Original Research Article

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Molecular detection and genotyping of Chlamydia trachomatis circulating in women of Western Cameroon: a cross-sectional study

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ABSTRACT

Background: In Cameroon, *C. trachomatis* screening is not routinely practiced, and its epidemiology is still unexplored. The present study aimed to determine the prevalence of *C. trachomatis* infection, its risk factors and the genotypes circulating in the West Cameroon region.

Methods: A cross-sectional study was carried out amongst patients in five district hospitals in the West region of Cameroon. Endocervical samples were collected from women visiting the hospitals forantenatal, prenuptial and contraception consultations and at least 18 years old, sexually active, and non-menstruating. The molecular detection of *C. trachomatis* was performed using conventional polymerase chain reaction (PCR) followed by sequencing of the *ompA* gene.

Results: The prevalence of *C. trachomatis* infection was determined to be 11.47%. Having sex for the first time between the ages of 15 and 17 (OR=1.683, 95% CI: 1.1-2.5), non-usage of condom (OR=1.622, 95% CI: 1.2-2.1), being single (OR=1.263, 95% CI: 1.0-1.5) and age range 18-30 years (OR=1.426, 95% CI: 1.1-1.8) were risk factors for *C. trachomatis* infection. Three genotypes of *C. trachomatis* circulated in West Cameroon viz. D (49%), E (29.4%) and G (21.6%).

Conclusions: This study revealed that, three genotypes; D (dominant), E and G were identified circulating in the population of the study area. This information may be important for controlling the dissemination of *C. trachomatis* infection in West Cameroon as well as strategizing the therapeutic approach.

Keywords: Women, West Africa, Chlamydia trachomatis, Endocervical swab, Genotype

INTRODUCTION

Chlamydia trachomatis (C. trachomatis) infection is a highly contagious sexually transmitted disease. C. trachomatis is an obligate intracellular gram-negative bacterium which infects approximately 127 million persons per year worldwide, making it the most prevalent sexually transmitted disease. This infection, most often asymptomatic, can cause tubal infertility and ectopic pregnancy, pelvic inflammatory disease, and

lymphogranuloma venereum.^{4,5} It leads to abortion, chorioamnionitis, premature rupture of the membrane, preterm labor, stillbirth and low birth weight and adverse neonatal sequelae.^{6,7}

Previous studies on *C. trichomatis* in Cameroon have been carried out in Yaoundé, Dschang and in the northern region and have strikingly shown divergent results. Per analysis with enzyme-linked immunosorbent assay (ELISA), a prevalence of 11.5% was reported among women with

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infertility in Yaoundé in 1986, while among prostitutes in the same town, the prevalence hiked to 38.3% in 1991.^{8,9} In 2003, while employing polymerase chain reaction (PCR), a prevalence of 3.78% was reported among students in Yaoundé. 10 In 2013, a prevalence of up to 42.5% was reported in the far North region following an ELISA screen.¹¹ Amongst students in Dschang, in 2015, a prevalence of 2% was also obtained based on ELISA test. 12 In 2016, a prevalence of 22.52% was determined among women consulting in Nkoldongo Hospital in Yaoundé via ELISA as well. 13 Furthermore, in 2018, an ELISAestablished prevalence of 40.8% was reported among women in the District Hospital of Dschang. 14 These results progressively changed in a jagged way and are therefore difficult to interpret and exploit for effective epidemiological control. These disparities undoubtedly may stem from the fact that in most of the reports, the ELISA technique was dominantly used for diagnosis and may also be due to the target populations in these studies. Indeed, a study has shown that the PCR technique is more sensitive and more specific than the ELISA technique, which was prone to false positive results. 15,16 Because this disease is very often silent and hospitals in the West Cameroon region often do not have equipment and qualified personnel for diagnosis, our working hypothesis was that the prevalence of C. trachomatis is high, and several genotypes of C. trachomatis circulate in this area. This study sought to answer the following research questions: what is the prevalence of C. trachomatis infection among women in West Cameroon, and what were the factors that increased the risk of infection among them? The objective of this study was to uncover epidemiological data that may serve as a useful tool for the better management of C. trachomatis infections in women in West Cameroon.

METHODS

Study design and setting

This was a cross–sectional and hospital-based study conducted in five district hospitals in the West region of Cameroon between January 2020 and July 2020. These hospitals include Dschang (235 women), Bafang (110 women), Mbouda (123 women), Bafoussam (109 women) and Bangangté (103 women) (Figure 1). The West region of Cameroon has a population of 1,785,285.

Study participants

Participants were recruited among women who came to the hospital for antenatal, prenuptial and contraception consultations. These participants were to be at least 18 years old, sexually active, had no sexual intercourse for at least 48 hours, were not under antibiotic treatment and were not menstruating. They were informed and invited to participate in the study. Those who agreed to participate signed a written informed consent form and were administered a questionnaire to record their

sociodemographic information and potential risk factors. This was done in turns sequentially.

Specimen collection

Endocervical swabs (680) were obtained from women using a non-lubricated speculum and a nonabrasive swab of the "bactopick". The collected samples were placed into a storage tube containing 1 ml of sterile saline (0.9% NaCl) and stored at -20 $^{\circ}$ C until further processing. 14

PCR diagnosis of C. trachomatis infection

DNA extraction

DNA was extracted from samples using the QIAamp mini kit.¹⁷ Briefly, the samples were removed from the freezer, left at room temperature for one hour and centrifuged at 15,000 rpm for 10 minutes. ATL buffer (180 µl) was added to the pellet and homogenized with a vortex mixer (iSwix-VT Neuation), and proteinase K was added followed by vortexing and incubation at 56 °C for 3 hours while homogenizing 2 to 3 times during incubation. After incubation, 200 µl AL buffer was added, and the mixture was homogenized using a vortex for 15 seconds and incubated at 70 °C for 10 minutes. Then, 200 µl ethanol was added and homogenized. The mixture was then introduced into minicolumns and centrifuged at 8,000 rpm for one minute. The filtrate was discarded, and the minicolumns were placed in new 2 ml tubes; buffer AW1 was added and centrifuged at 8,000 rpm for one minute, and the filtrate was discarded. Buffer AW2 was added to minicolumns and centrifuged at 14,000 rpm for 3 minutes, and the filtrate was discarded. The minicolumns were placed in new 2 ml tubes and then centrifuged at 14,000 rpm for one minute. After centrifugation, the minicolumns were placed in new tubes, and 50 µl of buffer AE was added and left at room temperature for 5 minutes. The tubes were centrifuged at 10,000 rpm for 3 minutes, and the extracted deoxyribonucleic acid (DNA) was stored at -20 °C for subsequent molecular analysis. The quantity and quality of the extracted DNA were estimated using a Nanodrop spectrophotometer (Thermo Scientific NanoDrop 2000 spectrophotometer).¹⁸

Amplification of cryptic plasmid and MOMP gene

The molecular identification of C. trachomatis was performed using two different pairs of primers: cryptic plasmic primer KL1/KL2 (KL1, 5'-5'-TCCGGAGCGAGTTACGAAGA-3'; KL2, AATCAATGCCCGGGATTGGT-3'),17,18 and MOMP primer (forward, 5'-CCTGTGGGGAAT CCTGCTGAA-3'; reverse, 5' GTC GAA AAC AAA GTC ACC ATA GTA 3').¹⁹ The amplification reactions were set for each primer pair in a 25 µl reaction volume containing 1X PCR buffer (10 mM Tris-HCl; 50 mM KCl; 1.5 mM MgCl2), 0.5 μM of each pair of primers, 200 μM dNTPs; 1 U of Taq DNA polymerase, 5 µl of DNA. The amplifications were carried out in a thermocycler (AB Veriti) with thermocycling conditions including an initial denaturation step at 95 °C for 10 minutes, followed by 50 amplification cycles each comprising a denaturation step at 95 °C for 30 seconds, annealing at 60 °C for 45 seconds, elongation at 72 °C for 1 minute and a final extension at 72 °C for 7 minutes. The amplicons were subjected to 1.5% agarose gel electrophoresis and observed on a UV transilluminator.

Identification of serovars

Amplification of ompA gene

Positive samples were used for the identification of different serovars of *C. trachomatis* using CT OMP 1F (5'-ATG AAA AAA CTC TTG AAA TCG G-3') and CT OMP 2R (5'-ACT GTA ACT GCG TAT TTG TCT G-3') primers. ¹⁹ This identification was performed by PCR in 25 μ l reaction medium containing 2.5 μ l of 1X PCR buffer (10 mM Tris-HCl; 50 mM KCl; 1.5 mM MgCl₂), 1.0 μ M of each primer, 200 μ M of dNTPs; 1.5 U of Taq DNA polymerase and 5 μ l of DNA. Thermocycling conditions constituted an initial denaturation step at 95 °C for 15 minutes, followed by 45 amplification cycles each comprising denaturation at 95 °C for 30 seconds, annealing at 55 °C for 45 seconds, elongation at 72 °C for 90 seconds and a final extension at 72 °C for 7 minutes.

OmpA gene sequencing

PCR products from CT OMP amplification were sequenced in a BigDye Terminator sequencing kit (Applied Biosystems, USA) on a 3500 Dx sequencing machine available in the department of medical microbiology, Post Graduate Institution of Medical Education and Research (PGIMER) Chandigarh.

Analysis of the sequences of the *C. trachomatis* omp1 nucleotide sequence was performed by comparing it to the nucleotide sequences of the known serovars of C. trachomatis using the basic local alignment search tool. All ompomp1 sequences were assembled into alignments using reference sequences from GenBank: B/TW-5 (M17342), C/TW-3 (M17343), D/UW-3/CX (AE00127), D/B-120 (X62918), E/Bour (X52557), F/ICCal3 (X52080), G/UW57 (AF063199), H/Wash (H/UW4), I/UW-12 (AF063200), J/UW36 (AF063202) and K/UW31 sequence Multiple alignment (AF063204). phylogenetic analysis were performed using MEGA X software package version 10.1.7.

Statistical analysis

The relationship between the prevalence and sociodemographic parameters in the study population was evaluated using the chi-square test (p≤0.05), and the risk factors were identified using multivariable logistic regression analysis. Odds ratios (ORs) with 95% confidence intervals were used to determine the degree of association between the infection and sociodemographic parameters. All these analyses were performed using IBM

statistical package for the social sciences (SPSS) version 19 software.

Ethical considerations

Ethical clearance was obtained from the Cameroon National Committee for ethics in human health (N° 2018/05/1022/CE/CNERSH/SP) and institutional ethics committee of PGIMER, Chandigarh in India (N° PGI/IEC/2020/001586) coupled to administrative authorization from the West regional delegation of public health and from each hospital.

RESULTS

Characteristics of the study participants

Table 1 presents the characteristics of study participants. Active medical surveys were performed in five district hospitals in the West region of Cameroon. A total of 687 women were screened, and 680 were enrolled. The age of the participants ranged from 18-49 years, with a mean age of 27.37±7.48 years. The most represented age ranges were [18-24 [(39.56% (269/680)) and [24-30 [(27.35% (186/680)). Very few participants (0.29%) did not go to school, while most of them had secondary (52.05% (354/680)) and university (36.02% (245/680)) educational levels. Among married women, 65.69% (157/239) were in monogamous relationships, and 34.30% (82/239) were in polygamous relationships. The regular and occasional use of condoms as a contraceptive measure was depicted by 41.76% (284/680) and 10% (68/680) of the participants, respectively, where 48.24% (328/680) did not use condoms. Most women (74.85%, 509/680) in the study did not know the transmission route of C. trachomatis infection, while only 23.82% (162/680) of women knew the real transmission route. Among these 74.85% of women, 22.05% (150/680) and 10.14% (69/680) thought the infection was transmitted through blood and saliva, respectively.

Variation in the prevalence of *C. trachomatis* infection with study population characteristics.

Table 2 presents relationship between *Chlamydia trachomatis* infection and risk factors.

Participants with a low level of education (primary) were significantly less infected (p=0.007) than participants with a higher level of education (secondary and university). The prevalence of C. trachomatis infection was significantly higher (p=0.029) in participants aged [1824[(14.86%) and [24-30[(12.90%), while women aged [42-49] (2.17%) were less infected [IC 95% (0.86-1.01)] and had the lowest prevalence. Single women (20.43%), women living in concubinage (11.36%) and women living apart together with a man (10.32%) showed a significantly higher (p=0.008) prevalence of C. trachomatis infection. The type of family also influenced the prevalence of this disease in the population, with women married in monogamic

families being significantly (p=0.02) more infected (12.10%). Participants who did not use condoms showed a significantly high (p=0.001) prevalence of infection (16.15%).

The other sociodemographic characteristics of the population did not influence the prevalence of this disease.

Table 3 presents association between *C. trachomatis* infections and risk factors in patients. Based on the results obtained in Table 2, risk factors were determined using logistic regression. It appears that age at first intercourse strongly predicted *C. trachomatis* infection (OR=1.68, 95% CI: 1.10-2.50), while the non-use of condoms (OR=1.62, 95% CI: 1.20-2.10) was significantly associated with *C. trachomatis* infection. Marital status (OR=1.26, 95% CI: 1.00-1.50) and age (OR=1.42, 95% CI: 1.10-1.80) were also significantly associated with a high prevalence of *C. trachomatis* infection (Table 3).

OmpA genotypes of C. trachomatis

Out of the 78 samples positive for C. trachomatis using PCR, 51 were successfully amplified with ompA primers and submitted to DNA sequencing and phylogenetic analysis. The gene tree shows the distance neighborjoining reconstruction based on the nucleotide sequences of the ompA gene (Figure 5). This tree demonstrated that three *C. trachomatis* genotypes circulate in the study areas: D (n=25; 49%), E (n=15; 29.4%) and G (n=11; 21.6%). The D strain (n=2; 4%) was the only strain found in participants in Bafang. The E strain was the most among participants in Bangangté (n=3; 6%) and Bafoussam (n=6; 12%), followed by D strains (n=2; 4% and n=2; 4%) and G (n=1; 2%, n=2; 4%), respectively. In Dschang and Mbouda, the D strain (n=10; 20% and n=9; 18%) had the highest prevalence among participants, followed by E (n=5; 10% and n=1; 2%) and G (n=4; 8% and n=4; 8%), respectively.

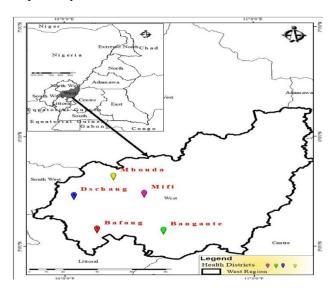


Figure 1: Map situating the West region of Cameroon and showing the study areas.

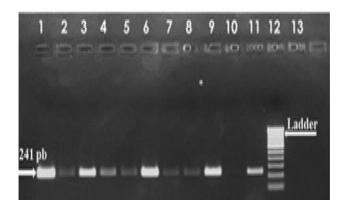


Figure 2: Polymerase chain reaction results showing positive samples of *C. trachomatis* using cryptic plasmid primers KL1 and KL2 on endocervical swab DNA extracts.

Lanes 1 to 9: positive (241 bp); lane 10: negative sample; lane 11: positive control; lane 12: DNA ladder (100 bp); and lane 13: negative control

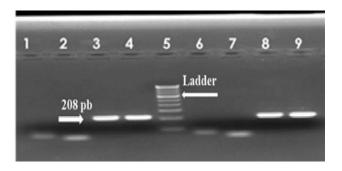


Figure 3: Polymerase chain reaction results showing positive samples of *Chlamydia trachomatis* using MOMP primers on endocervical swab DNA extracts. Lanes 3, 4 and 8: positive (208 bp); lane 5: DNA ladder (100 bp); lane 7: negative control; lane 9: positive control; lanes 1, 2, 6 and 7: negative samples

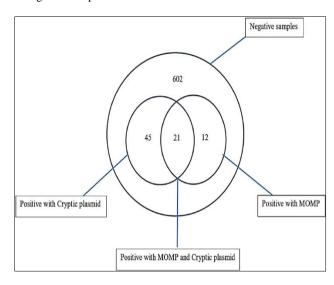


Figure 4: Summary of *Chlamydia trachomatis* identification using cryptic plasmid and MOMP primers on endocervical swab DNA extracts.

Table 1: Characteristics of study participants (n=690).

Variable	Total (%)
Level of education	
None	2 (0.29)
Primary	79 (11.61)
Secondary	354 (52.05)
University	245 (36.02)
Knowledge of STI	2 13 (30.02)
No	97 (14.26)
Yes	583 (85.73)
Knowledge of transmission route	303 (03.73)
No	299 (43.97)
Sexual intercourse	162 (23.82)
Blood	150 (22.05)
Saliva	69 (10.14)
Age range	07 (10.14)
18-24	269 (39.55)
24-30	186 (27.35)
30-36	125 (18.38)
36-42	54 (7.94)
42-49	46 (6.76)
Marital status	40 (0.70)
Single	137 (20.14)
Married	250 (36.76)
Concubinage	132 (19.41)
Living apart together	155 (22.79)
Divorced	4 (0.58)
Widow	2 (0.29)
Type of family	2 (0.23)
Monogamy	157 (23.08)
Polygamy	82 (12.05)
Age at first intercourse (years)	82 (12.03)
<15	28 (4.11)
15-17	346 (50.88)
≥18	306 (45)
Condom usage	300 (43)
	328 (48.23)
No Occasionally	68 (10.00)
Always	284 (41.76)
Number of sexual partner	204 (41.70)
More than one partner	195 (28.67)
One partner	485 (10.72)
Occupation	10.72)
No	144 (21.17)
University student	135 (19.85)
Secondary student	62 (9.11)
Trader	87 (12.79)
Famer	87 (12.79) 87 (12.79)
Others	
Previously infected with STD agents	165 (24.26)
Yes	184 (27.05)
No No	496 (72.94)
INU	470 (12.74)

Table 2: Relationship between C. trachomatis infection and risk factors.

Characteristics	Positive PCR	Number of	Prevalence	P value	Confidence
Level of education		participants	(%)		intervals, (95% C.I.)
None	1	2	50		<u>-</u>
Primary	4	79	5.06	0.007*	0.85-1.01
Secondary	34	354	9.60		0.87-0.96
University	39	245	15.92		0.85-0.98
Knowledge of STI		213	10.72		0.03 0.70
No	9	97	9.27		0.86-0.99
Yes	69	583	11.83	0.46	0.88-0.96
Knowledge of transmis			11.00		
No	30	299	10.03		0.88-0.98
Sexual intercourse	27	162	16.66		0.87-1.00
Blood	14	150	9.33	0.12	0.79-0.97
Saliva	7	69	10.14		0.82-1.03
Age range	,	- 0,	10.11		0.02 1.03
18-24	40	269	14.86		0.82-0.97
24-30	24	186	12.90		0.80-0.97
30-36	8	125	6.40	0.029*	0.88-1.00
36-42	5	54	9.25	0.02)	0.80-1.01
42-49	1	46	2.17		-
Marital status		10	2.17		
Single	28	137	20.43		0.19-1.06
Married	19	250	7.6		0.90-0.96
Concubinage	15	132	11.36	_	0.58-1.17
Living apart together	16	155	10.32	- 0.008*	0.67-1.13
Divorced	0	4	0	_	-
Widow	0	2	0		_
Type of family	0		0		
Monogamy	19	157	12.10		0.94-1.01
Polygamy	2	82	2.4	0.02*	0.85-0.94
Age at first intercourse		62	2.4		0.03-0.74
<15	5	28	17.5		0.51-1.21
15-17	48	346	13.87	0.04*	0.87-0.96
≥18	25	306	8.16		0.88-0.97
Condom usage	23	300	0.10		0.00-0.77
No	53	328	16.15		0.82-0.94
Occasionally	5	68	7.35	0.001*	0.82-0.94
Always	20	284	7.04		0.87-1.03
Number of sexual parts		204	7.04		0.92-1.0
More than one partner	26	195	13.33		0.80-0.98
One partner	52	485	10.72	0.33	0.89-0.96
Occupation	32	463	10.72	0.33	0.89-0.90
No	19	144	12 10		0.78-0.96
University student	22	135	13.19 16.29		0.78-0.96
Secondary student	11	62	17.74	0.05	0.81-1.01
	6	87			
Trader	7		6.89		0.85-1.01
Farmer		87	8.04		0.84-1.01
Others	13	165	7.87		0.92-1.01
Previously infected with		0.4	10.22	·	0.05.004
Yes	19	84	10.32	0.56	0.85-0.94
No Significant.	59	496	11.89		0.85-0.91

^{*}Significant.

Table 3: Association between *C. trachomatis* infections and risk factors in patients.

Variable	Odds ratio (95% CI)	P value
Age range	1.42 (1.10-1.80)	0.003*
Marital status	1.26 (1.00-1.50)	0.04*
Type of family	0.20 (0.04-0.90)	0.037
Condom usage	1.62 (1.202.10)	0.001*
Age of first intercourse	1.68 (1.10-2.50)	0.013*
Level of education	0.59 (0.40-0.80)	0.009

^{*}Significant association

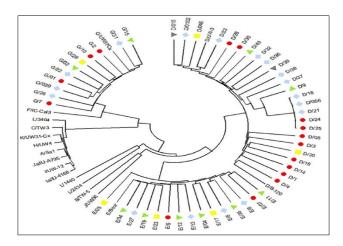


Figure 5: Distance neighbor-joining reconstruction of the phylogenetic tree based on the *C. trachomatis* ompA nucleotide sequence from 51 genotypes.

The neighbor-joining method was used in MEGA 10.1.7 software to generate unrooted phylogenetic trees for ompA from DNA sequences. The number of bootstrap replication values was 1,000. Initially, multiple sequence alignment was generated using ClustalW.

DISCUSSION

The prevalence of *C. trachomatis* was found to be 11.47%, which was comparable to some results obtained in South Africa, Tanzania and Brazil. 20-22 Such a high prevalence of C. trachomatis can be attributed to the asymptomatic nature of the infection, leading to late clinical manifestations, giving time to C. trachomatis to migrate to the upper genital tract, which could further lead to various sequelae in women and transmission to their partners.⁵ Young age associated with other risk factors identified may explain this prevalence rate. These risk factors include age of first intercourse, marital status (single more affected) and non-condom usage. According to Nicolai et al., condom usage is effective in preventing C. trachomatis infection.²³ In contrast, occupation and level of education were not associated with C. trachomatis infection, confirming the results obtained by Fogue et al in Dschang District Hospital in 2018, but contradictory to the results of Ngonde et al who demonstrated that the level of education was significantly associated with C. trachomatis infection in a study carried out in Yaoundé-Cameroon. ^{12,14} Single participants were found to be significantly more infected by *C. trachomatis*. In accordance with Morhason-Bello et al in Nigeria, this could be linked to multiple sex partners. ²⁴ However, it is not superfluous to point out that Nwankwo et al in Nigeria and Yirenya-Tawiah et al in Ghana reported that there was no relation between marital status and infection by *C. trachomatis*. ^{25,26}

According to the Cameroon national strategic plan for the fight against human immunodeficiency virus (HIV), acquired immunodeficiency syndrome (AIDS) and sexually transmitted infections (STIs) 2011-2015, the prevalence of Chlamydia infection was 8% before 2010, coming in third after gonococcus and syphilis.²⁷ The prevalence obtained within the framework of this study therefore shows that this prevalence has increased over time; therefore, the strategies put in place need to be revised and fully implemented. Furthermore, previous studies in Cameroon have reported prevalence varying between 2% and 40%, depending on diagnostic methods and study population.⁸⁻¹⁴ C. trachomatis is detected in urine and vaginal swabs using different techniques. Some results published in Cameroon may not reflect reality due to false positives related to the choice of diagnostic method. Indeed, the PCR that we used in this study is as sensitive and specific as cell culture and therefore is a recommended method. Furthermore, the target population of these studies can justify the significant differences observed in the prevalence published. For example, girls aged under 25 years and women above 25 years as well as women with new or multiple sex partners have higher prevalences.²⁸ This study showed that the cryptic plasmid primers were more sensitive than the MOMP primers, which could be due to the presence of multiple copies of cryptic plasmid genes (7-10 copies/bacterial cell) compared to the MOMP gene, which has only one.²⁹

The present study revealed three circulating genotype variants of *C. trachomatis* in the West region of Cameroon: genotype D (commonest), genotype E and genotype G. The presence of genotype D as the commonest genotype variant has been reported by previous studies in Hungary, China and India.³⁰⁻³² The identified genotypes are known to be commonly associated with urogenital infections.³³ The genotypes identified in our study show some differences from the prototype strains, which can be due to genetic recombination.³⁴ Of the 19 known genotypes, only 3 were identified in participants in this study, carried out in the West Cameroon region. It should be noted that this region is the smallest in the country, and the distances between cities and therefore health district centers are shorter: Dschang-Mbouda: 57.8 km, Dschang-Bafoussam: 52.5 km, Dschang-Bangangté: 90.4 km, Dschang-Bafang: 74.8 km, Bafoussam-Mbouda: 30.2 km, Bafoussam-Bangangté: 49.7 km, Bafoussam-Bafang: 59.0 km, Mbouda-Bangangté: 76.7 km, Mbouda-Bafang: 85.9 km, and Bafang-Bangangté: 47.4 km. Nevertheless, the mixing of populations is increased but dominated by the same tribe (Bamiléké) and could justify the low diversity of C.

trachomatis strains in this area, although Helm et al found that differences in prevalence are not ethnic group-linked.³⁵ This is more plausible since a similar study carried out in Yaoundé, Center region, among students identified up to 5 genotypes, with genotype E as the most prevalent.¹⁰ Yaoundé is a cosmopolitan city that may justify a greater shuffling of the genes of this bacterium.

CONCLUSION

The overall prevalence of *C. trachomatis* infections using PCR detection was 11.47% and was associated with marital status, age at first intercourse and condom usage as risk factors. Only three genotypes, D (dominant), E and G, were identified circulating in the population of the study area. This information may be important for controlling the dissemination of *C. trachomatis* infection in West Cameroon as well as strategizing the therapeutic approach.

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Institutional Ethics Committee

REFERENCES

- Rowley J, Vander HS, Korenromp E, Low N, Unemo M, Abu-Raddad LJ, et al. Chlamydia, Gonorrhoea, trichomonas and syphilis: Global prevalence and incidence estimates, 2016. Bull World Health Organ. 2019;97(8):548-62.
- 2. Eggert-Kruse W. Prevalence of Chlamydia trachomatis in subfertile couples. Fertility and Sterility. 2003;80(3):660-3.
- 3. World Health Organization. Growing antibiotic resistance forces updates to recommended treatment for sexually transmitted infections. Available at: https://www.who.int/news/item/30-08-2016-growing-antibiotic-resistance-forces-updates-to-recommended-treatment-for-sexually-transmitted-infections. Accessed on 15 February 2021.
- 4. Newman L, Rowley J, Vander Hoorn S, et al. Global Estimates of the Prevalence and Incidence of Four Curable Sexually Transmitted Infections in 2012 Based on Systematic Review and Global Reporting. Plos One. 2015;10:e0143304.
- Sunil S, Amit R, Shubha G, Venkatesan LS, Bagga R. Detection of Chlamydia trachomatis infections by polymerase chain reaction in asymptomatic pregnant

- women with special reference to the utility of the pooling of urine specimens. Indian J Med Res. 2017;146(7):59.
- 6. Adachi K, Nielsen-Saines K, Klausner JD. Chlamydia trachomatis Infection in Pregnancy: The Global Challenge of Preventing Adverse Pregnancy and Infant Outcomes in Sub-Saharan Africa and Asia. Biomed Res Int. 2016;1-21.
- 7. Sende P, Abong, T, Garrigue GP. Chlamydia trachomatis: a prevalence study among pregnant and infertile female patients and among men suffering from chronic urethritis. Afr J Sex Transm Dis. 1986;2:72-4.
- 8. Kaptue L, Zekeng L, Djoumessi S, Monny-Lobe M, Nichols D, Debuysscher R. HIV and chlamydia infections among prostitutes in Yaounde, Cameroon. Arch Genitourin Med. 1991;67(2):143-5.
- Ngandjio A, Clerc M, Fonkoua M, Thonnon J, Njock F, Pouillot R, et al. Screening of Volunteer Students in Yaounde (Cameroon, Central Africa) for Chlamydia trachomatis Infection and Genotyping of Isolated C. trachomatis Strains. J Clin Microb. 2003;41(9):4404-7.
- Noatina NB, Kagmeni G, Nimpa MM, Moungui HC, Tarini A, Zhang Y, et al. Prevalence of Trachoma in the Far North Region of Cameroon: Results of a Survey in 27 Health Districts. PLOS Negl Trop Dis. 2013;7(5):e2240.
- Ngondé EMC, Nsawir BJ, Nana RD, Thonnon J, Njock F, Pouillot R, et al. Etude séroepidémiologique de trois infections sexuellement transmissibles (Chlamydia Trachomatis, Hépatite B, Syphilis): cas de l'Hôpital de District de Nkoldongo à Yaoundé. Pan Af Med J. 2016;25.
- 12. Sanou SM, Donfack JH, Onohiol J-F, Mbongue G, Watcho P, Fokam J, et al. Prevalence of HIV, HBV and Chlamydia Infections in Cameroonian University Context: Case of the University of Dschang, in the Western Region. IJHSR. 2015;5:265-73.
- 13. Fogue P, Djeudong G, Bouting G, Aglago E, Simo G, Lueong S, et al. Molecular characterization of lower vaginal swabs for Human papilloma virus in association with Chlamydia trachomatis infection in Cameroonian Women. J Infect Public Health. 2018;11(3):314-20.
- 14. Detailed STD Facts Chlamydia. Chlamydia CDC Fact Sheet (Detailed). Available at: https://www.cdc.gov/std/chlamydia/stdfact-chlamydia-detailed.htm. Accessed on 22 July 2021.
- 15. Ajani TA, Anaedobe CG, Oluwasola TA, Ajani MA, Fayemiwo SA, Bakare RA. Polymerase chain reaction versus enzyme-linked immunosorbent assay in detection of Chlamydia trachomatis infection among gynaecological patients in South-Western Nigeria. Afr J Clin Exper Microb. 2018;9(2):76-83.
- 16. Santos C, Teixeira F, Vicente A, Astolfi-Filho S. Detection of Chlamydia trachomatis in endocervical smears of sexually active women in Manaus-AM, Brazil, by PCR. Braz J Infect Dis. 2003;7(2):91-5.

- Mazen AO, Wafa IE, Khalid AE. Molecular Detection of Chlamydia trachomatis among Sexual Transmitted Infections patients in Khartoum. Afr J Med Sci. 2018;3.
- Margaretha J, Lars F, Hans F. Characterization of Chlamydia trachomatis omp1 Genotypes among Sexually Transmitted Disease Patients in Sweden. J Clin Microbiol. 2001;39:3915-9.
- 19. Francis SC, Mthiyane TN, Baisley K, Mchunu SL, Ferguson JB, Smit T, et al. Prevalence of sexually transmitted infections among young people in South Africa: A nested survey in a health and demographic surveillance site. Plos Med. 2018;15:e1002512.
- Hokororo A, Kihunrwa A, Hoekstra P, Kalluvya SE, Changalucha JM, Fitzgerald DW, et al. High prevalence of sexually transmitted infections in pregnant adolescent girls in Tanzania: a multicommunity cross-sectional study. Sex Transm Infect. 2015;91(7):473-8.
- 21. de Borborema-Alfaia APB, de Lima FNS, Filho SA, Borborema-Santos CM. Chlamydia trachomatis infection in a sample of northern Brazilian pregnant women: prevalence and prenatal importance. Brazilian J Infect Dis. 2013;17:545-50.
- 22. Niccolai LM. Condom effectiveness for prevention of Chlamydia trachomatis infection. Sex Transm Infect. 2005;81(4):323-5.
- 23. Morhason-Bello IO, Ojengbede OA, Oladokun A, Adedokun BO, Ajayi A, Adeyanju AA, et al. The prevalence and outcome of asymptomatic chlamydial infection screening among infertile women attending gynecological clinic in Ibadan, South West Nigeria. Ann Med Health Sci Res. 2014;4(2):253.
- 24. Nwankwo E, Magaji N. Prevalence of Chlamydia trachomatis infection among patients attending infertility and sexually transmitted diseases clinic (STD) in Kano, North Western Nigeria. Af Health Sci. 2014;14(3):672.
- 25. Yirenya-Tawiah D, Annang TN, Apea-Kubi KA, Lomo G, Mensah D, Akyeh L, et al. Chlamydia trachomatis and Neisseria Gonorrhoeae prevalence among women of reproductive age living in urogenital schistosomiasis endemic area in Ghana. BMC Res Notes. 2014;7(1).

- 26. National AIDS Control Committee. National Strategic Plan to fight HIV, AIDS and STIs 2011-2015. Yaoundé, Cameroon. 2010;120.
- 27. Batool HR, Leili CT, Fedyeh H, Mahmood JT, Mohammed MN, Mamak S, et al. Effects of Chlamydia trachomatis infection on fertility, a case control study. J Reprod Fertility. 2013;14:67-72.
- 28. Mahony JB, Luinstra KE, Sellors JW, Chernesky MA. Comparison of plasmid- and chromosome-based polymerase chain reaction assays for detecting Chlamydia trachomatis nucleic acids. J Clin Microb. 1993;31(7):1753-8.
- 29. Chen Y, Chen J, Yang L, Yanming J, Li L, Wenjuan Y, Lifang L, et al. Distribution of Chlamydia trachomatis Genotypes in Infective Diseases of the Female Lower Genital Tract. Med Sci Monitor. 2017;23:4477-81.
- 30. Rawre J, Dhawan B, Khanna N, Sreenivas V, Broor S, Chaudhry R, et al. Distribution of Chlamydia trachomatis omp A genotypes in patients attending a sexually transmitted disease outpatient clinic in New Delhi, India. Ind J of Med Res. 2019;149(5):662.
- 31. Petrovay F, Balla E, Németh I, Gönczöl É. Genotyping of Chlamydia trachomatis from the endocervical specimens of high-risk women in Hungary. J Med Microb, 2009;58(6):760-4.
- 32. Centers for Disease Control and Prevention. Sexually Transmitted Diseases Treatment Guidelines. MMWR. 2015;64:106.
- 33. Taheri Beni B, Motamedi H, Ardakani MR. Genotyping of the prevalent Chlamydia trachomatis strains involved in cervical infections in women in Ahvaz, Iran. J Med Microb. 2011;60(3):396.

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