(International Print/Online Journal)

SJIF IMPACT FACTOR: 5.565
PUBMED-National Library of Medicine ID-101739732

ISSN (Print): 2209-2870
ISSN (Online): 2209-2862

International Journal of Medical Science and Current Research (IJMSCR)
Available online at: www.ijmscr.com
Volume 4, Issue 4, Page No: 261-265
July-August 2021

IJMSCR

Vulvovaginal candidiasis: The infection should explain itself

Zahraa Faisal Nama[1], Ali Abdul Hussein S. AL-Janabi[1], Hameedah Hadi AbdulWahid[2]
[1]Dept. of Microbiology, College of Medicine, University of Karbala, Iraq
Karbala Obstetrics and Gynecology Teaching Hospital, Karbala, Iraq[2]

***Corresponding Author:**
Professor Ali Abdul Hussein S. AL-Janabi
Dept. of Microbiology, College of Medicine, University of Karbala, Iraq

Type of Publication: Original Research Paper
Conflicts of Interest: Nil

Abstract

Vulvovaginal Candidiasis (VVC) is one of the common infections among women of reproductive age.It caused by different species of *Candida* than living as a member of the normal vaginal flora after the transition from harmless commensal to pathogenic fungi.Many predisposition factors associated with the host or fungi encourage the development of CVV. *C. albicans* and various species of non-albicans *Candida* are responsible for VVC.The VVC can be divided into two types depending on clinical characters; complicated and uncomplicated VVC. These two types differ in their symptoms, etiology and response to treatment. The diagnosis of VVC is mainly dependent on history of infection, clinical examination, and microbiological tests.

Keywords: NIL

INTRODUCTION

Various species of *Candida* situated as a normal flora commensalism in different sites of the human body such as skin and mucosal surfaces of nasal cavity, esophagus, gastrointestinal tract and vagina of healthy individuals [1-11]. Inducing excessive growth of *Candida* spp. through any disorder in the human body can promote it to become a pathogenic fungus and cause the infection called Candidiasis [1,7, 12-14]. Host disorders and virulence factors of *Candida* are all associated with developing candidiasis [2, 7, 9, 13, 15-17]. The abnormal host conditions and virulent factors of *Candida* are all associated with the onset of candidiasis [2, 7, 9, 13, 15-17]. One of the common types of candidiasis is vulvovaginal candidiasis (VVC), which develops in the lower genital tract of healthy women of childbearing age [12, 18-19]. The VVC affected millions of women annually and 75% of women once in their lives [20-23]. Many species of *Candida*, including *C. albicans* and non-albicans Candida (NAC), are responsible to the VVC [19]. *C. albicans* is the most causative agent of 90% of VVC [5, 18-20, 24-25]. Infection with NAC species has recently increased, especially by *C. glabrata*, *C. tropicalis*, *C. parapsilosis* and *C. krusei*[5, 21, 25]. The exact mechanism of VVC development is not clearly identified, but the infection can encourage by many predisposing factors such as pregnancy, uncontrolled diabetes, immunodeficiency, HIV infection, genetic, and long therapy with corticosteroids, antibiotics or estrogen oral contraceptive pills [12, 21, 23, 26]. The diagnosis of VVC depends mainly on three sequences: medical history, clinical characteristics and microbiological tests [27]. The main characters of VVC have been discussed in this review.

Candida infection

Many species of *Candida* living as saprophyte fungi and may form a commensalism relationship with humans through associated with other different normal flora in various parts of the human body such as skin, gastrointestinal tract, and mucous surfaces of nasal cavity, esophagus and vagina of healthy individuals

[1-11]. About 50% of population has *C. albicans* as a normal flora [9]. The growth of *Candida* spp. in humans is typically controlled by other microbiota, the human immune response, and layers of epithelial tissue [15]. This group of fungi has a potential ability to transition from innocuous fungi to pathogenic fungi under specific conditions causing numerous fungal infections called candidiasis in healthy and immunocompromised individuals [1,7, 12-14]. Thus, candidiasis considers a common type of opportunistic fungal infections worldwide [5, 9].

About 20 commensal species of *Candida* are capable of becoming pathogenic agents [12].*C. albicans*, which can isolate from 30-50% of healthy individuals, is the most common pathogenic species of *Candida* spp. since 1839 and responsible for different types of candidiasis [6, 12, 15-17, 26].Other pathogen species called Non-albicans Candida (NAC) comprise 19 species with six common pathogens; *C. parapsilosis*, *C. tropicalis*, *C. glabrata*, *C. krusei*, *C. guilliermondii* and *C. lusitaniae* [2, 6, 17, 28].The first five species together with *C. albicans* are responsible for 90-95% of invasive candidiasis [7, 29]. Depending on the level of the species, the incidence of candidiasis is a geographical variable between higher infection by *C. glabrata*in Asia-Pacific and the European Union and three times higher caused by *C. tropicalis*in Africa and the Middle East than in the European Union [29]. Clinical manifestations of NAC are similar to those of *C. albicans*, but differ in epidemiology, susceptibility to antifungal drugs and virulence factors [17].

Candida spp. can cause several types of infections in the human body ranging from minor candidiasis in the mucosal layers to sever life-threatening diseases such as candidemia as systemic infections [4-5,9, 12-13, 15, 17].*Candida* infection is common in immunocompromised patients with neutropenia as a result of immunosuppressive therapy or chemotherapy for cancer or organ transplantation [1,7, 12, 14, 15-16]. Other factors may also associate with Candidal infections such as long-term antibiotic treatment, long-term hospitalization, indwelling vascular or urinary catheters, abdominal surgery, diabetes, age, parenteral nutrition, and cancer [7, 9, 15-16]. In addition, *Candida* spp. has many virulence factors associated with increased pathogenicity such as the ability to adhere to host tissue, secretion of ectohydrolyases enzymes, and biofilm formation [9, 14]. However, the pathogenesis of *Candida*spp. depends principally on its virulence factors, the site of infection and the immune status of humans [2, 13, 17].

The filamentous forms (hyphae or pseudohyphae) are regarded as the infective stage of *Candida* spp., while the commensal stage is represented by the yeast form [16, 26]. Pathogenesis of *Candida* spp. usually starts with a change or transition from the yeast form to the hyphae [15]. Thus, *C. albicans*which has such a transition considers more pathogenic than NAC which have no hyphae form [30].

Vulvovaginal candidiasis

Vulvovaginal candidiasis (VVC) is one of the common fungal infections in the lower genital tract of healthy women of childbearing age [12, 18-19]. It affects millions of women annually and 75% of women once in a lifetime [20-23]. The infection is not lethal, but it leads to a high rate of morbidity, discomfort and pain with a health care cost [5]. Several species of *Candida* including *C. albicans* and NACare responsible for the development of VVC [19]. These species are normally found in the vagina as a member of the vaginal community which together with other natural vaginal flora represents less microbiota than that of the intestine [26]. External sources are also associated with increased density of *Candida* spp. in the genital tract, such as propagation from the perineum or gastrointestinal tract and sexual transmission [12]. However, the normal occurrence of *Candida* spp. in the vagina does not make VVC a sexually transmitted disease [24]. *C. albicans,* in the form of yeast, normally colonizes the genital tract of 10% to 55% of females of childbearing age and it can be isolated from 80% of VVC cases [12, 26]. It is most commonly yeast type causing 90% VCV [5, 18-20, 24-25]. VVC caused by NAC species is steadily increasing in current days, particularly by *C. glabrata, C. tropicalis, C. parapsilosis* and *C. krusei*[5, 21, 25].In general, NAC, especially *C. glabrata* cause less than 10% of all VVC cases [27]. In some cases, two species of *Candida* can be found in the same VVC caseas with *C. albicans* and *C. glabrata* and elimination of the sensitive one like *C. albicans* by treatment leading to leaving the resistance *C. glabrata* to cause infection [27].

There are two types of VVC; uncomplicated and complicated, with many differences between them [21, 25]. The uncomplicated VVC is characterized by mild to moderate severity with less than 4 episodes per

Volume 4, Issue 4; July-August 2021; Page No 261-265
© 2021 IJMSCR. All Rights Reserved

year and mainly caused by *C. albicans* [21, 25]. This type of infection makes up 90% of VVC cases [5]. Complicated VVC which accounted for 10% of VVC is characterized by severe clinical symptoms with more than 4 episodes per year and it is often due to NAC species in abnormal conditions such as diabetes [5, 21, 25]. The response of uncomplicated infection to topical and oral antifungal drugs available therapy mostly good and need low doses, while complicated is more difficult and needs more doses (7 to 14 days) to cure [5, 23-24].

The mechanism for VVC development by *Candida* spp. is not clear up to now. In general, it results from a disturbance of the balance of colonization of *Candida* spp. resulting from a change in the physiological, non-physiological or genetic factor of the host [20-21]. The presence of *Lactobacillus* spp. bacteria in the vagina has a role to play in regulating the growth of *Candida* spp. through its antimicrobial products such as hydrogen peroxide and lactic acid [31]. In addition, increased levels of glycogen in the vagina as a result of reproduction hormones may provide a source of carbon to promote overgrowing of *Candida* spp. [12]. This growth is primarily associated with the transition from harmless commensal yeast to the hyphae form which causes VVC [26].

Many predisposing factors contribute to the development of VVC, such as pregnancy, uncontrolled diabetes, immunodeficiency, HIV infection, genetic, long therapy with corticosteroids, antibiotics or estrogen oral contraceptive pills, intrauterine device, spermicides and condoms [12, 21, 23, 26]. The increase in VVC rates caused by NAC may be related to the increase in the use of over-the-counter antifungal drugs which are most often used inappropriately or as an incomplete course of treatment and all of which reduced normal susceptible *C. albicans* and increased NAC-resistant species [24-25, 32].

The diagnosis of VVC generally depends on several steps starting with medical history, then clinical characteristics and ending with microbiological tests [27]. The most common symptoms of VVC detected by clinical examination are whitish or curd like discharge without odor, grey-white pseudomembrane, epithelial erythema (eczematoid dermatitis), itching with swelling of labia and vulva, and burning [12, 24, 27, 33]. The pH value of vaginal discharge is also important for differentiating Candidal infection from bacterial or parasitic infection, where the pH value of more than 4.7 may rule out fungal infection [22].Microscopic examination of the wet smear of the vagina may help identify 50% to 80% of cases by observing the form of yeast or hyphae, while any uncertain diagnosis can be confirmed by culturing a vaginal specimen on special fungal media such as SDA [22-24, 27].Serology tests are not significant in the diagnosis of VVC due to low levels of specific antibodies [27].

In conclusion; understanding the global distribution of VVC needs obtaining adequate information on the disease type, the etiologic agent and effective diagnosis. This is important in reducing disease progression. Predisposing factors for VVC should be monitored with historical determination of the number of episodes.

References:

1- Ciurea CN, Kosovski I, Mare AD, Toma F, Pintea-Simon IA, Man A. *Candida* and candidiasis-opportunism versus pathogenicity: a review of the virulence traits. Microorganisms. 2020, 8, 857. DOI:10.3390/microorganisms8060857.

2- Moris DV, Melhem MSC, Martins MA, Mendes RP. Oral *Candida* spp. colonization in human immunodeficiency virus-infected individuals. J Venom Anim Toxins Incl Trop Dis. 2008, 14:224-257.

3- Gow NAR, van de Veerdonk FL, Brown AJP, Netea MG. *Candida albicans* morphogenesis and host defence: discriminating invasion from colonization. Nat Rev Microbiol. 2013, 10:112-122.

4- Molero G, Díez-Orejas R, Navarro-García F, Monteoliva L, Pla J, Gil C, Sánchez-Pérez M, Nombela C. *Candida albicans*: genetics, dimorphism and pathogenicity. International Microbiol. 1998, 1:95-106.

5- Dabas PS. An approach to etiology, diagnosis and management of different types of candidiasis. J Yeast and Fungal Research. 2013, 4:63-74.

6- Hameed AR, Ali SM, Ahmed LT. Biological study of *Candida* species and virulence factor.

Volume 4, Issue 4; July-August 2021; Page No 261-265
© 2021 IJMSCR. All Rights Reserved

International J Advanced Research in Engineering & Technology. 2018, 1:8-16.

7- Dadar M, Tiwari R, Karthik K, Chakraborty S, Shahali Y, Dhama K. *Candida albicans*-biology, molecular characterization, pathogenicity, and advance in diagnosis and control-a update. Microbial Pathogenesis. 2018, 117:128-138.

8- Sardi JCO, Scorzoni L, Bernardi T, Fusco-Almeida AM, Giannini MJS. *Candida* species: current epidemiology, pathogenicity, biofilm formation, natural antifungal products and new therapeutic options. J Med Microbiology. 2013, 62:10-24.

9- Talapko J, Juzbašić M, Matijević T, Pustijanac E, Bekić S, Kotris I, Škrlec I. *Candida albicans*-the virulence factors and clinical manifestations of infection. J Fungi. 2021, 7, 79. DOI.org/10.3390/jof7020079.

10- Sudbery PE. Growth of *Candida albicans* hyphae. Nature Review: Microbiology. 2011, 9:737-748.

11- Bhattacharya S, Sae-Tia S, Fries BC. Candidiasis and mechanisms of antifungal resistance. 2020, 9, 312. DOI:10.3390/antibiotics9060312.

12- Surain P, Aggarwal NK. *Candida*, a human pathogen and major types of candidiasis. International J Pharmaceutical Sciences and Research. 2020, 11:41-67.

13- Kabir MA, Hussain MA, Ahmad Z. *Candida albicans*: a model organism for studying fungal pathogens. ISRN Microbiology. 2012, ID 538694. DOI:10.5402/2012/538694.

14- Deorukhkar SC, Roushani S. Virulence traits contributing to pathogenicity of *Candida* species. J Microbiology & Experimentation. 2017, 5. 00140. DOI: 10.15406/jmen.2017.05.00140.

15- Höfken T. *Candida* and candidiasis. Chapter 5, Microbial Pathogenesis: Infection and Immunity. Edit Uday Kishore and Annapurna Nayak. Published by Landaes Bioscience and Springer Science + Business Media. New York. 2013, pp: 82-114.

16- Noble SM, Gianetti BA, Witchley JN. *Candida albicans* cell-type switching and functional plasticity in the mammalian host. Nature Reviews: Microbiology. 2016, 15:96-108.

17- Deorukhkar SC, Roushani S. Identification of *Candida* species: conventional methods in the era of molecular diagnosis. Ann Microbiol Immunol. 2018, 1,1002:1-6.

18- Sustr V, Foessleitner P, Kiss H, Farr A. Vulvovaginal candidosis: current concepts, challenges and perspectives. J Fungi. 2020, 6, 267. DOI:10.3390/jof6040267.

19- Willems HME, Ahmed SS, Liu J, Xu Z, Peters BM. Vulvovaginal candidiasis: a current understanding and burning questions. J Fungi. 2020, 6, 27. DOI:10.3390/jof6010027.

20- Rosati D, Bruno M, Jaeger M, Oever JT, Netea MG. Recurrent vulvovaginal candidiasis: an immunological perspective. Microorganisms. 2020, 8, 144. DOI:10.3390/microorganisms8020144.

21- Gonçalves B, Ferreira C, Alves CT, Henriques M, Azeredo J, Silva S. Vulvovaginal candidiasis: epidemiology, microbiology and risk factor. Crit Rev Microbiol. 2016, 42:905-927.

22- Lema VM. Recurrent vulvo-vaginal candidiasis: diagnostic and management challenges in a developing country context. Obstet Gynecol Int J. 2017, 7:00260. DOI: 10.15406/ogij.2017.07.00260.

23- Dovnik A, Golle A, Novak D, Arko D, Takač I. Treatment of vulvovaginal candidiasis: a review of the literature. Acta Dermatovenerol APA. 2015, 24:5-7.

24- Sobel JD, Faro S, Force RW, Foxman B, Ledger WJ, Nyirjesy PR, Reed BD, Summers PR. Vulvovaginal candidiasis: epidemiologic, diagnostic, and therapeutic considerations. Am J Obstet Gynecol. 1998, 178: 203-211.

25- Fidel PL, Vazquez JA, Sobel JD. *Candida glabrata*: review of epidemiology, pathogenesis and clinical disease with comparison to *C. albicans*. Clin Microbiol Rev. 1999, 12:80-96.

Volume 4, Issue 4; July-August 2021; Page No 261-265
© 2021 IJMSCR. All Rights Reserved

26- Cassone A. Vulvovaginal *Candida albicans* infections: pathogenesis, immunity and vaccine prospects. BJOG. 2015, 122:785-794.

27- Mendling W. Guideline: Vulvovaginal candidosis (AWMF 015l072). S2k (excluding chronic mucocutaneous candidosis). Mycoses. 2015, 58:1-15.

28- Wiederhold NP. Antifungal resistance: current trends and future strategies to combat. Infection and Drug Resistance. 2017, 10:249-259.

29- Turner SA, Butler G. The *Candida* pathogenic species complex. Cold Spring Harb Perspect Med. 2014, 4:a019778:1-17.

30- Kadosh D, Mundodi V. A re-evaluation of the relationship between morphology and pathogenicity in *Candida* species. J Fungi. 2020, 6, 13. DOI:10.3390/jof6010013.

31- Ramírez-Lozada T, Espinosa-Hernández VM, Frías-De-León MG. Update of vulvovaginal candidiasis in pregnant and non-pregnant patients. Curr Fungal Infect Rep. 2019, 13:181-190.

32- Sheary B, Dayan L. Recurrent vulvovaginal candidiasis. Australian Family Physician. 2005, 34:147-150.

33- Willems HME, Ahmed SS, Liu J, Xu Z, Peters BM. Vulvovaginal candidiasis: a current understanding and burning questions. J Fungi. 2020, 6, 27. DOI:10.3390/jof6010027.

Volume 4, Issue 4; July-August 2021; Page No 261-265

© 2021 IJMSCR. All Rights Reserved