

BACTERIOLOGICAL STUDY OF VAGINAL FLORA IN MOTHERS AT TERM

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ABSTRACT

The female genital tract is a complex ecosystem containing an abundance of microorganisms. The composition of the vaginal flora is not constant, suffering variations in response to exogenous and endogenous factors. The vaginal microflora appears to be so critical to health and disease. In cases of recurrent UTI the dominant organisms are the uropathogens, generally *Escherichia coli*; in recurrent bacterial vaginosis, these are anaerobic Gram negative rods, generally *Gardnerella vaginalis*. *Lactobacillus acidophilus* was the dominant member of a healthy vaginal microflora. Samples were collected by a trained faculty of Dept. of Obstetrics & Gynaecology. Sample processing and Identification of bacteria were done by standard

procedures. Most commonly isolated aerobic bacteria was CoNS (43.4%) and anaerobic bacteria was *Bacteroides fragilis* (26%). Most common pathogenic bacterial isolate was *Staphylococcus aureus* (42%)

Key Words: Vaginal microflora, *Bacteroides fragilis*, CoNS, Anaerobic Culture.

INTRODUCTION

The female genital tract is a complex ecosystem containing an abundance of microorganisms. The healthy vaginal flora in reproduction age is usually predominant by *Lactobacillus* species, a genus of Gram-positive, non-motile rod-like bacteria. Vaginal microbiota protects the mucosa against the establishment of pathogenic microorganisms through complementary mechanisms: specific adherence to the epithelium which blocks colonization of pathogens, production of antimicrobial compounds and co aggregation with pathogens [1].

In a fertile woman, the desquamated vaginal epithelial cells release glycogen, which supplies the main bacteria (*Lactobacillus*) with nutrients. These bacteria degrade glycogen and create an acidic environment, which restricts the growth of pathogenic microorganisms [2]. Thus, at fertile age the normal pH in the vagina ranges from 3.5 to 4.5, with a typical value of 4.2 [3]. The vaginal secretion also contains antimicrobial components of the immune system and leukocytes [4, 5].

One of the difficulties found for a broader characterization of the vaginal microbial flora is the presence of biofilms. Biofilms are formed by colonies of microorganisms that adhere among themselves and cover a solid surface. Biofilms have already been identified in the surface of vaginal cells, more known in women with bacterial vaginosis, where species of *Gardnerella vaginalis* and *Atopobium* predominate [6].

Possible racial/ethnic differences in the composition of the 'normal' microflora of the vagina have also not received appropriate research attention. The occurrence of hydrogen-peroxide-producing lactobacilli, purportedly active in antimicrobial defense is lower in black women. It has been reported that the vaginal pH of Black women is higher than that of White women among subjects who were not diagnosed as having bacterial vaginosis.

The composition of the vaginal flora is not constant, suffering variations in response to exogenous and endogenous factors. These factors include the different phases of the menstrual cycle, gestation, use of contraceptives, frequency of sexual intercourse, use of showers or deodorant products, use of antibiotics or other medications with immune-suppressive properties. For example, studies have related the loss of *Lactobacillus* to sexual intercourse or to the use of antibiotics. Nevertheless, another study has demonstrated that the sexual act without the use of condom had no effects upon the *Lactobacillus*, but increased the level of *Escherichia coli* and facultative gram- negative bacilli [7].

The vaginal microflora appears to be so critical to health and disease. In cases of recurrent UTI the dominant organisms are the uropathogens, generally *Escherichia coli*; In recurrent bacterial vaginosis, these are anaerobic Gram negative rods, generally *Gardnerella vaginalis*. *Lactobacillus acidophilus* was the dominant member of a healthy vaginal microflora; *Lactobacillus crispatus*, *Lactobacillus iners* most commonly isolated organism [8].

Among the anaerobic bacteria, Peptostreptococci and Bacteroides species were the dominating ones whereas the coagulase negative staphylococci were the most prevalent aerobic bacteria.^[5] Enterococcus faecalis, Escherichia coli and Staphylococcus epidermidis were the bacteria found in the pregnant women [9].

MATERIALS AND METHODS

This study was conducted over a period of 1 year, from February 2011 to January 2012. Total 69 pregnant women were included in this study. Two vaginal swabs were collected, by a trained faculty of Dept. of Obstetrics & Gynaecology, from the pregnant women at term for aerobic and anaerobic culture and were placed in aerobic and anaerobic Cary- Blair transport medium respectively. Samples were inoculated on different culture media i.e. Blood agar, MacConkey agar, Chocolate agar and Anaerobic Blood agar plates and incubated aerobically at 37°C for 24-48 hours except Anaerobic Blood agar plates, which were incubated in anaerobic jar using GasPak system. Identification of bacteria was done by Gram Staining and different standard biochemical tests [11, 12].

RESULTS

A total of 69 women fulfilled the criteria of full term birth. Specimens were obtained from vagina just after the delivery of the baby. Women were divided into two categories, the first category included women who underwent Normal vaginal delivery (NVD) and the latter included lower section caesarean section (LSCS). The age of the volunteers ranged from 18 – 32 years.

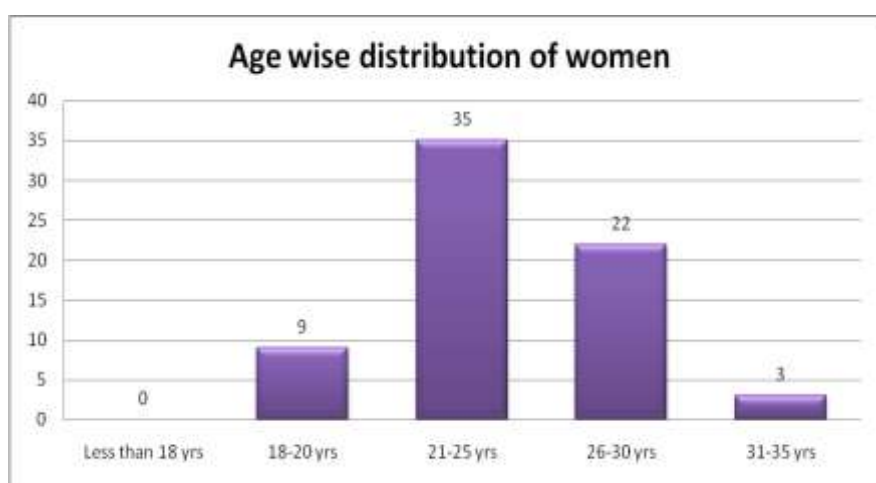


Fig 1: Age wise distribution of women in the study.

Out of total 69 women, 49 underwent NVD and 20 underwent LSCS. A total 246 bacteria were isolated from 69 samples. Out of which, 174 were aerobes and 72 were anaerobes.

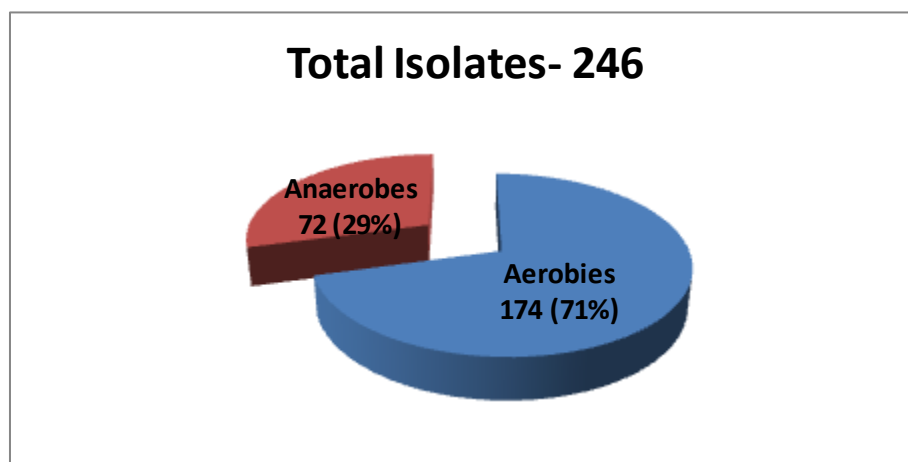


Fig 2: Distribution of aerobic and anaerobic bacterial isolates.

Table 1: Table showing number various aerobic organisms from vaginal swabs in NVD and LSCS cases.

S. No	Organism Isolated	NVD Samples n=49	LSCS Samples n=20	Total Samples n=69	%age n=174	%age n=69
1	CoNS	21	9	30	17.2	43.4
2	Staphylococcus aureus	19	10	29	16.6	42.0
3	Escherichia coli	13	7	20	11.4	28.9
4	Streptococcus spp.	12	3	15	8.6	21.7
5	Citrobacter diversus	11	3	14	8.04	20.2
6	Micrococci	0	0	0	0	0
7	Klebsiella Spp.	10	0	10	5.7	14.4
8	Acinetobacter spp.	9	2	11	6.3	15.9
9	Diphtheroids	8	2	10	5.7	14.4
10	GNNF	4	2	6	3.4	8.6
11	Enterococcus spp.	10	2	12	6.8	17.3
12	Enterobacter aerogenes	3	1	4	2.2	5.7
13	Bacillus spp.	1	0	1	0.5	1.4
14	Citrobacter spp.	2	1	3	1.7	4.3
15	Pseudomonas spp	3	1	4	2.2	5.7
16	Klebsiella pneumonia	5	0	5	2.8	7.2
Total		131	43	174		

Table 2: Table showing number various anaerobic organisms from vaginal swabs in NVD and LSCS cases.

S. No	Organism Isolated	NVD Samples n=49	LSCS Samples n=20	Total Samples n=69	%age n=72	%age n=69
1	Bacteroides fragilis	12	6	18	25.0	26.0
2	Porphyromonas spp.	11	5	16	22.2	23.1
3	Prevotella spp.	10	3	13	18.0	18.8
4	Veillonella	7	4	11	15.2	15.9
5	Peptostreptococcus spp.	5	1	06	8.3	8.6
6	Propionibacterium spp.	5	0	05	6.9	7.2
7	Bifidobacterium spp.	3	0	03	4.1	4.3
Total		53	19	72		

Table 3: Number of pathogenic organisms isolated from vaginal swabs from NVD and LSCS cases.

Pathogenic organisms	NVD Cases (n = 49)	LSCS Cases (n = 20)	Total
Staphylococcus aureus	19	10	29
Escherichia coli	13	07	20
Citrobacter diversus	11	03	14
Klebsiella spp.	10	00	10
Klebsiella pneumonia	05	00	05
Enterobacter aerogenes	03	01	04
Citrobacter spp.	02	01	03
Total	63	22	85

DISCUSSION

In the present study, a total of 69 women fulfilled the criteria of full term birth. Specimens were obtained from vagina just after the delivery of the baby. Women were divided into two categories, the first category included women who underwent Normal vaginal delivery (NVD) and the latter included Lower segment Caesarean section (LSCS). The age of the volunteers ranged from 18 – 32 years and majority of the women were in the age group of 21 – 25 years.

The quality and quantity of the cultivable microflora varies and changes from site to site, but in general the types of bacteria that colonise the various anatomical sites are remarkably consistent.

Gram staining of the swabs revealed the most abundant organism as Gram positive cocci in both NVD & LSCS samples. The Gram positive bacilli morphologically resembled *Lactobacillus* spp. Majority of the smears showed epithelial cells, scanty pus cells and predominance of thick GPB. None of the samples showed the presence of 'Clue cells'.

Staphylococcus aureus (16.6%), Coagulase negative staphylococci (17.2%) and *E.coli* (11.4%) were isolated from vaginal swabs in both NVD and LSCS cases. This observation was similar to the study of Shabeen Naz et.al where in they observed the most common organism found in vagina was *E.coli* (16.3%) followed by CONS (9.5%) [13].

It can be understood that the majority of pathogens were isolated from women with normal vaginal delivery when compared with women who had undergone Caesarean. *S.aureus*, *E.coli* and *Citrobacter diversus* were isolated in highest frequency in both the cases. This can be correlated with the study done by Manigeh et.al. The group found *S.aureus* and *E.coli* to be predominant pathogens in vagina [14].

In a study done by I.J Slotnick et.al, highest number of organism isolated from vaginal sample was *Enterococcus* (49.36%) followed by *Streptococcus* (24.05%) and *E.coli* (11.39%). However in the present study CONS (43.4%) was isolated in the most samples which was followed by *S.aureus* (42.0%) and *E.coli* (29.8%) in the vaginal samples [15].

In the study done by Catherine M. Corbishley highest number of organism isolated from vaginal sample was CONS (89%) followed by Diphtheriods (69%) and *S.aureus* (17%). However in the present study Diphtheriods were isolated in 14.4% of the vaginal samples [16]. Result of this study was also supported by a study done by A N Masfari et.al, who reported that highest number of organism isolated from vaginal sample was CONS (59%) followed by *Streptococcus* (41%).

The observation and results obtained in this study has allowed a detailed understanding of the microbial flora present in the vagina of the women soon after delivery. Identification of potential pathogens will help in appropriate treatment such that intranatal and postnatal infections in the new born child can be prevented.

CONCLUSION

Staphylococci , *streptococci* , diphtheriods ,and anaerobes seem to be common inhabitants of the normal as well as of the diseased vaginal tract .Other pathogens like *Psuedomonas* Spp.,

Klebsiella pneumonia were also grown in many samples. While in case of anaerobic organism, Bacteroides fragilis frequently found from the vaginal region.

Both patients and clinicians can incorrectly interpret the symptoms of vaginitis and patients often indulge in self medication with over the counter medications or home remedies for treatment, which can lead to many dangerous medical outcomes.

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