips using OraQuick ADVANCE[™] rapid HIV- 1 / 2 antibody testing. Any sample positive on screening was re-tested with enzymelinked immunosorbent assay (ELISA) and confirmed by western blot analysis. Approval for the study was obtained from UI/UCH ethics review committee.

Data Analysis

Data analysis was done using SPSS software, version 17.0 (SPSS Inc., Chicago, IL, USA). Summary statistics such as proportions for categorical variables; means and standard deviation for continuous variables were estimated. The variables included for the analysis were women's age, educational level, religion, ethnicity, marital status, occupation, age of sexual debut, numbers of sexual partners by the women, numbers of multiple partners of their spouses, types of contraceptives and prevalence of candidiasis. Frequency distribution tables for each of the variables were analysed. Odds ratio and confidence interval were calculated to evaluate the association between sexual behaviour, hormonal contraception and prevalence of candidiasis. Multivariate analysis was used to assess the effect of the confounding variables. Statistical significance was set at P < 0.05.

RESULTS

During the study period, a total of one hundred and sixteen women attending family planning clinic at the University College hospital; that fulfilled the inclusion criteria and using different hormonal contraceptives were included in the analysis. Table 1 shows the sociodemographic characteristics and the rate of candidiasis of the women. The mean age of the women was 28.70 years (SD = 6.72, range = 19 –54). Sixty-six (66, 56.9%) were in the 20-29 age range and more than half (16 of 27, 59.3%) of this age group were infected with candidiasis. Nearly half of them also (57, 49.1%) were

secondary school leavers and fifty of them (50, 43.1%) were neither married nor living with a partner. Table 1.

with their casual friends and school mates while only 30 (25.9%) initiated sex with their spouses. (Table 2)

The mean age of sexual debut of the women was 19.2 years (SD = 2.96) Fifty-five of them had their sexual debut

Characteristics	Category	Frequency (n=116) (%)	Candidiasis (n=27) (%)	P -value
Age in years	10-19 20-29 30-39 40-49 50-59	4 (3.4) 66 (56.9) 38 (32.8) 6 (5.2) 2 (1.7)	0 (0.0) 16 (59.3) 9 (33.3) 2 (7.4) 0 (0.0)	0.557
Level of Education	No formal education Primary school Secondary school Polytechnic / Colleges of Education University	2 (1.7) 15 (12.9) 57 (49.1 21 (18.1) 21 (18.1)	0 (0.0) 2 (7.4) 14 (51.9) 4 (14.8) 7 (25.9)	0.576
Marital Status	Not married, Not living with a partner Not married, Living with a partner Married , Not living with a partner Married , Living with a partner	50 (43.1) 9 (7.8) 17 (14.7) 40(34.5)	10 (37.0) 1 (3.7) 5 (18.5) 11 (40.7)	0.614
Social Class	Class I Class II Class III Class IV Class V Class VI	2 (1.7) 27 (23.3) 9 (7.8) 1 (0.9) 33 (28.4) 44 (37.9)	1 (3.7) 9 (33.3) 2 (7.4) 1(3.7) 8 (29.6) 6 (22.2)	0.160

TABLE 1: SOCIO-DEMOGRAPHIC CHARACTERISTICS OF THE PARTICIPANTS

Choice of hormonal contraceptives was statistically significant for younger women (Mean= 22.5 years). Younger age of sexual debut also influenced the choice of hormonal contraceptives especially the emergency contraceptives pills. Table 3 shows that thirty-six (31.0%) of the women preferred injectable hormonal contraceptives while thirty (25.9%) were taking oral contraceptives. Those women on oral contraceptive had the highest rate of VVC (11 of 27,

40.1%). The odds of women on oral contraceptive having VVC are slightly higher but are not statistically significant. (Table 3)

The prevalence of vulvo-vaginal candidosis in this study was 23.3% (27 of 116), Nineteen (70.4%) were *C. albicans* while eight were non-albicans Candida.

Variables	Catagorias	Engranding	Condidication $= 27(0/)$	D maluo
variables	Categories	rrequency		r-value
		N=116 (%)		
Age of sexual debut	11-15	4 (3.4)	1 (3.7)	0.457
°	16-20	81 (69.8)	19 (70.4)	
	21-25	26 (22.4)	6 (22.2)	
	26-30	5 (4.4)	0 (0.0)	
		· · ·	()	
Age of co-habiting with	16-20	22 (19.0)	4 (14.8)	0.934
a partner	21-25	49 (42.2)	15 (55.6)	
•	26-30	14 (12.0)	3 (11.1)	
	31-35	1 (0.9)	0 (0.0)	
	No cohabiting	30 (25.9)	5 (18.5)	
	0	~ /	× ,	
No of sexual partners in the	0	13 (11.2)	2 (7.4)	0.345
last one month	1	62 (53.4)	12 (44.4)	
	2	33 (28.4)	9 (33.3)	
	3	6 (5.2)	3 (11.1)	
	4	2 (1.7)	1 (3.7)	
		、 <i>`</i>	. ,	
Spouses with multiple partners	Ves	23 (19.8)	6 (22 2)	0.400
opouses with multiple particles	No	33 (28.4)	10(370)	0.100
	Don't know	60 (51.8)	11 (40 7)	
	DOILT KIIOW	00 (31.0)	11 (10.7)	

TABLE 2: SEXUAL AND REPRODUCTIVE HISTORY OF THE WOMEN

TABLE 4:

TABLE 3: TYPES OF HORMONAL CONTRACEPTIVES

Types of Hormonal Contraceptives	Frequency (N=116)	Percentage (%)
Oral Contraceptives	30	25.9
Injectable	36	31.0
Emergency contraceptives	48	41.4
Norplant implant	2	1.7

TABLE 4: PATTERN OF VULVO-VAGINAL CANDIDIASIS AND OTHER STIS AMONG WOMEN USING HORMONAL CONTRACEPTIVES.

Infections	Frequency (N=116)	Percentage (%)
Vulvo-vaginal candidiasis	27	23.3
Bacterial vaginosis	28	24.1
Trichomoniasis	12	10.3
Chlamydia trachomatis	9	7.8
Gonorrhoea	3	2.6
Genital warts	7	6.0
HIV infection	14	12.1

Other sexually transmitted infections diagnosed include bacterial vaginosis (24.1%), trichomoniasis (10.3%), *Chlamydia trachomatis* infection (7.8%), Gonorrhea (2.6%), genital warts (6.0%) and HIV infection (12.1%) as shown in Table 4. There was no significant association between the women infected with candidiasis and acquisition of HIV infection. Five (18.5%) of the women with vulvovaginal candidiasis were diagnosed with HIV infection. (P =

0.24). However, two (66.7%) of the patients with gonorrhoea were infected with HIV infection. Gonorrhoea was found to be significantly associated with HIV acquisition P = 0.003). The odds ratio of

hormonal contraceptive users infected with gonorrhoea acquiring HIV infection was 16.8 (1.4-199.8). Other STIs were not associated with acquisition of HIV. (Table 5)

Infection	HIV Infection		P Value	OR (95% CI)
	Negative Frequency (%)	Positive Frequency (%)		
Vulvo-vaginal candidiasis	22 (81.5)	5 (18.5)	0.24	2.02 (0.61-6.6)
Bacterial vaginosis	25 (89.3)	3 (10.7)	0.801	0.84(0.22-3.2)
Trichomoniasis	9 (75.0)	3 (25.0)	0.146	2.82 (0.66-11.9)
Chlamydia trachomatis	7(77.8)	2 (22.2)	0.330	2.2 (0.421-12.1)
Gonorrhoea	1(33.3)	2 (66.7)	0.003*	16.8 (1.4-199.8)
Genital warts	6 (85.7)	1 (14.3)	0.850	1.23 (0.137-11.05)

TABLE 5: ASSOCIATION OF VULVOVAGINAL CANDIDIASIS AND OTHER STIS WITH HIV INFECTION

TABLE 6: ASSOCIATION OF VULVO-VAGINAL CANDIDIASIS WITH HORMONAL CONTRACEPTIVES TYPE AND OTHER RISK FACTORS

Infection	Vulvo-vaginal candidiasis		P Value	OR (95% CI)
Types of Contraceptives /	Positive Frequency (%)	Negative Frequency (%)		
Risk factors	110 4 unity (70)	riequency (70)		
Oral Contraceptives	8 (26.7)	22 (72.3)	0.610	0.78 (0.30-2.03)
Injectable	8 (22.2)	28 (77.8)	0.857	1.06(0.426-2.78)
Contraceptives				
Norplant implant	0 (0.0)	2 (100.0)	0.432	2.82 (0.66-11.9)
Emergency	11 (22.9)	37 (77.1)	0.939	1.04 (0.43-2.46)
Contraceptives				
Multiple sexual	26 (42.6)	35 (57.4)	0.261	1.04 (0.96-1.12)
partners				
Douching	7 (16.3)	36 (83.7)	0.171	1.94 (0.74-5.06)
Vaginal discharge	23 (45.1)	28 (54.9%)	0.001	12.5 (3.939.5)
Vaginal pruritus	17 (53.1)	15 (46.9)	0.001	2.2 (1.4-3.7)
HIV Infection	5 (35.7)	9 (64.3)	0.24	2.02 (0.61-6.6)
Trichomoniasis	3 (25.0)	9 (75.0%)	0.88	1.01(0.87-1.18)
Bacterial vaginosis	10 (35.7)	18 (64.3)	0.56	2.3 (0.91-5.9)
Chlamydia Cervicitis	3 (33.3)	6 (66.7)	0.46	1.7 (0.42-7.4)

In this study, Eleven (40.7%) of the women infected with vulvovaginal candidiasis were regular emergency oral contraceptive users. Acquisition of VVC was observed more in women who had multiple sexual partners in the preceding one month before the study, though not statistically significant (P = 0.068). 96.3% (26 of 27) of women infected with VVC had multiple sexual partners. Douching was also found to increase the risk of acquisition of VVC. 25.9% of women with VVC usually practice douching (P= 0.171). (Table 6)

DISCUSSION

Vulvovaginal candidiasis is a common gyneacological health problem that is usually diagnosed in women of child bearing age;(24) and it has been associated with profound morbidity in all strata of women all over the world.(11) In our study, the prevalence of vulvovaginal candidosis was 23.3% among women attending the family planning clinic in University College Hospital, Ibadan, Nigeria. This is the second most common infection after bacterial vaginosis (24.1%). The results of previous studies have confirmed similar rates that ranged from 18.5-30%. (25, 26) However, this rate is much lower than 84.5% discovered in Kano, Nigeria (27); 45.0% obtained by Namkinga et al in Dar es Salaam (28) and 40% found by Ibrahim and his colleagues in Maiduguri, Nigeria (29). This finding may not be unconnected with the fact that some of the women could have some underlying asymptomatic co-morbidity especially diabetes mellitus. The prevalence of yeast infections has also greatly increased worldwide because of indiscriminate of antibiotics use and immunosuppressive treatment.(30) Tarry et al have established that the use of oral contraceptives with high oestrogen content could encourage increased vaginal colonisation with *Candida* spp (31)

In this study, we found out that more than half (56.9%) of those seeking contraceptive use are in their active reproductive age (20-29 years old) and only 6.9% are in the 40-59 years age bracket. The mean age of women in this study is 28.7 years. This result is not unexpected as most of these young women were single, sexually active and prefer hormonal contraceptives. The finding is in concordance with previous study by Fisher and Boroditsky that examined sexual activity of single Canadian women aged 15-29.(32). Vulvovaginal candidiasis (VVC) was more common in women aged 20-29 years (59.3%) and lowest in 40-59 years (7.4%). This finding was also in agreement with other study that showed that the incidence of vulvovaginal candidiasis usually peaks in the third decade of life and reduces in women older than 40 years of age.(19) Despite the higher number of single women using hormonal contraceptives, prevalence of VVC was noticed more in married women living with their spouses. This might not be unconnected with increased sexual activities with married women. This finding agreed with Okungbowa et al who reported similar findings among married women.(19)

Sexual risk behaviours that have been documented to influence the acquisition of VVC were not statistically significant in our study. Early age of sexual debut (16-20 years) accounted for higher rate of VVC (16 of 27, 70.4%) but is not significantly associated with the infection. Women that engage with at least two or more casual sex partners also had increased rate of VVC (13 of 27, 48.1%) with no significant association for the acquisition of VVC. This was not in agreement with the findings of Hellberg *et al* and Rathod *et al* that reported age of sexual debut; casual sex partners

and regular oral sex being associated with repeated VVC. (33, 34) However, this is in agreement with the findings of Corsello et al that believed that increased number of sexual partners, age of sexual debut and increased frequency of sexual intercourse were not significantly risk factors associated with VVC.(35) Douching has been documented to be an important risk factor for the acquisition of vulvovaginal candidosis in previous studies (34, 36) .In our study, seven (25.9%) of the women who had VVC usually practice douching , however, this was not found to be statistically significant (p=0.171). Vaginal discharge was the commonest presentation (51 of 116, 44.0%) closely followed by vaginal pruritus (32 of 116, 27.6%). Some of these women also presented with the combination of vaginal discharge and vulvo-vaginal pruritus at the time of study. Almost all women that presented with vaginal pruritus (31 of 32, 96.9%) also had vaginal discharge. It was noticed that more than half of women (17 of 27, 53.1%) that presented with pruritus had VVC. Vaginal pruritus has been found to be significantly associated (p=0.001) with the occurrence of VVC in our study. These findings were in tandem with the results of similar studies that reported either combination of the symptoms or vaginal pruritus alone. (27, 37) (Table 6)

Types of hormonal contraceptives could also influence the acquisition of VVC. In this study, it was found that usages of oral and emergency contraceptives were found to be the commonest; however none of the hormonal contraceptive methods in this study was significantly associated with the acquisition of VVC. Eleven (22.9%) of the 48 women using emergency contraceptives had VVC and this is not statistically significant. This finding is similar to some studies that believed oral contraceptive alone may not influence the recurrence of VVC (16, 38). However, this is not in agreement with the findings of another study that found that users of oral contraceptive pills are at increased risk for acquisition of VVC.(6)

Vulvo-vaginal candidiasis has been linked as risk factor for the increased acquisition of HIV in hormonal contraceptive users. However, in our study there was no significant association between VVC and acquisition of HIV (P=0.24), only five (18.5%) of those women infected with VVC were seropositive for HIV infection. Our finding is not in agreement with the study of Martins *et al* that found a strong trend of association between the use of high dose of oral contraceptive pills and HIV acquisition. (5) The prevalence of Chlamydia cervicitis and gonococcal cervicitis in this study was 7.8% and 2.6% respectively. There was no significant association between the acquisitions of VVC and Chlamydial infection (P= 0. 46). This result was in tandem with

the previous studies regarding use of combined oral contraceptives and cervical Chlamydia infections (6, 39, 40). However, few of these studies reported conflicting results. In a prospective cohort study in the U.S. it was found that women using COCs were not at increased risk of developing gonorrheal or chlamydial cervical infection compared with women using non-hormonal contraception (39). Other infections like bacterial vaginosis, genital warts and trichomoniasis were not strongly associated with development of VVC in women using hormonal contraceptives in this study.

Young age, education, Christianity, non-marital status, and lower social class; influenced the choice and use of different hormonal contraceptive method though no significant association. Hormonal contraceptives users were associated with increased prevalence of vulvovaginal candidiasis in this study though not statistically significant. Vaginal discharge and vulvovaginal pruritus are the commonest

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symptoms that are strongly associated with VVC. There is need for public health enlightment programme to educate women using hormonal contraceptives methods to adopt safer sexual behaviours, as well as seeking early diagnosis and treatment of VVC and other sexually transmitted infections. The main limitation in this study was the lack of speciation of the non-albicans strains of *Candida* and was due to unavailability of Chromogenic Agar (CHROM agar) and other molecular diagnostic facilities in our center then. Temporal causality could not be established since this is a cross sectional study. Our small size limitation could also have interfered with the ability to fully explore the various associations.

Acknowledgement

We would like to appreciate the support from the resident doctors, medical laboratory scientists and public health nurses during the period of study.

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ORIGINAL ARTICLE

AFRICAN JOURNAL OF CLINICAL AND EXPERIMENTAL MICROBIOLOGY JANUARY 2018 ISBN 1595-689X VOL19 No.1 AJCEM/1907 COPYRIGHT 2018 https://dx.doi.org/10.4314/ajcem.v19i1.7 AFR. J. CLN. EXPER. MICROBIOL. 19 (1): 47-57

SCREENING AND PARTIAL PURIFICATION OF AMYLASE FROM ASPERGILLUS NIGER ISOLATED FROM DETERIORATED TOMATO (LYCOPERSICON ESCULENTUM MILL.) FRUITS

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ABSTRACT

Amylases (EC 3.2.1.1) are cellwall degrading enzymes associated with the pathogenicity of microorganisms in the spoilage of tomato fruits. The use of amylase in many industries has made it very important to optimize production process to achieve maximum yields. Screening and partial purification of Amylase from Aspergillus niger isolated from tomato (Lycopersicon esculentum Mill.) fruits was studied. Amylase producing fungi were isolated from fresh tomatoes kept at ambient temperature (28±1°C). Isolates were characterized on the basis of their morphological and cultural techniques. Partial purification of amylase was carried out by anmonium sulphate precipitation. The enzyme activity was determined and optimum conditions were obtained. The molecular weights of the crude and partially purified Amylase were determined by SDS PAGE method. A total of five isolates were obtained using basic screening technique for amylase activity, one of the isolates (Isolate code F2) exhibited maximum amylase activity. The fungi isolate code F2 was identified as Aspergillus niger. Optimum conditions for Amylase AMY F2 were ascertained at pH 6.0; temperature 30°C; substrate concentration of 0.3mg/ml, and time of heating of less than 10min. The molecular weights of the crude and partially purified Amylase AMY F2 were found to be 55kDa and 35kDa respectively by SDS PAGE method. Microorganisms had been an encouraging means of economical production of enzymes in large scale for the food and drug industry.

Keywords: Amylase, Partial Purification, Enzyme, Tomato Fruits

RENDEMENT ET PURIFICATION PARTIELLE DE L'AMYLASE DE ASPERGILLUS NIGER ISOLÉ À PARTIR DE TOMATE DÉTERIORÉ (LYCOPERSICON ESCULENTUM MILL.) FRUITS

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ABSTRAIT

Les amylases (EC 3.2.1.1) sont des enzymes dégradant les parois cellulaires associées à la pathogénicité des microorganismes dans la détérioration des fruits à la tomate. L'utilisation de l'amylase dans de nombreuses industries a rendu très important d'optimiser le processus de production pour obtenir des rendements maximaux. Le dépistage et la purification partielle de l'amylase d'Aspergillus niger isolés à partir des fruits à la tomate (Lycopersicon esculentum Mill.) Ont été étudiés. Les champignons producteurs d'amylase ont été isolés à partir de tomates fraîches conservées à température ambiante ($28 \pm 1 \circ C$). Les isolats ont été caractérisés en fonction de leurs techniques morphologiques et culturelles. La purification partielle de l'amylase a été réalisée par précipitation au sulfate d'ammonium. L'activité enzymatique a été déterminée et des conditions optimales ont été obtenues. Les poids moléculaires de l'Amylase brut et partiellement purifiée ont été déterminée par un procédé SDS PAGE. Au total, cinq isolats ont été obtenus en utilisant une technique de dépistage basique pour l'activité amylase, l'un des isolats (code isolé F2) présentait une activité amylase maximale. Le code isolant F2 des Fusions a été identifié comme Aspergillus niger. Les conditions optimales pour Amylase AMY F2 ont été déterminées à pH 6,0; température 30 ° C; concentration de substrat de 0,3 mg / ml et temps de chauffage de moins de 10 min. On a trouvé que les poids moléculaires de l'amylase brute et partiellement purifiée étaient respectivement de 55 kDa et 35 kDa par le procédé SDS PAGE. Les microorganismes ont été un moyen encourageant de production économique d'enzymes à grande échelle pour l'industrie alimentaire et pharmaceutique.

Mots-clés: Amylase, Purification partielle, Enzyme, Fruits tomates

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INTRODUCTION

Tomato (Lycopersicon esculentum Mill.) has fleshy endocarp which belongs to the berry class (1). They are rich in nutrients such as vitamins, minerals, dietary fiber and protein (2). Tomato fruits have 95% water and 4.5% carbohydrate (3). In view of these, the tomato fruit is often attacked by microorganisms most especially during and after harvest, which makes tomato spoilage to occur often (4). Microorganisms which are related with the deterioration of tomato fruits can attack them after harvesting; or during the process of storage and distribution (5). The spoilage usually occurs on the fruits after a period of time (6). The plant cell wall which is a protective layer that coats the outer surface usually plays many roles, including controlling movement of water into the fruit (7). It also filters potentially damaging UV light, and limits attack by pathogens (5). In Nigeria, tomatoes are kept at the open markets; the fruits are often displayed in baskets and on benches for the prospective customers, thereby exposing them to opportunistic microbial infections especially mycotoxins (8) . Post-harvest Infections in tomato fruits could occur during storage, transportation, packaging and distribution (loading and offloading) at various point of sale at which bacteria and fungi are present (9). Adequate knowledge and careful handling procedure of the tomatoes can reduce wastage of the fruits (10). Previous study on deterioration of tomatoes by microorganism showed that post-harvest damages are mostly due to attack by fungi such as Aspergillus niger, Aspergillus flavus and Rhizopus stolonifer of up to 90% prevalence (7,11). Thus, there is need for constant research to isolate the fungi associated with tomato fruits deterioration with the view to providing suitable solutions of preserving the tomato fruits, keeping them fresh up to when they reach the consumers (12). This helps to ensure all year round availability and to protect the public health (13).Contamination of fresh tomatoes by microorganisms occurs naturally because the fruits are exposed to the environments during harvest, transportation and storage (7). Hence, the tomato normal flora and pathogen contamination often occurs at different points (14). Tomato micro flora which are mostly fungi found on fresh tomato fruits are the yeasts and molds (8). Microorganisms are present everywhere and around us (15). Pathogens such Escherichia coli and Listeria monocytogenes may be found on the cell wall of the fresh tomato fruits and this are of public health impact (7). Enterobacteriaceae and Gram negative bacteria of the genus *Pseudomonas* may also be found the surface of tomato fruits. Yeast of the genus Saccharomyces populations of 105-106 cfu/ml had been reported (8, 16). Bacterial populations

ranging from 104 - 109 cfu/ml and mold from the genus Aspergillus and Rhizopus with population ranging from 10⁴ - 10⁹ spores/ml in fresh tomatoes had also been reported (5). Growth of pathogenic microorganisms on the intact surface of fresh tomato is not common as the microbes cannot produce cell wall degrading enzymes until they gain entrance into the tomatoes where they can get nutrients and water (17). Damage to the cell wall of the tomato fruits therefore helps the food borne pathogens to grow and multiply, most especially under room temperatures (7). Refrigerator temperature arrests the growth of microorganisms while those that could survive extremely low temperatures still grow when the cell walls are broken due to the fact that released fluids serve as nutrients for the microorganisms (8,18).

Fungi such as Aspergillus niger can produce different cell wall degrading enzymes that breaks down large polysaccharides into simple reducing sugars which are used up for growth and multiplication (19). These enzymes have a lot of industrial and environmental importance. For example, they are used in brewery, food processing and bioremediation of organic pollutants (19,20). Amylases (EC 3.2.1.1) are extracellular enzymes which catalyzes starch hydrolysis (21). The enzyme catalyzes the breakdown of a-1,4-O-glycosidic bonds in polysaccharides leaving by a-anomeric configuration in the resulting compounds (22). The amylase family exists in two forms as either starch modifying enzymes or starch hydrolyzing enzymes (7). Amylases can be recovered from different sources of plants, animals and microorganisms origin (23). Some amylases require calcium ions (Ca²⁺) for their optimum activity and structural stability (21). Amylases have a wide range of industrial application which ranges from production of dextrins, sugar syrup and sweeteners (23). They are usually imported because of their application in the breweries, bakery and factories making soaps and detergents (24). Amylase makes up to 40% of enzyme production in the world (23). However, prolonged storage of amylases often results in reduced activity (21).

MATERIALS AND METHODS

One hundred and eighty (180) fresh tomato fruits were purchased from the Ota market, Ota, Ogun State, Nigeria. They were sorted, washed and transported to the microbiology laboratory of the Department of Biological Sciences, Covenant University, Ota, Ogun State in sterile polythene bags. Sixty (60) samples designated as P were stored in a locally made post-harvest storage system, the second set of sixty (60) fruits designated R were stored in the refrigerator and the last set of sixty (60) fruits designated C were stored at ambient temperature in the laboratory. All samples were analyzed and sampling was done for a period of fourteen days.

Isolation of microorganisms from the tomato fruit samples

The total spore count was determined by pour plate method, each tomato fruit samples was diluted using sterile distilled water. One (1) milliliter of the dilution of 10⁴ was plated onto Sabroaud Dextrose Agar (SDA) and incubated at room temperature for 3-5 days for the fungal population.. **Fungal samples** were collected from the center of the growth covering the plates with the aid of sterile inoculating needle. The samples were smeared on glass slides and stained with lactophenol cotton blue (9).

Identification of the fungal isolates

The fungi isolated in this research were identified using identification methods contained in the illustrated Handbook of Fungi (25). The colony color, pattern of growth, and sporulation style were observed (6). Microscopic observation was carried out on the mature sporulating growths five days after plates. inoculation on SDA Morphological characteristics like arrangement and shape of spores, type of sporangia, and type of hyphae, presence or absence of septa on hyphae were examined under the high power objective of a compound binocular microscope (26). Microscopic examination was carried out after Gram staining the Yeast isolates, while Lactophenol blue staining was carried out on the remaining fungal isolates which are molds (27).

Preparation of fungal spore suspension for production of enzymes

A spore suspension containing 15ml of sterile distilled water and three drops of tween 80 solution was used to obtain the spore from a 120 h-old culture of each fungal isolate. The suspension was centrifuged at 4000rpm for 6 minutes. The supernatant was discarded and replaced with 10ml of sterile distilled water. The spore suspension was diluted serially from 10⁻¹ to 10⁻⁷. The fungal spores were counted using the Neubauer Counting Chamber according to the method of (28).

Growth of Isolated Fungi in Basal Salt Medium Containing Starch

The Basal Salt Medium, for the growth of the isolated fungi and the enzyme production, was prepared according to the method of (29) containing (in one liter): $KH_2PO_4 - 2.0g$, $(NH_4)_2SO_4 - 1.4g$, $MgSO_4 .7H_2O - 0.3g$, $CaCl_2 - 0.3g$, Urea - 0.3g, Tween 80 - 1ml, Yeast extract - 0.4g, FeSO₄ .7H₂O - 5mg, MnSO₄ - 1.6mg,

 $ZnSO_4$ - 1.4mg, $CoCl_2$ - 2.0mg. The medium was supplemented with 1% (w/v) soluble starch. One hundred milliliters of growth medium was inoculated with 1 ml of an aqueous spore suspension containing approximately 5 x 10⁶ spores/ml, 8 x 10⁶ spores/ml and 10 x 10⁶ spores/ml of isolated fungi F1, F2 and F3 respectively. Experimental flasks contained the inoculated sterilized medium while control flasks contained only the sterilized medium. Both experimental and control flasks were incubated without shaking according to the method of (30) for eight days at room temperature (25°C).

Crude Enzyme Extraction by Filtration

To separate the liquid enzyme mixture and the mycelia mat along with the spore bodies' filtration technique was employed. The mixture was filtered through Whatman No. 1 filter paper and then centrifuged at 5,000 rpm for 30 minutes according to the method of (31). This served as the crude enzyme.

Amylase Assay

Amylase activity was determined using the method described by (21) whereby the reaction mixture consisted of 2 ml of 0.2% (w/v) starch in 0.2M citrate phosphate buffer at pH 6.0 as substrate and 0.5 ml of enzyme. The control experiments consisted of only 2 ml of the prepared substrate. The content of the experimental and control test tubes were incubated at 35°C for 20 minutes. The reaction in each test tube was terminated with 3 ml of 1N Hydrochloric acid. The enzyme (0.5 ml) was then added to the control tube. Two milliliters of the mixture from each of the set of experimental and control was transferred into new set of clean test tube. 3ml of 0.1N Hydrochloric acid was added into the content of each new test tubes after which 0.1 ml of iodine solution was added. The optical density reading was taken at 670nm. One unit of enzyme activity was defined as the amount of enzyme which produced 0.1 percent reduction in the intensity of the blue color of starch iodine complex under conditions of the assay. Specific activity was calculated as enzyme units per milligram protein.

Ammonium sulphate precipitation

Ammonium sulphate precipitation was done according to the method described by (31). Solid Ammonium sulphate of analytical grade was added to crude enzyme preparation to 90% saturation. The solution was then kept at 4°C for 24h. After 24 h, the precipitate was removed by centrifuging at 5000rpm for 30 minutes, the supernatant was decanted and the precipitate was then dissolved again in 1ml of 0.2M citrate phosphate buffer (pH 6.0). The enzyme solution was dialyzed overnight against five changes of the similar buffer. Dialysis was done in acetylated cellophane tubing prepared from Visking dialysis tubing (Gallenkamp) as described by (32). The protein content of the dialysate was determined by the method of (33,34). Enzyme assay of the dialysate was also determined as described above.

Effect of Temperature on Amylase AMY F2

To determine the optimum temperature for the amylase production, the partially purified enzyme were subjected to various temperatures; 20°C, 25°C, 30°C, 35°C, 40°C and 45°C for 20 min. The enzyme activity was determined as previously described by (21)

Effect of pH on Amylase AMY F2

The effect of pH on the enzymes activity was determined by varying the pH of the substrate from 4.5 to pH 8. The substrate consisted of 0.2% (w/v) of soluble starch dissolved in 0.2M citrate phosphate buffer pH 6.0 of varying pH. Incubation was at 35°C for 20 min. Amylase activity was determined as previously described by (23).

Effect of Substrate Concentrations on Amylase AMY F2

The effect of various substrate concentrations was determined using various concentrations of starch in 0.2M citrate phosphate buffer; 0.05%, 0.1%, 0.15%, 0.2%, and 0.25%. The reaction mixture contained 1ml of starch and 0.5ml of enzyme incubated at 35°C for 20 min. Amylase activity was determined as previously described by (30).

Effect of Time of Heating on Stability of Amylase AMY F2

The effect of time of heating on the stability of Amylase enzyme was determined. Samples of partially purified enzyme was heated at 80°C for different periods of time (0, 5, 10, 15, 20, 25, 30 min) respectively. The reaction mixtures consisted of 1 ml of starch and 0.5ml of the enzyme solutions. Amylase activity was determined as previously described by (21).

Molecular weight determination of Amylase AMY F2

The crude enzyme and ammonium sulphate precipitated amylase sample were loaded on SDS-PAGE and a protein profile was obtained according to the method of (35). The molecular weight of the enzyme was determined by comparing them with the molecular weight marker. The ammonium sulphate precipitated sample was run on native PAGE. The native gel placed over the Starch agar gel was then subjected to zymogram staining as described by (35).

RESULTS

Enumeration of Fungal Population

The total fungal spore count for the tomato fruits stored in the post-harvest storage system was within the range of $1.0 \times 10^5 - 4.0 \times 10^6$ spores/ml while those fruits stored in the refrigerator had fungal spore count range of $1.0 \times 10^5 - 3.0 \times 10^6$ spores/ml and fungal spore count of $2.0 \times 10^2 - 4.0 \times 10^{11}$ spores/ml for the fruits stored at ambient temperature (Table 1).

Days	Post-Harvest Storage System (P)	Refrigerator	Ambient temperature
	spores/ml	(R)	(C)
		spores/ml	spores/ml
2	1.0 X 10 ⁵	1.0 X 10 ⁵	1.2 X 10 ⁵
3	3.0 X 10 ⁵	4.0 X 10 ⁵	2.0 X 10 ⁵
4	3.0 X 10 ⁵	2.0 X 10 ⁵	4.0 X 10 ⁵
5	5.0 X 10 ⁵	1.0 X 10 ⁵	1.0 X 10 ⁶
6	3.0 X 10 ⁶	4.0 X 10 ⁵	2.0 X 10 ⁹
7	4.0 X 10 ⁶	2.0 X 10 ⁶	2.0 X 10 ⁹
8	3.0 X 10 ⁶	3.0 X 10 ⁶	5.0 X 10 ⁹
9	4.0 X 10 ⁶	2.0 X 10 ⁶	1.0 X 10 ¹¹
10	4.0 X 10 ⁶	1.0 X 10 ⁶	2.0 X 10 ⁶
11	4.0 X 10 ⁶	1.0 X 10 ⁶	1.0 X 10 ⁶
12	2.0 X 10 ⁶	1.0 X 10 ⁶	2.0 X 10 ⁶
13	1.0 X 10 ⁶	NG	4.0 X 10 ⁶
14	1.0 X 10 ⁶	NG	2.0 X 10 ²
	T/		

TABLE 1: ENUMERATION OF FUNGAL POPULATION

KEY: NG – No growth

Identification of Fungal Isolates

The result revealed five pure fungal isolates from tomato fruits (*Lycopersicum esculentum* Mill.). Gram reaction result revealed presence of yeast (*Saccharomyces cerevisae*) while the molds were identified to be *Aspergillus flavus*, *Aspergillus niger*, *Rhizopus stolonifer*, and *Aspergillus fumigatus* (Table 2).

Production of Amylase

The amylase produced by fungal isolate code F2 obtained from tomato fruits stored at the ambient temperature on day 7 produced amylase with a total activity of 0.266 units/ml, protein content of 0.338 mg/ml and a specific activity 0.787 units/mg proteins and a yield of 63% after ammonium sulphate precipitation (Table 3).

TABLE 2: IDENTIFICATION OF THE	E FUNGAL	ISOLATES
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Isolate	Colony	Nature of	Asexual spore	Somatic	Identity of Fungi
code	Colour	hyphae		structure	Isolates
F1	Deep green colony	Septate	Globose conidia	Filamentous	Aspergillus flavus
F2	Blackish colony	Septate	Globose conidia	Filamentous	Aspergillus niger
F3	Cotton white	Non septate	Sporangiospore	Filamentous	Rhizopus stolonifer
F4	Light green colony	Septate	Globose conidia	Filamentous	Aspergilus fumigatus
F5	Shiny milky colony (moist)	No hyphae	Budding cells	Unicellular	Saccharomyces cerevisae

TABLE 3: PARTIAL PURIFICATION OF AMYLASE OBTAINED FROM MICROORGANISMS ISOLATED FROM

TOMATO (Lycopersicon esculentum MILL.) FRUITS							
Enzyme	Protein step	Total	Activity	Protein	Specific	Yield	Purification fold
code	-	(units/ml)	-	(mg/ml)	activity	(%)	
					(units/mg)		
AMY F2	Crude extract	0.27		0.34	0.79	100.00	1.00
	Ammonium	0.17		0.02	9.33	63.00	1.86
	sulphate						
	precipitation						

Characterization of Enzymes

Effect of Temperature on Amylase AMY F2 The temperature of incubation affected the amylase activity tremendously. The activity of amylase AMY F2 increased with an increase in incubation temperature until an optimum was reached (Figure 1). Subsequent increase in temperature beyond the optimum temperature led to reduction in the enzyme activity. The optimum temperature for amylase AMY F2 was 30°C.

Effect of pH on Amylase AMY F2

The pH of the reaction mixtures had effect on the activities of the amylase produced both by the fungi isolate F2. The enzyme activities increased as the pH increases and also decreased when the optimum pH value was reached. The optimum pH for amylase AMY F2 was at pH 6.0 (Figure 2).







FIGURE 2: EFFECT OF PH ON PARTIALLY PURIFIED AMYLASE AMY F2

Effect of Substrate Concentration on Amylase AMY F2

The activity of the amylase produced by fungi F2 isolated from tomato fruits increases with an increase in concentration of the substrate. This continued to increase until an optimum concentration of substrate was attained (Figure 3). The optimum substrate concentration of AMY F2 was 0.30 mg/ml.

Effect of Heat on Amylase AMY F2

The activity of amylase on heating at 80°C decreased with an increase in the time of heating. When the amylase was subjected to heat for 2 minutes, activities of approximately was lost. Amylase AMY F2 was completely inactivated after 10 minutes of heating (Figure 4).



FIGURE 3: EFFECT OF SUBSTRATE CONCENTRATION ON PARTIALLY PURIFIED AMYLASE AMY F2



FIG. 4: EFFECT OF HEAT (80°C) ON PARTIALLY PURIFIED AMYLASE AMY F2



PLATE 1: ASPERGILLUS NIGER ISOLATED FROM TOMATO (LYCOPERSICON ESCULENTUM MILL.) FRUITS



PLATE 2: SDS PAGE OF THE CRUDE AMYLASE AMY F2



PLATE 3: SDS PAGE OF THE PARTIALLY PURIFIED AMYLASE AMY F2

Molecular Weight Determination of Amylase AMY F2

Molecular weight of the crude Amylase and partially purified Amylase AMY F2 are 55KDa and 35KDa respectively (Plate 2 and 3).

DISCUSSION

The result of this research had the total fungal population ranges between 1.0 x 10⁵ and 4.0 x 10⁶spores/ml for the tomato fruits stored in the postharvest storage system, those in the Refrigerator ranges between 1.0×10^5 and 3.0×10^6 spores/ml while the tomato fruits stored at ambient temperatures had fungal population range of 2.0 x 10² and 4.0 x 10¹¹spores/ml. This results is similar to the finding of (36) having an average fungal counts ranging between 1.3 x 10³ and 2.0 x 10³spores/ml and identified them to be Aspergillus niger, Rhizopus Fusarium oxysporium, Saccharomyces stolonifer, cerevisiae, Alternaria alternate, Penicillium digitatum and Geotrichum candidum. (37) also reported an average fungal count of 5.4 x 105spores/ml and 2.0 x 10³spores/ml for Penicillium notatum and Aspergillus flavus at ambient temperature for tomato samples from new Benin Market in Edo State, Nigeria.

The fungi isolated from the tomato fruits were members of the yeast family *Saccharomyces cerevisae* and the mold family *Aspergillus niger, Aspergillus flavus, Aspergillus funigatus, Rhizopus stolonifer.* (21) reported *Aspergillus* sp. and *Saccharomyces cerevisae* as the fungi associated with spoilage of tomato fruits. (38) also reported two fungi, *Aspergillus flavus* and *Rhizopus stolonifer* after five days of storage of fresh tomatoes at ambient temperatures.

The result of this research revealed the ability of some fungal isolates to produce Amylase. (31) and (39) reported production of amylase from fresh tomato fruits. The production from fungi and yeasts has also been reported by (21). The production of amylase from microorganisms isolated from other sources were also reported from other fruits and vegetables (40), bread (28), Irish potato (30) and even soil (41).

Members of the genera *Aspergillus*, *Rhizopus* and *Saccharomyces* were reported by (7,42,43) for their potentials to secrete a number of cell wall degrading enzymes.

The optimum temperature of amylase produced in this study was 30°C. This is in support of the reports of (23,39). (28) had earlier reported that the optimum temperature for amylase production by *Penicillium citrinum* ranges from 30°C - 35°C depending on source. However, this report contrasts with earlier

reports by (23) and (44) which reported that amylase production by was optimum at 37°C. Optimum pH was identified as 6.0 for Amylase AMY F2. This result confirmed that of previous researchers that who reported that amylase was most active between pH 5.0 and 6.0 (43). The optimum substrate concentration for the starch was 0.25mg/ml. (23) reported optimum substrate concentration of 0.20mg/ml for amylase. In this research, the effect of time of heating was investigated at 80°C over a period of 30min revealed loss of enzyme activity within 10min of heating. This confirmed earlier reports by (23,28,45). (30) revealed that amylase was active for over 5min of heating at 80°C. There was continuous reduction in the enzyme activity as heat was applied. After 10min of heating, enzyme activity was completely lost in all enzymes as was also revealed by (21).

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This research work recommends that tomato fruits could be potential source of amylase enzyme needed for various industrial processes. The Potential use of amylase has made it very important to optimize production process to achieve maximum yields.

Acknowledgements: The authors hereby acknowledge the technologists in Department of Biological Sciences, Covenant University for assisting in laboratory

Funding Information: This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Conflicts of Interests: There is no conflict of interest

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REVIEW ARTICLE

AFRICAN JOURNAL OF CLINICAL AND EXPERIMENTAL MICROBIOLOGY JANUARY 2018 ISBN 1595-689X VOL19 No.1 AJCEM/1908 http://www.ajol.info/journals/ajcem

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CANDIDA AURIS INFECTION: HOW PREPARED IS NIGERIA FOR THIS EMERGING FUNGAL AGENT?

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ABSTRACT

Reports from Asia and other parts of the world have demonstrated that the incidence of *Candida auris* infection is on the rise. *Candida auris* is a fungal pathogen causing a wide variety of infections affecting people of all age groups. *Candida auris* was first described in 2009 and has since emerged as an important cause of invasive fungal infection, most importantly healthcare-associated candidaemia. Large outbreaks have been reported worldwide, with therapeutic failure and associated high mortality rates recorded.

The emergence and spread of *C. auris* raises public health concerns because of some characteristics of this pathogen. First it is resistant to many antifungal agents making this infection very difficult to treat. It is also associated with horizontal transmission in health care settings causing outbreaks among hospitalized individuals with high mortality rates. Furthermore, identification of *C auris* is a challenge. Routine identification methods usually misidentify the organism as other yeasts especially *Candida haemulonii*.

This review discusses the current knowledge on the epidemiology, treatment and control of this infection. The urgent need for the stakeholders in Nigerian tertiary hospitals to set machinery in motion for prompt diagnosis, management and prevention of transmission of this infection are also discussed.

INFECTION À CANDIDA AURIS: COMMENT LE NIGERIA EST-IL PRÉPARÉ POUR CET AGENT FONGIQUE ÉMERGENT?

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ABSTRAIT

Des rapports en provenance d'Asie et d'autres parties du monde ont démontré que l'incidence de l'infection à Candida auris est en augmentation. Candida auris est un pathogène fongique causant une grande variété d'infections affectant les personnes de tous les groupes d'âge. Candida auris a été décrit pour la première fois en 2009 et est depuis apparu comme une cause importante d'infection fongique invasive, surtout la candidémie associée aux soins de santé. De grandes épidémies ont été signalées dans le monde entier, avec des échecs thérapeutiques et des taux de mortalité élevés associés enregistrés.

L'émergence et la propagation de C. auris soulèvent des préoccupations en matière de santé publique en raison de certaines caractéristiques de ce pathogène. D'abord, il est résistant à de nombreux agents antifongiques rendant cette infection très difficile à traiter. Il est également associé à la transmission horizontale dans les milieux de soins de santé, ce qui provoque des éclosions parmi les personnes hospitalisées avec des taux de mortalité élevés. De plus, l'identification de C auris est un défi. Les méthodes d'identification de routine confondent généralement l'organisme avec d'autres levures, en particulier Candida haemulonii.

Cette revue discute les connaissances actuelles sur l'épidémiologie, le traitement et le contrôle de cette infection. Le besoin urgent pour les parties prenantes des hôpitaux tertiaires du Nigeria de mettre en place un système de diagnostic rapide, de prise en charge et de prévention de la transmission de cette infection est également discuté.

INTRODUCTION

Candidaemia and candidiasis are usually caused by *Candida albicans* but infections due to non albicans *Candida* species have been on the increase globally. (1) Cases of invasive non albicans candidiasis have been reported from many parts of the world. Among the

non albicans *Candida* species; *C. glabrata* and *C. tropicalis* have emerged as important opportunistic pathogens with other species being reported to a lesser degree.

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In 2009, a novel yeast species belonging to the genus *Candida* was isolated from the external ear canal of a patient admitted in a Japanese hospital. (2) DNA analysis revealed this new species to be closely related *Candida ruelliae* and *Candida haemulonii* in the Metschnikowiaceae clade. It was thereafter named as *C. auris* based on its first isolation from an ear infection. (2)

Candida auris is an unusual *Candida* species first found in human ear specimens. It is capable of hospital acquired transmission leading to large outbreak in health care settings. (3) It has emerged as a significant pathogen in hospitals and accounts for 8.6% to 30% of cases of candidaemia in a recent report. (4)

Contaminated surfaces was thought to be the source of dissemination of *C. auris*, however, urogenital colonization from an indwelling urinary catheter could also result in dissemination to the blood stream causing fungemia. (5, 6)

EPIDEMIOLOGY

Candida auris has become an important nosocomial pathogen with widespread dissemination across several Asian countries and other parts of the world. (7) The actual global picture remains unclear as the current commercial methods of laboratory diagnosis misidentify *C. auris* (8)

Since it was first reported in Japan in 2009, C auris has been reported in many other regions of the world. (2) In South Korea, it was isolated in fifteen cases of chronic otitis media and subsequently in three patients with blood stream infections across three different hospitals. (9) Candidaemia caused by C. auris has also been reported in India and South Africa, with an estimated prevalence of 0.3%. (10) (6) The first cases in the United Kingdom were recorded in 2013 from blood cultures, thereafter there have been many others documented including outbreaks in 2013 and 2015-2016. (3, 7) In the United States, C. auris has been identified from over 122 patients, 77 clinical cases and 45 patient contacts. Majority of the cases were in New York. (11) Whole-genome sequencing of C. auris isolates has shown, clustering into four distinct clades. (11) Studies have found that isolates from within each geographical region are highly related to one another whereas isolates from different regions did not exhibit such relatedness. (11, 12) These suggest independent emergence of C. auris within geographical regions followed by local transmission. (11, 12) This geographically specific clustering of C auris has also been demonstrated in a study involving samples from the India, South Africa, Japan, Korea and Brazil. (13)

PATHOGENESIS

C. auris has an innate pliability for survival and persistence in the hospital environment; it is able to rapidly colonize patients' skin and is highly transmissible within the healthcare setting. (3). This has led to serious and protracted outbreaks. C. auris does not produce hyphae and produces only rudimentary pseudohyphae, however many strains are highly pathogenic with some as pathogenic as C albicans. (7), (14) Various virulence factors are responsible for the ability of *C. auris* to easily survive and persist in infection sites. Phospholipases are extracellular hydrolytic enzymes which help in adherence and invasion of host cells and this has been demonstrated in C. auris. (14, 15) C. auris also produces heamolysin leading to invasive disease and widespread infection. (15) Proteinase activity has also been demonstrated in C. auris and is said to be in higher proportion than phospholipase production. (15)(14)

Some isolates of *C. auris* have been noted to form large aggregates as a result of failure of budding yeast to separate. This observation was found in cases of lethal infection and it is thought that aggregation might be a mode of immune evasion and tissue persistence. (7) (16)

Earlier studies had also reported the lack of biofilm production by *C. auris* compared to its counterpart *C. haemulonii*. (17) Subsequent researches have however demonstrated that *C. auris* is able to differentially adhere to polymeric surfaces, form biofilms, and resist antifungal agents. (18) These biofilms are, however, much thinner than those formed by *C. albicans* and have a limited amount of extracellular matrix. (14) *C. auris* is also able to grow at high temperatures of 37°C-42°C and exhibit lethality and tissue invasion close to that of *C. albicans*, the most pathogenic *Candida* species. (16)

RISK FACTORS

Individuals at extreme ages have been noted to be at high risk of infection. (9) Presence of foreign bodies such as central venous catheters, urinary catheters and mechanical ventilation also increase the risk of infection. (9) (19) (6) Concomitant use of broadspectrum antibiotics and use of antifungals puts the patient at higher risk. (6, 13) A case series involving many countries has found intensive care stay to be a major risk factor for *C. auris* infections which is similar to other studies. (3, 13, 19)

Comorbidities and immunosuppressive conditions such as diabetes mellitus, chronic kidney disease, cancer chemotherapy, hematologic malignancies, and bone marrow transplantation have also been identified. (1) (20) Additional risk factors are erythrocyte transfusion, parenteral nutrition, abdominal surgery, hemodialysis, pancreatitis and HIV infection. (9) (13) (19) (20)

Neutropenia does not appear to carry appreciable risk according to available reports. (9), (1)

A study found longer ICU stay, underlying respiratory disease, vascular surgery, medical intervention and exposure to antifungals as the major risk factors for acquiring *C. auris* infection. (21)

CLINICAL CONDITIONS

C. auris is an emerging fungal pathogen that can cause a wide range of human infections especially in intensive care settings (22), (4) The clinical spectrum of C. auris infections has expanded from minor cases of superficial infections to highly invasive bloodstream infections. (8) It is a source of multiresistant health-care associated infections with a high potential for horizontal transmission in the hospital setting. (23) Many studies including that by Schelenz et al have demonstrated such transmission in hospitalized patients. (3) Candida auris is a recognized cause of chronic otitis media, wound infections, including diabetic foot. (22) (7). The occurrence of candidaemia due to C auris appears to be on the increase and is associated with high mortality of up to 50%. (3) (7) (11) C. auris accounted for 30% of the annual candidaemia cases in a tertiary care general hospital; most of the patients had persistent candidaemia with overall mortality rates of 30- 50%. (6) C auris had also been reported as a cause of bronchopneumonia. (22), (11) Other sites where C auris has been cultured are urine, bile fluid, bone and jejunum. (11)

LABORATORY DIAGNOSIS

Specimens for laboratory diagnosis depend on clinical presentation and include blood, sputum, swabs, urine and others. On Sabouraud dextrose agar (SDA), colonies of C. auris are white to cream colored and smooth. (9), (4) Microscopic examination shows ovoid to globose budding yeast cells in singles or pairs. (4) C. auris does not form chlamydoconidia or pseudohyphae on cornmeal agar. (4) (14) It failed to form Chlamydospores even after 3 days of growth on Cornmeal agar at 30°C. (6) It grows well at 37 and up to 42°C but does not grow at 45°C. (9) (6) No growth has been observed on cycloheximide-containing medium. (9) Urease test and nitrate assimilation test are both negative in C. auris. (9) In contrast to C. auris, C. haemulonii and C. duobushaemulonii isolates produce pseudohyphae and do not grow at 42°C. (4) Assimilation of N-acetylglucosamine (NAG) is quite variable and therefore not valid in differentiating C. auris from C. pseudohaemulonii. (4) (6) It appears pink on CHROM-agar Candida medium and grows at 37°C and 42°C. (6)

Although *C. auris* is close phylogenetically to *Candida haemulonii* and *Candida ruelliae* in the Metschnikowiaceae clade analyses of the 26S rDNA D1/D2 domain, nuclear ribosomal DNA ITS region sequences, and also chemotaxonomic studies have indicated that it represents a new species. The taxonomic description of *Candida auris* sp. nov. was proposed in 2009. (2)

Unfortunately, the usual phenotypic tests are unable to correctly identify *C auris* which is misidentified as one of the closely related Candida species especially *C haemulonii*.

The Vitek 2 system is unable to differentiate between isolates of *C. auris* and those of *C. haemulonii* and *Candida pseudohaemulonii* identifying them as *C. haemulonii* or *C. famata.* (9), (6), (10)

In addition, the API 20C system, identified isolates of *C. auris* as *Rhodotorula glutinis*, or *C. sake* while *C. haemulonii* and *C. pseudohaemulonii* were identified as *Kodamaea ohmeri*.(9) (6)

Currently, the reliable methods for definitive identification of *C. auris* are molecular based methods such as PCR, sequencing analysis, amplified fragment length polymorphism (AFLP) fingerprinting and MALDI-TOF biotyping. (1, 3, 13) Internal transcribed spacer (ITS) region sequencing is used to confirm the identity of suspected isolates as *C. auris*. (6), (1), (3), (4)

Matrix assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) can be used to identify related species of Candida. (4) AFLP has been shown to reliably distinguish C. auris from other closely related species such as C. haemulonii, C. pseudohaemulonii and C. duobushaemulonii. (3) In addition, REAG-N can be used for epidemiologic typing of *C. pseudohaemulonii* and *C. auris* isolates. (17) A cheap method was devised by Kumar et al for identifying C. auris among isolates identified by VITEK2 as members of C. haemulonii complex. CHROMagar Candida medium is supplemented with Pal's agar and on this medium C. auris strains show confluent growth of white to cream colored smooth colonies both at 37°C and 42°C without pseudohyphae production. On the contrary, C. haemulonii complex isolates show poor growth of smooth, light-pink colonies later becoming semiconfluent with pseudohyphae production. (24)

ANTIFUNGAL RESISTANCE

C. auris has a phylogenetic relationship with *Candida krusei*, *C. haemulonii*, and *C. lusitaniae*. These species are known to have either intrinsic or inducible resistance to antifungal agents such as fluconazole and amphotericin B. (12) There are at present no epidemiological cutoff values (ECVs) or clinical

breakpoints defined for *C. auris*, thus non species-specific breakpoints are usually used. (25)

C. auris isolates are resistant to fluconazole with high MICs observed in virtually all reports. (6), (1) (10) (4) Among the other azoles, isavuconazole, posaconazole, itraconazole and voriconazole, potent activity against C. auris has been demonstrated. (1).(26) The results are however inconsistent as variable results have been observed depending on the study. One study found posaconazole to have the most potent activity in vitro followed by isavuconazole then itraconazole. (25) Reduced susceptibility voriconazole has been demonstrated in some isolates but with excellent activity of isavuconazole and posaconzole. (10), (4) In contrast, another study observed resistance to itraconazole but susceptibility to voriconazole. (15) Flucytosine also shows excellent in vitro activity. (6)

In most investigations, Amphotericin B showed excellent activity against *C auris* athough a few cases of resistance have been observed. (1), (6), (10), (15), (25)

The echinocandins, caspofungin, anidulafungin and micafungin, have excellent activity against the organism.(1, 6, 10) *C. auris* resistant to all classes of antifungals including echinocandin has been reported, thereby emphasizing the importance of antifungal susceptibility testing. (13)

In summary, *C auris* exhibits uniform resistance to fluconazole, variable susceptibility to the other azole antifungals and a low acquired resistance to amphotericin B and the echinocandins. (25)

ANTIFUNGAL THERAPY

The first-line therapy is an echinocandin, pending the results of susceptibility testing, which should be carried out without delay. (27) Duration of antifungal therapy is like other infections caused by other Candida spp. In candidaemia, treatment should be continued for 14 days after resolution of symptoms attributable to candidaemia and also documented evidence of clearance of Candida from the bloodstream. (27) A novel drug, SCY-078, the first orally bioavailable 1, 3- β -D-glucan synthesis inhibitor, has demonstrated potent antifungal activity against various *Candida* spp including *C. auris*. (14)

INFECTION PREVENTION AND CONTROL

Similar to other *Candida* infections, *C. auris* infections appear to be hospital acquired, occurring several days to weeks into a patient's hospital stay. (12, 27) This suggests an exogenous rather than endogenous source of infection and a breach of infection control procedures. In cases of infections, environmental sampling has showed persistent presence of *C. auris* around bed space areas. (3) Implementation of strict infection control is therefore of paramount importance in the control of this infection. (11)

Cases and their contacts should be cohorted / isolated; and patient housed in a private room. Before de-isolating the patient, a series of three negative screens taken 24 hours apart is advocated. (27) To decrease the risk for transmission, health care personnel in acute care settings should use Standard and Contact Precautions. Personal protective clothing including cuffed long-sleeved disposable gowns, gloves and aprons should be worn by health care workers. (3) Decolonization of C. auris infected patients can be performed using chlorhexidine formulations depending on the site. Oral nystatin can also be prescribed if oropharyngeal colonization is present. (3) Environmental decontamination can be implemented using chlorine-based products and hydrogen peroxide vapour. (3)

When transferring colonized patients to other health care facilities, the receiving facilities need to be notified of the presence of this multidrug-resistant organism so as to ensure that appropriate precautions are adhered to. There should be thorough daily and, also on discharge of patient, terminal cleaning of rooms of patients infected with C. auris infections, using a disinfectant active against *Clostridium difficile* spores. (11, 20) Equipment used for patients should be cleaned and disinfected with hydrogen peroxide vapour. (3) Screening for C. auris in units having patients with ongoing infections or patients coming from other affected hospitals/units or patients at risk for candidiasis may be conducted. Suggested screening sites are: Nose, throat, and groin, urine/urethral swab, perineal or low vaginal swab, sputum/endotracheal secretions, wounds and other appropriate sites. All screen-positive patients should be isolated or cohorted. (27)

PROGNOSIS

Candida auris is an emerging healthcare-associated fungal pathogen associated with high mortality rate of 40-70%. (12) (1) Patients may have therapeutic failure with persistent candidaemia in spite of antifungal treatment which results in fatal outcomes. (6, 9, 20)

Recurrent *C. auris* candidaemia occurring 3 to 4 months after the initial episode of infection is another complication that may be encountered *C. auris*. (20)

Overall outcome is usually better when infection prevention measures are in place. (18)

LEVEL OF PREPAREDNESS IN NIGERIA AND FUTURE DIRECTIVE

Nosocomial outbreaks as well as recovery of laboratory confirmed isolates of *C. auris* have not been reported in Nigeria. More assertive infection control measures and steps should be put in place to prevent

the transmission of the organism in our health care settings. *Candida auris* infection should be suspected when the isolate is recovered from the critically ill patients in different Intensive Care units (ICU) in our tertiary hospitals. According to the recommendation of Centre for Disease control (CDC), all *Candida* isolates recovered from sterile sites should be identified to the species level so that initial empirical treatment can be administered on species -specific antifungal susceptibility patterns(28, 29). All healthcare facilities in Nigeria with high clinical suspicion of inpatients with *C. auris* should contact the local authority as well as the Federal Ministry of Health (FMoH) for notification.

Medical laboratories should emphasise the importance of accurate species identification for Candida to a species level. Many Medical Microbiology laboratories do not routinely speciate non-Candida albicans isolates or utilize yeast identification methods such as chromogenic agar, biochemical tests (API) or automated systems such as VITEK which do not speciate this pathogen or may misidentify C. auris as yeasts such as Candida haemulonii, Candida sake, and Rhodotorula mucilaginosa.(30) Clinical laboratories should be encouraged to forward C. haemulonii isolates and isolates not identified beyond Candida spp. by conventional methods to tertiary or public health laboratories in Nigeria for further characterization.

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Antifungal resistance is an important concern in managing invasive Candida infections, Therefore, understanding drug susceptibility of these different species can help develop protocols for appropriate empirical treatment of these infections. We recommend that each hospital should put in place good antimicrobial stewardship programme and monitor the antifungal susceptibility pattern against this organism. In addition, each hospital should develop their guidelines and policies for the control and prevention of *C. auris* infection.

CONCLUSION

There should be high level of clinical suspicions when non-albicans *Candida* are isolated in high risk patients admitted in intensive care units. Antifungal susceptibility testing should be initiated and performed routinely in all our tertiary hospitals and public medical microbiology laboratories. If there should be any report of positive cases, infected patients should be cared for in an isolated single room to prevent transmission of the pathogen.

Other aggressive infection control measures should be implemented in the hospitals. These include stringent hand hygiene procedures before and after touching the patients and items around the bed sides; cleaning of affected clinical areas with high strength chlorine-based agents and prompt treatment of patients with antifungal agents.

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ORIGINAL ARTICLE

AFRICAN JOURNAL OF CLINICAL AND EXPERIMENTAL MICROBIOLOGY JANUARY 2018 ISBN 1595-689X VOL19 No.1 AJCEM/1909 COPYRIGHT 2018 https://dx.doi.org/10.4314/ajcem.v19i1.9 AFR. J. CLN. EXPER. MICROBIOL. 19 (1): 64-69

RESULT OF 2004 EXTENDED TRYPANOSOMOSIS SURVEY OF RUMINANTS AT KACHIA GRAZING RESERVE, NORTH CENTRAL NIGERIA

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Running Title: Ruminant Trypanosomosis Prevalence in Nigeria

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ABSTRACT

Tsetse fly and trypanosome prevalence in ruminants were estimated in April and August, peak months of the dry and rainy seasons in the Kachia Grazing Reserve (KGR) of Kaduna State, North Central Nigeria. This study was subsequent to reports of seasonal outmigration of semi nomadic Fulani from the grazing reserve due to death of cattle from trypanosomosis. Result of blood samples showed an overall parasitological infection rate of 17.4%. Infection rates in cattle, sheep and goats were, 18.6%, 9.5% and 5.1% respectively. Over all higher infection rate in the rainy season was attributed to abundance of tsetse and other hematophagus flies. Infection rate in younger animals (21.9%) was higher compared to those of older animals (16.5%). *Trypanosoma vivax* was the dominant infecting trypanosome specie followed by *T. congolense* and *T. brucei*.

It was concluded that tsetse fly and trypanosomosis constituted dual plagues limiting economic livestock production and settling of the pastoralists in the grazing reserve. This warrants application of sustainable integrated control measures to enhance utilization of abundant fodder at the reserve.

Key words: Kachia grazing reserve, trypanosomosis, ruminants, infection rates, Nigeria.

RÉSULTAT DE L'ENQUÊTE DE TRYPANOSOMOSE EXTENSION DE 2004 DES RUMINANTS À LA RÉSERVE DE PISCINE KACHIA, NIGERIA CENTRALE DU NORD

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ABSTRAIT

La prévalence de la mouche tsé-tsé et du trypanosome chez les ruminants a été estimée en avril et août, les mois de pointe des saisons secanes et pluvieuses dans la réserve de pâturage de Kachia (KGR) de l'État de Kaduna, dans le nord du centre du Nigeria. Cette étude a été postérieure à des rapports d'émigration saisonnière de Fulani semi-nomades provenant de la réserve de pâturage en raison de la mort de bovins de la trypanosomose. Le résultat des échantillons de sang a montré un taux global d'infection parasitaire de 17,4%. Les taux d'infection chez les bovins, les ovins et les chèvres étaient respectivement de 18,6%, 9,5% et 5,1%. Le taux d'infection plus élevé pendant la saison des pluies a été attribué à l'abondance de mouches tsé-tsé et d'autres mouches hématophobes. Le taux d'infection chez les animaux plus jeunes par plus (21,9%)était plus élevé rapport à ceux des animaux âgés (16,5%). Copyright ©2017 AJCEM. This work is licensed under the Creative Commons Attribution 4.0 International License CC-BY

Trypanosoma vivax était le trypanosome infectant dominant suivi de T. congolense et T. brucei.

On a conclu que la mouche tsé-tsé et la trypanosomose constituaient des fléaux doubles limitant la production d'élevage économique et la colonisation des pasteurs dans la réserve de pâturage. Cela justifie l'application de mesures de contrôle intégrées durables pour améliorer l'utilisation de fourrages abondants dans la réserve.

Mots clés: réserve de pâturage de Kachia, trypanosomose, ruminants, taux d'infection, Nigeria.

INTRODUCTION

Tsetse flies and Animal African trypanosomosis constitute major threats to livestock value chains and food security with resultant underdevelopment in several parts of sub-Saharan Africa including Nigeria, in spite of decades of attempts at chemotherapeutic and vector control (1, 2). In Nigeria, tsetse flies had been shown to infest about 80% of the nation's agro ecological land mass including the high lands of Jos, Mambilla and Obudu plateau, previously known to be tsetse free (3). Impact of the disease arise from not less than 3 million livestock deaths in Africa each year and reduced calving rate, livestock numbers, milk off -take, meat off take, animal draft power and mixed farming (1, 4). Conflict among farmers and pastoralists induced by freshwater scarcity (5) has strengthened the need for development of Nigeria's grazing reserves as panacea. The Nigerian Institute for Trypanosomiasis Research had over the years received reports of outbreaks of animal trypanosomosis in southern parts of Kaduna State (6) with resultant deaths of cattle and migration of semi nomadic Fulani out of the area. For this reason an extended survey was undertaken in the Kachia Grazing Reserve, located within this area, to assess the status of trypanosome infection in ruminants in the grazing reserve for application of appropriate control measures that will permit the settling of more herds in this area and exploitation of the abundant fodder for large scale livestock production. This study was undertaken in 2004 but could not be published due to problems initially encountered in the retrieval of data from storage systems. Even though many works have since been done in this reserve, the data is here presented for the purpose of referencing.

MATERIALS AND METHODS

2.1		S	Aı	rea		
The	Kachia	(Ladduga)	Grazing	Reserve	(KGR)	is

situated at Latitude 10°03' and10°13'N and Longitude 7°55' and 8°06'E within the Northern Guinea savanna (Fig. 1) and spans an area of 88,411 hectares, forming parts of Kufana , Kachia and Kamuru Ikulu lands in Chikun, Kachia and Zangon Kataf Local Government Areas respectively in Kaduna State, North Central Nigeria. The Grazing Reserve is divided into six blocks each comprising of an earth dam (Fig. 2) used for the watering of animals. The reserve is inhabited by settled semi nomadic Fulani who apart from cultivation of crops like maize, guinea corn, millet, yams, cocoa yam, groundnuts and cassava, keep cattle, sheep and goats. The Reserve comprised also of nomadic primary and secondary schools, a market, veterinary clinic and health center at the central area of the Reserve. The animals settle here in most part of the year and migrate out to neighboring states following the drying up of the dams and streams at the onset of the dry season which begins in October.



FIG. 1: VEGETATION MAP OF NIGERIA SHOWING THE KACHIA GRAZING RESERVE (ARROWED) IN THE WOODLAND AND TALL GRASS SAVANNAH



FIG. 2: MAP OF KACHIA GRAZING RESERVE SHOWING GRAZING BLOCKS SAMPLED AND THEIR EARTH DAMS

Animal Sampling

A systematic random sampling of all animals was used to obtain a sample size of 1,641 animals from all blocks made up of 1445 cattle, 137 sheep and 59 goats. Cattle of one year and below were considered young calves whereas those over one year old were regarded as adults while sheep and goats under 5 months were regarded as young and those above 5 months old as adults. The cattle were made up mostly of White Fulani (Bunaji) breed while those of sheep and goats were those of the Yankasa and Red Sokoto breeds respectively. From each of the animals, 5 milliliters of jugular blood were obtained into specimen bottles containing ethylene diamine tetra acetic acid (EDTA) dispensed as one milligram powder per milliliter of blood and conveyed in cold boxes with ice packs to the field laboratory for analysis. The samples were analyzed using buffy coat dark ground/ phase contrast technique (7) and Giemsa-stained thin smears. Trypanosome species were identified based on their morphological structures from Giemsastained thin films. Consent was sought from the Kaduna State Ministry of Agriculture and Natural Resources, Chairman of Kachia Local Government as well as the herd owners and their chiefs before the animals were sampled. All parasitological positive cases were treated the following day with Diaminazene aceturate (Berenil) at the dose of 3.5mg /Kg body weight. The study covered the months of April and August which were peak periods of the dry and wet seasons respectively.

Statistical analysis

The data analysis was done using Microsoft Excel 2010. Values between infected and uninfected animals were compared using student t – test. Values between the infected ruminant species were compared using one way Analysis of Variance (ANOVA). In all cases values of P<0.05 were considered significant.

RESULTS

The trypanosome infection rates in all ruminants sampled from the Kachia Grazing Reserve is summarized on Table I. The overall infection rate in ruminants was 17.4%. Higher infection rate of 18.9% was observed in the rainy season as against 15.7% in the dry season. This was the general pattern in all ruminant species sampled. Infection rate of 18.6% (P<0.05) in cattle was highest followed by 9.5% and 5.1% in sheep and goats respectively. Infection rate in young animals (21.9%, Table II) was higher compared to that of adult animals (16.5%). Infection rate in females (17.8%) was similarly higher than that in males (16.0%, Table III). Of the total number of

parasitological positive infections, 94.3% was due to single infections while 5.8% was due to mixed infection. Infections due to *T. vivax, T. congolense, T. brucei* were 44.6%, 37.8% and 0.5% respectively. Of the mixed infection cases, 30.8% was due to *T. brucei* and *T. congolense,* 38.5% due to *T. vivax* and *T. brucei*, and 30.8% due to *T. vivax and T. congolence* mixed infections. Ruminant population encountered in the rainy season was more than those observed in the dry season as many herds migrated out of the Reserve in search of water as most of the dams and seasonal streams had dried up at the peak of the dry season between the months of March and April.

TABLE I: TRYPANOSOME INFECTION RATES IN RUMINANT SPECIES AT THE KACHIA GRAZING RESERVE.

Ruminant Species	Season	No. Animals	No. Positive	Infection Rate(%)
Cattle	Dry	682	116	17.0
	Rainy	763	`153	20.1
		(1445)	(269)	18.6
Sheep	Dry	34	2	5.9
	Rainy	103	11	10.7
	`	(137)	(13)	9.5
Goats	Dry	36	0	0.0
	Rainy	23	3	13.0
		(59)	(3)	5.1
Total	Dry	752	118	15.7
	Rainy	889	167	18.9
		(1641)	(285)	17.4
TABLE II: AGE DEPENDENT TRYPANOSOME INFECTION RATES AMONG RUMINANT SPECIES AT KACHIA GRAZING RESERVE

Ruminant Species	Age	No. Animals	No. Positive	Infection Rate (%)
Cattle	Adult	1173	208	17.7
	Young	272	61	22.4
Sheep	Adult	137	13	9.5
	Young	0	0	0.0
Goats	Adult	52	3	5.8
	Young	7	0	0.0
Total	Adult	1362	224	16.5
	Young	279	61	21.9

TABLE III: SEX DEPENDENT TRYPANOSOME INFECTION RATES AMONG RUMINANT SPECIES AT KACHIA GRAZING RESERVE

Ruminant Species	Sex	No. Animals	No. Positive	Infection Rate (%)
Cattle	Male	409	68	16.8
	Female	1036	201	19.4
Sheep	Male	38	5	13.2
	Female	99	8	8.1
Goats	Male	17	1	5.9
	Female	42	0	0.0
Total No.	Male	464	74	16.0
	Female	1177	209	17.8

DISCUSSION

This study showed that tsetse and animal trypanosomosis were prevalent in the Kachia Grazing Reserve. The overall trypanosome infection rate of 17.4% in ruminants was by far higher than the 4.3% over all prevalence rate for Nigeria obtained from the country wide survey by EEC-Trypanosomiasis

control project between 1980- 1996 (3). This suggests that trypanosomosis was a major problem in the grazing reserve. Higher infection rate recorded in cattle than in small ruminants suggests the preference of tsetse and other biting flies for bovine blood than those of small ruminants or the larger size of moving cattle attracted more biting flies compared to small ruminants which are smaller in size. Differences in the infection rates in sheep and goats suggest that husbandry practice played roles in trypanosomosis risk in small ruminants. Whereas sheep were taken along with cattle for grazing, goats were tired around hamlets during the dry and rainy seasons thereby leading to more exposure of the sheep to infection than goats.

Higher infection rates were observed in the rainy season compared to dry season suggesting that this was associated with concurrent increase in tsetse infestation and that of other biting flies at the reserve there by making the risk of trypanosomosis higher in the rainy season. The role of rainy season in abundance of tsetse and other biting flies in trypanosomosis outbreak in livestock in Kaduna State had been described by Maikaje (8). Further analysis of the result showed that trypanosome infection of goats occurred only in the rainy season suggesting that there was encroachment of tsetse on settlement areas which also exposed humans to tsetse bites and trypanosomiasis (sleeping sickness). Kaduna State previously known to be an endemic focus for the human disease was controlled to below endemic proportions (9, 10). Although there had been general resurgence in sleeping sickness in parts of the country (11), the true situation in Kaduna State is not known. Trypanosome infection rate at the grazing reserve was also higher in young animals which suggests that these were current infections acquired probably from the Grazing Reserve with consequent effects on rearing of livestock in the reserve. This may have resulted in reduced herd sizes from death of young animals, growth retardation and infertility in the older animals (1).

The dominance of *T. vivax* infection in the Grazing Reserve may equally have been as a result of prevalent infestation of the area by other biting flies beside tsetse as these have been associated with prevalence of *T. vivax* in the absence of tsetse flies and spread of African trypanosomes beyond tsetse belts of Africa and parts of Asia and Latin America (12, 13).

CONCLUSION

Trypanosomosis was prevalent in Kachia Grazing Reserve and constituted a major threat to economic production of livestock in the area with higher infection rates in the rainy season, young and female animals. This called for strategic and integrated seasonal approaches to tsetse and other hemophagus flies as well as trypanosomosis control in order to limit the impact of the disease and enhance the settling of more pastoralists in the grazing reserve. Integrated seasonal approach to tsetse fly control means the application of different tsetse fly control techniques which include use of insecticide impregnated screens, epicutenous application of insecticides and Sterile Insect Technique depending on patterns of tsetse fly distribution which varies between dry and wet seasons. This will help limit the

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conflicts among farmers and pastoralists in this part of Kaduna state and other parts of the country. At the time of this study there was no sustainable tsetse fly control programme in the grazing reserve and the herdsmen migrated out of the reserve seasonally.

CONFLICTOFINTERESTThe authors declare that there was no conflict ofinterest in the course of this investigation.

ACKNOWLEDGEMENT

This study was funded by the Nigerian Institute for Trypanosomiasis Research, Kaduna.

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ORIGINAL ARTICLE

AFRICAN JOURNAL OF CLINICAL AND EXPERIMENTAL MICROBIOLOGY JANUARY 2018 ISBN 1595-689X VOL19 No.1 AJCEM/1810 COPYRIGHT 2018 https://dx.doi.org/10.4314/aicem.p19i1.10

COPYRIGHT 2018 <u>https://dx.doi.org/10.4314/ajcem.v19i1.10</u> AFR. J. CLN. EXPER. MICROBIOL. 19 (1):70- 75

FIRST MOLECULAR INVESTIGATION OF CAPSULAR SEROTYPING AND HYPERVIRULENT (HVLP) OF *K. PNEUMONIAE* IN UNIVERSITY HOSPITAL CENTER OF YOPOUGON COTE D'IVOIRE

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ABSTRACT

Klebsiella pneumoniae is a well known human pathogen. Although infectious in most nosocomial infections with a high level of resistance, capsular types and circulating hypervirulent strains in our context are not documented. The aims of this study are to identify capsular serotypes and hypervirulent strains circulating at the Yopougon University Hospital in Abidjan. 51 strains of *Klebsiella* were collected at Chu de Yopougon. The capsular serotypes were determined using PCR and the serotypes K1, K2 and K5 were searched. The hypervirulent strains were also investigated by PCR and by string test. The predominant serotypes were non-K1 / K2 (46/51, 90%). The serotypes found K5 and K2 in (4/51, 7.8%) and (1/51; 1.9%) respectively. The rmpA gene linked to hyperviscosity or hyperviscosity was not found although 25.5% (12/51) were positive for the stretch test. The capsular distribution of strains of *Klebsiella pneumoniae* seems different from Asian authors. The determination of non-K1non types K2 remains to be elucidated.

Keyvords: Klebsiella pneumoniae, capsular serotype - hypervirulence

PREMIERE ETUDE D'INVESTIGATION MOLECULAIRE DE SEROTYPAGE CAPSULAIRE ET DE GENE D'HYPERVIRENCE DE *KLEBSIELLA PNEUMNIAE* AU LABORATOIRE DU CHU DE YOPOUGON EN COTE D'IVOIRE

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Résumé

Klebsiella pneumoniae est un pathogène nosocomial humain bien connu. Bien qu'incriminé dans la plus part des infections nosocomiales avec un niveau élevé de résistance, les types capsulaires et les souches hypervirulentes circulantes dans notre contexte ne sont pas documentés. L'objectif de cette étude est d'identifier les sérotypes capsulaires et les souches hypervirulentes circulant au CHU de Yopougon Abidjan., 51 souches de *Klebsiella* ont été collectés au Chu de Yopougon. Les sérotypes capsulaires ont été déterminée à l'aide de la PCR et les sérotypes K1, K2 et K5 ont été recherchés. Les souches hypervirulentes ont été recherchées également par PCR et par le test d'étirement ou string test. Les sérotypes prédominants étaient les non K1/K2 (46/51; 90%). Les sérotypes retrouvés K5 et K2 dans respectivement (4/51; 7,8%) et (1/51; 1,9%). Le gène rmpA lié à l'hyperviscosité n'a pas été retrouvé bien que 25,5% (12/51) étaient positives au test d'étirement. La distribution capsulaire des souches de *Klebsiella pneumoniae* semble différente des auteurs asiatiques. D'ou l'intérêt de travaux plus approfondies afin de déterminer les types capsulaire des souches non K1 non K2.

Mots clefs : Klebsiella pneumoniae - serotype capsulaire - Hypervirulence

INTRODUCTION

Klebsiella pneumoniae is an opportunistic pathogen responsible for community infections and nosocomial infections such as pneumonia, septicemia, suppurative and urinary infections, particularly in patients admitted to intensive care **(1)**.

The capsule is considered to be a major virulence factor for *Klebsiella*. It intervenes in the formation of biofilm and in the increase of the anti-opsonised effect allowing the bacterium to escape the immune response of the host (2,3,4) Currently, 78 capsular antigens of *K. pneumoniae* are

listed and the serotypes most frequently involved in human infection are serotypes K1, K2, K5, K54

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Several reports have revealed that capsular types Some of these have reported a correlation between serotypes K1, K2 and abscesses of the liver, but serotypes are not the only determining factor in the occurrence of liver abscesses (4). Although the first case of a patient with liver abscess was described in China in the 1980s (5), this strain of K pneumoniae responsible for liver abscess has been reported in Taiwan, Japan, Europe, North America, and Korea. (6,7,8). This characterized emergent infection is often complicated by septic meningitis and purulent endophthalmitis. This new strain called "Klebsiella *pneumoniae hypervirulent* or HvKP["] is a variant of the classical strain in terms of aspects of the colonies on the different agar plates. These strains are characterized by a hyperproduction of the capsule mediated by the rmpA / rmpA2 gene which gives these strains a hypervisic aspect. The association of hyperviscosity with the presence of the magA gene is also found, particularly in strains of serotypes K1, K54 and K2, K5, K20, K57 (9.10)In Ivory Coast, K pneumoniae is involved in various infections (11) in human infection and in the colonization of area in hospitals (12). 2010. Although the antibiotic resistance of Klebsiella pneumoniae has often been studied (13), data on circulating serotypes and hypervirulent strains are non-existent. The aims of this study are to identify capsular serotypes and hypervirulent strains circulating at the Yopougon University Hospital in Abidian.

MATERIALS AND METHODS

are related to the severity of infection. This study was carried out at the Bacteriology-Virology Unit of the Central Laboratory of the Yopougon University Hospital for Classical Bacteriology and at the Molecular Biology Platform of the Pasteur Institute of Côte d'Ivoire for the molecular analysis of the strains of January To March 2016.

14. Study population

51 strains of which 47 were of human origin and four of environmental origin (1, 2, 34, and 36) were studied. 7 strains of *K oxytoca*, 17, 24, 33, 44, 48, 53, 55) were associated in molecular analyzes to investigate the specificity of *K pneumoniae* identification primer 15. *Bactériologie*

Isolates where biochemically identified by conventional bacteriology tests.Susceptibility testing for the strains was performed using the Kirby-Bauer disk diffusion test on Mueller-Hinton agar. Results were interpreted according to the recommendations and definitions from Comité Antibiogramme de la Société Française de Microbiologie (CASFM 2016) *E. coli* ATCC 25922 was used as the MIC reference strain.

A string test was performed to distinguish hvKP from cKP according to **Fang** study [8].

16. PCR assay

The" *K.pneumoniae* Pf/*K.pneumoniae* Pr1 "primer pair included in the multiplex PCR is for the identification of *K. Pneumoniae*. The following genes were targeted: *rmpA*, and the K1 K2 and K5 capsular serotypes. The primers targeting the capsular serotype specifying genes were previously described (Table 1).

SEROTYPE	PRIMER	SEQUENCE	PRODU CT SIZE (PB)	REFERENCES
K1	MAGAF1	GGTGCTCTTTACATCATTGC	1283	FANG ET AL. (2004)
	MAGAR1	GCAATGGCCATTTGCGTTAG		
K2	K2WZY-F1	GACCCGATATTCATACTTGACAGAG	641	TURTON ET AL. (2008)
	K2WZY-R1	CCTGAAGTAAAATCGTAAATAGATGGC		
K5	K5WZXF360	TGGTAGTGATGCTCGCGA	280	TURTON ET AL. (2008)
	K5WZXR639	CCTGAACCCACCCCAATC		
RMPA	RMPAF	ACTGGGCTACCTCTGCTTCA	516	NADASY ET AL. (2007)
	RMPAR	CTTGCATGAGCCATCTTTCA		
K.PNEUMONIAE 16S-23S ITS	PF	ATTTGAAGAGGTTGCAAACGAT	130	LIU ET AL. (2008)
	PR1	TTCACTCTGAAGTTTTCTTGTGTTC		

TABLE 1: PRIMERS USED IN THE MULTIPLEX PCR

Extraction of DNA was carried out by thermal shock by a freezing cycle (-20 $^{\circ}$ C. for 1 hour and then heating on thermo block for 10 minutes at 95 $^{\circ}$ C. The GoTag G2 Flexi DNA polymerase kit

(Promega Corporation, USA) was used for the PCR mixes containing 0.2μM of each primer, 7.5μM, MgCl, 0.5μM dNTPs, 3 unit Taq polymerase, 1X of buffer and 5μl of DNA template for a final volume

of 50µl. Amplification onditions were :95°C 15 min (1 cycle), (95°C 30 s ,58°C 90 s, 72°C 90s) (35cycles), 72°C 10 min (1 cycle). The revelation was made on a GelDoc Bioanalyzer (BioRad) after electrophoresis on 1.5% agarose gel.

RESULTS

Concerning the source of ours isolates, (92%) were isolated from clinical sources and (8%), from hospital environment. 31% were isolated from biological products in the pediatric and 23% from intensive care unit. Of the 47 clinical isolates, 33(65%) were from urine and 7 (14%) from sputum (tableau II)

TABLE II: DISTRIBUTION OF BACTERIAL BY SPECIMEN AND WARDS

Wards	Value (n)	%
Surgery	3	6
Endocrinology	7	14
Médecine	3	6
Nephrology	4	8
Pediatric	16	31
Intensive care unit	12	23
Over	6	12
Specimen		
Aspirates	2	4
Catheter tip	2	4
hospital's environment	4	8
CSF	1	2
Sputum	7	14
Blood	2	4
Urine	33	65
Total	51	100

The bacterial isolates exhibited a high resistance to the antibiotics tested. In our study 14% of *strains* are resistant to at least three families of antibiotic at a time. The proportion of resistance to third generation céphalosporins, ciprofloxacine and gentamicin was 49%, 45% and 33%, respectively, (Table 5). The prevalence of ESBL producing strains was 30% in *K. pneumoniae*

TABLEAU III: DISTRIBUTION OF ANTIBIOTICS RESISTANCE

Antibiotic	Value (n)	%
Amoxicilline+Acide clavulaniqueR CefoxitineR	25/51	49
CeftriaxoneR	25/51	49
ImipénèmeR	1/51	2
CiprofloxacineR	23/51	45
GentamycineR	17/51	33
AmikacineR	2/51	3,9
FosfomycineR	2/51	3,9

The molecular identification all (41) isolates gave positive results and identified as *K. pneumoniae*. Results of PCR amplification confirmed that all isolates were *K. pneumoniae*. Serotype of 9.8% where be identified by primers used whose 7,8% of K2 (Figure 1 and 2) and 2% of K5. Five of idenfied serotype came from urine 12% (4/33) and sputum 14,28% (1/7) .Of the 5 strains serotyped 2 had a positive String test (40%) however rmpA gene linked to hyperviscosity has not been found.





FIGURE 2: STRAINS 16 AND 30 WITH SEROTYPE K2 (PB = 641)



MP = Molecular weight marker, wells CP, CPK and K5 contain ampicons of K pneumoniae already confirmed by PCR = positive controls and wells 6 and 31 contain water for injectable preparation = Negative controls

DISCUSSION

Most gave a band for the *K. pneumoniae* 16S-23S internal transcribed spacer region. Amplification of the 16S rRNA gene represents a highly accurate and versatile method for the identification of bacteria to the species level, even when the species in question is notoriously difficult to identify by biochemical methods (17). The K1 serotype was not found in our study. It is disagreed with results elucidated by other workers (15,16) who noticed that serotypes K1, K2 and Non-K1/K2 accounted for 14.3 % (7/49), 38.8 % (19/49) and 46.9 % (23/49) of all *K. pneumoniae* isolates, respectively. Our results were in agreement with those who reported that *K. pneumoniae* serotype K1 is dominant on the other serotypes and find K1 and serotype K2 was 52.3% and 22.7% (18 **19**).

This could be related to the isolation site of our strains, more than 70% are non-invasive strains. Otherwise the capsular serotype K1 is recognized as the most virulent and the most encountered throughout the world especially in the countries of Asia where it is correlated to hepatic abscesses (17). In a study of strains of K. pneumoniae from 11 Asian countries serotype K1 are findings were 27,5%, 12,6% and 9,6% in Taiwan, Korea and Vietnam respectively. Although cases have been reported in South Africa and Nigeria, no case of Liver Abscesses has been described in our context. This could explain the absence of serotype K1 in our series. But the absence of serotype K1 could also be related to the size of our sample. K. pneumoniae serotype K2, it was found in (4/51)7.8% of the strains.

Our results were in agreement with some workers (18,19,20) who reported that *K. pneumoniae* serotype K2 is dominant (64%) on the over serotypes of the three serotypes K1 K2 et K5 researched. Serotype K2 is one of the most common and most invasive capsular serotypes described

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throughout the world. A similarly wide range of capsular serotypes has been demonstrated in other studies. However, there are differences in the serotypes that appear most frequently in some countries. Non-K1/K2 strains constituted a very important proportion of the strains of our study with more than 90%. Our results were in agreement with Adam et al. (2006)(21) in Australia who noticed high prevalence of non K1/K2 strains in 96% of 293 strains. They are by far from Lin et al. (2010)(22,) who also found in their series a predominance of non-K1 / K2 serotypes (46.9%. However, they remain discordant with those of many Asian authors in whom serotypes K1 and K2 are predominant (23). In general, there is a variable global distribution of Klebsiella capsular serotypes

The rmpA gene is the regulator of capsular synthesis; many studies have suggested that this gene could be responsible for the hypervirulent phenotype of K. pneumoniae characterized by the hypervisic character of the strains and found the gene more often associated with serotypes K2 than K1 and non-K1 / K2 serotypes (24). This gene was not found in our study

Conclusion

Capsular serotypes Non-K1/K2 were the most recovered hence the interest of more studies in order to identify them. Moreover, the determinants of hyper virulence were not found despite the presence of strains positive to the string test.

Acknowledgements

We are grateful to Molecular biology platform of institut Pasteur of Ivory Coast for collaboration

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