ISSN: 0975-833X

Available online at http://www.journalcra.com

International Journal of Current Research
Vol. 11, Issue, 10, pp.7721-7727, October, 2019

DOI: https://doi.org/10.24941/ijcr.36892.10.2019

INTERNATIONAL JOURNAL OF CURRENT RESEARCH

RESEARCH ARTICLE

PREVALENCE OF LOWER GENITAL TRACT INFECTIONS IN WOMEN: CASE OF SAINT CAMILLE HOSPITAL OF OUAGADOUGOU FROM 2015 TO 2018

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ARTICLE INFO

Article History:
Received 24th July, 2019
Received in revised form
19th August, 2019
Accepted 15th September, 2019
Published online 30th October, 2019

Key Words:
Low genital tract infection,
Candida albicans,
Candida spp., Enterococcus spp,
Burkina Faso.

ABSTRACT

Background: Vaginal infections remain a major public health problem in Burkina Faso. A retrospective study was conducted at Saint Camille Hospital of Ouagadougou (HOSCO) to determine the prevalence and risk factors associated with vaginal infections in women seen at gynecological consultation between 2015 and 2018. **Methods**: This is a retrospective analysis of women seen at gynecological consultation for vaginal infections at HOSCO from June 2015 to June 2018.The antibiogram and antifongigram of microorganisms isolated were determined using standard procedures. **Results:** The study population consisted of 4168 women aged 10 to 65 years with a mean of 29.0 ± 7.8. The overall prevalence of vaginal infections was 83.2% (3469/4168) in the study population with 517 cases of coinfections. Women from 19 to 45 years accounted for 92.8% of the study population and was the most exposed to *C. albicans* ($p < 0.001$) and *Escherichia coli* ($p = 0.002$). More than 50.0% (1770/3469) of yeast infections with 70.3% (1245/1770) of *Candida albicans* and 29.7% (525/1770) of *Candida spp.* were found while *Enterococcus spp.* was involved in 15.9% of vaginal infections. Antifongigram revealed higher sensitivity for Nystatin, Econazole, Clotrimazole and Miconazole. The highest resistance rates were observed for Fluconazole, Miconazole and Amphotericin B. **Conclusion:** This study has shown that *Candida albicans* and *Enterococcus spp.* are the most common pathogens involved in lower genital tract infections in women in Ouagadougou. We also report increased resistance to Fluconazole, Miconazole and Amphotericin B and suggests surveillance of antimicrobial resistance for better management of patients.

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***Citation: Tovo S. Frida, Ouattara Abdoul Karim, Zohoncon M. Theodora, Obiri-Yeboah Dorcas, Yonli A. Theophane, Djigma W. Florencia, Sangaré Lassana and Simpore Jacques.* 2019.** "Prevalence of lower genital tract infections in women: case of saint Camille Hospital of Ouagadougou from 2015 to 2018.", *International Journal of Current Research*, 11, (10), 7721-7727.

INTRODUCTION

Clinical symptoms of genital tract infections in women account for half of the reasons for female consulting in a hospital setting. They refer to all infections of the female genital tract. Two forms can be distinguished, namely lower genital tract infections (LGTIs) and upper genital tract infections (UGTIs). Their complications can lead to sexually transmitted infections (STIs), causing many deaths worldwide (Olombel, 2005). According to the WHO, the daily incidence of STIs in 2016 was more than one million cases in the world (OMS, 2018). STIs still occur in developing countries, especially in Sub-Saharan Africa. Female genital tract infections (FGTIs) have long been considered unalarming illnesses; but due to their consequences on the reproductive health of women, they are currently a public health concern. Vaginal infections are associated with high risk of human immunodeficiency virus (HIV), human papillomavirus (HPV), hepatitis B virus (HBV), hepatitis C virus (HCV) and transmission of many other STIs. Previous studies have shown that vaginal infections increase HIV infectivity and susceptibility of contracting as well as transmitting that STIs (Simpore, 2006; Ilboudo, 2010 ; Simpore, 2004). Studies have been conducted on the prevalence of LGTIs; especially bacterial vaginosis in HIV-infected women worldwide as well as in Africa and Burkina

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Faso. The prevalence range for bacterial vaginosis was from 60% to 70% according to the authors, study populations and clinical and/or microbiological criteria (Olombel, 2005; Anagounou, 1994; Tamboura, 2004). Approximately 35% of women were found consulting clinics for STIs with 15 to 20% of pregnant women. This rate would exceed 50 % in the general population of women. Genital tract infections are associated with increasing HIV prevalence in Africa (Lewis, 2011; OMS, 2018). Indeed, African tropical climatic conditions are favorable for the development and proliferation of microorganisms involved in vaginal infections and endemic pathologies. In Burkina Faso, *Candida albicans* is the most common germs (almost 50% in most studies) reported in vaginal infections. However, a relatively high frequency of *Gardnerella vaginalis; candida spp.*; *enterococcus spp, E. coli, Staphylococcus aureus, Streptococcus agalactiae, Trichomonas vaginalis,* group B Streptococcus, genital herpes, genital condyloma, HPV, HIV and HBV infections have also been reported (Tamboura, 2004 ; Traore, 2016 ; Sanou, 2014). These different microorganisms involved in vaginal infection were associated or not with HIV infections (Simpore, 2004; Sagna et al., 2010). Management of infected patients is required for adequate treatment through the administration of antibiotics (ATB) and antifungals (ATF).

Due to the increasing resistance of microorganisms to ATB, such as betalactamins (Ceftriazone); tetracyclines and quinolones (Ciprofloxacin); macrolides (Erythromycin) and phenicoles (Chloramphenicol), the issue of bacterial resistance should be one of the major concerns of the research studies in sub-Saharan Africa. Previous studies conducted in Burkina Faso by Nadembega *et al.* and Karou et *al*. early discussed female genital tract infections and antibioresistance (Nadembega, 2017; Karou, 2012). The present retrospective study within the same timeline reports the epidemiology of lower genital tract infections in women from 2015 to 2018. The study purpose was to highlight the resistance profile of microorganisms responsible for vaginal infections in women attending gynecological consultation at HOSCO for better management of patients and a considerable reduction in the transmission of STIs.

MATERIAL AND METHODS

Patients and setting: The present retrospective analysis which aimed to determine the prevalence of microorganisms responsible for vaginal infections and their resistance profile to available antimicrobials was approved by the Internal Ethics Committee of HOSCO. This comprehensive sample study population consisted of women seen at gynecological consultation for vaginal infections regardless clinical symptoms from June 2015 to June 2018 at HOSCO, Ouagadougou, Burkina Faso. The socio-demographic (age) and clinical data(Imbalance of the bacterial flora, risk factors for bacterial proliferation such as excessive use of some toiletries, inappropriate underwear, ant biotherapy, excess or lack of hygiene, Unprotected sex with or without itching, abnormal vaginal discharge…) of the patients were obtained through the registers of the gynecology department. The socio-professional data of patients were missing. Women in menstrual period, having performed a vaginal toilet or had sex the day before sampling were excluded from the study.

Sampling: Abnormal vaginal secretions (Vaginal discharge or leucorrhoea) were collected by cervical swabbing. For each patient, two swab collections were done; the first on endocervix for the detection of pathogenic bacteria and the second on exocervix for microscopic examination in the fresh state.

Culture and identification of the microorganisms

Antifongigram: The antifungals considered in this study were selected according to their availability and accessibility in the Burkina Faso: These were Fluconazole, Nystatin, Miconazole, Clotrimazole, Amphotericin B, Ketoconazole and Econazole. These molecules were tested on samples positive for *Candida albicans* and *Candida spp.*

Antibiogram: The antibiotics such as Ampicillin (AM); Amoxicillin + Acidic clavulanic (AMC); Oxacillin (OX); Ceftriaxone (CRO); Ceftazidime (CAZ); Cefoxitin (FOX); Tetracycline (YOU); Doxycycline (DO); Kanamycin (K); Netilmicin (CLEAN); Tobramycin (TM); Ofloxacin (OFX); Ciprofloxacin (CIP); Erythromycin (E); Trimethoprim + sulfonamides (SXT); Colistin (CS); Chloramphenicol (C), were tested on bacterial strains detected after agar culture.

Statistical analyses: Standard descriptive analysis was performed using Epi Info version 7 and IBM SPSS 25.0 (SPSS Inc., Illinois, USA) softwares. The chi-square test and Fisher's exact test was used to compare categorical variables while continuous variables were analysis using Student's t-test and the differences between groups were considered statistically significant for $p \leq 0.05$.

RESULTS

Sociodemographic characteristics of the study population: The population of the present study consisted of 4168 women aged 10 to 65 years with a mean of 29.0 ± 7.8 years. The age range of most women (92.8%) was from 19 to 45 and the latter was the most exposed group for vaginal infections. (Table I) The prevalence of *Candida albicans* ($p < 0.001$) and *Escherichia coli* infection ($p = 0.002$) was significantly higher in this age group compared with those under 19 years and over 45 years of age.

Prevalence of vaginal infections and microorganisms involved: Out of 4168 patients included in this study, 3469 were positive for low vaginal infection with an overall prevalence of 83.2 %. The results demonstrated that *Candida albicans* was the most common microorganism and accounted for 35.9 % of infections followed by *Enterococci spp.* (15.9 %), *Candida spp.* (15.1 %) and *Gardnerella vaginalis* (11.0 %). The prevalence of other microorganisms was less than 2 % while no infection with *Chlamydia trachomatis* and *Mycoplasma genitalium* were found in our study population. (Table II)

Prevalence of coinfections: The results of this study revealed multiple infection cases among the infected women (3469/4168). An overall prevalence of 14.9% (517 /3469) of coinfections were found in our study population. Coinfections with *C. albicans*/*Enterococcus spp.* (130/3469) and *GV*/*C. albicans* (122/3469) were the most prevalent while the lowest coinfections were observed with *GV/Staphylococcus aureus* (13/3469) and *GV/Enterococcus spp.* (10/3469) (Figure 1).

Table 1. Distribution of vaginal infections according to age groups

	Age Groups N (%)				
Parameters	X ≤ 18	19 – 45	X > 45	P	Total
Microorganisms	N = 129 (03.09)	N = 3869 (92,83)	N = 170 (04.08)		N = 4168 (100)
Candida albicans	44 (1.10)	1181 (28.33)	20 (0.48)	< 0.001	1245 (29.87)
Enterococcus spp.	16 (0.38)	505 (12.12)	31 (0.74)	0.137	552 (13.24)
Candida spp.	18 (0.43)	488 (11.71)	19 (0.46)	0.769	525 (13.00)
Gardnerella vaginalis	14 (0.34)	357 (8.57)	9 (0.22)	0.172	380 (9.12)
Escherichia coli	7 (0.17)	180 (4.32)	18 (0.43)	0.002	205 (4.92)
Staphylococcus aureus	7 (0.17)	166 (3.98)	10 (0.24)	0.516	183 (4.39)
Staphylococcus spp.	3 (0.07)	132 (3.17)	9 (0.22)	0.326	144 (3.45)
Streptococcus agalactiae	3 (0. 07)	58 (1.39)	4 (0.09)	0.527	65 (1.56)
Klebsiella pneumonia	2 (0.04)	39 (0.94)	2 (0.04)	0.820	43 (1.03)
Trichomonas vaginalis	1 (0.02)	40 (0.96)	0 (0.00)	0.397	41 (0.99)
Streptococcus spp.	0 (0.00)	31 (0.74)	1 (0.02)	-	32 (0.77)
Staphylococcus epidermidis	2 (0.04)	49 (1.18)	0 (0.00)	0.320	21 (0.50)
Pseudomonas spp.	1 (0.02)	2 (0.04)	0 (0.00)	-	3 (0.07)
Chlamydia trachomatis	0 (0.00)	0 (0.00)	0 (0.00)	-	0 (0.00)
Mycoplasma genitalium	0 (0.00)	0 (0.00)	0 (0.00)	-	0 (0.00)

Table 2. Frequency of different microorganisms in positive samples

Microorganisms	Positive	%
Candida albicans	1245	35.9
Enterococcus spp.	552	15.9
Candida spp.	525	15.1
Gardnerella vaginalis	380	11.0
Escherichia coli	205	5.9
Staphylococcus aureus	183	5.3
Staphylococcus spp.	144	4.1
Streptococcus agalactiae	65	1.9
Staphylococcus epidermidis	51	1.5
Klebsiella pneumoniae	43	1.2
Trichomonas vaginalis	41	1.2
Streptococcus spp.	32	0.9
Pseudomonas spp.	3	0.1
Chlamydia trachomatis	0	0.0
Mycoplasma genitalium	0	0.0
Total	3469	100.0

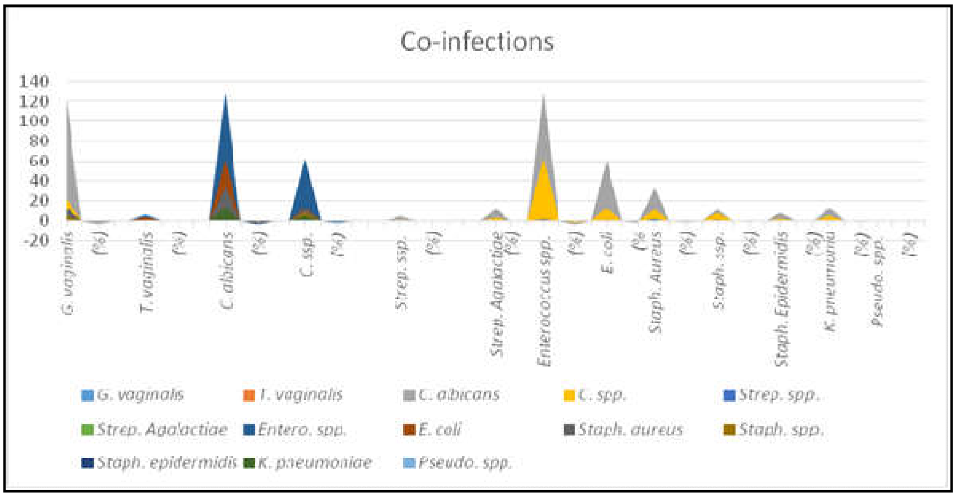

Figure 1. Profile of co-infections in the study population

Resistance profile from yeasts to antifungals (ATF)

Susceptibility of yeast strains to ATF: A total of 1770 cases of yeast were isolated with 1245 strains of *Candida albicans* and 525 strains of *Candida spp*. The antifongigram assay were performed using these strains. For most yeast strains tested on the different antifungal discs used, a high sensitivity was observed for Nystatin, Econazole, Clotrimazole and Miconazole while the highest resistances were recorded for Fluconazole, Miconazole and Amphotericin B (Figure 2).

Antibiotics and bacterial resistance profile: The antibiotics used in this study were divided into three (3) groups. The beta-lactamase group was composed of: Ampicillin (AM); Amoxicillin + clavulanic acid (AMC); Oxacillin (OX); Ceftriaxone (CRO); Ceflazidine (CAZ); Cefoxitin (FOX); The group of tetracycline aminoglycosides and quinolones included: Tetracycline (TE); Doxycycline (DO); Kanamycin (K); Netilmicin (NET); Tobramycin (TM); Ofloxacin (OFX); Ciprofloxacin (CIP); while Erythromycin (E); Trimethoprim +

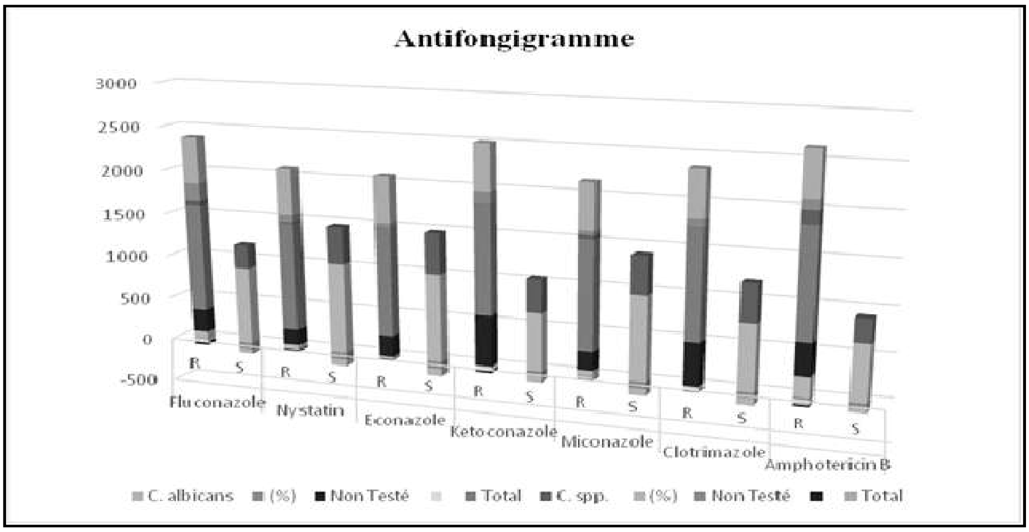

Figure 2. Susceptibility of yeasts: *candida albicans* and *candida spp* to antifungals

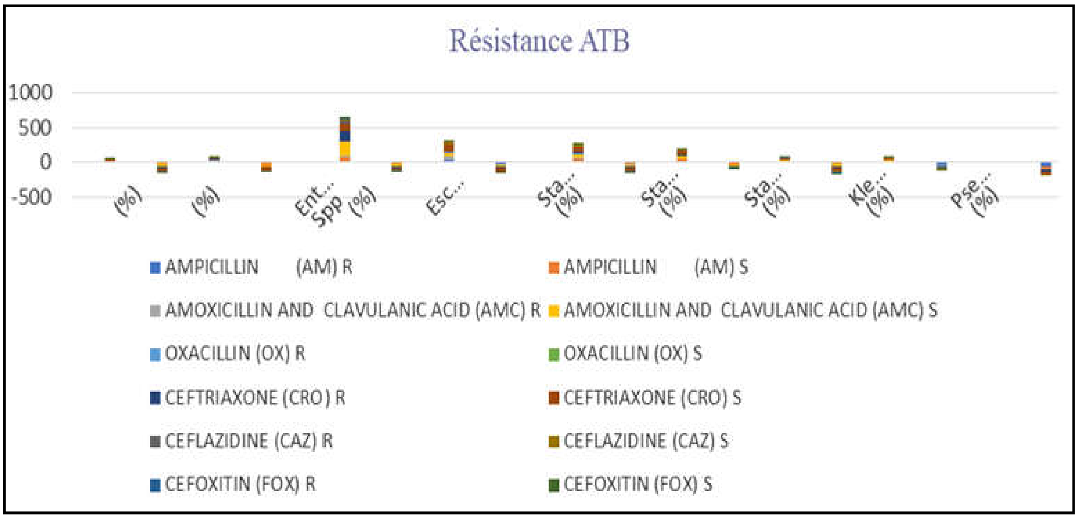

Figure 3. Susceptibility of bacteria to beta-lactamases

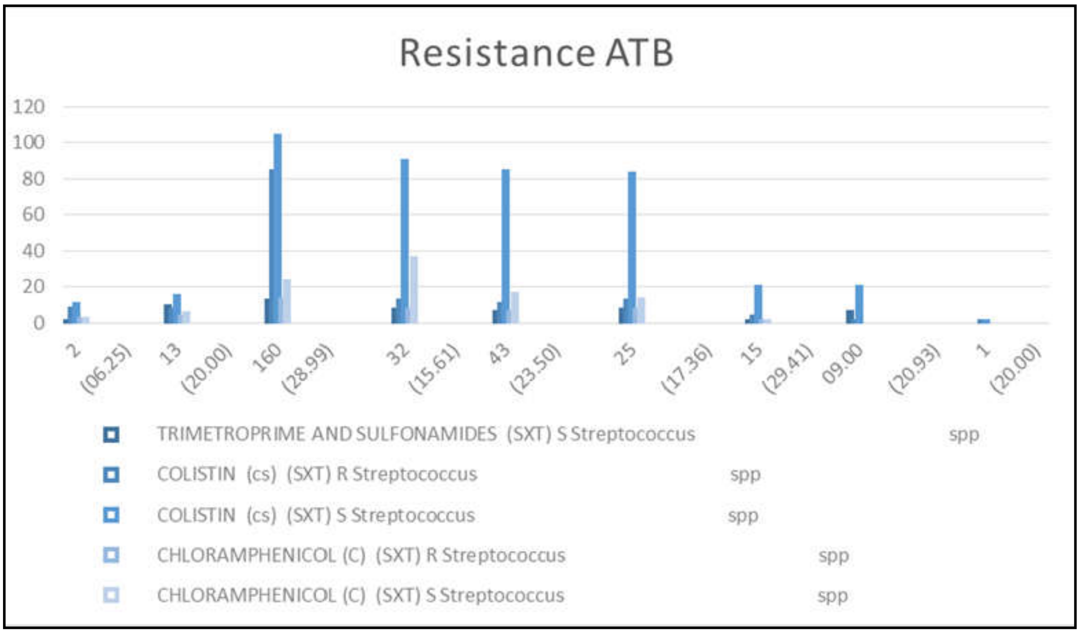

Figure 4. Susceptibility of bacteria to tetracyclines - aminoglycosides and quinolones

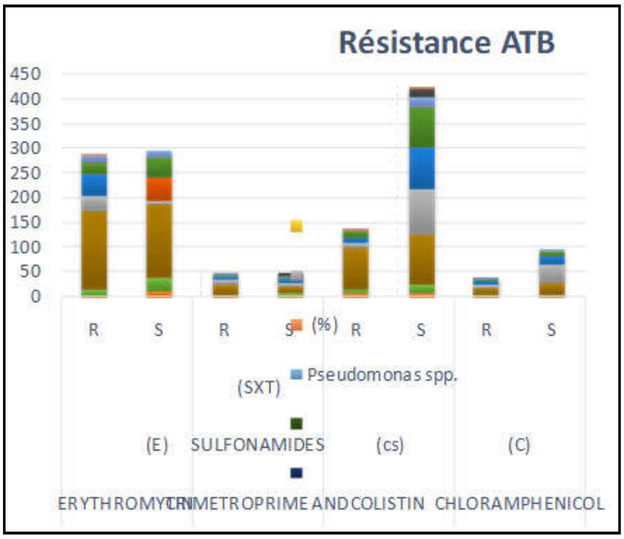

Figure 5. Susceptibility of bacteria to macrolides -sulfonamides and combinations - polypeptides and phenicol

Sulfonamides (SXT); Colistin (CS); Chloramphenicol (C) comprised the macrolide group - sulfonamides + associated - polypeptides and phenicoles.

Susceptibility of bacterial strains to beta-lactamases: In the beta-lactamase group, amoxicillin, Ceftriazone, and ampicillin presented the best susceptibility levels on the bacterial strains tested. More resistance was found with *Enterococcus spp.* to Ceftriazone, Ceflazidine and Cefoxitin (Figure 3).

Susceptibility of bacteria strains to tetracycline-aminoglycosides and quinolones: In the group of tetracyclines-aminoglycosides and quinolones the highest sensitivity was observed for ciprofloxacin against *Enterococci spp* and *Escherichia coli*. High resistance of Enterococci strains to Kanamycin and Tetracycline was also observed in this study (Figure 4).

Susceptibility of bacteria strains to macrolides-sulfonamides + associated - polypeptides and phenicoles; For this class of antibiotics, we noted that Erythromycin and Colistin disks tested against *Enterococci* showed sensitivity on 148 and 104 strains respectively against 160 and 84 resistant strains. Colistin was also highly sensitive to *Escherichia coli* (90); *Staphylococcus aureus* (84) and *Staphylococcus spp* (83) (Figure V)

DISCUSSION

Sociodemographic characteristics of the study population: The population of the present study consisted of 4168 women aged 10 to 65 years with a mean of 29.0 ± 7.8 years. The age group 19 to 45 years was the most exposed to infections and accounted for 92.8% of the study population. Similar results have been reported by Anagounou (64.0%) in Benin (among pregnant women) and Faye-Kette (82.5%) in Abidjan although their study population was consisted of women less than 30 years of age (Anagounou, 1994; Faye-Kette Achi, 1992). It is noteworthy that age group includes most of the sexually active women. The minimum age of 10 years in our study could be explained by early sexual intercourse among adolescents in Burkina Faso. Indeed, Traore et al. in their study on HPV infections, reported in 2015 a case of first sexual intercourse at 7 years of age in Orodara (Traore, 2016). The most representative and most exposed age group to lower genital tract infections of our study population ($P < 0,05$) was from 19 to 45 years. The literature reports that this age group from adolescence to menopause is the high sexual activity period of women with increase wish for a child. During this sexually active period, women are at high risk of sexually transmitted infections (Moodley, 2002). In a study conducted in Burkina Faso from 2010 to 2011, Nadembega *et al.* reported a prevalence of 58.5% of women with clinical symptoms of vaginal infections and most of them were sexually active (Nadembega, 2017). Indeed, early sexual intercourse and the lack of sexual hygiene are associated with an increased risk of opportunistic and vaginal infections (Traore, 2016). However, the results of our study are different from those reported by Koueke in Cameroon where women with vaginal infections were 24 to 31 years of age (Koueke, 1996). This difference could be explained by characteristics and low size of their study population. Our results suggest that low vaginal tract infection is associated with age (Table 1).

Distribution of the population according to the frequency and prevalence of exposure to pathogens: An overall prevalence of low genital tract infections in women of 83.2% (3469/4168) was found in our study population. Our results revealed a high prevalence of *Candida albicans* (35.9 %) infection in woman and confirm the previous studies that have demonstrated that is the most prevalent yeast species in vaginal infections. Meda et *al.* in 1995 found a prevalence of 17.0 % for *Candida albicans* in a sample of 220 women in Bobo-Dioulasso (Meda, 1995; Djigma, 2008). Vulvovaginal candidiasis is widespread in sexually active and inactive women. Indeed, previous studies reported that the two most common vaginal infections (candidiasis and vaginosis) are caused by *Candida albicans* and other fungi (25.0 - 44.0%) and bacteria (18, 0 - 37.0%). The etiologic agent of vaginitis *Trichomonas vaginalis* is scarce and dependent on environment and hygiene conditions. *Enterococcus spp* (15.9 %) was the second most prevalent pathogen in our study population followed by *Candida spp* (15.1 %) and *Gardnerella vaginalis* (11.0%).

Escherichia coli (5.9%); *Staphylococcus aureus* (5.3%) and *Staphylococcus ssp* (4.1%) had low infection rates. Low prevalence of *Streptococcus agalactiae* infection (1.9%); *Staphylococcus epidermidis* (1.5%); *Klebsiella pneumonia* (1.2%); *Trichomonas vaginalis* (1.2%); *Streptococcus spp.* (0.9%); *Pseudomonas spp* (0.1) was also found. Most of these bacteria are associated with other pathogens for vaginal infection and *Gardnerella vaginalis* is the most prevalent in bacterial vaginosis. In the present study it was the fourth most common microorganism. Our results are different from those of Nicand et *al.* and Sedallan *et al.* who reported a predominance of *Gardnerella vaginalis* in their study population (Nicand, 1994; Sedallian, 1995). Tamboura also found a predominance of *Candida spp.* followed by *Gardnerella vaginalis* in Ouagadougou while it was the third most common pathogen in the studies of Fofana and Hovette *et al.* respectively in Burkina and Djibouti (Tamboura, 2004; Burkina Faso, 1993; Hovette et al., 1999). Altogether our results confirm that *Gardnerella vaginalis* surveillance is required for the control of bacterial vaginoses. No *Chlamydia trachomatis* and *Mycoplasma genitalium* were found in the present study.

The prevalence of coinfections: Our study reports 517 cases of coinfection out of the 3469 infected women with 122 cases of *GV*/*C. albicans*and 22 cases of *GV*/*C spp.*

These results are different from those reported by Djigma *et al.* On association between *C. albicans* and urogenital mycoplasmas. GV was reported to be rarely associated to coinfection (Djigma, 2008). *C. albicans*/*Enterococcus spp* was the most common coinfection (130 patients) in our study population followed by *GV*/*C. albicans* (122 patients). *Candida albicans* is the best-known species of the genus Candida found in 80.0% of the population as commensal species although it can cause opportunistic infections of the digestive and gynecological mucosa. Its coinfection with pathogens such as *Enterococcus spp*, *Streptococcus agalactiae*; *E. coli*; *Klebsiella pneumoniae* could lead to severe complications (Camacho-Gonzalez, 2013).

Resistance profile of strains isolated to antifungals (ATF) and antibiotics (ATB)

Sensitivity and resistance of yeast strains to ATF: A total of 1770 cases of yeasts were isolated with 1245 (35.9%) strains of *Candida albicans* and 525 (15.9%) cases of *Candida spp.* These antifungal strains gave us remarkable sensitivities to Nystatin, Econazole, Clotrimazole and Miconazole. The highest resistance was observed for Fluconazole, Miconazole and Amphotericin B. Nadembega *et al.* also reported a similar result with sensitivity of yeasts to Clotrimazole and the Econazole and resistance to Miconazole while Sanou and *al.* (2017); (2014) found a different result in Bobo-Dioulasso with sensitivity to Fluconazole and resistance to Nystatin and Miconazole (Sanou, 2014).

Sensitivity and resistance of bacteria strains to available ATB: In the present study beta-lactamases such as Amoxicillin, Ceftriazone and Ampicillins were found with the highest sensitivity against bacteria strains tested. *Enterococcus spp.* was sensitive to Ciprofloxacin; Kanamycin, Tetracycline; Erythromycin and the Colistin. However, as reported by Nadembega et *al. Enterococcus spp.* were found with a high resistance rate to Ceftriazone in our study population. This resistance is due to the hydrolysis of antibiotics by the sebeta-lactamases producing bacteria [26]. *Staphylococcus aureus* and *Staphylococcus spp.* were susceptible to Colistin and *Escherichia coli* to Ciprofloxacin and Colistin. Most of the previous studies reported antibiotic resistance which remain a public health concerns worldwide and especially in sub-Saharan Africa (Karou, 2012; Bere *et al*., 2009; Simpore, 2008; Bonfiglio, 2002). Although the retrospective collection of samples has some limit due to the missing data (for example we were not able to determine the most exposed social class to vaginal infections), this study give and overview on vaginal infections prevalence in women from Ouagadougou, Burkina Faso.

Conclusion

The present study which purposed to determine the prevalence of low genital tract infections in 4168 women attending gynecological consultation at HOSCO from 2015 to 2018, reports a frequency of 83.2 % of infected women. The main etiological agents were *C. albicans, C. spp*., *Gardnerella vaginalis*, and associated infections with bacteria such as: *Enterococci spp.*, *E. coli*, *Staphylococcus aureus* and *Staphylococcus spp.* were also found in this study. Women with low genital tract infections are at high risk of sexually transmitted diseases especially HIV infection. Our results also reported resistance of strains studied to some antibiotics and antifungals tested and suggest a combined action between health authorities for better management of patients as well as populations to avoid excessive used of unprescribed dugs in order to reduce antibiotic resistance.

Acknowledgement: Our sincere thanks to the patients who voluntary participated in this study and laboratory staff of Biomedical Laboratory of the Saint Camille Hospital of Ouagadougou for their assistance.

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