
“STUDY OF VAGINAL MICROBIOME IN WOMEN ADMITTED FOR DELIVERY TO A TERTIARY CARE HOSPITAL”

Thesis Submitted to
KLE ACADEMY OF HIGHER EDUCATION AND RESEARCH
(Deemed-to-be -University)

[Declared as Deemed-to-be-University u/s 3 12B of the UGC Act, 1956 vide
Govt. of India Notification No.F.9-19/2000-U.3 (A)]

Accredited ‘A⁺’ Grade by NAAC (3rd Cycle)

Placed in Category ‘A’ by MoE (GoI)



**For the award of the degree of
Doctor of Philosophy
In the Faculty of Nursing**

By

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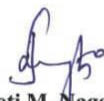
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ACKNOWLEDGMENT

“As with all commandments, gratitude is a description of a successful mode of living. The thankful heart opens our eyes to a multitude of blessings that continually surround us.” – James E. Faust

Many people have blessed me and generously offered their assistance, which has helped me complete this thesis project effectively. I would particularly like to take this opportunity to express my gratitude to everyone who has helped with this project.

I want to thank **Almighty God**, the greatest teacher of all, first and foremost. I promise to always remember how fortunate I am to be here, even though it comes with a responsibility and a lesson.

I am thrilled to formally thank my research guide, **Dr. Sangeeta N. Kharde**, Dean and Professor of KAHER Institute of Nursing Sciences, Belagavi, for her essential support in helping me finish my study work. It is an honour for me to serve under her excellent leadership. I will be indebted to her forever.

With great pleasure, I would like to convey my sincere appreciation to my research co-guide, **Dr. Anita Dalal**, Professor in the Department of Obstetrics and Gynaecology at JNMC, Belagavi, for her guidance and insightful advice.

I would like to extend my sincere gratitude to **Dr. Sudha A. Raddi**, Assistant Professor, Ministry of Education, University of Bisha, College of Applied Medical Sciences, Kingdom of Saudi Arabia for her guidance in the research work.

I would like to extend my sincere gratitude to **Dr. Suneel Dodamani, Scientist –I, Dr. Prabhakar Kore’s Basic Science Research Center** and all the staffs of BSRC

who have directly and indirectly extended a big help and kind support during my research work.

I would like to extend my sincere gratitude to **Dr. Tyagi** and **Dr. J B Prasad**, **former faculties of** Department of Epidemiology and Biostatistics, KAHER JNMC, Belagavi; additionally, I would like to thank Dr. Javali, Professor in the Department of Epidemiology and Biostatistics at KLE-USM, Belagavi, for the careful and patient assistance with the statistical work that was required for the study.

I am grateful for the administrative assistance provided by **Dr. Nitin Gangane**, the Honourable Vice Chancellor of KAHER, **Dr. V. A. Kothiwale**, the Registrar, and **Dr. N. S. Mahantshetti**, the Dean of the Faculty of Medicine of KAHER.

I am extremely grateful to **Professor (Dr.) Daksha Dixit**, Former Director Academic Affairs, and **Dr. Roopa Bellad**, Director Academic Affairs, KAHER, Belagavi for her patience, encouragement and support.

I sincerely thank Prof. Veereshkumar Nandagaon, Principal of KAHER INS, Belagavi, for serving as a role model and for the unwavering encouragement, professional counsel, and assistance. I would like to express my special gratitude to my colleagues **Asha mam, Shubharani mam, Nirmala mam, Uma Mam, Babita and Shweta** for their insightful comments and encouragement.

I wish to sincerely thank **Dr. Sheela Podar**, labor room In-charge, **Sister Mariyamma and Sister Malashree**- of labor room for the help rendered during the sample collection which enabled me to complete the assignment.

The support and unwavering faith of my parents, **Heikham Omor Singh** and **Heikham Sanayaima Devi**, my husband- **Anand Patil**, my sister- **H. Amita Devi**, my

brothers, **H. Somendro Singh and H. Jonathan Singh**, and my son- **Vivaan**, have lifted a heavy burden off my shoulders. Words cannot express how much I appreciate them. I would like to express my sincere gratitude to **Ms. Shivani Tendulkar** for her unwavering support, direction, inspiration, and assistance in getting my work done on schedule.

Words cannot express how appreciative I am that all of you have stood by me with love and support without condition.

Mrs. Heikham Gineta Chanu

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ABBREVIATIONS

Sr. No	Abbreviations	Expanded forms
1.	HIV	Human immunodeficiency virus
2.	SRS	Sample Registration System
3.	NICU	Neonatal Intensive Care Unit
4.	HDP	Hypertensive Disorders of Pregnancy
5.	LBW	Low Birth Weight
6.	BP	Blood Pressure
7.	ANC	Antenatal Care
8.	CI	Class Interval
9.	GHTN	Gestational Hypertension
10.	ACOG	American College of Obstetricians and Gynaecologists
11.	RR	Relative risk
12.	PCR	Polymerase Chain Reaction
13.	PTB	Pre-Term Birth
14.	HTN	Hypertension
15.	PE	Pre Eclampsia
16.	NFHS	National Family Health Survey
17.	CI	Confidence Interval
18.	AOR	Adjusted Odds Ratio

19.	ICU	Intensive Care Unit
20.	FGR	Fetal Growth Retardation
21.	OR	Odds Ratio
22.	GDM	Gestational Diabetes mellitus
23.	HTN	Hypertension
24.	ANC	Antenatal Care
25.	VLBW	Very Low Birth Weight
26.	CINAHL	Cumulated Index To Nursing And Allied Health Literature
27.	RR	Risk Ratio
28.	IEC	Institutional Ethical Committee
29.	EMBASE	Excerpta Medica Database
30.	PIH	Pregnancy Induced Hypertension
31.	ARR	Adjusted Risk Ratio
32.	RCT's	Randomized controlled trials
33.	ANC	Antenatal Care
34.	DM	Diabetes Mellitus
35.	GDM	Gestational Diabetes Mellitus
36.	CHC	Community Health Centre
37.	LSCS	Lower Segment Caesarean Section
38.	APGAR	Appearance, Pulse, Grimace, Activity, And Respiration
39.	ARDS	Acute Respiratory Distress Syndrome

40.	FGM	Fetal Growth Monitoring
41.	IVF	In Vitro Fertilization
42.	CHTN	Chronic Hypertension
43.	MNH	Maternal And Newborn Health Registry
44.	KLES	Karnataka Lingayat Education Society
45.	IMVIC	Indole, Methyl red, Voges Proskauer and Citrate test
46.	CST	Community State Types
47.	PTDW	Pre term delivered women
48.	TDW	Term delivered women
49.	SPTB	Spontaneous Preterm Birth
50.	IL	Interleukin
51.	TNF-alpha	Tumor necrosis factor alpha
52.	PcoA	Principal Co-ordinate Analysis
53.	ds DNA	Double stranded Deoxyribonucleic acid
54.	ssDNA	Single stranded Deoxyribonucleic acid
55.	EONS	Early onset neonatal sepsis
56.	BV	Bacterial vaginosis
57.	AV	Aerobic vaginitis
58.	PROM	Premature Rupture of Membrane
59.	PPROM	Pre-labour Premature Rupture of Membrane
60.	rDNA	Recombinant Deoxyribonucleic acid

61.	PCAM	Predictive Chorioamnionitis
62.	AVF	Aberrant Vaginal flora
63.	RNA	Ribonucleic acid
64.	MRS	Man, Rogosa and Sharpe
65.	mt DNA	Mitochondrial Deoxyribonucleic acid
66.	qPCR	Quantitative PCR
67.	HPV	Human Papillomavirus
68.	NG	Neisseria Gonorrhoea
69.	CT	Chlamydia trachomatis
70.	TV	Trichomonas Vaginalis
71.	MG	Mycoplasma genitalium
72.	VMB	Vaginal Microbiome
73.	Hsp	Heat Shock protein
74.	VMTs	Vaginal microbiota transplants
75.	QIIME	Quantitative Insights Into Microbial Ecology
76.	QIAGEN	Quality, Ingenuity and Accessibility-Germany
77.	NMDS	Non- metric multi-dimensional scaling
78.	INSPIRE project	Innovation in Science Pursuit for Inspired Research Project
79.	GAS	Group A Streptococcal infection
80.	ddNTPs	dideoxynucleoside tri- phosphates
81.	dNTPs	deoxy-nucleotide triphosphates

82.	ddATP	2',3'- Dideoxyadenosine 5'- triphosphate
83.	ddTTP	dideoxythymidine 5'-triphosphate
84.	ddGTP	2', 3'- Dideoxyguanosine 5'-triphosphate
85.	ddCTP	2', 3' – Dideoxycytidine 5'-triphosphate

ABSTRACT

Background: The adverse outcome of pregnancy either on the mother or fetus remains to be still high despite improvements in healthcare services. This is due to various factors including medical, environmental or socio-economic factors. Vaginal microbiome is the micro organism which colonizes the vagina and plays an important role in health and disease state of women. The microbiome starts to develop from uterus and is further influenced by various factors like timing of birth, environmental exposures, diet, inflammatory immune responses, clinical infection, sexual and hygiene practices. Bacterial vaginosis, a condition where normal vagina flora is replaced by anaerobic bacteria. is present in about 20% of pregnant women and majority of them are asymptomatic. It is associated with premature rupture of membranes, preterm delivery, chorioamnionitis and intra uterine death. It also leads to adverse neonatal outcomes like assisted ventilation or respiratory distress at birth, neonatal Intensive care unit admission, fetal and infant mortality, neonatal sepsis, chronic lung disease and delayed development.

Objective of the study: To study the vaginal microbiome in women admitted for delivery beyond 28 weeks of gestational age and its outcome on mother and immediate newborn.

Methods: The study design adopted for the present study is case series research design. Using the consecutive sampling technique, 300 mothers were included in the study. Participants were selected based on the inclusion criteria like all mothers with or more than 28 gestational weeks delivering in tertiary care hospitals of Belagavi city. Data was collected by using tools on socio-demographic profile and questionnaire on Maternal and neonatal health outcome. Data was analyzed by using descriptive statistics, Chi-square test and multiple logistic regression analysis.

Vaginal swabs were collected from posterior vaginal fornix and placed in a sterile tube and immediately stored at -70°C until assayed. The swabs were streaked on MRS agar plate and incubated at 37°C in anaerobic chamber for 24 hours. Biochemical test (Gram staining and IMViC test) was performed for the samples followed by DNA extraction using QIAamp® DNA Mini Kit. After the amplification, the samples were analyzed by Sanger Sequencing.

Results: Gram staining was performed for all the samples followed by IMVIC test. Out of all samples, **106** were Voges-Proskauer test positive and **69** were citrate test positive. In the study, 18 samples (6%) were gram negative and 282 samples (94%) were gram positive. After identifying the samples with similar characteristics, representatives were selected for DNA isolation and then sanger sequencing was performed. The result showed that the women who had full term delivery showed more abundance of *L. crispatus* (39.3%), *L. jensenii* (27.8%), *L. iners* (26.3%), *Bacillus cereus* (6.6%); and the women who had preterm delivery showed the presence of *Lactobacillus iners* (48.8%), *L. Gasseri* (7.3%), *Atopobium vaginae* (4.9%) and *Enterococcus faecalis* (39%).

Among the 300 respondents, majority (47%) of the mothers belongs to the age group of 24-29 years, 79% of them are Hindu, 48.67% have completed Pre-University Course, 98.33% are home maker, 67.33% had a non consanguineous marriage and 62.33% are non vegetarian. In the study, 62.33% had vaginal delivery, 58% were primipara and 52.67% of them were pregnant for the first time.

The study found a significant association between the age and education level of the mother along with maternal and neonatal outcome; there was no significant association between the gestational age (Preterm and term) with demographic

characteristics. Multiple logistic regression analysis showed that women who had delivered vaginally, those pregnant for the third time have good maternal outcome and women who had 11-13 antenatal visits have good neonatal outcomes. Also, women with either maternal or fetal conditions have equal chance of undergoing Cesarean section. Birth weight and length of the baby is associated with the gestational age of the mother at the time of delivery.

Conclusion: Early diagnosis of bacterial vaginosis and aerobic vaginitis in pregnancy may help to identify women at risk of developing premature labour who could benefit from measures aimed at recreating a normal vaginal flora. To determine whether treating vaginal dysbiosis in asymptomatic pregnant women will significantly affect the start of premature labour, a large population study will be required. The study suggests imparting awareness towards health care professionals and all women of reproductive age group regarding the importance of maintaining healthy vaginal microbiome. The study gives a overview of the relationship between the socio-demographic characteristics of the women and the maternal and neonatal outcome. This study will also help in preventing the adverse maternal and neonatal outcome by encouraging to identify it at the earliest.

Keywords: Vaginal microbiome, Full term labour, preterm labour, low birth weight, childbirth, Maternal Outcome, Neonatal Outcome, Preterm Birth, Associations.

TABLE OF CONTENT

SR. NO	PARTICULARS	PAGE NO
1	INTRODUCTION	1-9
2	REVIEW OF LITERATURE	10-42
3	MATERIALS AND METHOD	43-56
4	DATA ANALYSIS AND RESULT INTERPRETATION	57-94
5	DISCUSSION	95-99
6	CONCLUSION	100-105
7	SUMMARY	106-108
8	BIBLIOGRAPHY	109-123
9	ANNEXURES	124-183

LIST OF TABLES

SR. NO	PARTICULARS	PAGE NO
1	Primers used for sequencing the DNA molecule	53
2	Steps of PCR Amplification	53
3	Biochemical Test for selected samples	58
4	Biochemical Test Result	59
5	PCR amplification result	65
6	Maternal characteristics of respondents	78
7	Association between socio demographic variables with maternal and neonatal outcome	79-80
8	Association between gestational age (Preterm and term) with demographic characteristics	83-84
9	Multiple logistic regression analysis of gestational age by maternal outcomes	85
10	Multiple logistic regression analysis of gestational age by neonatal outcomes Table 10 Multiple logistic regression analysis of gestational age by neonatal outcomes	87

11	Multiple logistic regression analysis of gestational age by other parameters	90
12	Comparison of gestational age (Preterm and term) with birth weight, head circumference, chest circumference and length by independent t test	92
13	Comparison of gestational age (Preterm and term) with APGAR scores at 1 min and 5 min by independent t test	94

LIST OF FIGURES

SR. NO	PARTICULARS	PAGE NO
1	Conceptual Frame work	9
2	Flow chart of data collection procedure	56
3	Gram Staining and IMVIC test	59
4	16SrRNA amplicon of selected samples	62
5	Sanger sequencing graph of selected samples	63-64
6	Phylogenetic tree analysis for <i>Lactobacillus iners</i>	66
7	Phylogenetic tree analysis for <i>Lactobacillus crispatus</i>	67
8	Phylogenetic tree analysis for <i>Lactobacillus jensenii</i>	68
9	Phylogenetic tree analysis for <i>Lactobacillus gasseri</i>	69
10	Phylogenetic tree analysis for <i>Atopobium vaginae</i>	70
11	Phylogenetic tree analysis for <i>Bacillus cereus</i>	71
12	Phylogenetic tree analysis for <i>Enterococcus faecalis</i>	72
13	Phylogenetic tree analysis for <i>Pantoea</i> species	73

LIST OF GRAPHS

SR. NO	PARTICULARS	PAGE NO
1	A pie graph showing percentage distribution of age of the mother.	74
2	A doughnut graph showing percentage distribution of age of the mother.	74
3	A column graph showing percentage distribution of educational level of the mother.	75
4	A column graph showing percentage distribution of occupation of the mother.	75
5	A bar graph showing percentage distribution of type of marriage of the mother.	76
6	A pie graph showing percentage distribution of age of the mother.	76

CHAPTER I

INTRODUCTION

Background: Reproductive health of women is important not only for her health but also for her partner/husband and child. Bacterial infections may affect the pregnant women from the time of implantation of fertilized ovum till delivery and also during postpartum period.¹

Pregnancy is a process where various changes takes place in the system in order to provide support for the growth of the unborn child including endocrine, metabolic and immune system where there is changes in the microbiome in the body during pregnancy.²

The content of the vaginal organisms affects the gestation. Thirty percent spontaneous premature childbirth are due to pre- term pre- labor rupture of membrane (PPROM), linked to increase in the bacterial communities in the vagina before its rupture.³

Vaginal bacteria is greatly impacted the host's age, menstruation, race/ethnicity, genetics, food, sexual activity, smoking, and other factors.⁴

The bacterial vaginal microbiome changes in structure during pregnancy. The vaginal microbiome's structure and makeup during pregnancy may make unfavourable pregnancy outcomes more common. Premature birth, group A streptococcal infection (GAS), and neonatal infections are the most frequent consequences.⁵

The nature of vaginal microbiota frequently influences the health of women and the result of pregnancy. This microbiota is a dynamic ecosystem made up of numerous bacteria in varying amounts and ratios that can either cause or protect the vaginal epithelium from various vaginal disease.⁶

PPROM linked to dysbiosis of the vagina, accounts for as much as one-third of preterm deliveries. Infection, inflammation, and successive ascending colonisation can cause important newborn morbidity, such as early-onset neonatal sepsis (EONS).⁷

Preterm birth is primarily caused by contamination of the reproductive system, most prevalent microorganisms causing this globally are *Fusobacterium* species, *Gardnerella vaginalis*, *Mycoplasma hominis*, *Ureaplasma urealyticum*, and *Streptococcus agalactiae*.⁸

The ecosystem of microbial species that makes up vaginal flora is well-balanced and can be classified as aerobic or anaerobic based on their metabolic traits.⁹

While hormonal fluctuations and immune system dysfunction might increase a gravid woman's susceptibility to diseases that could endanger the health of the mother, the child, or both, pregnancy is a normal state of health. Numerous risk factors, such as drug or alcohol abuse, smoking, poor care during pregnancy, inherited predisposition, age of the mother, increase in blood pressure, poor dietary condition, diabetes mellitus and infections in the bladder might contribute to pregnancy complications. Long-lasting genital infections can also raise a woman's risk of macrosomia, PTB, and spontaneous abortion if she has had an infection prior to becoming pregnant.¹⁰

Almost all women have 10 *Lactobacillus* species in their vaginal microbiota; the relative amounts and ratios of these species vary depending on the woman's race. There are more than 250 kinds of bacteria known to exist in the vagina, with the genus *Lactobacillus* often being the most common commensal bacteria in a healthy human vagina.¹¹

In fact, physiological changes brought on by elevated oestrogen and progesterone levels during pregnancy also influence the composition of VMB. But as the pregnancy draws to a conclusion and oestrogen levels drop, particularly after delivery, a shift to a more diversified and non-*Lactobacillus* dominated VMB community is typical. Poor VMB (*Lactobacillus* species) and increased VMB richness and diversity in the third trimester have been linked to unfavourable pregnancy results. Pregnancy-related interactions among genital pathogens, pathobionts, and VMB are complicated and mostly unknown.¹²

Human micro-organisms is very important for the mother and the child's health result.¹³ It also helps to prevent vaginal infections, Sexually transmitted infections, etc.^{14, 15}

Vaginal microbiome or vaginal flora is the micro organisms which colonizes the vagina.^{16,17} A reproductive women produces vaginal secretion of around 1ml to 4ml comprising of 10^6 to 10^8 bacterium per millilitre.¹⁶

Vaginal microbiome is dynamic due to the composition that changes during pregnancy, menstruation and diseases like bacterial vaginosis.¹⁷ The microbiome starts to develop from utero and is further influenced by various factors like timing of birth, weeks of pregnancy, methods of childbirth, consumption of antibiotics, breast-

milk feeding;¹⁸ environmental exposures, diet, nutrition, inflammatory immune responses, clinical infection, disease state;¹⁹ sexual and hygiene practices.²⁰

Lacto- bacillus has the ability to reduce infection during pregnancy and the presence of lactobacilli may give good pregnancy outcome.²¹

Bacterial vaginosis is present in about 20% of pregnant women and majority of them are asymptomatic. It is related to chorioamnionitis and intra uterine death. Studies have shown that poor pregnancy outcome is higher among pregnant women with bacterial vaginosis and urinary tract infections.^{1, 22, 23, 24} The health of fetus and newborn may also be affected.¹³

Out of the various reason of perinatal death and morbidity in all nations, premature childbirth is one amongst them.²⁵

Vaginal microbiome varies among the asymptomatic women belonging to reproductive age group.^{26, 27} Globally, BV is prevalent of 4 to 64 percent. It is very common among the reproductive women.²⁸

Studies have shown that management of BV in pregnancy inorder to minimize associated complications is not much effective although there is no clear evidence.^{29, 30} Urogenital infection and dysbiosis especially bacterial vaginosis affects around 1 billion women each year disturbing their reproductive health and well being.³¹

Hence, the purpose of conducting the study is to determine the influence of vaginal microbiome on the gestational age and results of vaginal microbiome on mother and the baby. This will also help to make a protocol and educate the women on prevention of vaginal infection so that further complications will be prevented to the mother and fetus.

NEED FOR THE STUDY

Lactobacillus lactis has an intravaginal cleansing effect during pregnancy that reduces the presence of common bacterial species. In some women, there may be some micro organisms other than the normal micro organisms that can cause complications.^{32, 33}

Vaginal microbiome when observed with bacterial vaginosis is associated more with preterm delivery and also pelvic inflammatory diseases.³⁴ Any disruption in microbiota may result in urogenital conditions.²⁰

Miscarriage, premature labour beginning, and tubal pregnancy are among the pregnancy issues linked to disruption of the female genital microbiome.³⁵

Many Lactobacillus species predominate in the healthy human vagina, and they are crucial in defending women from genital infections. But sometimes infections can be caused by a shortage in lactobacilli, upsetting the microbial balance in the vagina.³⁶

Bacterial vaginosis may result in untoward/ negative neonatal outcome like foetal or newborn mortality, likelihood of getting the child admitted to a neonatal intensive care unit, respiratory difficulty at birth, neonatal sepsis, chronic lung disease and delayed development.^{1, 24}

Even though BV doesn't cause symptoms, it has been linked to unfavourable reproductive outcomes, such as low birthweight, early pregnancy loss, late miscarriage, preterm delivery, and infertility.³⁷

The colonisation of the female vaginal canal by bacteria has been the subject of in-depth research for a very long period. A significant amount of information

regarding the bacteria that live in the vaginal tracts of healthy women and those linked to illness which pose a risk to the success of pregnancy has been gathered as a result of these investigations.

In order to determine the bacteria causing genital infections and implement the proper treatment, pathogens are typically tested for by culture. However, in many cases, this method has not been able to provide a diagnosis since genital tract swab cultures do not develop. By using modern sequencing techniques that are independent of culture, our understanding of this microflora has significantly increased, leading to a significant rise in the number of taxa that have been observed in the female reproductive organs.¹⁰

It was proposed that abnormal makeup of the mother's gut and organisms in the vagina raise the possibility of early onset labour, which raises the incidence of premature delivery. However, large degree of interpersonal variability in microbiomes of healthy people occurs, which makes it difficult for scientists to find causal relationships in their studies.³⁸

Round about fifteen million are prematurely born every year all over the world and 1 million dies due to complications.³⁹ This is one of the major reason of infant death and sufferings to those who survives.⁴⁰

According to WHO Report, globally around 10.6% of all births are preterm.⁴¹ Within India, according to the estimates, 33.4 lakh preterm babies are born that contributes to 22% of world's preterm birth.⁴² 27% of neonatal death are mostly due to preterm birth and 36% are due to sepsis and pneumonia. Preterm birth can cause motor and sensory deficits, learning disabilities and most commonly respiratory disorders.⁴³

Many studies have been done on the vaginal microorganisms and their links to preterm birth, but considerably less research has been done to see the transitions taking place in the vaginal organisms in late pregnancy and childbirth. Thus, an interesting area of study is the potential correlations between the vaginal microbiome in late pregnancy, shortly before childbirth, and at the commencement of labour.⁴⁴

Determining the vaginal health will be achievable owing to research on vaginal microorganisms and its reproductive outcomes. The mothers will gain a better understanding of the significance of maternal reproductive health for successful pregnancy outcomes from this study.

Objectives of the study:

1. To study the vaginal microbiome in women admitted for delivery beyond 28 weeks of gestational age and its outcome on mother and immediate newborn.
2. To find the association between socio-demographic variables with maternal and neonatal outcome.

Operational Definitions:

- **Vaginal microbiome:** In the present study vaginal microbiome are the micro organisms present in the vagina that may or may not affect the gestational age or health status or of the women and also the health of the fetus and newborn.
- **Bacterial vaginosis:** In the present study, bacterial vaginosis means any imbalance of normal vaginal flora or micro organisms.
- **Preterm birth:** In the present study, preterm birth means delivery of babies prior to completion of 37 gestational weeks.

- **Vaginal smear:** In this study, vaginal smear means the sample collected from the vagina in the cotton swab.
- **PCR:** PCR or polymerase chain reaction is a technique used to find gene material from a particular organism, such bacteria or a virus.
- **Lactobacilli:** In the present study, lactobacilli means the normal vaginal flora.
- **Women admitted for delivery:** In the present study, women admitted for delivery refers to the pregnant women beyond 28 weeks of gestational age admitted for delivery in the selected tertiary care hospital.

Conceptual Frame work: The conceptual frame work prepared by Nkechi Martina Odugwu et.al. and published in the year 2020 directs the present study.

According to the conceptual framework, the vaginal microbiota is directly impacted by circulating levels of progesterone and oestrogen, sex, nutrition or diet, and behavioural health practices. Additionally, experts anticipate that the vaginal microbiome may either exclude or promote pathogens as a result, thereby affecting the outcome for both mothers and newborns based on the framework.

In this study, demographic variables include the following: Age, Religion, Educational level of the mother, Occupation of the mother, Type of marriage and Diet.

The study believes that the above selected Sociodemographic variables will have a impact upon vaginal micro-biome of the women among selected population i.e it will cause disturbance within the micro - organisms present in the vagina. This means that the imbalance may either be increase in the various microbial species or decrease in the microbial species. This either situation may lead to adverse health

outcomes during the pregnancy. The adverse health outcomes includes maternal outcomes like mode of delivery, risk of Operative delivery (forceps and vacuum delivery) and age of gestation at the time of labour; and neonatal outcomes like alive or dead, birth weight, anthropometric measurements, APGAR Score, need for resuscitation, NICU admission and need for oxygen mask.

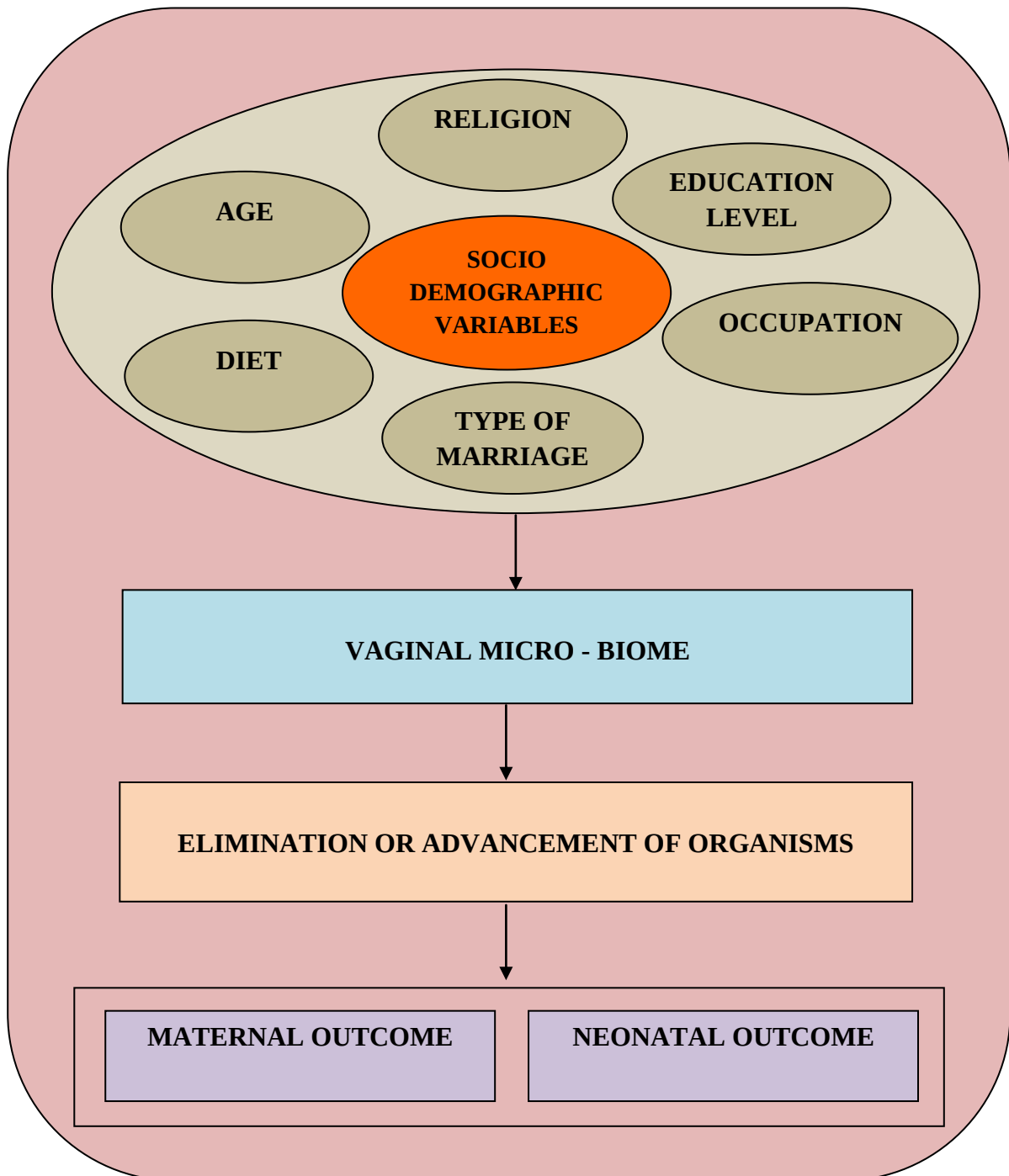


Figure 1: Conceptual Frame work

CHAPTER II

REVIEW OF LITERATURE

An investigation of written works that provide information relevant to the study's topic is called a review of the literature. It involves suitable, methodical inquiry, inspection, and summarization of the content under examination. The following reviews provide an explanation of summarised data:

A. Studies related to Vaginal Microbiome of mothers with preterm delivery

The incidence of atypical vaginal bacteria in pregnant women by trimester and whether abnormal vaginal colonisation is linked to a higher risk of miscarriage or premature delivery were the subjects of a retrospective investigation. The study examined the delivery results based on the specific type of microorganisms. Pregnant women who had a vaginal culture performed as part of a standard prenatal check-up were included in study. There were 593 singleton pregnancies in this study. Depending on which trimester a vaginal culture was conducted, participants were divided into three groups: 1st, 2nd and 3rd trimesters. With each passing trimester of pregnancy, the abnormal vaginal colonisation rate dramatically dropped (21.7% for the first, 21.0% for the second, and 14.5% for the third; $P = 0.048$). Preterm delivery before 28 weeks of gestation was significantly more common when abnormal vaginal colonisation was found in the second trimester but not in the first (6.9% vs. 0%; $P = 0.006$). *Klebsiella pneumonia* was found to be a major bacterium linked to preterm delivery before 28 weeks of gestation among aberrant vaginal flora isolated in the second trimester. The study found a link between premature delivery before 28 weeks and aberrant vaginal colonisation found in the second trimester. It has been determined that *K. pneumonia* is the most likely causal microbe.⁴⁷

A study on the vaginal micro – biota of women hospitalised for early labour and delivery was carried out. The study compared the microbiome of individuals who responded to tocolytic treatment with that of those who did not respond and delivered prematurely. It analysed hospital data from 245 women admitted for preterm labor, with duration of pregnancy between 24 to 36 weeks and 6 days. Results of the vaginal-swabs taken upon admission was assessed, and the records were examined. All of the women who were hospitalised for early labour had vaginal dysbiosis, as evidenced by the presence of pathogenic microbial species and a decrease or lack of lactobacilli. Of the 245 women, 200 (81,63%) showed improvement after receiving the tocolytic medication, while 45 (18,36%) did not show improvement and gave birth before 37 full weeks. *Gardnerella vaginalis*, *Streptococcus agalactiae*, *Candida albicans*, and *Ureaplasma urealyticum* were the most common microbial species. Comparative analysis revealed significant dysbiosis in non-responders, indicating reduced lactobacilli presence. The two groups exhibited significant differences in vaginal flora dysbiosis severity ($p < 0.05$).⁹

A study aimed to assess whether vaginal microbiota could predict the risk of chorioamnionitis (CAM) in cases of preterm delivery. Vaginal samples were collected from eighty-three pregnant women admitted for premature labor and categorized into two groups according to Blanc's classification: those with CAM (stage II; $n = 46$) and those without CAM (stage I; $n = 37$). Sequencing and analysis of 16S rDNA amplicons (V1–V2) from these samples were performed. A random forest algorithm was used to identify bacterial species associated with CAM, leading to the development of a predictive CAM (PCAM) scoring system. The CAM group showed significantly higher α diversity compared to the non-CAM group ($P < 0.001$). The PCAM score had an area under the curve of 0.849 for patients under 35 weeks of

gestation. The PCAM group (n = 22) experienced a significantly shorter prolonged gestation period compared to the non-PCAM group (n = 25; P = 0.022). Additionally, multivariate analysis indicated significant developmental differences among 3-year-old children.⁷⁰

A retrospective study was conducted to evaluate the impact of excessive vaginal colonization by aerobic bacteria and fungi on various postnatal factors, such as the length of pregnancy and the duration of neonatal hospital stays. The research included 899 participants, with the control group consisting of 413 patients who exhibited normal vaginal biocenosis. In contrast, the experimental group comprised 396 patients who showed significant proliferation of aerobic bacteria and fungi, with samples taken during the gestational week of 26 and 42. Due to missing data, 248 patients, or 23.46% of the total, were removed from the research. According to the study, patients with aberrant vaginal flora (AVF) were more likely than patients with balanced microflora (5.31%) to give birth prematurely (9.09%), with a p-value of 0.038. An Apgar score of less than four was more commonly obtained by newborns of moms using AVF. In the study group, the proportion of eutrophic newborns was lower, at 82.08%, compared to 88.65% among the controls. Infants born to mothers with AVF experienced longer hospital stays, averaging 6.30 ± 9.87 days, while those from the control group averaged 5.06 ± 5.30 days. Additionally, perinatal infections were more prevalent among newborns of mothers with AVF, occurring in 23.97% compared to 15.94% among the controls. Among the experimental group, four infants died, whereas no deaths were reported in the control group. Frequently identified organisms included 39.64% *Candida* spp., 9.85% *Klebsiella* spp., 7.32% *Staphylococcus aureus*, and 57.32% *Streptococcus agalactiae* (GBS). Newborns whose mothers were infected with *Klebsiella* spp. Exhibited higher rates of infection

symptoms (35.90% vs. 19.16%; $p = 0.011$). Furthermore, GBS carriers had a greater incidence of premature births. The study concluded that a marked increase in aerobic bacteria during the 3rd trimester of pregnancy heightens the risk of preterm birth, leads to infection symptoms in infants, elevates mortality rates, and extends hospital stays.⁷¹

A study investigated the complex species and strain dynamics of the vaginal microbiome during pregnancy and the postpartum period, and its link to premature birth. Researchers performed a metagenomic analysis on the diverse vaginal ecosystem using a large longitudinal cohort of U.S. women, with initial samples taken during the third trimester. The main findings were confirmed with a second group of women, who were sampled during the 2nd trimester. The study identified specific species and the strains, examined their co occurrence patterns and explored the connection between key species and pre- term birth (PTB) outcomes. Additionally, an mtDNA-bacterial species association analysis was conducted as part of the study to ascertain how human heredity shapes the ecology of vaginal microbes in relation to PTB. The study also investigated the clinical applicability of metagenomics in pathobiont group B Streptococcus detection and co-occurrence patterns. The study's results highlight that detailed analyses of vaginal ecology both before and after pregnancy showcase the power of metagenomics in revealing intricate aspects of the vaginal microbial ecosystem. Additionally, it provides valuable insights into the dynamics of both structural and functional communities within that framework.⁷⁴

In order to ascertain whether placental or vaginal microbiota and preterm birth are related, a study was done. Women in labour who arrived at the research hospital with an estimated gestational age of 26 weeks to 36 weeks plus six days were included in the study. Upon the patient's admission during active labor, a vaginal sample was collected, and when feasible, a placental sample was also obtained. The

16S rRNA gene's variable regions V6, V7, and V8 were amplified using PCR primers to create libraries, which were subsequently analysed with QIIME2 2022.2 and sequenced with an Illumina MiSeq device. Of the 49 women who gave birth before their due date, 23 matched case-control pairs had enough sequencing information to compare. Lactobacilli were present in all subjects, ranging in abundance from less than 1% to more than 99%. *Lactobacillus crispatus* and *Lactobacillus iners* were the most commonly found species. *Gardnerella* and/or *Prevotella*, which have been linked in prior research to premature birth, were found in more than half of the vaginal samples. There were nearly equal amounts of certain *Lactobacillus* species and genera associated with dysbiosis found in both preterm and full-term delivery mothers, with no statistically significant differences noted. The majority of placental samples had poor DNA recovery and included a mixture of contaminants, sequencing artefacts, and microorganisms that were probably introduced during birth canal passage. Nonetheless, major evidence of the placental-infecting *Streptococcus* species was found in many placental samples. The study came to the conclusion that there was no connection between preterm birth and the makeup of the vaginal microbiota.⁸²

An investigation of the vaginal microbiota's prognostic potential for sPTB was carried out. In a comprehensive study involving longitudinal sampling with 514 controls and 257 cases (totalling 2,976 samples), researchers conducted the largest investigation into the vaginal microbiota. The findings revealed that only early premature pre-labor rupture of membranes (PPROM) occurring prior to 34 weeks of gestation was linked to both the microbiota and spontaneous preterm birth (sPTB). Starting from the early stages of pregnancy, higher proportions of *Mobiluncus*, *Prevotella*, *Sneathia* and *Anaerococcus*, along with increased microbial diversity, were observed in cases of early PPRM when compared to the control group.

Additionally, data collected prior to 24 weeks was effective in predicting PPRM with delivery occurring before 30 weeks, while random forest models utilizing data from before 28 weeks showed a prediction accuracy for early PPRM. According to the study, tracking the vaginal microbiota profile could be useful in the therapeutic setting to find a group of women who will deliver preterm child.⁸⁴

An investigation was carried out to evaluate the condition of the vaginal microbiome in women who were susceptible to spontaneous preterm labour. In the study, 150 women who were of reproductive age participated. Preterm birth risk factors or the possibility of preterm birth were the study's inclusion criteria. The status of the vaginal microbiota was evaluated by bacterioscopic, molecular biology, and pH measurement of the vaginal contents. According to the research findings, there is a connection between an increased risk of preterm birth and imbalances and inflammatory alterations in the vaginal flora. For expectant mothers who have risk factors for preterm birth, the OR rises to 8.120, and it reaches 10.133 for those diagnosed with impending preterm delivery. Consequently, alterations in the vaginal microbiota are recognized as a significant risk factor for both spontaneous and threatened premature births. This indicates how urgently new diagnostic and treatment approaches must be developed aimed at preventing premature pregnancy terminations and reducing the occurrence of obstetric and perinatal complications.⁸¹

A study was done to find out how the vaginal microbiota's microbial diversity related to the success of pregnancy. The general and reproductive health of a woman is greatly influenced by her vaginal microbiome. A healthy vaginal microbiome is usually not very diverse and is dominated by lactic acid-producing *Lactobacillus* species. Sexual activity, the use of antibiotics, and hormonal fluctuations are some of the factors that can upset the balance of the vaginal microbiota and cause diseases like

bacterial vaginosis. The mother's and the fetus's vaginal microbiota changes and becomes more significant throughout pregnancy, acting as a barrier to prevent infections. Although the bacteria that live in the vagina are very important, little is known about how differences in their diversity and composition may affect the course of a pregnancy. This study examined 749 pregnant participants from the InSPIRe project who were in their third trimester and represented a diverse group. The results demonstrated the significance of lactobacilli, in particular *L. crispatus*, in preserving low diversity and suggested a connection between their lack and the risk of preterm birth. The study also demonstrated that the entire diversity of the vaginal microbiota, rather than a specific species, is the most reliable risk indicator.⁸⁶

The relationship between vaginal microbiota and spontaneous preterm birth (sPTB) in pregnant women who are at high risk of recurrence was investigated in a study. Twenty six individuals (16.9%) out of the 154 had repeated spontaneous pregnancy termination before 37 weeks of gestation. The make up of the vaginal microbiota showed no association with sPTB. Interestingly, the percentage of *Lactobacillus iners* increased from the first to the second trimester, at the expense of a more varied microbiota. This modification occurred concurrently with the bacterial vaginosis (BV) treatment, indicating a similar alteration in the microbiota after the intervention. The makeup of the vaginal microbiota in this high-risk group did not correlate with recurrent sPTB. BV therapy most certainly had an impact on the mid-gestational decrease in diversity and the observed elevation in the *L. iners*-dominated microbiota.⁸⁹

In women with cervical incompetence, a study looked at the typical microbiological spectrum and the impact of different vaginal infections on preterm birth. The analysis revealed seven distinct types of bacteria in the vaginal microbiota,

with *E. coli* and *Ureaplasma* spp. Being the most common. Among 327 participants, 217 had bacterial colonization while 110 did not. *Ureaplasma* spp. Were most frequently found in women who delivered before 34 weeks, while *E. coli* was more common in those who delivered after that gestational age. However, there was no discernible difference in the prevalence of these bacterial taxa between individuals who experienced preterm birth and those who did not.⁹⁰

B. Studies related to Vaginal Microbiome of mothers with term delivery

To evaluate the vaginal microbiota during a term normal conception, a longitudinal study was carried out. The study focused on 12 healthy women who were planning to conceive and delivered at term (38–42 weeks) without any complications. About 10 million reads were obtained through sequencing on the Illumina MiSeq. Before and during pregnancy, members of the Firmicutes phylum predominated, with Proteobacteria making up the majority until puerperium. Although the *Lactobacillus* species was prevalent both prior and pregnancy period, the vaginal microbiota diversity changed after delivery. The species – level analysis showed that *Lactobacillus crispatus* was obviously dominant in a healthy vaginal microbiome prior or during pregnancy. Additionally, PcoA analysis revealed differences in composition of the bacteria between the *Lactobacillus* species (two levels) both before pregnancy and during pregnancy. However, after the delivery, there is reduce in *Lactobacillus* species that act as protective barriers, leaving the vaginal micro-ecological barrier susceptible to illness. Furthermore, one significant environmental factor influencing the vaginal microbial community was the pH of the vagina.⁶⁰

To determine the prevalence of aerobic bacterial colonisation of the vagina in low- risk mothers in active labour and its correlation with early- onset neonatal- sepsis (AEONS) and postpartum infection, a study was carried out in a tertiary hospital. Low

– risk childbearing women in active labour with intact- membranes were enrolled in the trial. To find aerobic bacteria, high vaginal swabs were obtained and cultivated according to usual procedures. Puerperal sepsis development and AEONS were the main results. The findings demonstrated that out of 920 low-risk participants, 484 (52.6%) had vaginal colonisation, with coagulase-negative *Staphylococcus* accounting for the majority of colonisers (13.2%) and *Escherichia coli* for the remainder (8.9%). In comparison to women who had many vaginal examinations, those whose sample was taken on the initial examination had a 0.34-fold decreased chance of colonisation. Progressive vaginal inspections were associated with a higher frequency of colonisation ($p<0.001$). None of the neonates born to colonised women experienced AEONS or puerperal sepsis, respectively. The study found no link between the vaginal colonisation of aerobic bacteria during vigorous labour and an increased risk of AEONS or puerperal sepsis.⁶⁴

A study explored the vaginal microbiome at the onset of labor and during the later stages of pregnancy. Researchers examined cross-sectional vaginal swab samples from 324 Finnish women who were between 37 and 42 weeks pregnant. The samples were collected before elective cesarean sections, at the onset of spontaneous labor, and during pregnancies that lasted 41 weeks. The study used 16S rRNA gene amplicon sequencing for analysis. To determine factors influencing microbial variation, the microbiota data was integrated with detailed clinical information. The results revealed a strong association between vaginal microbiota composition and both gestational age and parity (the number of previous births). *Lactobacillus crispatus* was found to be the predominant species in the vaginal microbiota, and its relative abundance increased in late-term pregnancies, especially among women who had never given birth before. The absence of prior births was a major predictor of this

relationship. The study determined that the increased abundance of *L. crispatus* linked to gynaecological health in pregnant women was caused by delayed pregnancy and reproductive –history.⁷³

C. Studies related to comparison of vaginal microbiome among mothers with preterm and term delivery

A retrospective cohort study analysed the vaginal micro- organisms of pregnant women who delivered at term (n = 170) versus those who experienced spontaneous preterm birth (sPTB) (n = 46). Vaginal swabs were collected from women between 11 and 16 weeks of gestation. The microbiota profiles were categorized into seven community state types. Women who delivered prematurely had more diverse and richer microbial communities compared to those who delivered at term, with a higher proportion of Mollicutes. The lack of clustering based on community state types (CST) between the two groups is likely due to the dominance of a single species influencing CST classification, overshadowing the impact of less common taxa. The study found variations in the microbiota's richness, diversity, and predominance of Mollicutes amongst groups, but it was unable to pinpoint a particular microbial community structure that is predictive of sPTB.²³

A case control study was conducted to find out if the microbes in the vagina of pregnant women who had a spontaneous preterm delivery differs from that of women who had a term delivery. Women who were expecting and gave birth spontaneously before 34 weeks of pregnancy (the case) and those who did so on term (the controls) were included in the study. A variety of statistical and bioinformatics tools, such as generalised estimating equations and linear mixed effects models, were employed. The study's findings showed that: 1) there were no differences in the relative abundance of bacterial taxa between women who delivered at term and those who

delivered prematurely; 2) the frequency of vaginal community state types (CST I, III, IV-B) was similar between the two groups; and 3) the vaginal microbiota composition during a normal pregnancy shifted with gestational age, with a decrease in anaerobic or strictly anaerobic microbial species as pregnancy advanced.⁴⁶

A prospective case control research was carried out to assess the relationship between genital tract colonisation with BV and PTB. Eighty-two women who had spontaneous preterm birth (cases) or term delivery (controls) were enrolled in the study and had a BV screening. The Nugent score system was used to diagnose BV. According to the study, women with PTB had a considerably greater BV than those with TB. Moreover, the risks of BV with PTB were higher among women with PTB than among those with TB, even after adjusting for a known variable, marital status, which varied significantly across women with preterm and TB. According to the study's findings, pregnant women who have BV are more likely to get PTB. Early BV screening and treatment could be a viable technique to minimize PTB and its effects, given the difficulties associated with preterm labour and PTB.²⁸

An observational study was carried out to ascertain the involvement of vaginal microbes in preterm prelabour rupture of the membranes. Pregnant women had vaginal swabs taken four times, both before and after erythromycin treatment, as well as after PPRM. The remaining women, controls, were formed and samples were taken, delivered at term, while the women who were sampled antenatally went on to develop PPRM. Out of the 91 pregnant women studied, three (25%) had a vaginal microbiome with an abundance of Gram-negative bacteria like *Prevotella* spp. (indicative of dysbiosis) and a deficiency in *Lactobacillus* spp. Before membrane rupture, the vaginal microbiome of the women who later developed PPRM (n=12) was primarily composed of *Lactobacillus iners* (7, 58%), *Lactobacillus jensenii* (1,

8%), and *Lactobacillus crispatus* (1, 8%). In contrast, the vaginal microbiome of the control group (n=39) was predominantly *Lactobacillus crispatus* (17, 43%), *Lactobacillus iners* (12, 31%), *Lactobacillus jensenii* (5, 13%), and *Lactobacillus gasseri* (5, 13%), with no signs of dysbiosis. After membrane rupture but before erythromycin treatment (n=17), the predominant vaginal microbiomes were *Lactobacillus iners* (8, 47%), dysbiosis (5, 29%), *Lactobacillus crispatus* (3, 18%), and a combination of *Lactobacillus iners* and *Lactobacillus crispatus* (1, 6%). In 18 women (74%), dysbiosis worsened and became the prevailing state following a 48-hour erythromycin treatment (n = 23). The study, suggests that *L. crispatus* may have a preventive role in preventing this pregnancy problem.⁴⁹

In a prospective pilot study, a group of women who were both asymptomatic and symptomatic were compared to their term counterparts to ascertain the variations in metabolite profiles and vaginal microbiota. Cervicovaginal fluid samples were studied. The results showed that *Lactobacillus* spp. Dominated five Community State Types (CST): CSTI- *Lactobacillus crispatus*, CSTII- *Lactobacillus gasseri*, CSTIII- *Lactobacillus iners*, CSTV- *Lactobacillus jensenii*, and the mixed anaerobes –CSTIV. At weeks 20–22 and 26–28, CSTV in the PTDW was more than twice as high as in the TDW. Compared to 28% of TDW, no PTDW at 26–28 weeks had a microbiome dominated by CSTII. At 20–22 and 26–28 weeks, samples with a CSTI predominance displayed greater lactate levels than CSTV, whereas samples with a CSTII predominance revealed increased succinate values than CSTV, at 26-28 weeks. Principal coordinates analysis, which showed significant metabolite grouping based on CST, validated these.⁴⁵

A case-control research was conducted on the Slovenian population in order to re-evaluate the function of the microbiomes in the vagina during PTD. According to

the study, compared to women who had term births, PTD women had higher levels of micro – organisms and alpha- diversity. According to the study, there was a notable difference in the overall makeup of the vaginal micro-organisms (beta-diversity) depending on the gestational age group at birth (Pweighted Unifrac < 0.001). Reduced *Lactobacilli* spp. Abundance was observed in preterm delivery women, however *Gardnerella* and other genera.⁴⁸

To characterize the vaginal bacterial composition over time, a study was conducted on women who were either at high risk (n=38) or low risk (n=22) for preterm birth and who later experienced preterm premature rupture of membranes (PPROM), as well as those who delivered their babies at term without any difficulties (n = 36). The investigation began as early as week 6 of gestation. In the comparison between women at moderate and high risk for preterm births and those who delivered at term, only 3% showed a decrease in *Lactobacillus* spp. Abundance and an increase in microbial diversity before experiencing PPRM. Pregnancy-related bacterial community structure instability was linked to PPRM, with a change towards greater diversity mostly taking place in the second trimester. This analysis uncovered a higher relative abundance of potentially harmful species, such as *Dialister*, *Peptoniphilus*, *Streptococcus*, and *Prevotella*. The study identified reduced abundance of *Lactobacillus* spp. And increased diversity of vaginal bacteria as early indicators of PPRM risk. It suggested that further interventional studies are needed to evaluate whether altering the vaginal bacterial composition could help prevent preterm births.⁶⁹

To determine whether vaginal microbiome is linked to preterm birth and threatening early labour, a study was done. 64 pregnant women participated, had their vaginal microbiomes analysed using the 16S ribosomal RNA sequencing method. Forty seven women who experienced imminent pre- term labour and 17 women with

other illnesses were included. 24 pregnancies had full-term deliveries and 23 pregnancies had preterm deliveries in a study of mothers at risk of pre-term labour. The vaginal micro-organisms of preterm and full-term delivery groups, as well as those of premature labour groups that were not threatened, were compared. The study found that while no differences are observed in the vaginal micro-organisms between the premature labourers who were threatened and those who were not, there were significant difference in the Nugent score. The results of univariate and multivariable analysis showed that among women whose premature labour was threatened, *Ureaplasma* species positive was a predictor of preterm delivery.⁵⁰

The effect of female genital tract bacteria on preterm birth risk was investigated through a study. MEDLINE, PubMed, and EMBASE were the three main search engines that were present. Articles exploring the relationship between the risk of SPTBs and vaginal microbiome were included. According to the study, therapies aimed at modifying the vaginal microbes may be able to lower the sexually transmitted infections (STBIs) by disrupting the mother's immune response during pregnancy. The most common vaginal microbiota in term pregnancies is *Lactobacillus* spp., yet this does not ensure a typical obstetric result. The majority of full-term, straightforward pregnancies have been linked to *L. crispatus* dominance, whereas 67% of early SPTBs are linked to increase in *L. iners* in 2nd trimester. There is conflicting data linking bacterial vaginosis to increased incidence of SPTB. Better obstetric outcomes are associated with high Nugent scores; The study came to the conclusion that large-scale research on ethnic and demographic groups may be able to assist in the development of standards for patients' vaginal microbiome profiles and their unique risk of developing SPTB. This obstetric issue should be resolved with the use of a creative and methodical strategy. Identification of women who are more

likely to acquire SPTB during pregnancy may improve obstetric outcomes through analysis of changes in the vaginal microbiome.⁵¹

To find out if vaginal microbiota and PTB are related, research was done. In order to determine whether the relationships varied between women who were swabbed at different gestational ages, the study examined these associations in a fresh cohort using post hoc analysis. The study examined the vaginal microbiomes of individuals. The study's findings demonstrated that no CST- diverse, lactobacillus – dominated, was linked to PTB when gestational age at sampling was disregarded. Women who have CSTs dominated by Lactobacillus are at a reduced risk than those with a diversified CST to have a PTB among those whose samples were collected before 12 weeks of gestation. According to the study's findings, the healthy vaginal microbiota varies by race and ethnicity, and more extensive study is needed to distinguish the effects of these differences throughout pregnancy.⁵²

To perform a longitudinal meta-analysis of the vaginal microbiome in preterm birth (PTB), five separate studies comprising 3,201 samples from 415 pregnant women who delivered either at term or preterm were included. The research discovered a statistically significant distinction in the microbiological within-sample variation among those who delivered term with those delivering preterm. The research findings indicate that there is a consistent within-sample variance throughout pregnancy. Using linear mixed effects regression, the study was also able to determine which bacterial genera were substantially correlated with the date of birth in each trimester. The study also discovered that many genera are linked to PTB and that Lactobacillus abundance is related to term delivery. Of them, two are new: Olsenella and Clostridium sensu stricto. The biggest risk factor was not BV but rather the absence of Lactobacilli.⁵³

To evaluate the link between maternal and newborn outcomes and aerobic vaginitis (AV) in late pregnancy, a prospective observational study was carried out. Results of pregnancies were tracked down and recorded. The relationship between AV and premature labour was the main finding. The study provided the odds ratio and 95% confidence interval for comparing the outcomes of mothers and their babies. The findings indicated a correlation between AV and preterm delivery as well as prelabor membrane rupture. AV was linked to a higher rate of neonatal ICU hospitalisation in terms of neonatal outcomes. The study found that preterm birth, PROM, and neonatal ICU admission are only a few of the adverse pregnancy outcomes that are associated with AV, which is frequent in late pregnancy. The findings recommended that during pregnancy, physicians give vaginal microbiome assessment more thought.⁵⁶

In a study, five community state types have been identified regarding the variety of the pregnancy-related vaginal microbiota, four of which are led by *Lactobacillus* and 5th by anaerobic species. There has also been an observed variance between species stability and gestational age. Anaerobic flora is more prevalent in the bodies of White, Asian, and Caucasian women, according to interspecies and racial variance studies. Both preterm and spontaneous labour are significantly influenced by the flora in the vagina during gestation. The post- partum period sees a significant decline in the *Lactobacillus*-rich microbiome and an increase in diversity. Other microbial communities have been identified in the human vagina in addition to the recognised bacterial communities. Vaginal viral virome makes up the majority of the fragment, and nothing is known about the vaginal microbiome. Research has shown that the vaginal microbiome is primarily composed of ds DNA viruses, with ssDNA and a small number of unknown viruses. There were very few eukaryotic viruses

found; the only harmful ones were Herpesvirales and Papillomaviridae. Babies are exposed to this flora through the breast milk, the mother's intestines, or the vagina.⁶¹

In a study, the cytokine environment and vaginal micro-biota of eighteen women who had delivered preterm and thirty-six controls who delivered at-term were examined longitudinally. The researchers identified a predictive vaginal microbiome profile for preterm birth (PTB) using 16S ribosomal RNA gene sequencing. This profile was detectable as early as the first trimester and was characterized by reduced levels of *Lactobacillus crispatus* and *Finegoldia*, increased levels of *Prevotella buccalis*, and lower concentrations of cytokines such as TNF- α , IL-4, and IFN- γ . The research findings indicate that variations in the local vaginal immunological milieu and vaginal microbial diversity are associated with chances of pre-term birth. The study emphasised novel approaches to anticipate PTB in ethnic minority Burman/Karen populations in high-resource locations, as well as poor socio-economic conditioned area who are most at risk of complications from un-expected PTB.⁶³

To find the bacterial taxa linked to PTB and term birth (TB) in Indian women, a study was carried out. Vaginal swabs were obtained from thirty-eight pregnant women who gave birth to 20 spontaneously term and 18 preterm neonates at each of the three trimesters of their pregnancy. Metagenomic DNA was extracted from vaginal swabs (n=115) for paired end-sequencing of the V3- V4 region of the 16S rRNA gene. Additionally, shotgun whole genome sequencing was performed on bacterial species associated with reproductive outcomes. To isolate genomic DNA and perform whole genome sequencing, *Lactobacillus* species were cultivated anaerobically using De Man, Rogosa, and Sharpe (MRS) agar medium. The alpha diversity indices in the vaginal microbiomes were comparable between the term and

preterm samples. The results exhibited birth outcomes being interrelated with the dominance of particular *Lactobacillus* species and a small number of other facultative anaerobes.⁷²

A research study was conducted to investigate the connections among race, the vaginal microbiome and instances of spontaneous preterm birth. The research involved 360 Black women (comprising 276 who had term births and 84 with spontaneous preterm births) and 464 White women (including 375 with term births and 89 experiencing spontaneous preterm births). The findings revealed that the vaginal microbiome of Black women showed higher alpha diversity, an increased prevalence of *Lactobacillus iners*, and a lower prevalence of *Lactobacillus crispatus*. Nonetheless, it was discovered that among women who douche, there were no appreciable racial variations in microbiota. *L. crispatus* was less abundant in the sPTB-associated microbiome, whereas *L. iners* and alpha diversity showed no significant correlation with sPTB. The multivariable-adjusted odds of spontaneous preterm birth (sPTB) decreased by about 20% for every tenfold increase in the normalized relative abundance of *Lactobacillus crispatus*. The study also revealed strong correlations among several maternal characteristics, such as age, race, socioeconomic status, education level, marital status, and douching practices. In univariate analyses, the effect sizes of the microbiome ranged between 1.8% and 5.2%. The findings indicated that White and Black women possess unique vaginal microbiomes. Furthermore, the vaginal microbiome was linked to spontaneous preterm birth (sPTB), with a lower abundance of *Lactobacillus crispatus* increasing the risk of sPTB, regardless of racial differences in microbial community composition. Moreover, the study showed that the connections between race, the

vaginal microbiome, and preterm birth were obscured by the practice of vaginal douching.⁷⁵

To investigate how different vaginal microbiota affect spontaneous preterm birth (sPTB), a case-cohort study was conducted involving 308 pregnant women from the same region serving as controls and 41 women experiencing sPTB. The prevalence of gestational diabetes mellitus (GDM) was the only significant difference found between the two groups; the control group was chosen at random at the beginning. Early in the second trimester, vaginal swabs were obtained, and the QIIME 2 platform with 16S amplicon sequencing was used for the primary bioinformatics study. The sPTB group and the control group's vaginal microbiome features were evaluated in the study. The results showed that the GDM rate in the sPTB group was greater (19.51%) than in the control group (7.47%). Additionally, there was more alpha diversity in the vaginal microbiota of pregnant women with sPTB. In addition to having higher alpha diversity, the sPTB group also had unique beta diversity characteristics when compared to the other group. A greater rate of sPTB was linked to the presence of *Lactobacillus paragasseri/gasseri*, *Streptococcus*, or *Proteobacteria* in the non-GDM subgroup. On the other hand, among all pregnant women, a lower incidence of sPTB was associated with a higher relative abundance of the new *L. mulieris*. In the end, the study found that because GDM may affect the association between vaginal taxa and sPTB, maternal GDM must be taken into account when utilising vaginal taxa to identify pregnant persons at an elevated risk for sPTB.⁷⁹

To investigate the relationship between lower vaginal lactobacilli levels and pregnant women's risk of preterm delivery, an ambispective case-control research was conducted. The research included total of 455 expectant mothers, aged 14 to 46 years, with 112 (25%) experiencing preterm pregnancies and 343 (75%) classified as

having term pregnancies. Vaginal secretions were obtained, and the quantity and kinds of lactobacilli were determined using Gramme staining under a microscope. The results were then analysed using Hay's criteria (grade I: normal, grades II and III: abnormal). The findings showed that the preterm group had a greater percentage of decreased vaginal lactobacilli than the term group ($p < 0.001$). The probability of a preterm delivery was found to be strongly correlated with lactobacilli grades II and III, even after controlling for age, pre-pregnancy body mass index, insufficient prenatal care, and other variables. In particular, the odds ratio for grade II and grade III lactobacilli were 3.6 and 17.8, respectively. The findings suggested that pregnant women who experienced preterm deliveries exhibited a higher percentage of depleted vaginal lactobacilli compared to those with term deliveries.⁸⁷

D. Studies related to vaginal microbiome of reproductive age group women, mode of delivery and among the pregnant mothers irrespective of gestational age.

A study was conducted to explore the vaginal microbiome of Indian women of childbearing age. The research revealed that the vaginal microbiome in fertile women exhibited a significant personal component and showed considerable variation in taxonomic, genomic, and functional characteristics across different ethnic groups. The most frequently identified bacterial species in their vaginal environment included *Lactobacillus iners*, *Lactobacillus crispatus*, *Lactobacillus gasseri*, *Lactobacillus jensenii*, and *Lactobacillus johnsonii*. Additionally, the genomes of four major *Lactobacillus* species were analysed to reflect the community state types (CSTs) and identify their potential roles in the intricate vaginal microbial ecosystem. This study represents the first documentation of the vaginal microbial ecology in Indian women

and provides genomic insights into the prevalent genital tract bacteria among women of reproductive age.⁵⁴

A study was conducted to understand the relationship of a childbirth mode and the organisms present in the vagina including 144 adult women. Nineteen ladies (19%) disclosed having a caesarean section. Overall, the study showed no correlation in caesarean section with Molecular BV, with *Prevotellabivia* being the most strongly correlated taxon with C-section. The research suggested a potential link between adult Molecular-BV and C-sections. The lesser sample and participant's age and various other characteristic comparability within the study locations hampered the analysis. The study indicates that larger samples of women could be recruited for future longitudinal studies, which could also mention the time-based dynamics of vaginal micro-organisms and investigate various other potential con-founders such as socioeconomic status, breastfeeding history, and maternal factors that may influence the relationship between vaginal microbiota and birth mode.⁵⁵

A study including 700 mother-child dyads was carried out to determine the degree of delivery mode-dependent transmission and the function that the mother's vaginal microbiota plays in seeding the child's microbiome. In the third trimester, the mother's vaginal microbiota was assessed and contrasted with the faecal and respiratory microbiota of the kids. *Firmicute*, *actinobacteria* and *proteobacteria* dominated the vaginal microbiota at 24 weeks of gestation. This matched *Lactobacillus* (81.9%) and *Gardnerella* (7.8%) at the genus level. Lactobacilli represented the majority of operational taxonomic units (OTUs), with *L. crispatus*, *L. iners*, *L. gasseri*, and *L. jensenii* being the most prevalent. According to the study's findings, a mother's vaginal microbiota has little effect on the early faecal and respiratory microbiome of her newborn. Although babies are exposed to the vaginal

microbiota of their mothers during childbirth through the vagina, the predominating microbe is not usually linked to the radically various habitats found in intestines and hypopharynx.⁵⁷

To investigate the impact of the pre-conceptional vaginal microbiome on the risk of spontaneous preterm birth, a case-cohort study was conducted. HIV-negative Pregnant Kenyan women were tracked from conception to birth and the early postpartum period. During the preconception phase, participants sent monthly vaginal specimens for the examination of vaginal microbiota. A swab was taken from in between the foetal membranes following delivery. Samples from the placenta and the umbilical cord were taken for histopathology. Deep sequencing and broad-range 16S rRNA gene PCR were employed to assess species-richness and changes in community in preconception vaginal samples from women who experienced spontaneous preterm birth (SPTB) compared to those with term births. Additionally, bacteria from fetal membrane samples were quantified using taxon-specific qPCR, and the correlation between bacterial counts and histological indicators of inflammation in the placenta, fetal membranes, and umbilical cord was examined. The study found that by emphasising the fact that pre- conceptional vaginal micro- organisms is the mediator of premature delivery, the findings could change the way that the pathways relating vaginal microbiota and preterm are thought to be thought of.⁵⁸

A study was done to find out if pro-inflammatory vaginal milieu in Ugandan pregnant women was related to a varied vaginal microbiome. The vaginal microbiota of expectant mothers receiving prenatal treatment was described in the study. The study examined the abundances and richness of commensal group of bacteria in the female vaginal canal. Dada2 plugin, Qiime2 version 2018, and Naive-Bayes classifier were used to analyse the data for taxonomic assignment. According to the study, the

vaginal microbiota profile of 19% (35/179) of pregnant women was dominant by *Lactobacillus*. The research findings indicate that the primary cervicotypes, or “CTs,” were *Lactobacillus non-iners* (CT1), *L. iners* (CT2), *Gardnerella* (CT3), and *Atopobium* (CT 4). The women with no *Lactobacillus* C T showed considerably greater amounts of the chemokines IL – 6 and I L – 8 along with the inflammatory cytokines IL – 1beta & TNF-alpha in their cervical lavage. Irrespective of HIV sero-status, pregnant women with highly variable cervicotype (CT4) were linked to inflammation, which is recognised as a promoter for HIV acquisition and transmission.⁵⁹

A review of research on infections during pregnancy and the mother’s microbiome was done. This review sought to elucidate the potential impact of infections and metabolic issues related to pregnancy on the dysregulation of maternal microbiome. According to the study, pregnancy causes distinct alterations in the immune system and metabolism of the mother. The fetus’s healthy growth is supported by the maternal body through drastic physiologic adaptation. Immune system control, metabolic control, and infection resistance are all heavily influenced by the gut microbiome. Research has indicated that pregnancy induces changes in the microbiomes of the mother’s gut, vagina, and oral cavity. However, it remains unclear whether and how these changes are linked to maternal immunity, metabolism, or susceptibility to infections. There is still a lack of coordinated adaptation of these various facets of human physiology to support a healthy pregnancy.⁶²

In order to evaluate the data about the correlation within imbalance in the vaginal organisms, B V, and A V, and late untoward pregnancy results in women, a systematic-review was carried out. Throughout the review, the suggested Reporting Items for Systematic Review and Meta-Analysis (PRISMA) guidelines were adhered

to. Three databases were searched: PubMed, Embase (Ovid), and Cochrane. These databases included observational and intervention studies conducted in sub-Saharan Africa (SSA) that linked vaginal microbiome dysbiosis, bacterial vaginosis (BV), or aerobic vaginitis (AV) to outcomes such as preterm birth, preterm rupture of membranes (PROM), low birth weight, small for gestational age, intrauterine growth restriction, intrauterine infection, intrauterine death, stillbirth, perinatal death, or perinatal mortality. Among 693 searches, the result indicated that twelve studies were included. According to one study, low birthweight and VMB dysbiosis are positively correlated. Studies identified a correlation between bacterial vaginosis (BV) and preterm birth, low birth weight, small-for-gestational age, and intrauterine infection, despite considerable variations in design of the study and outcome- reporting. Neither intrauterine growth retardation (1/1) nor pregnancy loss (5/5) were linked to any of the studies that could be retrieved.⁶⁵

Cohorts from five distinct studies with longitudinal vaginal microbiota data were analysed meta-analytically. In the study, samples collected between 9 and 13 weeks of gestation were classified as 1st trimester, those collected between 14 and 25 weeks as 2nd trimester, and those collected between 26 and 36 weeks as 3rd trimester. The quantity of the species (bacteria) in the microbiome was compared between women who gave birth on time and those who did not. In all, 415 women's samples, or 3,201 samples, were evaluated for the study. According to the study, there was more within-sample variation in the abundance of microbes in the vagina among preterm women, especially in 1st trimester. Researchers found that several microbial taxa, including *Olsenella* and *Clostridium sensu stricto*, which had not previously been connected to premature birth, were associated with preterm birth after longitudinally modelling the data. According to the study, while earlier research has

linked an abundance of *Lactobacillus* to full-term birth, its absence alone, in conjunction with the presence of other bacteria, may be a predictor of preterm birth.⁶⁶

A research study was conducted to analyse data from a diverse group of women at various stages of pregnancy and from different ethnic backgrounds, with the aim of identifying specific bacteria associated with preterm births. Higher vaginal microbial diversity has been linked to early birth, especially in 1st trimester of gestation, according to the study. Through the integration of five distinct data sets, totalling over three thousand samples from over four hundred women, the researchers discovered unexpected connections within the micro- organisms in vagina, particular bacteria, and preterm birth. Additionally, the researchers discovered particular microorganisms linked to preterm birth. Previous research have brought attention to some, such *Lactobacillus*, which is more common in women who give birth fully term, whereas others, like *Olsenella* and *Clostridium sensu* are linked to preterm delivery.⁶⁷

A research study was carried out to examine the makeup and evolution of the vaginal microbiota throughout pregnancy and childbirth. Along with analysing the vaginal microbiota of fifty-seven women during weeks 24, 36, and during the time of birth- after the membranes splits but prior to delivery, the study also examined the content of the micro- biota in the infant's sto-mach and airways, comparing the two. Bacterial diversity and taxonomic distribution saw significant alterations in the vaginal community structure. According to the study, from 24 weeks of pregnancy until child- birth, the abundance of most bacterial taxas climbed stepwise, while *Lacto- bacillus* gradually decreased. The study indicated that mother- to – child vertical transfer occurs; with the highest transfer observed for *Clostridiales*, followed by *Lactobacillales* and *Enterobacteriales*.⁶⁸

A research study was conducted on Pemba Island in Tanzania to investigate the makeup of the vaginal microbiome (VMB), the prevalence of genital pathogens and how these elements relate to women who are pregnant and those in the postpartum period. Ninety women participated in the study, and vaginal swabs were taken once after delivery, if feasible, and at two different stages during pregnancy (less than 20 weeks GA and more than 20 weeks GA). VMB characterisation was performed using the IS-pro assay. Quantitative PCR (qPCR) methods were employed to detect the presence of *Human papillomavirus (HPV)*, *Mycoplasma genitalium (MG)*, *Trichomonas vaginalis (TV)*, *Neisseria gonorrhoeae (NG)* and *Chlamydia trachomatis (CT)*. During pregnancy, the majority of VMB were *Lactobacillus* dominant; after delivery, they were non-*Lactobacillus* dominating. The investigation's findings revealed a significant decrease in VMB richness for both paired and unpaired samples throughout pregnancy. Within unpaired samples, Shannon diversity was notably lower during pregnancy compared to the postpartum period. At every assessment point, the two most commonly identified pathobionts were *Klebsiella species* and *Streptococcus anginosus*. The study concluded that women whose VMB was not predominantly composed of *Lactobacillus* exhibited a higher abundance of pathobionts. The investigation added to the body of knowledge regarding the composition of VMB, its alterations during and after pregnancy, and its relationships to genital pathogens and pathobionts.¹²

In order to determine the possible causes of each woman's unique microbiome changes throughout the pregnancy to postpartum transition, a study was carried out. 48 pregnant women participated in the study, which assessed vaginal samples taken during the first, third, and postpartum phases of the pregnancy. The study identified the composition of species within vaginal communities and assessed the levels of

chemicals in vaginal fluid that influence alterations in the immune system and host physiology at various time points. *Prevotella bivia* and *Streptococcus anginosus* were found in much higher quantities than *Lactobacillus*, which was less abundant. Postpartum vaginal secretions were also shown to be changed by the study. Small amounts of D- & L- lactic acid isomers were detected, alongside elevated levels of hyaluronan and Hsp70. The research indicates that these differences stem from alterations in the vagina following childbirth, which notably transform the host environment and consequently impact the ability of different bacterial species to thrive and proliferate.⁷⁶

A prospective case control study was carried out to investigate how the vaginal microbiome of pregnant women changed during COVID -19. The research involved matching twenty-nine healthy controls with nineteen pregnant women diagnosed with COVID-19 based on age and gestational week. Vaginal swabs were taken while the infection was at its worst and once more a month later. Longitudinal samples were obtained prior to, during, and following the infection in three patients. The microbiome alterations were analysed using 16S rRNA gene sequencing. The findings indicated that COVID-19 was associated with vaginal dysbiosis during pregnancy, as evidenced by a heightened alpha diversity index. Specifically, there was a significant reduction in Firmicutes and *Lactobacillus*, alongside an increase in Bacteroidetes within the COVID-19 group. Additionally, women classified as moderate/severe showed higher levels of *Ureaplasma* and lower levels of *Lactobacillus gasseri* compared to those with asymptomatic or mild cases. During the active phase of the longitudinal study, an increase in Actinobacteria was observed, while levels of Firmicutes and Bacteroides were reduced. The study concluded that vaginal dysbiosis, characterized by low *Lactobacillus* levels and elevated

Bacteroidetes, may have implications for adverse pregnancy outcomes related to SARS-CoV-2 infection.⁷⁷

A narrative review was conducted to explore the impact of the microbiome within the vagina and potential rehabilitative techniques on the well-being of mothers. The study showed that commensal bacteria, including *Lactobacillus*, which lower pH and thwart pathogenic invasion, are important for vaginal health during pregnancy. The role of vaginal bacteria in a number of prenatal and perinatal diseases has been investigated, and the restoration and modification of the vaginal microbiome is a rapidly developing field in women's health. Preterm labour (PTL) prevention may be the main benefit of these repairs. Pregnant women at risk for postpartum hemorrhage (PTL) might find therapeutic benefits from using vaginal and oral probiotics, which serve as effective supplementary treatments for bacterial vaginosis (BV)- a condition that increases Pre-term labour. Vaginal microbiota transplants (VMTs) represent an innovative restorative approach that involves transferring a woman's cervicovaginal secretions to another individual. The analysis made clear that more investigation into recurrent BV is required to ascertain whether VMTs can safely establish a healthy vaginal flora dominated by *Lactobacillus*. It also cautioned against hastily establishing a direct connection between vaginal dysbiosis and various health issues, as the root causes of dysbiosis are often unclear. This review's main focus was on the impact of vaginal microbiota on pregnancy outcomes, including preeclampsia, gestational diabetes, PTL, and infertility.⁷⁸

To investigate potential variations in the vaginal microbiome between miscarrying and normally pregnant women, a prospective observational study was carried out. The study included twenty-four first-trimester pregnant participants. Using an Illumina MiSeq instrument and QIAGEN reagents, a sequencing analysis of

the V4 region of the 16S rRNA gene was performed to characterise the vaginal microbiomes. Furthermore, relationships between clinical data on pregnancy and the vaginal flora were examined. The ordination plots presented in the study illustrated the differences in microbiota composition between the control group and women who experienced miscarriages. Among nulliparous women, 50% had *Lactobacillus crispatus* as their dominant bacterial species. In contrast, only 15% of women with no miscarriage history had *Lactobacillus iners* as their predominant bacterium, whereas it was found in 50% of women with a history of miscarriages and those who miscarried during the study. Moreover, the quantity of functional taxa and the richness of the microbiota in women who had miscarriages were found to be significantly different from those in mothers who had term deliveries. Different relative abundances of eight species were discovered in the two groups of women. According to the study's findings, a woman's past pregnancies affect the vaginal microbiome's composition.⁸⁰

In vitro fertilisation (IVF) pregnant women's vaginal microbiota (VM) and its dynamic alterations were studied, along with the relationship between VM and premature birth. Six women conceived spontaneously and sixteen who had IVF were enrolled for the study. During the initial, second, and third trimester of gestation, vaginal samples were taken from each participant. The observed species of VM and the alpha-diversity indices Chao1 were considerably greater in T1 than in T2 or T3 for every subject. According to non-metric multi-dimensional scaling (NMDS) study of beta-diversity, the VM structure of the IVF and control groups was substantially dissimilar at T1, although it gradually converged during T3. In T1, the IVF group exhibited a greater presence of potentially harmful bacteria and a lower presence of beneficial bacteria in comparison to the control group. Furthermore, preterm birth mothers who did IVF had greater abundances of *Lactobacillus_iners*,

Escherichia coli, and *Alloscardovia omnicolens*. The study found that in both healthy individuals and women who had IVF, the VM diversity declined with increasing gestation.⁸³

A thorough review was carried out to gather the most recent information about the vaginal microbial ecosystem and its significance for women's health and reproductive outcomes. An extensive examination of the typical vaginal microbiome was given by this study, explored its connection to pregnancy results, and examined its influence on various gynecological conditions. The review also sought to increase knowledge about the significance of preserving a healthy vaginal microbiome for improved reproductive health and the avoidance of gynaecological problems among the general public and healthcare professionals. Many pregnancy outcomes, such as intra-amniotic infections, spontaneous preterm births, miscarriages, early membrane rupture, preeclampsia, and procedures like in vitro fertilisation and embryo transfer, have been linked to the vaginal microbiota, an essential part of the human microbiota. It also contributes to the development of various gynecological issues, such as bacterial vaginosis. The study looked at how the vaginal microbiota changed under different circumstances and found that it was important for women's health, especially reproductive health, which has a big impact on how well women get pregnant. The findings suggest that a closer look and more focused investigation into the relationship between vaginal microbiome and pregnancy outcomes are necessary, along with the mechanisms at play, can lead to a better understanding. This is true even in light of the limitations and deficiencies in current research.⁸⁵

An investigation was carried out to look at how South African women's vaginal microbiomes changed during and after pregnancy. From their first prenatal visit until the third trimester (24–36 weeks of gestation), 60% of women classified as

having Gardnerella-dominant community state types (CSTs) switched to Lactobacillus-dominant CSTs. On the other hand, during the third trimester and postpartum (averaging 17 days after delivery), 80% of individuals with Lactobacillus-dominant CSTs switched to non-Lactobacillus-dominant CSTs, with a significant proportion switching to facultative anaerobe-dominant CSTs. According to STI diagnosis, the microbiome's composition also varied, showing that women with STIs were more likely to be in CSTs dominated by Gardnerella or L. iners. In conclusion, there was a tendency towards Lactobacillus dominance throughout pregnancy, and in the postpartum period, a unique and extremely varied anaerobe-dominant microbiota profile emerged.⁸⁸

A study was carried out to investigate modifications in the maternal microbiota during last trimester of pregnancy and the factors that affect the formation of the newborn microbiota after an elective cesarean section. In healthy pregnancies, the vaginal and rectal microbiomes of the mother remain stable during the third trimester. Additionally, there were no indications of microbial colonization in the newborn before birth. The microbial composition of the neonatal microbiomes in infants born via cesarean section was found to be different from that of the mother's vaginal and rectal microbiomes at the time of birth, indicating that exposure to the environment outside the womb is the primary element affecting how the newborn microbiota develops in this group.³⁸

JUSTIFICATION

- Globally, the rate of preterm births is over 10%.
- Frequent microorganisms that impact pregnancy results consist of *Gardnerella*, *Mycobacterium hominis*, *Escherichia/Shigella*, *Prevotella*, *Atopobium*, *Sneathia*, *Gemella*, *Ureaplasma*, *Mycoplasma*, *Dorea*, and *Streptococcus*.
- Infants exposed to Bacterial Vaginosis (BV) at term have an increased likelihood of experiencing meconium during birth, a higher chance of needing assisted breathing, respiratory distress at birth, NICU admission, and newborn sepsis in babies born full-term. BV exposure is linked to a higher likelihood of NICU hospitalisations in preterm newborns.
- Those who give birth prematurely have a greater incidence of bacterial vaginosis (BV) during pregnancy when compared to those who give birth on time.
- Regular screening of pregnant women leads to a reduction in negative pregnancy outcomes.
- In healthy term pregnancies, *Lactobacillus* species are the dominant type of vaginal bacteria, although their presence does not guarantee a positive obstetric result.
- The *Lactobacillus* species that are most frequently found in Indian women's vaginal flora are *L. iners*, *L. crispatus*, *L. gasseri*, and *L. jensenii*.
- Variables like gestational age, number of pregnancies, socioeconomic situation, education level, marital status, and douching behaviours affect the composition of the vaginal microbiome.

- There is a positive correlation between low birth weight and vaginal microbiome imbalance; a vaginal microbiota dominated by *Lactobacillus crispatus* is more common in late-term pregnancies and is highly correlated with a lack of previous births. During the third trimester, there is a lower presence of *Lactobacillus* and a markedly greater presence of *Streptococcus anginosus* and *Prevotella bivia*.
- Vaginal microbiome changes during pregnancy have been connected to the COVID-19 pandemic; among individuals affected, there has been a noticeable decrease in Firmicutes and *Lactobacillus* and an increase in Bacteroidetes.
- Probiotics for the vagina and mouth are beneficial in preventing preterm labor. Additionally, vaginal microbiome transplants (VMTs), which involve transferring cervicovaginal secretions from one woman to another, have shown effectiveness.
- Although the significance of vaginal microorganisms is recognized, the way shifts in their composition and diversity affect pregnancy outcomes is not well understood.
- The vaginal and rectal microbiomes of mothers in healthy pregnancies generally remain stable during the third trimester.
- *Ureaplasma* species were the most prevalent bacteria in women who had preterm births before 34 weeks, whereas *E. coli* was the most common in those who delivered preterm after 34 weeks. Nonetheless, there was no discernible difference in the prevalence of these bacterial species between individuals who gave birth prematurely and those who did not.

CHAPTER III

MATERIALS AND METHODS

The various actions that the investigator took are covered in this chapter. It includes a detailed overview of the methodology, research framework, target population, environment, sample characteristics, and size, along with the sampling technique and criteria. Additionally, it outlines the selection of tools, the process for collecting data, and the strategy for analysing the data.

Research Approach: This study employed an evaluative method to examine the vaginal microbiome in women who were admitted for childbirth.

Study Design: This study utilizes a case series study design to study the topic.

Study Population: Pregnant mothers delivering in labour ward of selected tertiary care hospital of Belagavi city.

Sampling Technique: Consecutive mothers delivering with gestation of 28 weeks or more.

Sample Size:

$$N = \frac{Z_{1-\alpha/2}^2 pq}{(10\%p)^2} \times 1.1$$

Where

$Z_{1-\alpha/2}$ = one tail standard normal variate assuming sample size at a 95% confidence level

P = Prevalence

Q = 1-p

Attrition = 15%

Considering the above formula, the sample size is calculated as **300**.

Sampling Criteria

Inclusion criteria:

1. All mothers with or more than 28 gestational weeks delivering in tertiary care hospitals of Belagavi city.
2. Mothers who have conceived naturally or mothers who became pregnant with IVF.

Exclusion criteria:

1. Use of vaginal antimicrobials or antibiotics
2. Women associated with medical conditions (hypertensive disorders in pregnancy, diabetes, heart disease, antepartum haemorrhage, sexually transmitted diseases).

Study Variables

Socio-demographic variables: Demographic characteristics included in the study are will be Age, Religion, Educational Qualification, Occupation, Type of marriage and Diet.

○ **Independent variable:**

- ✓ Vaginal microbiomes

○ **Dependent variables:**

- ✓ Gestational age,
- ✓ Health of the mother
- ✓ Birth outcome like the weight of the newborn, Apgar score and anthropometric measurements.

○ **Extraneous variables:**

- ✓ Biological factors: Gestational age, Parity, Mode of conception, Genetic factors.
- ✓ Lifestyle and environmental factors: Diet, Hygiene practices, Sexual activity, Stress level
- ✓ Hospital related factors: Vaginal examinations, method of collecting swabs, use of antiseptic solutions

Study Location/ setting:

This study took place at the postnatal ward and labor ward of KLE's Dr. Prabhakar Kore Hospital and Medical Research Centre, located in Nehru Nagar, Belagavi, Karnataka, India.

Patients from all throughout the nation come to this tertiary care hospital.

Ethical and administrative deliberations

Approval from the Institutional Ethical Committee (IEC): The Institutional Ethical Committee of KLE University, Belagavi granted ethical approval for the study. (Appendix I).

Hospital authority: The Medical Superintendent of the chosen tertiary care hospital in Belagavi granted official authorization for this project (Annexure II).

Patient's consent: The mothers gave their written approval to take part in the research. After receiving a full explanation of the procedures involved and their role in the research (Annexure III).

Data collection instruments and Procedure

- Socio-demographic variables
- Maternal and Newborn Information (Modified MNH Registry)
- Identification of bacteria:
 - Collection of sample (vaginal swab)
 - Morphology testing
 - Biochemical testing
 - DNA Isolation
 - PCR (Polymerase Chain Reaction Test)

STEP I: ADMINISTRATION OF TOOL ON MODIFIED MATERNAL & NEWBORN HEALTH (MNH) REGISTRY

This standardized tool, originally developed by the Global Network for Women's and Children's Health Research, was adapted for the purposes of this study (Annexure III). It has five Sections.

Section I: Socio- demographic information of mother (Age, religion, Education level, occupation, type of marriage and diet)

Section II: Maternal Past Antenatal information

Section III: Maternal Present Antenatal information

Section IV: Maternal Intranatal information

Section V: Maternal and Newborn Outcomes

Procedure of data collection:

1. First self-introduction was done to the mother and the purpose of the interaction was explained clearly. After obtaining the written consent, the information related to demographic variables and Modified Maternal & Newborn Health (MNH) Registry were collected. The mother is then explained regarding the process of sample collection.
2. Preparation of equipment: Before patient preparation, ensure that all necessary tools and materials are available and properly sterilized.
 - Sterile vaginal swab
 - Sterile speculum (preferably non-lubricated,) for visualization if needed.
 - Sterile gloves.
 - Biohazard-labeled collection tube for sample transport.
 - Labeling materials
3. Preparation of the Patient: The procedure was explained in simple terms, emphasizing that: It is painless but may cause slight discomfort, it involves inserting a sterile swab into the vagina for a few seconds and the sample will help in microbiome analysis.
 - a. The mother was asked to empty her bladder for comfort.
 - b. The mother was positioned in Dorsal Lithotomy Position (Patient lies supine with knees bent and feet resting on stirrups or bed, a disposable drape is placed for privacy and comfort.)

4. Vaginal Swab Collection:

- Wash hands thoroughly and wear sterile gloves.
- Prepare a sterile vaginal swab and transport tube with patient label.
- Gently separate the labia minora using a sterile-gloved hand. Insert a sterile speculum (without lubrication) to visualize the posterior fornix.
- Gently insert the sterile swab approximately 5 cm into the vaginal canal, ensuring it reaches the posterior fornix.
- Rotate the swab to ensure adequate sample collection.
- Carefully withdraw the swab without touching external genitalia to avoid contamination.
- Immediately place the swab into the transport medium and secure the cap.
- Label the tube with patient ID/code, date, and time of collection.
- Place the sample in a cold transport box (microbiome analysis).

5. After care of the procedure

- Remove the speculum gently and offer tissues or a sanitary pad if needed.
- Ensure mother's comfort and address any discomfort.
- Wash hands.

Time duration for data collection:

- The time taken for each sample to administer the tool and collect the sample (vaginal swab) along with preparation of the patient is 25 minutes.

STEP II: IDENTIFICATION OF BACTERIA:

Sample Collection: Before being tested, vaginal swabs from the posterior vaginal fornix were collected, sterilised, and rapidly stored at -70°C.

After swabbing the MRS agar plate, they were incubated at 37⁰C in anaerobic chamber for 24 hours. These samples were subjected to gram staining and biochemical test (IMViC test).

Gram staining:

The steps of gram staining are as follows:

1. A loopful of tap water was added to the slide to create a thin, even layer of microorganisms. A loop was used to touch a colony, mixing the bacteria with the water, and the liquid was spread as widely as possible. The sample was left to air dry.
2. The slide was then heated to fix the sample and then cooled afterward.
3. After fully staining the slide for a minute with Crystal Violet, the slide was washed.
4. The slide was covered for a minute with an iodine solution as a thorough stain, followed by rinsing.
5. The slide was carefully decolorized using Gram Stain Decolorizer for three seconds and then immediately rinsed with water.
6. After applying a 30-second safranin counterstain, the slide was washed with water
7. The slide was placed between the pages of a bibulous paper book to dry. After drying, the slide was taken out, and immersion oil was used to observe the organisms under the microscope.⁹¹

Biochemical test (IMViC test):

In-dole Test –

The bacteria that can change the amino acid tryptophan into indole can be found with this assay.

Procedure:

1. Agar medium deep tubes are filled with bacterial sample, which is then incubated at 37° for one to two days.
2. Kovac's reagent is applied sparingly to the test tube.
3. The colour red denotes a favourable outcome.
4. Several types of bacteria produce indole, including *Haemophilus influenza*, *Aeromonas hydrophila*, *Aeromonas punctata*, and *E. coli*.

Methyl-red test –

This test detects the presence of bacteria that ferment glucose to generate acid. In an acidic environment, the methyl red indicator turns red; whereas in a non-acidic environment, it displays an orange hue.

Procedure:

1. A bacterial sample is cautiously added to the MR-VP medium. Two to three days are spent incubating the culture.
2. The test tubes are filled with methyl red indicator.

The favourable outcomes are indicated by the red colouring. *Proteus vulgaris* and *E. coli* are examples of MR test positive.

Voges Proskeuer test-

Certain microbes can convert pyruvic acid into neutral end products such as acetyl methyl carbinol. This test can be used to identify these kinds of organisms

Procedure:

1. An MR-VP media is inoculated with the sample.
2. It then incubated for one to two days.
3. The culture is enriched with Barrit's reagent.
4. The presence of VP-positive organisms is indicated by the deep rose colour.

The VP test showed positive results for several bacterial species, including *Enterobacter*, *Klebsiella*, *Serratia marcescens*, *Vibrio cholera*, and *Vibrio alginolyticus*.

Citrate utilization test-

When no other carbon sources are available, certain microorganisms can get their energy from citrate owing to the enzyme citrate permease. Citrase changes citrate into acetate and oxaloacetic acid, which are then transformed into carbon dioxide and pyruvic acid. Sodium carbonate, a basic compound, forms when carbon dioxide reacts with sodium and water. The bromothymol blue indicator turns intense Prussian blue from green as a result of this reaction.

Procedure:

1. A properly prepared sample of the bacteria is introduced in Koser's citrate media, that includes bromothymol blue.
2. The prepared slant is then incubated for a period of one to two days.
3. A deep blue hue denotes a favourable outcome, whereas a green hue denotes an unfavourable outcome.

Bacteria such as *Serratia marcescens*, *Proteus mirabilis*, *Citrobacter freundii*, *Enterobacter*, *Klebsiella pneumoniae*, and *Providencia* are known to test positive for citrate utilization.⁹²

DNA Isolation: DNA extraction was performed using the QIAamp ® DNA Mini Kit, adhering to the following steps:

- To begin with, the materials were moved into a 1.5 ml microcentrifuge tube. To ensure full lysis, 20 µl of Proteinase K and 180 µl of Buffer ATL were added, vigorously mixed by vortexing, and incubated at 56°C for 3 hours.
- After that, 200 µl of Buffer AL was added, and 15 seconds of vigorous vortexing were required. After that, this mixture was incubated for ten minutes at 70°C. For a brief period, the tube was centrifuged to eliminate any droplets from the lid.
- 200 µl of 96–100% ethanol was then added, and the mixture was vortexed for 15 seconds. To remove any droplets from the cap, a quick centrifugation was performed on the tube. After that, the mixture was pipetted onto a QIAamp Mini spin column that had been put in a 2 ml collection tube. The column was then spun for one minute at 6000 x g (8000 rpm). The collection tube and flow-through were thrown away.
- After that, 500 µl of Buffer AW1 was added to a fresh 2 ml collection tube containing the QIAamp Mini spin column. For one minute, the tube was centrifuged at 6000 x g (8000 rpm).
- The collecting tube and flow-through were thrown away once more. After that, 500 µl of Buffer AW2 was added to a fresh 2 ml collection tube containing the QIAamp Mini spin column.

- After that, the tube was centrifuged for three minutes at maximum speed (20,000 x g; 14,000 rpm). The collection tube and flow-through were thrown away. Following that, the QIAamp Mini spin column was moved to a fresh 1.5 ml microcentrifuge tube. After adding distilled water, the tube was allowed to sit at room temperature for one minute.
- To extract the DNA, the tube was then centrifuged for one minute at 6000 x g (8000 rpm).
- Ultimately, a 1.0% agarose gel was used to evaluate the purity of the extracted DNA. The effective extraction of high-molecular weight DNA was confirmed by the observation of a single band.⁹³

PCR Amplification:

The primers used for sequencing the DNA molecule are as follows:

S.No	Primer Name	Sequence 5' to 3'	Length
1)	16S rRNA- F	F (5'-AGAGTTTGATCCTGGCTCAG-3')	20
2)	16S rRNA- R	R (5'-GGTTACCTTGTTACGACTT-3')	19

Table 1: Primers used for sequencing the DNA molecule

PCR Cycles	Temperature	Time
De- naturation	90° C	30 secs
Annealing	62° C	60 secs
Extension	72° C	120 secs

Table 2: Steps of PCR Amplification

Denaturation: Two single-stranded DNA templates are produced when the H-bond between two DNA strands breaks.

Annealing: The polymerase enzyme gets its starting point when the primers attach to the templates for single-stranded DNA.

Extension: By incorporating the nucleotides into the DNA template, the polymerase enzyme lengthens the primers and produces a new double stranded DNA molecule.

The steps of PCR Amplification are as follows:

1. Using the 16SrRNA-F and 16SrRNA-R primers, a portion of the 16S rRNA gene was amplified. On an agarose gel, a single, discrete band with a PCR amplicon size of 1500 bp was seen.
2. Purification was performed on the PCR amplicon to remove any impurities.
3. Using the 16SrRNA-F and 16SrRNA-R primers, a DNA sequencing reaction was carried out for both the forward and reverse strands of the PCR amplicon on the ABI 3730xl Genetic Analyser. The BDT v3.1 Cycle sequencing kit was employed.
4. Using alignment software, the forward and reverse sequencing data were combined to create the consensus sequence for the 16S rRNA gene.
5. The 'nr' database in the NCBI GenBank was searched using BLAST on the 16S rRNA gene sequence. Based on the greatest identity score, the top 10 sequences were chosen and aligned using the Clustal W multiple alignment program. Using MEGA 10, a distance matrix and phylogenetic tree were produced.⁹⁴

Phylogenetic Tree:

A phylogenetic tree shows the relationships between species graphically.

The sequence obtained from the sequencing analysis was subjected to BLAST on NCBI. Nucleotide blast was carried out. The forward and reverse nucleotide sequence was entered in the accession section. The organism was added in the allotted section and later clicked on blast. Similarly in the same section we also found the distance between the trees.

Statistical Analysis:

- Descriptive statistics
- Chi-square test
- Multiple logistic regression test
- Independent t test

Conclusion

This chapter has covered the research methodology, study design, variables involved, research setting, target population, sample selection, sampling method, creation of the instrument, details about the instrument, and the data collection process.

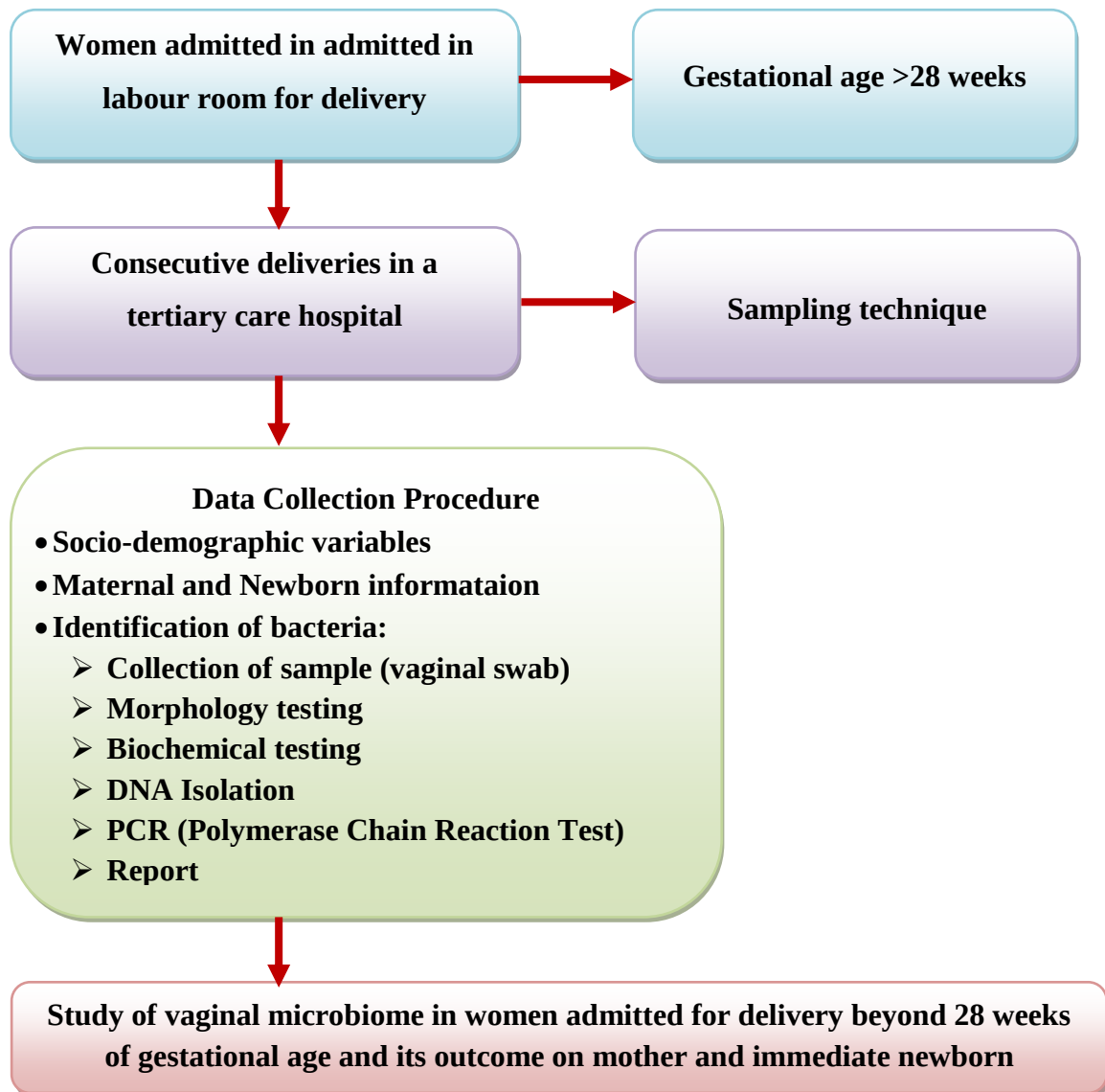


Figure 2: Flow chart of data collection procedure

CHAPTER IV

DATA ANALYSIS AND RESULT INTERPRETATION

This study investigated the vaginal microbiome of 300 mothers who delivered at a tertiary care hospital. The purpose of the data collection was to help the researchers understand the makeup of the vaginal microbiome in these individuals. They employed descriptive statistics, such as frequency and proportion for categorical variables, to analyse the data. Furthermore, an analysis of binary logistic regression was performed to evaluate the correlation between the explanatory factors and the result variables. With the use of odds ratios and 95% confidence intervals, the strength of these connections was assessed. A statistically significant relationship between an explanatory variable and an outcome variable was defined as having a p-value of less than 0.05. IBM SPSS version 22 was used for all statistical analyses.

The study aimed to...

1. To study the vaginal microbiome in women admitted for delivery beyond 28 weeks of gestational age and its outcome on mother and immediate newborn.

The results are presented in tables and figures below:

Section I: Study of vaginal microbiome in women admitted for delivery.

Section II: Socio-demographic variables and its associations with maternal and neonatal outcome.

4.1 SECTION I: STUDY OF VAGINAL MICROBIOME IN WOMEN ADMITTED FOR DELIVERY.

Biochemical Test: Gram staining was performed for all the samples followed by IMViC test. The analysis of the biochemical test were collected and reported.

Sample	Gram Staining			IMViC Test			
	Colour	Shape	Gram Reaction	Indole - test	Methyl - red test	Voges - Proskauer test	Citrate-utilization test
1.	Violet	Rod	Gram +	-	-	-	-
2.	Blue	Rod	Gram +	-	-	-	-
3.	Blue	Rod	Gram +	-	-	-	-
4.	Purple	Rod	Gram +	-	-	-	-
5.	Blue	Rod	Gram +	-	-	-	-
6.	Purple	Rod	Gram +	-	-	+	+
7.	Purple	Rod	Gram +	-	-	+	+
8.	Blue	Oval	Gram +	-	-	+	-
9.	Blue	Oval	Gram +	-	-	+	-
10.	Blue	Oval	Gram +	-	-	+	-
11.	Blue	Rod	Gram +	-	-	-	-
12.	Blue	Rod	Gram +	-	-	-	-
13.	Blue	Rod	Gram +	-	-	-	-
14.	Blue	Rod	Gram +	-	-	-	-
15.	Violet	Rod	Gram +	-	-	-	-

Table 3: Biochemical Test for selected samples

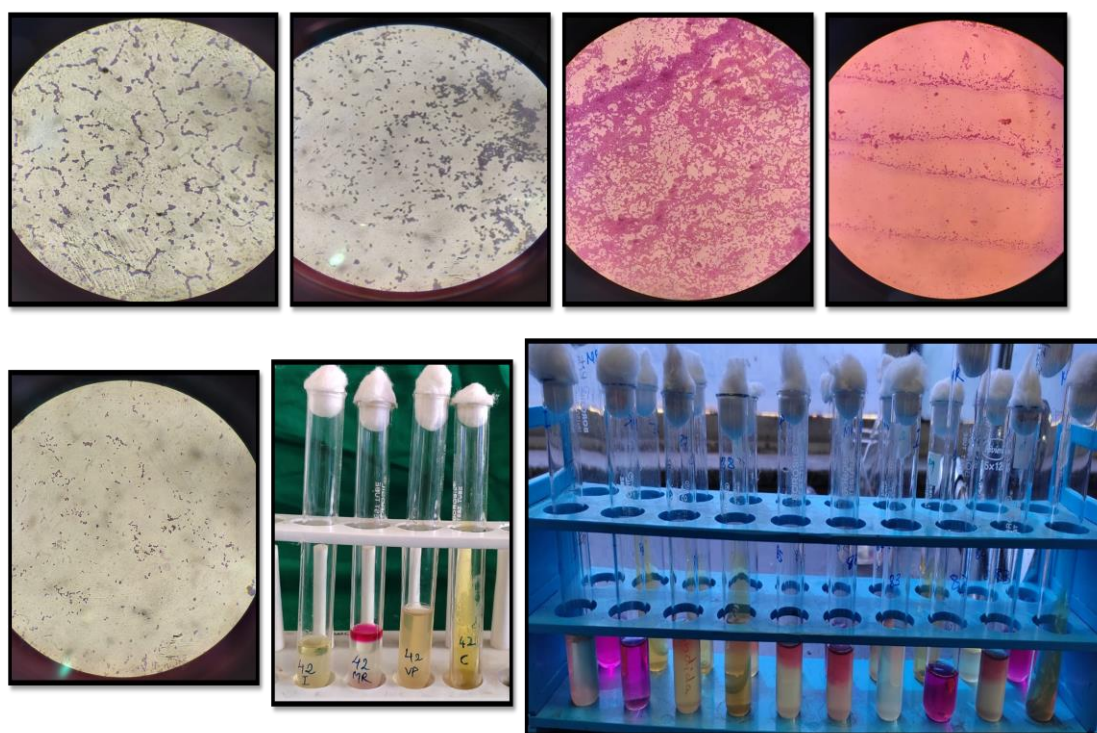


Figure 3: Gram Staining and IMVIC test

Bacteria	n	%
Gram Negative	18	6
Gram Positive	282	94
Total	300	100

Table 4: Biochemical Test Result

Out of all samples, **106** were Voges-Proskauer test positive and **69** were citrate test positive.

16S rRNA Amplification: After identifying the samples with similar characteristics, representatives were selected for DNA isolation and sent for sanger sequencing. In the analysis, the following universal primer was used:

S.No	Primer Name	Sequence 5' to 3'	Length
3)	16S rRNA- F	F (5'-AGAGTTTGATCCTGGCTCAG-3')	20
4)	16S rRNA- R	R (5'-GGTTACCTTGTTACGACTT-3')	19

Sanger Sequencing:

Sanger sequencing remains the gold standard for DNA sequencing, widely employed in labs worldwide. The technique takes advantage of a number of characteristics of a DNA polymerase, including its capacity to replicate a DNA molecule exactly, its enzymatic synthesis directionality, the DNA polymerase requires a strand of DNA, called a "primer," to act as a starting point. And this primer must have 3' hydroxyl (OH) group at its end, to attach new nucleotides.

The polymerase is unable to stretch the DNA strand in the absence of a 3' OH. The polymerase incorporates a dideoxynucleotide (ddNTP – ddATP, ddTTP, ddGTP, ddCTP), a base analogue without a 3' OH, into the developing strand of an enzymatic sequencing reaction.

The polymerase's ability to extend the DNA strand is halted when a ddNTP is incorporated. This happens because ddNTPs lack the 3' hydroxyl group that's crucial for the polymerase to attach further nucleotides. However, the polymerase still follows the standard base pairing rules when incorporating ddNTPs. Consequently, G couples with C and A pairs with T, ensuring the ddNTP is added to the correct location in the growing DNA strand.

Chain extension concludes when the polymerase incorporates a ddNTP. For every template, four reactions are carried out in order to ascertain the relative location of a given base along the DNA strand. We call this process "DNA sequence determination." To help with the procedure, each reaction contains a distinct dideoxynucleotide in addition to DNA polymerase, DNA primer, and dNTPs. The ratio of ddNTP to dNTP affects the average number of nucleotides that the polymerase can add to the DNA molecule before adding a ddNTP and stopping chain elongation. Radiation or other markers can be used to label the DNA primer, ddNTPs, or dNTPs in order to facilitate the detection of the freshly synthesised DNA strands. When a collection of molecules undergo these reactions, the reaction mixture is electrophoresed to produce a series of extension products that show the bases' locations along the DNA strand. By electrophoresing the products from various reaction tubes in adjacent lanes on a sequencing gel, the DNA sequence is obtained and the findings may be identified and analysed. The sequence of the expanded DNA strand from 5' to 3' can be found by examining the identities of the increasingly longer products, since DNA polymerase adds bases in the 5' to 3' direction. The bases nearest to the 5' end are identified by the smaller fragments. Usually, 300–400 bases can be determined by a single (manual) reaction.

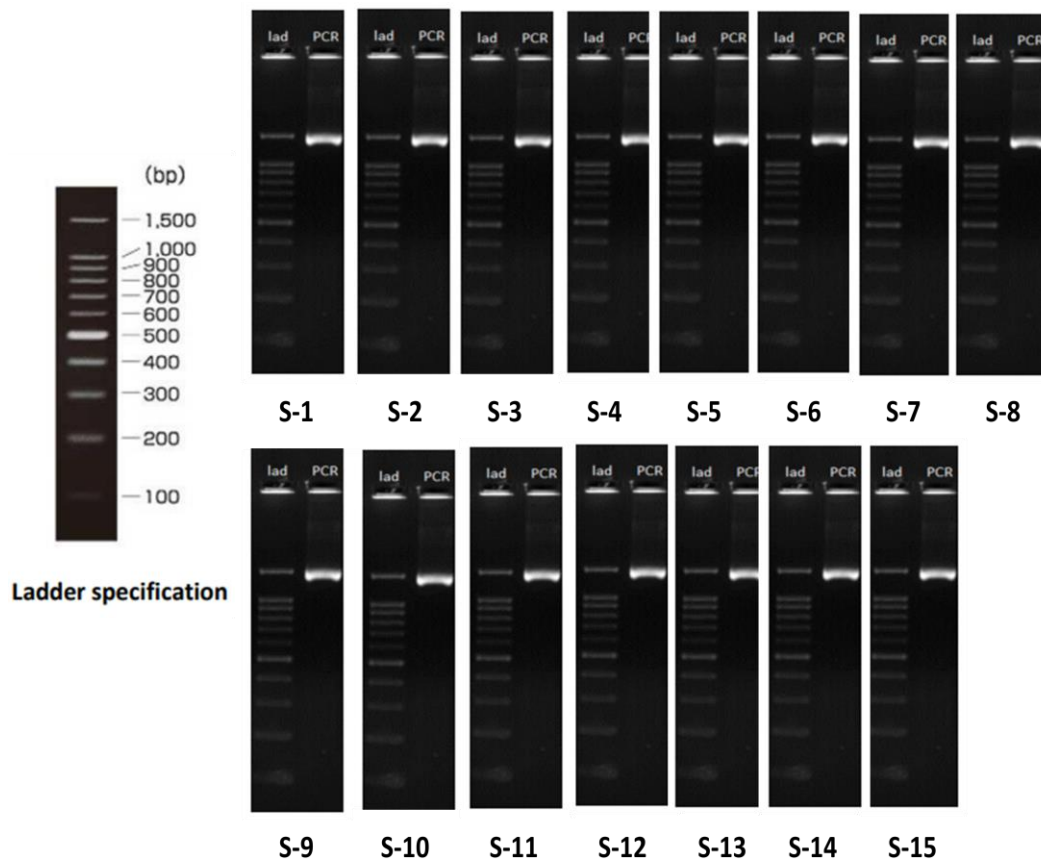
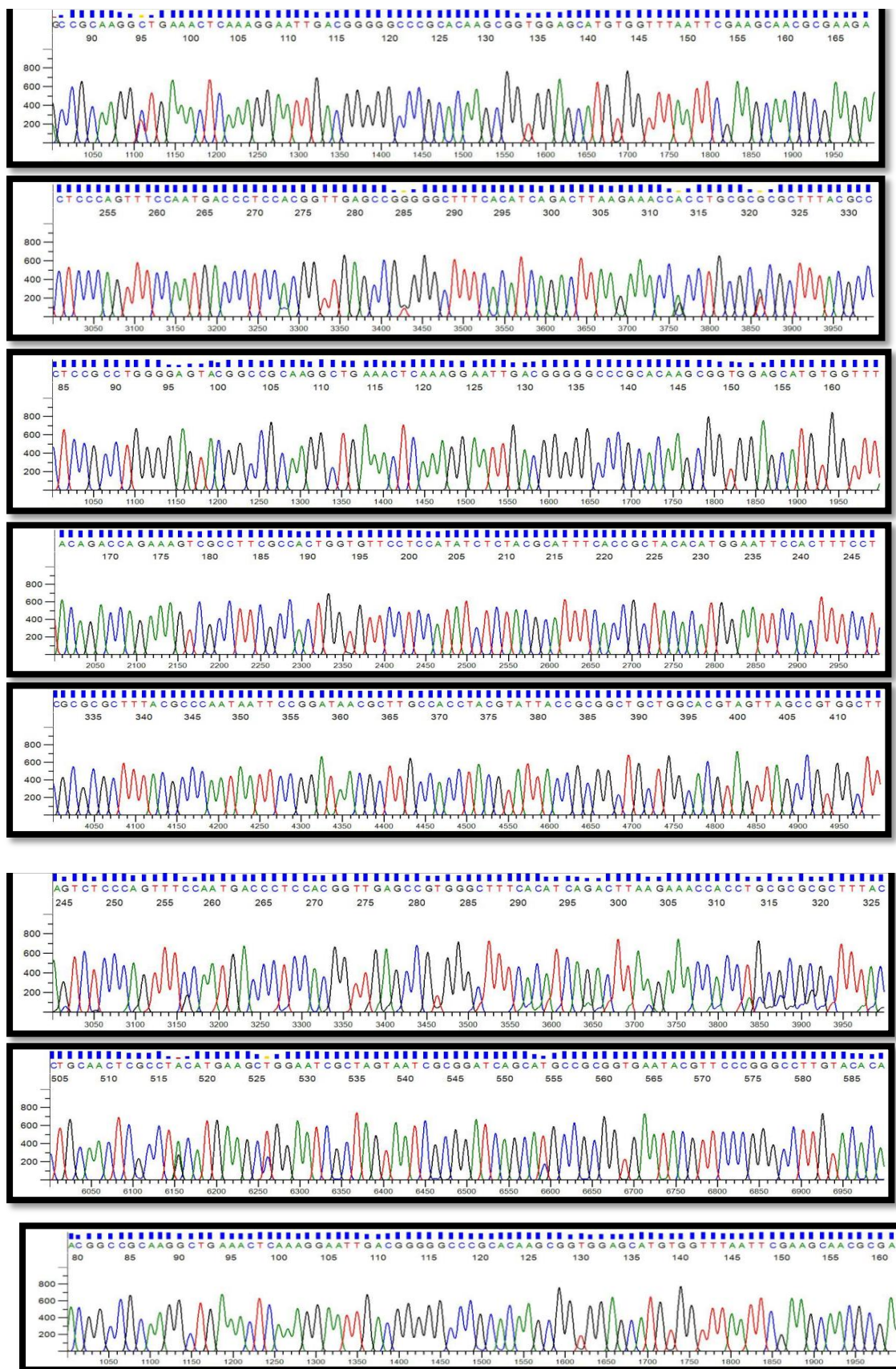


Figure 4: 16SrRNA amplicon of selected samples (S1: *Lactobacillus iners*, S2: *Lactobacillus crispatus*, S3: *Lactobacillus jensenii*, S4: *Lactobacillus gasseri*, S5: *Atopobium vaginae*, S6 & 7: *Bacillus cereus*, S8, 9 & 10: *Enterococcus faecalis*, S11 & 12 *Lactobacillus crispatus*, S13& 14: *Lactobacillus jensenii*, S15: *Pantoea sp*)

In the above figure, the primer binds at 500 base pair.



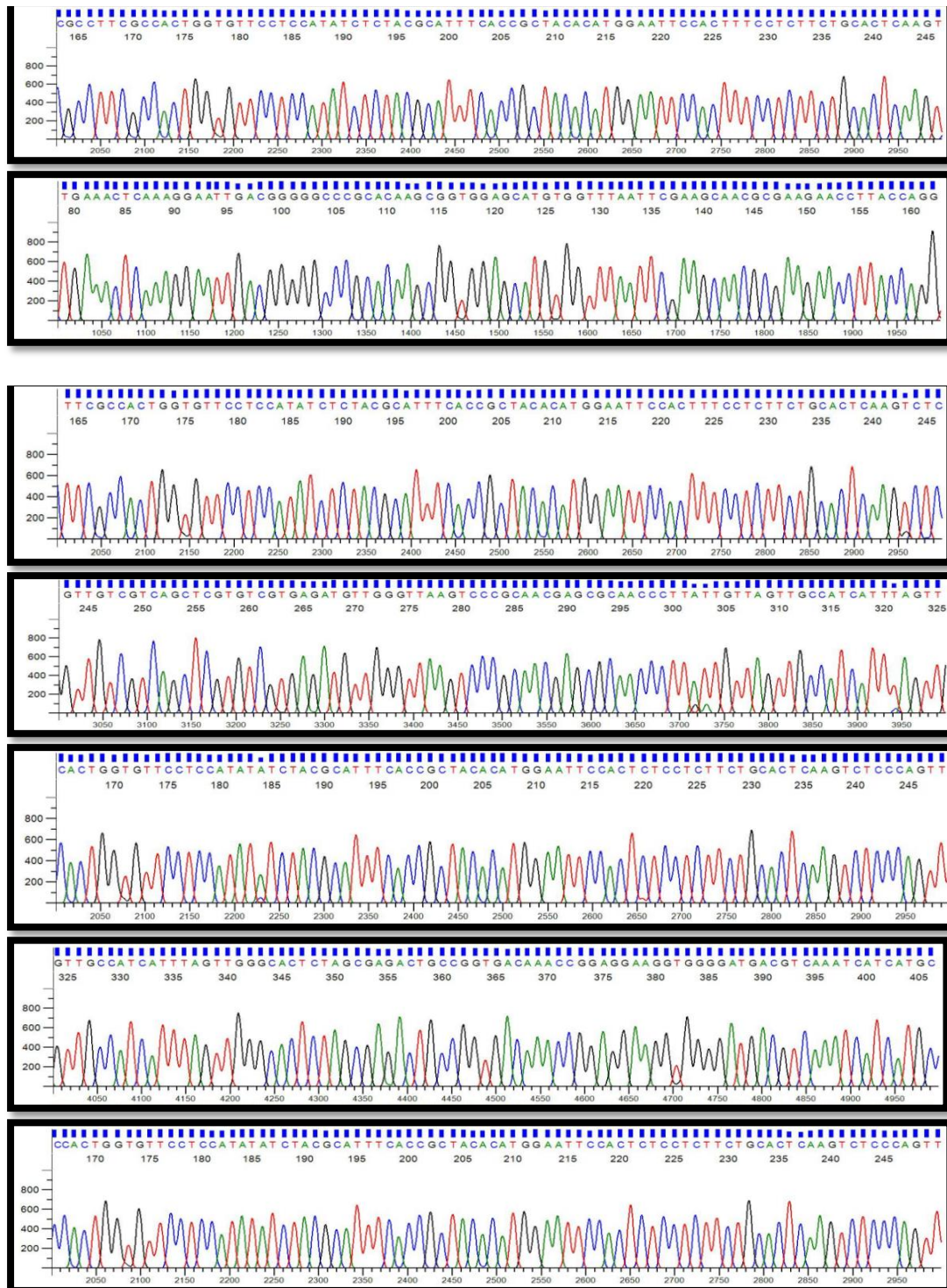


Figure 5: Sanger sequencing graph of selected samples

The peak of ATGC, whose waves are amplified, is shown in the above figures as the range where the nucleotide has a high expression level.

Preterm	n	%	Term	n	%
L. iners	20	48.8	L.iners	68	26.3
L.gasseri	3	7.3	L. crispatus	102	39.3
Atopobium vaginae	2	4.9	L. jensenii	72	27.8
E. fecalis	16	39	Bacillus cereus	17	6.6
Total	41	100	Total	259	100

Table 5: PCR amplification result

After the amplification, the samples were analyzed by Sanger Sequencing. The samples showed the presence of *Lactobacillus Crispatus*, *Lactobacillus jensenii*, *Lactobacillus inners*, *L. Gasseri*, *Bacillus cereus*, *Bacillus sp. Firmi*, *Bacillus sp. Strain*, *Atopobium vaginae*, *Enterococcus sp. Strain* and *Enterococcus faecalis*.

In the study, the women who had full term delivery showed more content of *L. crispatus*, *L. jensenii*, *L. iners*, *Bacillus cereus*, *Bacillus sp. Firmi* and *Bacillus sp. Strain*; and the women who had preterm delivery showed the presence of *lactobacillus iners*, *L.Gasseri*, *Atopobium vaginae*, *Enterococcus sp. Strain* and *Enterococcus faecalis*.

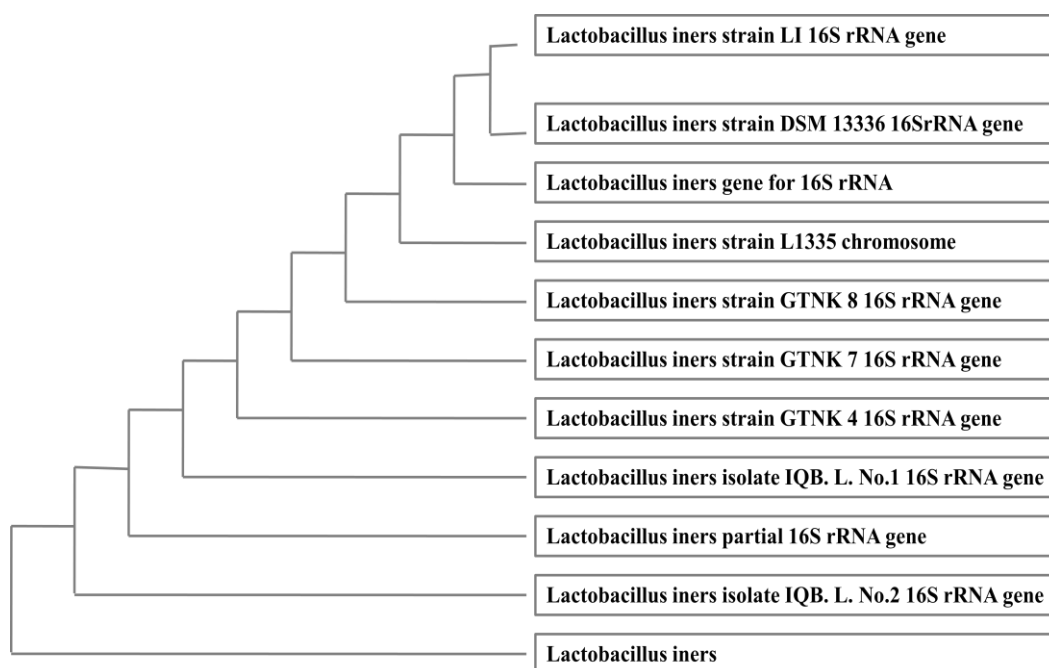
Phylogenetic tree analysis:

In the phylogenetic tree analysis, we found

- i. *Lactobacillus iners*
- ii. *Lactobacillus crispatus*
- iii. *Lactobacillus jensenii*

- iv. *Lactobacillus gasseri*
- v. *Atopobium vaginae*
- vi. *Bacillus cereus*
- vii. *Enterococcus faecalis*
- viii. *Pantoea* species

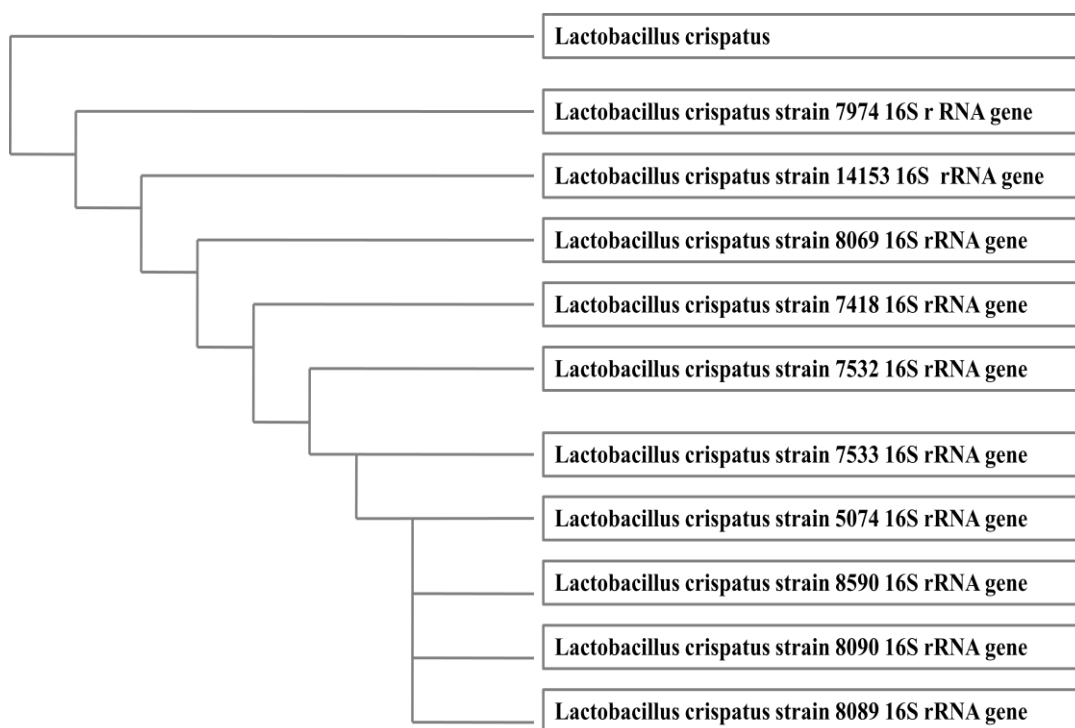
Following are the phylogenetic tree of selected samples:



S-1

Figure 6: Phylogenetic tree analysis for *Lactobacillus iners*

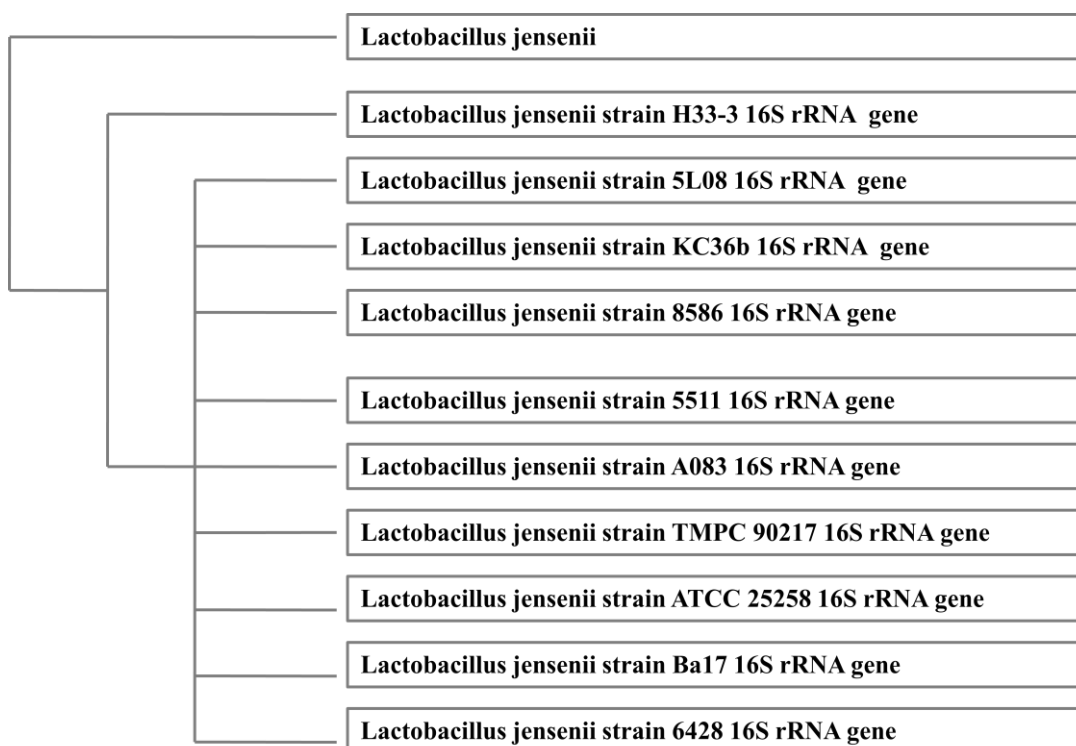
In the phylogenetic tree analysis for *Lactobacillus iners*, *Lactobacillus iners* strain LI 16S rRNA gene, *Lactobacillus iners* strain DSM 13336 16SrRNA gene, *Lactobacillus iners* strain L1335 chromosome, *Lactobacillus iners* strain GTNK 8 16S rRNA gene, *Lactobacillus iners* strain GTNK 7 16S rRNA gene, *Lactobacillus iners* strain GTNK 4 16S rRNA gene, etc were found.



S-2

Figure 7: Phylogenetic tree analysis for *Lactobacillus crispatus*

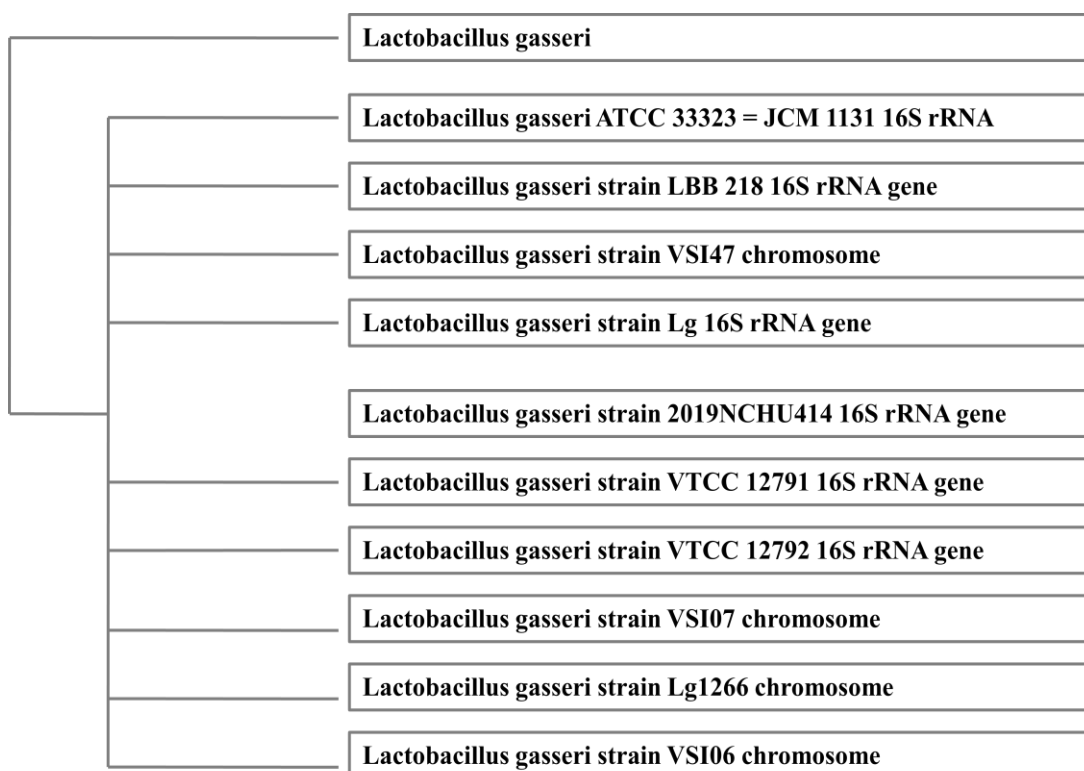
In the phylogenetic tree analysis for *Lactobacillus crispatus*, *Lactobacillus crispatus* strain 7974 16S rRNA gene, *Lactobacillus crispatus* strain 14153 16S rRNA gene, *Lactobacillus crispatus* strain 8069 16S rRNA gene, *Lactobacillus crispatus* strain 7418 16S rRNA gene, *Lactobacillus crispatus* strain 7532 16S rRNA gene, *Lactobacillus crispatus* strain 7533 16S rRNA gene, *Lactobacillus crispatus* strain 5074 16S rRNA gene, *Lactobacillus crispatus* strain 8590 16S rRNA gene, *Lactobacillus crispatus* strain 8090 16S rRNA gene, *Lactobacillus crispatus* strain 8089 16S rRNA gene, etc were found.



S-3

Figure 8: Phylogenetic tree analysis for *Lactobacillus jensenii*

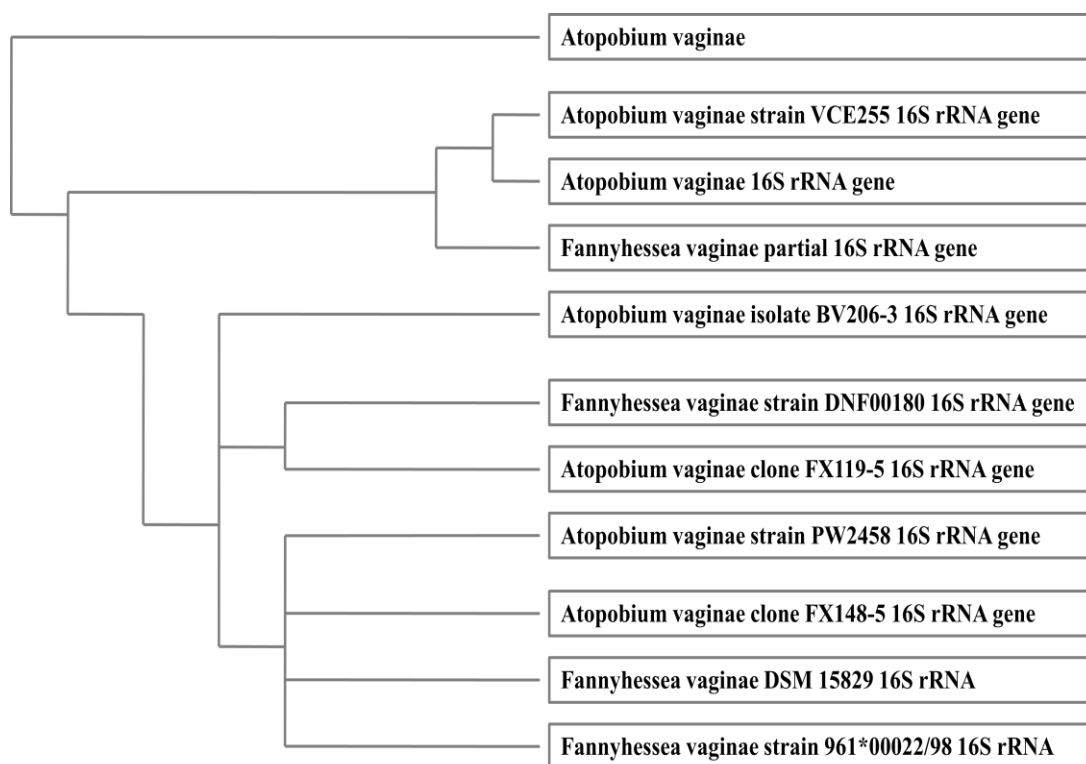
In the phylogenetic tree analysis for *Lactobacillus jensenii*, *Lactobacillus jensenii* strain H33-3 16S rRNA gene, *Lactobacillus jensenii* strain 5L08 16S rRNA gene, *Lactobacillus jensenii* strain KC36b 16S rRNA gene, *Lactobacillus jensenii* strain 8586 16S rRNA gene, *Lactobacillus jensenii* strain 5511 16S rRNA gene, *Lactobacillus jensenii* strain A083 16S rRNA gene, *Lactobacillus jensenii* strain TMPC 90217 16S rRNA gene, *Lactobacillus jensenii* strain ATCC 25258 16S rRNA gene, *Lactobacillus jensenii* strain Ba17 16S rRNA gene, *Lactobacillus jensenii* strain 6428 16S rRNA gene, etc were found.



S-4

Figure 9: Phylogenetic tree analysis for *Lactobacillus gasseri*

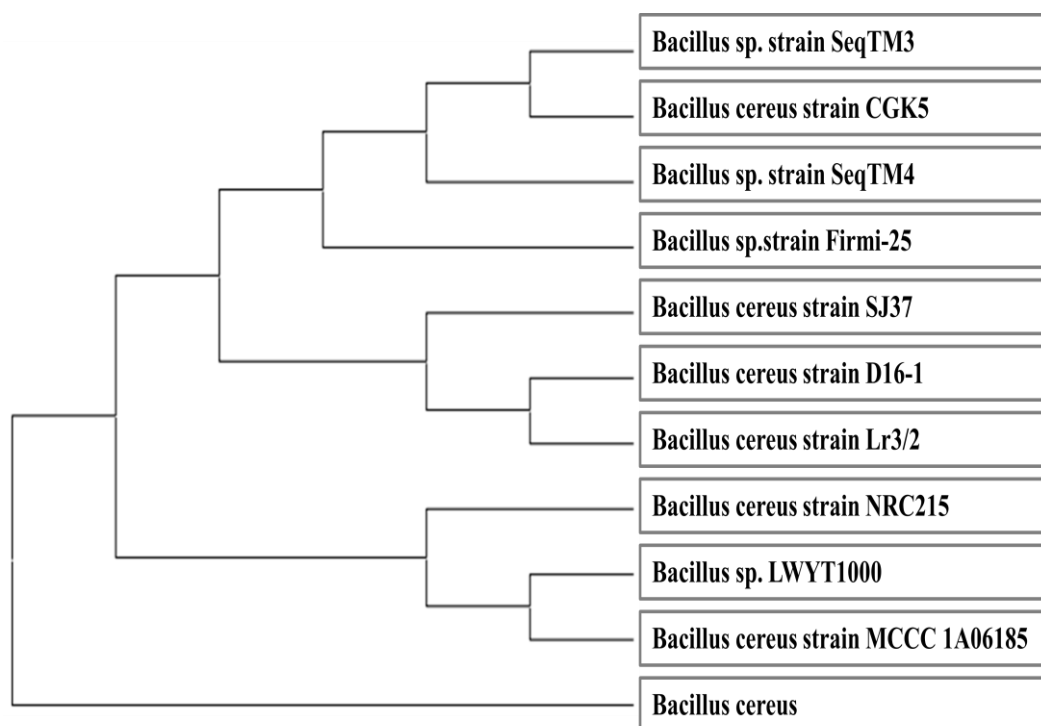
In the phylogenetic tree analysis for *L. gasseri*, *L. gasseri* ATCC 33323=JCM 1131 16S rRNA, *Lactobacillus gasseri* strain LBB 218 16S rRNA gene, *Lactobacillus gasseri* strain VSI47 chromosome, *Lactobacillus gasseri* strain Lg 16S rRNA gene, *Lactobacillus gasseri* strain 2019NCHU414 16S rRNA gene, *Lactobacillus gasseri* strain VTCC 12791 16S rRNA gene, *Lactobacillus gasseri* strain VTCC 12792 16S rRNA gene, *Lactobacillus gasseri* strain VSI07 chromosome, *Lactobacillus gasseri* strain Lg1266 chromosome, *Lactobacillus gasseri* strain VSI06 chromosome, etc were found.



S-5

Figure 10: Phylogenetic tree analysis for *Atopobium vaginae*

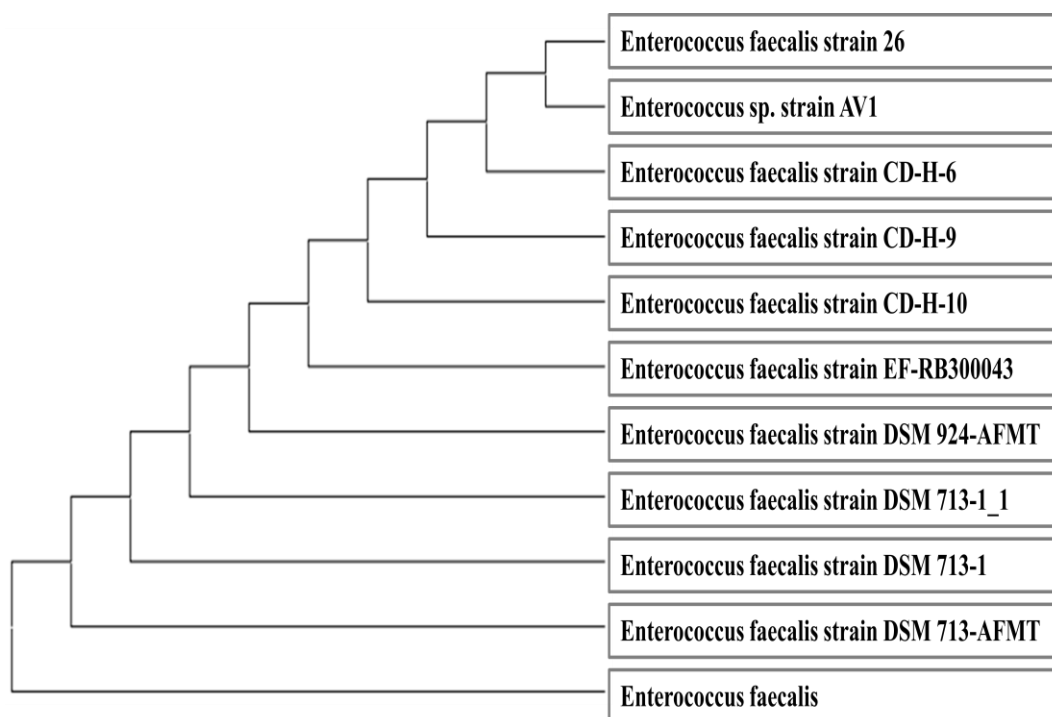
In the phylogenetic tree analysis for *Atopobium vaginae*, *Atopobium vaginae* strain VCE255 16S rRNA gene, *Atopobium vaginae* 16S rRNA gene, *Fannyhessea vaginae* partial 16S rRNA gene, *Atopobium vaginae* isolate BV206-3 16S rRNA gene, *Fannyhessea vaginae* strain DNF00180 16S rRNA gene, *Atopobium vaginae* clone FX119-5 16S rRNA gene, *Atopobium vaginae* strain PW2458 16S rRNA gene, *Atopobium vaginae* clone FX148-5 16S rRNA gene, *Fannyhessea vaginae* DSM 15829 16S rRNA, *Fannyhessea vaginae* strain 961*00022/98 16S rRNA, etc were found.



S-6

Figure 11: Phylogenetic tree analysis for *Bacillus cereus*

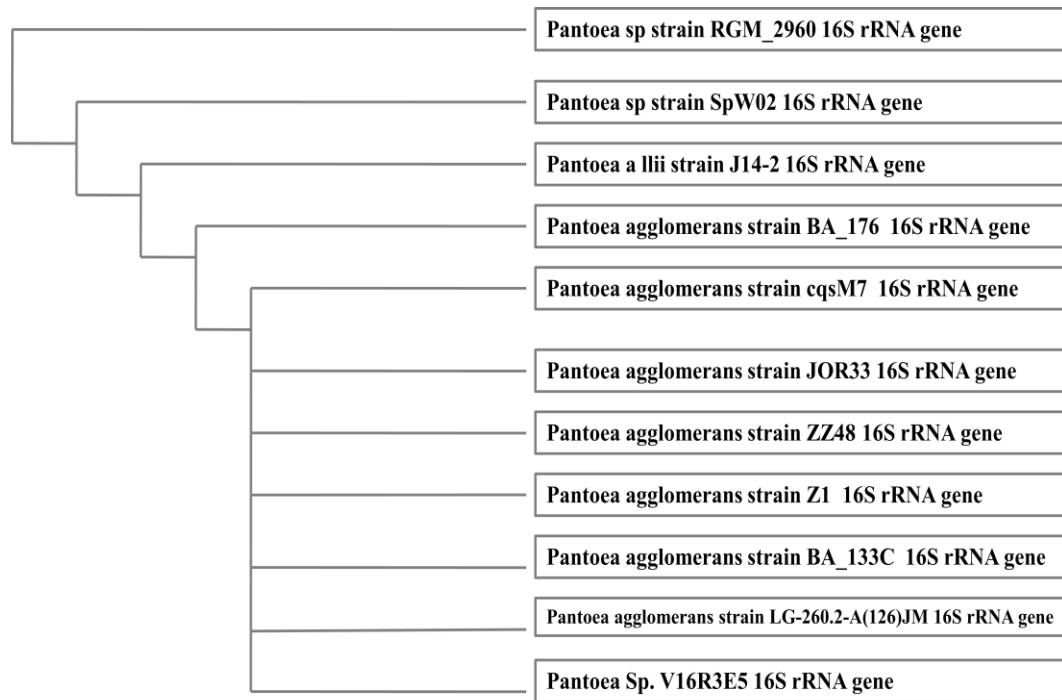
In the *Bacillus cereus* phylogenetic tree analysis, *Bacillus sp. strain SeqTM3*, *Bacillus cereus strain CGK5*, *Bacillus sp. strain SeqTM4*, *Bacillus sp. strain Firmi-25*, *B. cereus strain SJ37*, *B. cereus strain D16-1*, *B. cereus strain Lr3/2*, *B. cereus strain NRC215*, *B. sp. LWYT1000*, *B. cereus strain MCCC 1A06185*, etc were found.



S-8

Figure 12: Phylogenetic tree analysis for *Enterococcus faecalis*

In the phylogenetic tree analysis for *Enterococcus faecalis*, *Enterococcus faecalis* strain 26, *Enterococcus* sp. strain AV1, *Enterococcus faecalis* strain CD-H-6, *Enterococcus faecalis* strain CD-H-9, *Enterococcus faecalis* strain CD-H-10, *E. faecalis* strain EF-RB300043, *E. faecalis* strain DSM 924-AFMT, *E. faecalis* strain DSM 713-1_1, *Enterococcus faecalis* strain DSM 713-1, *Enterococcus faecalis* strain DSM 713-AFMT, etc were found.



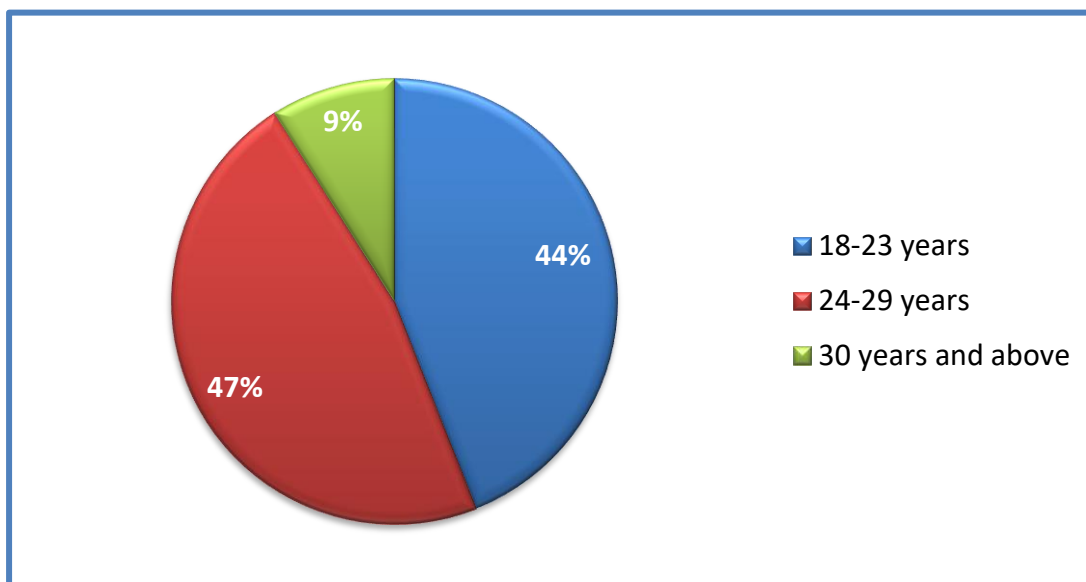
S-15

Figure 13: Phylogenetic tree analysis for *Pantoea* species

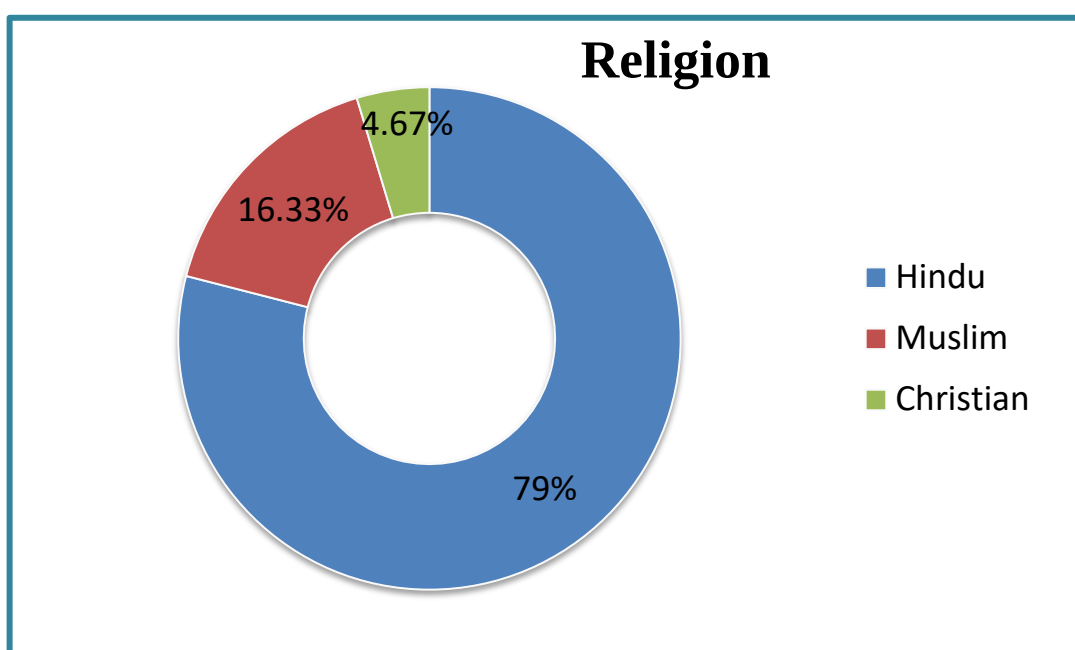
In the phylogenetic tree analysis for *Pantoea* species, *Pantoea* sp strain RGM_2960 16S rRNA gene, *Pantoea* sp strain SpW02 16S rRNA gene, *Pantoea a llii* strain J14-2 16S rRNA gene, *Pantoea agglomerans* strain BA_176 16S rRNA gene, *Pantoea agglomerans* strain cqsM7 16S rRNA gene, *Pantoea agglomerans* strain JOR33 16S rRNA gene, *Pantoea agglomerans* strain ZZ48 16S rRNA gene, *Pantoea agglomerans* strain Z1 16S rRNA gene, *Pantoea agglomerans* strain BA_133C 16S rRNA gene, *Pantoea agglomerans* strain LG-260.2-A(126)JM 16S rRNA gene, *Pantoea* Sp. V16R3E5 16S rRNA gene, etc were found.

SECTION II: SOCIO-DEMOGRAPHIC VARIABLES AND ITS ASSOCIATIONS WITH MATERNAL AND NEONATAL OUTCOME.

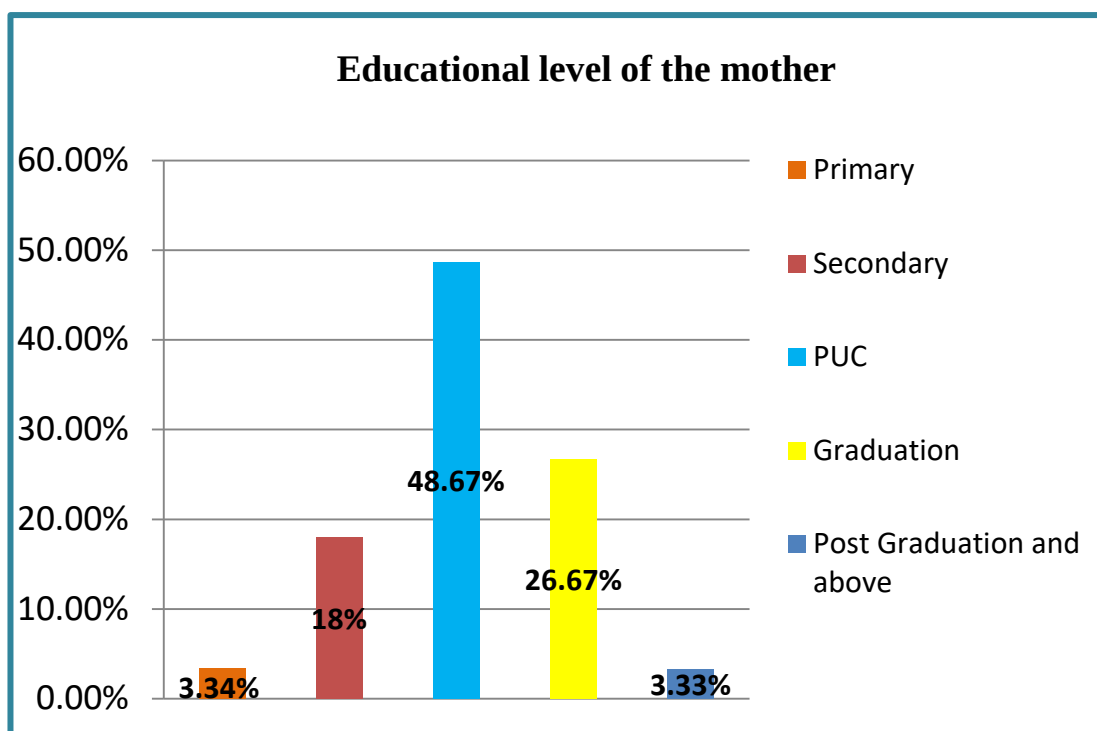
A. Demographic characteristics of respondents:



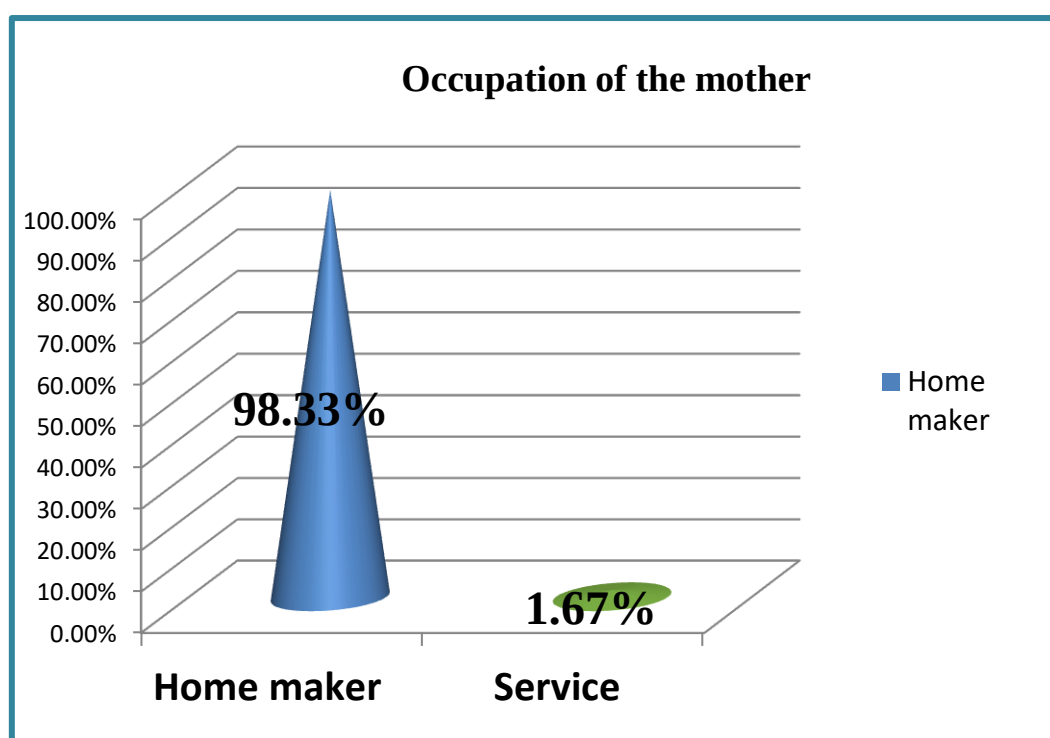
Graph 1: A pie graph showing percentage distribution of age of the mother.



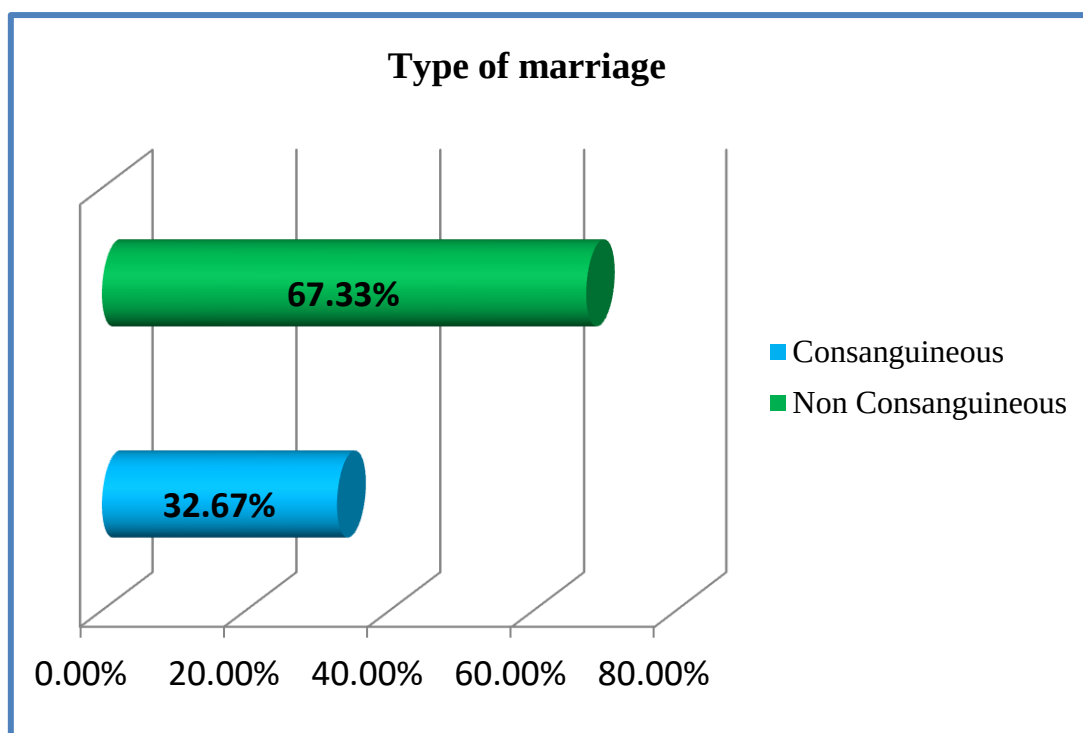
Graph 2: A doughnut graph showing percentage distribution of age of the mother.



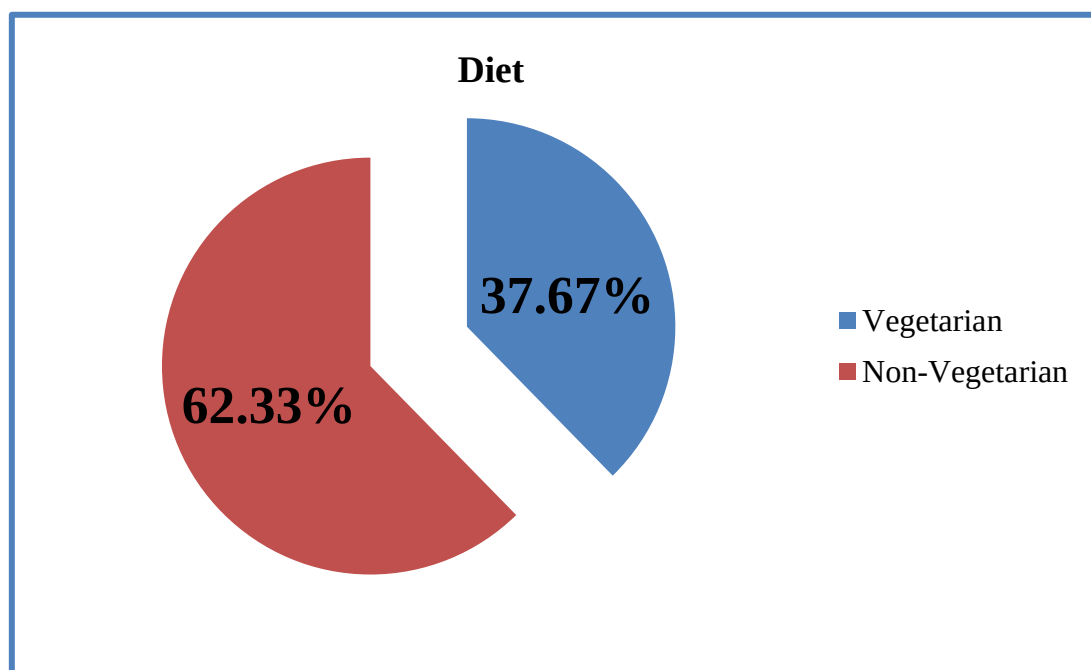
Graph 3: A column graph showing percentage distribution of educational level of the mother.



Graph 4: A column graph showing percentage distribution of occupation of the mother.



Graph 5: A bar graph showing percentage distribution of type of marriage of the mother.



Graph 6: A pie graph showing percentage distribution of age of the mother.

Graph 1-6 depicts the demographic characteristics of the respondents, among 300, majority (47%) of the mothers belongs 24-29 years of age group, 44% belongs to the age group of 18-23 years and 9% belongs to 30 years and above; 79% of them are Hindu, 16.33% Muslim and 4.67% Christian; 48.67% have completed Pre-University Course and few (3.33%) completed post-graduation and above; 98.33% are home maker and 1.67% are employed (service); 67.33% had a non- consanguineous marriage while 32.67% had consanguineous marriage; and 62.33% are non-vegetarian whereas 37.67% are vegetarian.

B. Maternal characteristics of respondents:**n=300**

Maternal characteristics	No of respondents	% of respondents
Mode of delivery		
Vaginal delivery	187	62.33
Cesarean section	113	37.67
Parity -		
Primipara	174	58.00
2	107	35.67
3	19	6.33
Gravida		
One	158	52.67
Two	89	29.67
Three	46	15.33
Four +	7	2.33
Total	300	100.00

Table 6 shows the maternal characteristics of 300 respondents, focusing on mode of delivery, parity, and gravida. Regarding the mode of delivery, the majority (62.33%) had a vaginal delivery, while 37.67% underwent a cesarean section. In terms of parity, 58% of respondents were primipara (first-time mothers), 35.67% had given birth twice, and 6.33% had given birth three times. Gravida, which refers to the number of pregnancies a woman has had, shows that 52.67% of respondents had been pregnant once, 29.67% twice, 15.33% three times, and only 2.33% had four or more pregnancies.

C. Association between socio demographic variables with maternal and neonatal outcome

n=300

	Age of the mother					Education level of the mother						
Health outcome	18-23 years	24-29 years	30 years+	%	χ^2 test, p-value	Prim ary	Secon dary	PUC	Degree	PG	%	χ^2 test, p-value
Mode of delivery												
Vaginal delivery	84	86	17	62.33	0.208,	7	39	96	40	5	62.33	9.058, 0.06
Cesarean section	48	55	10	37.67	0.901	3	15	50	40	5	37.67	
Parity												
Primipara	103	62	9	58	45.232,	6	23	87	51	7	58	13.25, 0.104
2	28	66	13	35.67	0.0001*	4	23	53	25	2	35.67	
3	1	13	5	6.33		0	8	6	4	1	6.33	
Gravida												
One	91	61	6	52.67	43.262,	6	16	85	44	7	52.67	26.569, 0.0090*
Two	33	47	9	29.67	0.0001*	0	20	41	26	2	29.67	
Three	8	29	9	15.33		3	16	18	8	1	15.33	
Four +	0	4	3	2.33		1	2	2	2	0	2.33	
No. of antenatal visits												
4-6 Visits	6	12	1	6.33	2.5,	3	6	9	1	0	6.33	17.23, 0.0280*
7-10 visits	29	28	7	21.33	0.645	1	12	33	17	1	21.33	
11-13 visits	97	101	19	72.33		6	36	104	62	9	72.33	

If underwent CS/ forceps/ vacuum delivery, what is the indication												
No	82	82	18	60.67	5.916, 0.206	8	39	93	37	5	60.67	14.721, 0.065
Maternal Cause	9	22	3	11.33		1	2	17	12	2	11.33	
Fetal Cause	41	37	6	28		1	13	36	31	3	28	
Is baby admitted to NICU-												
Yes	26	18	3	15.67	2.945, 0.229	0	8	30	6	3	15.67	10.114, 0.0390*
No	106	123	24	84.33		10	46	116	74	7	84.33	
Reason for NICU admission Immediately after birth												
Prematurity	3	1	0	1.33	8.667, 0.193	0	1	2	1	0	1.33	39.729, 0.0001*
Asphyxia	2	6	0	2.67		0	1	4	0	3	2.67	
Others	21	11	3	11.67		0	6	24	5	0	11.67	
NA	106	123	24	84.33		10	46	116	74	7	84.33	
Is baby treated with Oxygen												
Yes	8	7	0	5	1.734, 0.42	1	3	7	1	3	5	16.101, 0.0030*
No	124	134	27	95		7	51	139	79	7	95	
Total	132	141	27	100		10	54	146	80	10	100	

Table no.7 presents the association between socio-demographic variables and maternal and neonatal outcomes. It categorizes data based on the mother's age and education level while analyzing different health outcomes.

Mode of Delivery: Among the total deliveries, 62.33% were vaginal, while 37.67% were cesarean sections. The chi-square test for mode of delivery based on education level showed no significant association ($p = 0.06$).

Parity: Primiparous mothers accounted for 58%, while those with two and three deliveries made up 35.67% and 6.33%, respectively. A statistically significant association was found between parity and maternal education ($p = 0.0001$).

Gravida: Mothers with a single pregnancy history represented 52.67%, while those with two, three, and four or more pregnancies constituted 29.67%, 15.33%, and 2.33%, respectively. A significant relationship was observed between gravida and education level ($p = 0.009$).

Antenatal Visits: Most mothers (72.33%) had 11-13 antenatal visits, while 21.33% had 7-10 visits, and only 6.33% had 4-6 visits. The number of antenatal visits was significantly associated with education level ($p = 0.028$).

Indications for CS/Forceps Delivery: Among those who underwent CS or forceps delivery, 60.67% had no indication, while 11.33% were due to maternal causes and 28% due to fetal causes. However, no significant association was found ($p = 0.065$).

NICU Admission: **About** 15.67% of neonates were admitted to the NICU, and the association with education level was statistically significant ($p = 0.039$).

Reasons for NICU Admission: Among admitted neonates, 1.33% were due to prematurity, 2.67% due to asphyxia, and 11.67% due to other causes. A highly significant association was found ($p = 0.0001$).

Oxygen Treatment for Neonates: Only 5% of babies required oxygen support, while 95% did not. A statistically significant relationship between education and neonatal oxygen treatment was observed ($p = 0.003$).

Thus, the table indicates that socio-demographic factors, particularly maternal education, have a significant impact on various maternal and neonatal health outcomes, including parity, gravida, antenatal visits, NICU admission, and neonatal oxygen treatment.

D. Association between gestational age (Preterm and term) with demographic characteristics

n=300

Characteristics	Preterm	%	Term	%	Total	%	χ^2 test, p-value	p-value
Age of the mother								
18-23 years	22	53.66	110	42.47	132	44.00	2.2130	0.3310
24-29 years	17	41.46	124	47.88	141	47.00		
30 years & above	2	4.88	25	9.65	27	9.00		
Religion								
Hindu	31	75.61	206	79.54	237	79.00	0.8000	0.6700
Muslim	7	17.07	42	16.22	49	16.33		
Christian	3	7.32	11	4.25	14	4.67		
Education level of the Mother								
Primary	0	0.00	10	3.86	10	3.34	6.3775	0.2711
Secondary	11	26.83	43	16.60	54	18.00		
PUC	22	53.66	124	47.88	146	48.67		
Graduation	8	19.51	72	27.80	80	26.67		
Post Graduation & above	0	0.00	10	3.86	10	3.33		
Occupation of Woman								
Home maker	41	100	254	98.07	295	98.33	0.8050	0.3700
Service	0	0.00	5	1.93	5	1.67		

Type of Marriage								
Consanguineous	10	24.39	88	33.98	98	32.67	1.4790	0.2240
Non Consanguineous	31	75.61	171	66.02	202	67.33		
Diet								
Vegetarian	15	36.59	98	37.84	113	37.67	0.0240	0.8780
Non-Vegetarian	26	63.41	161	62.16	187	62.33		
Total	41	100	259	100	300	100.0		

Table no.8 describes the association between gestational age (preterm and term births) and various demographic factors among 300 participants. The analysis includes maternal age, religion, education, occupation, type of marriage, and diet, using the chi-square (χ^2) test to determine statistical significance.

Results show that most preterm births occur in mothers aged 18-29 years, with no significant difference across age groups ($p = 0.3310$). Religion-wise, Hindu mothers had the highest proportion of preterm births, but the association was not significant ($p = 0.6700$). Education levels revealed the highest preterm births in PUC-educated mothers, though not statistically significant ($p = 0.2711$). Nearly all preterm births were among homemakers, with no impact of occupation ($p = 0.3700$).

Regarding type of marriage, consanguinity did not significantly affect gestational age ($p = 0.2240$). Similarly, dietary habits showed no influence on preterm birth ($p = 0.8780$).

Overall, none of the demographic factors analyzed had a statistically significant impact on gestational age, suggesting that other medical, genetic, or environmental factors might be more influential.

E. Multiple logistic regression analysis of gestational age by maternal outcomes

Maternal outcomes	Adjusted OR	95% CI for OR		p-value
		Lower	Upper	
Mode of delivery				
Vaginal delivery	0.32	0.19	0.54	0.0001*
Cesarean section	Ref.			
Parity				
Primipara	Ref.			
2	1.03	0.20	5.23	0.9690
3	0.82	0.05	13.68	0.8880
Gravida				
One	Ref.			
Two	0.25	0.06	1.16	0.0760
Three	0.10	0.01	0.75	0.0250*
Four +	0.19	0.01	2.84	0.2290

Table no.9 explains the relationship between maternal outcomes and different variables such as Mode of Delivery, Parity, and Gravida. Vaginal delivery was found to be significantly associated with a reduced likelihood of the maternal outcome compared to cesarean section. The adjusted odds ratio (OR) of 0.32 (95% CI: 0.19 - 0.54, $p = 0.0001$) suggests that vaginal delivery decreases the odds of the outcome by 68%. The confidence interval does not include 1, indicating statistical significance, and the highly significant p-value further supports the strength of this association.

Parity was not found to have a significant association with maternal outcomes. Women with two previous births had an odds ratio (OR) of 1.03 (95% CI: 0.20 - 5.23, $p = 0.9690$), indicating no meaningful difference compared to primipara women. The wide confidence interval suggests a high degree of uncertainty, and the non-significant p -value further supports the lack of association. Similarly, women with three previous births had an OR of 0.82 (95% CI: 0.05 - 13.68, $p = 0.8880$), indicating a slight reduction in odds, but the extremely wide confidence interval reflects a lack of precision, and the non-significant p -value suggests no strong evidence of an effect.

Regarding gravida, women with two pregnancies had an OR of 0.25 (95% CI: 0.06 - 1.16, $p = 0.0760$), suggesting a 75% reduction in odds compared to primigravida women, but the confidence interval crossing 1 and the non-significant p -value indicate that the association is not strong. In contrast, women with three pregnancies had an OR of 0.10 (95% CI: 0.01 - 0.75, $p = 0.0250$), signifying a 90% reduction in odds. The confidence interval does not include 1, and the p -value is significant, making this a strong finding. However, for women with four or more pregnancies (OR = 0.19, 95% CI: 0.01 - 2.84, $p = 0.2290$), although the odds ratio suggests a reduction in odds, the wide confidence interval and non-significant p -value indicate high variability and a lack of strong association.

Hence, vaginal delivery significantly reduces the odds of maternal outcomes compared to cesarean section. Parity does not show a significant effect on maternal outcomes. Gravida three is significantly associated with reduced odds of maternal outcomes. Other gravida categories do not show strong statistical significance.

F. Multiple logistic regression analysis of gestational age by neonatal outcomes

n=300

Neonatal outcomes	Adjusted OR	95% CI for OR		p-value
		Lower	Upper	
No. of antenatal visits				
4-6 Visits	Ref.			
7-10 visits	2.08	0.69	6.30	0.1950
11-13 visits	0.51	0.27	0.96	0.0360*
If underwent CS/ forceps/ vacuum delivery. What is the indication				
No	Ref.			
Maternal Cause	0.10	0.03	0.34	0.0001*
Fetal Cause	0.18	0.09	0.33	0.0001*
Is baby admitted to NICU-				
No	Ref.			
Yes	1.83	0.80	4.20	0.1540
Reason for NICU admission Immediately after birth				
Prematurity	Ref.			
Asphyxia	-	-	-	-
Others	0.52	0.03	8.04	0.6380
Is baby treated with Oxygen				
No	Ref.			
Yes	3.61	0.37	35.48	0.2710

Table no.10 indicates the relationship between various neonatal outcomes and their predictors, including antenatal visits, mode of delivery, NICU admission, and oxygen treatment.

For antenatal visits, the reference group consists of mothers who had 4-6 visits. Compared to them, those who had 7-10 visits had higher odds of the neonatal outcome (OR = 2.08), but this result was not statistically significant ($p = 0.1950$). However, mothers who had 11-13 visits had significantly lower odds of adverse neonatal outcomes (OR = 0.51, $p = 0.0360$), suggesting that frequent antenatal care may contribute to better neonatal health.

Regarding the mode of delivery, when operative delivery (CS/forceps/vacuum) was performed for maternal or fetal indications, both conditions were associated with significantly lower odds of neonatal complications. Specifically, maternal indications were associated with an OR of 0.10 ($p = 0.0001$), while fetal indications had an OR of 0.18 ($p = 0.0001$). These findings suggest that timely intervention for maternal or fetal distress may reduce the likelihood of adverse neonatal outcomes.

The analysis also examined whether NICU admission influenced neonatal outcomes. Babies admitted to NICU had 1.83 times higher odds of experiencing neonatal complications compared to those not admitted, but this association was not statistically significant ($p = 0.1540$). Among the reasons for NICU admission, prematurity was the reference category, while other reasons (such as asphyxia or miscellaneous conditions) did not show a significant effect on neonatal outcomes ($p = 0.6380$).

Lastly, the analysis explored whether babies requiring oxygen treatment had different odds of adverse outcomes. While oxygen-treated infants had an OR of 3.61, the wide confidence interval (0.37 - 35.48) and a non-significant p-value (0.2710).

Hence, more antenatal visits (11-13) are associated with a significantly reduced risk of adverse neonatal outcomes (OR = 0.51, $p = 0.0360$). Delivery interventions (CS/ forceps/ vacuum) due to maternal or fetal causes are protective against adverse neonatal outcomes (both $p < 0.05$). NICU admission, reasons for NICU admission, and oxygen treatment show no statistically significant associations with neonatal outcomes.

Overall, the results highlight the importance of adequate antenatal care and timely obstetric interventions in improving neonatal health. However, factors like NICU admission and oxygen treatment did not show strong associations with neonatal outcomes, potentially due to sample size limitations or confounding variables.

G. Multiple logistic regression analysis of gestational age by other parameters

Others	Adjusted OR	95% CI for OR		p-value
		Lower	Upper	
Birth weight	0.07	0.03	0.18	0.0001*
Head circumference	0.78	0.56	1.08	0.1310
Chest circumference	0.97	0.68	1.37	0.8490
Length	1.43	1.16	1.77	0.0010*
APGAR Score at 1 min.	1.07	0.67	1.73	0.7730

Table no.11 examines the relationship between gestational age and several neonatal parameters, including birth weight, head circumference, chest circumference, length, and APGAR score at 1 minute.

Birth weight shows a strong negative association with gestational age, with an adjusted OR of 0.07 (95% CI: 0.03 - 0.18) and a highly significant p-value (0.0001). This suggests that lower birth weight is strongly linked to lower gestational age, meaning that preterm infants are significantly more likely to have lower birth weights.

Head circumference has an OR of 0.78 (95% CI: 0.56 - 1.08) with a p-value of 0.1310, indicating no significant association between head circumference and gestational age. This suggests that variations in head circumference may not be a strong predictor of gestational age.

Chest circumference has an OR of 0.97 (95% CI: 0.68 - 1.37) and a p-value of 0.8490, meaning there is no statistically significant relationship between chest

circumference and gestational age. This implies that chest circumference remains relatively stable across different gestational ages.

Length is positively associated with gestational age, with an adjusted OR of 1.43 (95% CI: 1.16 - 1.77) and a significant p-value (0.0010). This indicates that longer neonatal length is significantly correlated with higher gestational age, meaning that full-term babies tend to be longer compared to preterm infants.

APGAR score at 1 minute has an OR of 1.07 (95% CI: 0.67 - 1.73) with a p-value of 0.7730, showing no significant association with gestational age. This suggests that the APGAR score at 1 minute does not strongly predict gestational maturity.

Hence, birth weight and length are significantly associated with gestational age. Head circumference, chest circumference, and APGAR score at 1 minute do not show a significant relationship with gestational age. Lower birth weight is strongly linked to lower gestational age, while greater length is associated with higher gestational age.

H. Comparison of gestational age (Preterm and term) with birth weight, head circumference, chest circumference and length by independent t test

Parameters	Preterm		Term		t-value	p-value
	Mean	Std.Dev.	Mean	Std.Dev.		
Birth weight	3.32	0.47	3.87	0.37	-8.6333	0.0001*
Head circumference	33.29	1.05	34.71	1.77	-4.9743	0.0001*
Chest circumference	31.39	1.26	32.70	1.79	-4.4943	0.0001*
Length	45.71	1.42	47.51	1.72	-6.3746	0.0001*

Table no. 12 The table presents a comparison of various anthropometric parameters—birth weight, head circumference, chest circumference, and length—between preterm and term neonates using an independent t-test. The mean values and standard deviations (Std. Dev.) for both groups are displayed, along with the t-value and p-value to determine statistical significance.

Birth Weight: The mean birth weight of preterm neonates is 3.32 kg with a standard deviation of 0.47, whereas term neonates have a higher mean birth weight of 3.87 kg with a standard deviation of 0.37. The t-value is -8.6333, and the p-value is 0.0001, indicating a statistically significant difference.

Head Circumference: The mean head circumference is 33.29 cm for preterm neonates (Std. Dev. = 1.05) and 34.71 cm for term neonates (Std. Dev. = 1.77). The t-

value of -4.9743 and p-value of 0.0001 suggest a significant difference between the groups.

Chest Circumference: Preterm neonates have a mean chest circumference of 31.39 cm (Std. Dev. = 1.26), while term neonates have a larger mean of 32.70 cm (Std. Dev. = 1.79). The t-value of -4.4943 and p-value of 0.0001 indicate statistical significance.

Length: The mean length of preterm neonates is 45.71 cm (Std. Dev. = 1.42), compared to 47.51 cm (Std. Dev. = 1.72) for term neonates. The t-value is -6.3746, with a p-value of 0.0001, confirming a significant difference.

Overall, the results demonstrate that term neonates have significantly higher birth weight, head circumference, chest circumference, and length compared to preterm neonates. The low p-values across all parameters indicate strong statistical significance, meaning the observed differences are unlikely to have occurred by chance.

I. Comparison of gestational age (Preterm and term) with APGAR scores at 1 min and 5 min by independent t test

Parameters	Preterm		Term		t-value	p-value
	Mean	Std.Dev.	Mean	Std.Dev.		
APGAR Score at 1 min.	7.24	0.83	7.57	0.78	-2.4431	0.0151*
APGAR Score at 5 min.	8.22	0.79	8.68	0.64	-4.1213	0.0001*

Table no. 13 presents a comparison of APGAR scores at 1 minute and 5 minutes between preterm and term neonates using an independent t-test. The mean APGAR score at 1 minute for preterm neonates is 7.24 with a standard deviation of 0.83, whereas for term neonates, it is slightly higher at 7.57 with a standard deviation of 0.78. The t-value for this comparison is -2.4431, and the corresponding p-value is 0.0151, indicating a statistically significant difference ($p < 0.05$). Similarly, at 5 minutes, the mean APGAR score for preterm neonates is 8.22 (SD = 0.79), while for term neonates, it is 8.68 (SD = 0.64). The t-value for this comparison is -4.1213, with a highly significant p-value of 0.0001 ($p < 0.05$). These findings suggest that term neonates have significantly higher APGAR scores at both 1 and 5 minutes compared to preterm neonates, indicating better overall neonatal outcomes in term births.

CHAPTER V

DISCUSSION

This chapter covers the conversations and provides a quick overview of the study's framework, conclusions, consequences, recommendations, and findings. Critical examination of the literature either confirms or refutes discussions.

The objective of the research was to study the vaginal microbiome in women admitted for delivery beyond 28 weeks of gestational age and its outcome on mother and immediate newborn and to find the association between socio-demographic variables with maternal and neonatal outcome.

Findings related to study of vaginal microbiome in women admitted for delivery

By controlling vaginal pH levels, a healthy vaginal microbiome—which is typified by a high prevalence of *Lactobacillus* species—is essential for preventing genital infections. On the other hand, an unbalanced microbial ecology in the vagina is associated with an increased risk of problems like trichomoniasis, bacterial vaginosis, STDs, premature labour, and different birth abnormalities. This microbial variety can be influenced by racial or ethnic background, pregnancy, hormone swings, sexual behaviour, cleanliness habits, and other factors.⁹⁵

Variations in the levels of *Lactobacillus* strains within the vaginal microbiome may be influenced by ethnic factors.⁹⁶ The primary *Lactobacillus* species found in the vaginal flora include *Lactobacillus Acidophilus*, *L. Crispatus*, *L. Gasseri*, *L. Jensenii*, and *L. Iners*. A disruption in the vaginal flora can lead to conditions such as aerobic vaginitis or bacterial vaginosis, characterized by an increase in anaerobic species like *Gardnerella*, *Mobiluncus*, *Bacteroides*, *Prevotella*, and *Peptostreptococcus*, along with

higher levels of Streptococcus, Staphylococcus, and Escherichia Coli. Women who are of reproductive age frequently contract bacterial vaginosis, and one of its indicators is a vaginal discharge that has a distinct ‘fishy’ smell, resulting from amines produced during bacterial metabolism.⁹

In the study, the women who had full term delivery showed more abundance of *L. crispatus*, *L. jensenii*, *L. iners* and *Bacillus cereus*; and the women who had preterm delivery showed the presence of *L. iners*, *L. Gasseri*, *Atopobium vaginae* and *Enterococcus faecalis*.

Similar study has been conducted by Sakabe Y et.al. where they observed that Lactobacillus was generally prevalent, with particularly high levels of *L. iners* and *L. crispatus*, while the population of *L. gasseri* was notably low in samples from preterm deliveries.⁹⁷

In a study conducted by L. Bayigga et.al, *L. crispatus* was the predominant bacterium in the vaginal microflora of healthy women prior to or during pregnancy. However, during the post- partum period, the situation varies, resulting in a drop in the number of disease-fighting Lactobacillus species, making the vaginal microecological barrier vulnerable to illnesses.⁷⁸

Also in a study, it was found that 40% of preterm delivering mothers lack *Lactobacillus species* whereas the full-term delivering mothers possesses one or more species of Lactobacillus- *L. crispatus* followed by *L. jensenii* and *L. gasseri*.⁹⁸

Whereas in contrast to the above similar results, the study conducted by Kyung-A Son, et.al⁴⁵ showed that Klebsiella pneumonia is the major bacterium linked to preterm delivery. Also in the study conducted by Kosti I et.al⁶⁶, it mentioned that

many genera are linked to PTB. Among them, *olsenella* and *clostridium sensu stricto* were new. It also added that BV was not the biggest risk factor but rather the absence of *Lactobacilli*.

Findings related to Socio-demographic variables and its associations with maternal and neonatal outcome

In the study, majority (47%) of the mothers belongs to the age group of 24-29 years, 79% of them are Hindu, 48.67% completed Pre-University Course, 98.33% are home maker, 67.33% had a non consanguineous marriage and 62.33% are non vegetarian.

Among the 300 respondents, 62.33% had vaginal delivery, 58% were primipara and 52.67% of them were pregnant for the first time.

The study showed that i) Age and mother's educational attainment are significantly correlated with both maternal and neonatal outcomes ($p < 0.05$); ii) Preterm and term gestational ages do not significantly correlate with demographic factors ($p < 0.05$).

Similar results were observed in the research conducted by Naik et al., which indicated that a significant portion of the participants (57.71%) came from urban areas, and 66.66% identified as Hindu. The study found that the rate of poor pregnancy outcomes exceeded 50% among women who were illiterate. Factors such as being from a low socioeconomic background, residing in rural areas, marrying before the age of 18, and having a history of consanguineous marriage were linked to adverse pregnancy outcomes. The research highlighted a notable correlation between pregnancy outcomes and variables such as education level, type of employment,

socioeconomic status, age at marriage, and consanguineous marriage. Additionally, significant relationships were found concerning maternal age and place of residence, while no significant correlations were noted with family type or access to transportation.⁹⁹

Multiple logistic regression analysis of gestational age by maternal outcomes showed that the women who had delivered vaginally and those who were pregnant for the third time have good maternal outcome ($p<0.05$); women who had 11-13 antenatal visits have good neonatal outcomes, and those women with either maternal or fetal conditions have equal chance of undergoing Cesarean section ; and Additionally, research has demonstrated a significant correlation ($p<0.05$) between the baby's length and birth weight and the mother's gestational age at the time of delivery. According to the research by Harrison, M.S., et al., women who have had at least four prenatal visits are less likely to experience adverse maternal outcomes. On the other hand, women who have malpresented foetuses, are deemed to be obstetrically high risk, have lower levels of education, or are dealing with maternal or obstetric issues are more likely to experience adverse outcomes.¹⁰⁰

The comparison of gestational age (Preterm and term) with birth weight, head circumference, chest circumference and length by independent t test showed that there is a significant association between gestational age (Preterm and term) with birth weight, head circumference, chest circumference and length by independent t test ($p<0.05$).

A similar finding is shown in the study conducted by Babilu et.al. which showed significant correlation between Foot length with GA and other anthropometric parameters in preterm babies and in term AGA and LGA babies.¹⁰¹

Also the comparison of gestational age (Preterm and term) with APGAR scores at 1 min and 5 min by independent t test showed a significant association between the gestational age (Preterm and term) of the mother with APGAR scores of the newborn at 1 min and 5 min by independent t test at 0.05 level of significance.

CHAPTER VI

CONCLUSION

Women who may benefit from interventions targeted at restoring normal vaginal flora and who are at risk of premature delivery can be identified with the aid of early detection of aerobic vaginitis and bacterial vaginosis in pregnancy. The study highlights the common vaginal microbiome present during the time of delivery and its effect on maternal and neonatal health outcomes. The study suggests imparting awareness to healthcare professionals and all women of reproductive age groups regarding the importance of maintaining a healthy vaginal microbiome.

To determine whether treating vaginal dysbiosis in asymptomatic pregnant women will significantly affect the start of premature labour, a large population study will be required.

An overview of the relationship between the women's sociodemographic characteristics and the results for their babies and mothers is given by the study. By early detection, this study will also contribute to the prevention of unfavourable consequences for mothers and newborns.

Implication for Nursing

a. Nursing Practice

Implementing findings from vaginal microbiome research into clinical practice requires a multi-tiered approach. In tertiary hospitals, advanced screening and precision medicine strategies can be adopted. Secondary hospitals can integrate focused interventions, while primary care settings should prioritize education, risk assessment, and referral systems. Private hospitals can leverage technology and

personalized care models, whereas public health programs can drive large-scale policy integration.

Based on the study result, preparation of a booklet on Antenatal Hygiene may help in imparting awareness to healthcare professionals including nursing officers and health assistants working in clinical sector and also the ASHA workers and ANMs working in the community sectors.

This will help the women of reproductive age groups, pre-pregnancy and early pregnancy till postpartum period learn to maintain hygiene thus maintaining a healthy vaginal microbiome. This will also help to prevent and treat early incase if affected, thus leading to reduction of maternal and newborn morbidity rate.

Nursing Education:

In order to address the mother's, infant's and family's physical, psychological, and social requirements, nurses are crucial as well as in promoting safe and effective care methods. Nursing students should be able to gain advanced knowledge and skills in the practice of maternal healthcare through the nursing curriculum. The study results indicate that the curriculum should include instruction on the vaginal microbiome, including how it changes throughout pregnancy and any potential negative effects on a mother's or baby's health as a result of a woman's unique microbiome. To avoid difficulties during and after pregnancy, in-service education programmes and lectures on health cleanliness, including hands, breasts, mouth, and perineal hygiene, should be held. This will improve the maternal and neonatal outcome. Nursing students should also be encouraged for the effective utilization of research-based practice in the clinical areas.

Findings from the study on the vaginal microbiome in women admitted for delivery have significant implications for nursing education. Nurses play a critical role in maternal and neonatal care and integrating microbiome-related knowledge into their skill set can enhance patient outcomes. Below are specific examples of how the study findings can influence skill development and competency-building among nurses.

1. Strengthening Nursing Assessment Skills

- **Microbiome Risk Screening:** Train nurses through guest lecture, seminar or hands on workshop to strengthen the overall knowledge and skills regarding assessing the risk factors and ruling out the chances of bacterial vaginosis and recurrent infections using history-taking and urine pH test in antenatal clinic during the visit.

2. Enhancing Infection Control Practices

- **Microbiome-Preserving Hygiene:** Plan and conduct in- service education programme for nurses working in maternity units on health and hygiene during peripartum period to prevent vaginal dysbiosis.

3. Clinical Decision-Making in Maternal Care

- **Probiotic & Prebiotic Counseling:** Develop nurses' ability to educate pregnant women on importance of antenatal diet and supplements for microbiome balance.

4. Advanced Nursing Interventions in Labor & Delivery

- **Vaginal Swab Collection:** Train nurses of maternity units regarding strict aseptic and asepsis techniques including universal precautions for microbiome

sampling. Teach neonatal nurses to observe infants for sepsis risks linked to maternal microbiome imbalances.

6. Leadership & Research in Nursing

- **Nurse-Led Research:** Encourage the nursing students of OBG Nursing department to participate in studies on microbiome-based maternal care.

b. Nursing Administration

In addition to overseeing the nurses, nurse administrators should be knowledgeable with the most recent developments in healthcare and be able to handle medical concerns in novel ways. It is recommended that the nurse administrator develop in-service or training programmes for nurses that emphasise the significance of educating them on the role of the vaginal microbiota during the prenatal, intranatal, and postnatal periods, as well as the potential impact on the health of mothers and newborns. This will support wellbeing and assist in averting difficulties.

c. Nursing Research

Nursing research on prenatal women is necessary in order to deliver high-quality care. Women of reproductive age are not consistently taught about the importance of the vaginal microbiome, how it changes throughout pregnancy, and how this affects both the mother and the unborn child.

Research elucidates novel tools for in-depth investigations of the numerous organisms found in the vagina. Nursing students must be taught the importance of research in key areas. Below are specific research methodologies and priority areas for future nursing-led studies.

Recommendations

- A comparable study with a bigger sample size might be conducted.
- A comparable study can be carried out in various environments.
- A comprehensive population study could be undertaken to determine if addressing vaginal dysbiosis in asymptomatic pregnant women significantly affects the likelihood of premature labor.

Priority Research Areas

1. **Microbiome & Pregnancy Outcomes:** Study links between vaginal microbiota and preterm birth, postpartum infections (e.g., cohort study on term vs. preterm deliveries).
2. **Nursing Interventions:** Assess the impact of probiotics or hygiene education on microbiome health (e.g., RCT on nurse-led probiotic use).
3. **Neonatal Health:** Investigate how maternal microbiome affects neonatal sepsis risk and early microbiome colonization (e.g., case-control study on newborn microbiota).
4. **Microbiome Screening:** Develop nurse-led screening protocols (e.g., pilot study on vaginal pH testing in pregnancy).
5. **Best Nursing Practices:** Evaluate how hygiene, labor room protocols, and antibiotic use impact microbiome stability (e.g., quality improvement project).

Recommended Methodologies

- **Cohort Studies:** Track microbiome changes across pregnancy.
- **RCTs:** Test effectiveness of nurse-led probiotic or hygiene interventions.
- **Case-Control Studies:** Compare microbiomes in women with vs. without pregnancy-related infections.
- **Qualitative Research:** Explore nurses' experiences in microbiome-based care.
- **Implementation Science:** Assess feasibility of nursing-led microbiome screening & education.

Limitation

- The research is restricted to women who are admitted at the time of childbirth.
- The research is limited to one tertiary care hospital, which may not be representative of the broader population.
- Lack of Longitudinal Data – Since it is a descriptive study, it does not track changes in the vaginal microbiome over time (e.g., before, during, and after delivery).
- Limited Generalizability – Findings may not be applicable to women from different geographic, ethnic, or socioeconomic backgrounds.
- Confounding Factors such as dietary habits, hygiene practices, and underlying health conditions may influence the vaginal microbiome but are not controlled.
- The accuracy of microbiome analysis depends on sample collection methods, storage conditions, and sequencing techniques, which could introduce variability.

CHAPTER VII

SUMMARY

The current study was undertaken by the investigator to study the vaginal microbiome in women admitted for delivery.

Objectives

1. To study the vaginal microbiome in women admitted for delivery beyond 28 weeks of gestational age and its outcome on mother and immediate newborn.
2. To find the association between socio-demographic variables with maternal and neonatal outcome.

The research study-design utilized for the present study is case series research design. Using the consecutive sampling technique, 300 mothers were included in the study. Participants were selected based on the inclusion criteria like all mothers with or more than 28 gestational weeks delivering in tertiary care hospitals of Belagavi city.

Approval for the study was granted by the Institutional Ethical Committee of KLE University in Belagavi. The mothers were provided with a detailed explanation of the procedure and their involvement in the research before giving their written informed consent. During the data collection process, the objectives of the study were communicated to the mothers and relatives, and consent was obtained from each participant involved.

Data collection was started by administering the tools on socio-demographic variables and modified Maternal and Newborn Health Registry. After removing vaginal swabs from the posterior vaginal fornices, they were promptly preserved at -

70°C in a sterile tube until analysis. After swabbing the MRS agar plate, they were incubated at 37°C in anaerobic chamber for 24 hours. Identification of bacteria by using:

- Gram Staining
- Biochemical test
- DNA isolation
- PCR (Polymerase chain Reaction) test

For categorical data, descriptive analysis was done using frequency and proportion. To look into the relationship between the explanatory factors and the result measures, a binary logistic regression analysis was carried out. The results include the odds ratio along with the corresponding 95% confidence interval. An relationship between an explanatory variable and an outcome variable is defined as a P-value < 0.05. Version 22 of IBM SPSS was employed for statistical analysis.

Findings related to study of vaginal microbiome in women admitted for delivery

In the study, the presence of *L. iners*, *L. gasseri*, *Atopobium vaginae*, and *Enterococcus faecalis* was found in the women who had preterm delivery, while the women who had full term delivery displayed higher abundances of *L. crispatus*, *L. jensenii*, *L. iners*, and *Bacillus cereus*.

Findings related to Socio-demographic variables and its associations with maternal and neonatal outcome

Of the mothers in the study, the majority (47%) are between the ages of 24 and 29; 79% are Hindu; 48.67% have completed a pre-university course; 98.33% are

home maker; 67.33% had non-consanguineous marriages; and 62.33% are non vegetarians.

Of the 300 participants, 62.33% delivered their babies vaginally, 58% were primipara, and 52.67% were expecting their first child.

The study's findings revealed that: i) there is a meaningful correlation ($p<0.05$) between the mother's age and level of education and the outcomes for both the mother and the newborn; ii) The population's demographics and gestational age (both term and preterm) do not significantly correlate ($p<0.05$).

A multiple logistic regression analysis of gestational age by maternal outcomes revealed that good maternal outcomes were experienced by women who delivered their babies vaginally and those who were pregnant for the third time ($p<0.05$); good neonatal outcomes were experienced by women who had 11–13 antenatal visits, and women with either maternal or foetal conditions had an equal chance of having a Caesarean section; additionally, it was shown that birth weight and length of the baby were related to the mother's age of gestation at the time of delivery ($p<0.05$).

An independent t-test comparison of gestational age (preterm and term) with birth weight, head circumference, chest circumference, and length revealed a significant ($p<0.05$) correlation between the variables. Furthermore, a significant correlation was found at the 0.05 level of significance between the mother's gestational age (preterm or term) and the APGAR scores of the newborn measured at 1 minute and 5 minutes, as determined by an independent t test comparing the two variables..

CHAPTER VIII**BIBLIOGRAPHY**

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ANNEXURE I**ETHICAL CLEARANCE LETTER**

 KLE EMPOWERING PROFESSIONALS ☎: 0831-2444444	KLE ACADEMY OF HIGHER EDUCATION AND RESEARCH (Formerly known as KLE University) (Deemed-to-be-University established u/s 3 of the UGC Act, 1956) Accredited 'A' Grade by NAAC (2nd Cycle) Placed in Category 'A' by MHRD (GoI) <i>JNMC Campus, Nehru Nagar, Belagavi-590 010, Karnataka State, India</i> FAX: 0831-2493777 Web: http://www.kledeemeduniversity.edu.in E-mail: info@kledeemeduniversity.edu.in
Ref.No.KAHER/EC/20-21/001/13	4 th September 2020
To, Ms. Heikham Gineta Chanu Part-Time Ph.D. Research Scholar, 2019-20 Batch, Faculty of Nursing, KAHER, Belagavi.	
Dear Research Scholar,	
The KAHER Ethics Committee on Human Subjects for Ph.D. Research Project met on Thursday, the 20th February, 2020 to consider your application for approval of the research project "Study Of Vaginal Microbiome In Women Admitted For Delivery To A Tertiary Care Hospital."	
As there are no ethical issues involved in your proposed research project, the committee has provided approval for this research project.	
You are requested to report to Ethical Committee of the following:	
1. Any deviation from or change of the protocol. 2. Any changes in study documents.	
 (Dr. Anita Dalal) Member-Secretary Ethical Committee (Human) for Ph. D. Research KAHER, Belagavi.	 (Dr. B.C. Kotintot) Chairman Ethical Committee (Human) for Ph. D. Research KAHER, Belagavi.
CC to: - The Director Research Foundation, KAHER, Belagavi. - The Director Academic Affairs, KAHER, Belagavi. - The Registrar, KAHER, Belagavi. - Special Officer to Hon. Vice Chancellor, KAHER, Belagavi.	

ANNEXURE II

PERMISSION LETTER FROM HOSPITAL AUTHORITY

LETTER SEEKING PERMISSION TO CONDUCT RESEARCH STUDY

From,

Mrs. Heikham Gineta Chanu
Asst. Professor & Ph.D Scholar,
Department of OBG Nursing
KAHER INS, Belagavi

To,

The Medical Superintendent
KLE's Dr. Prabhakar Kore Charitable Hospital
Nehru Nagar, Belagavi

(Through Proper Channel)

Subject: Request for permission to conduct research study

Respected Sir,

With reference to the subject cited above, I would like to request you to kindly grant me permission to conduct a research study for my Ph.D work. I am pursuing my Ph.D at KLE Academy of Higher Education and Research, Belagavi under the guidance of Dr. Sudha A Raddi, Principal, KAHER Institute of Nursing Sciences, Belagavi. The topic of my study is **"Study of vaginal microbiome in women admitted for delivery to a tertiary care hospital"**. Samples for my study are mothers delivering baby with gestation of 28 weeks or more. The data collected will be kept confidential and used only for my Ph.D study work. Hence I request you to kindly permit me to conduct the research study at your esteemed hospital.

Kindly do the needful.

Thanking You,

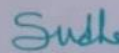
(Enclosure: Ethical Clearance Letter)

Date: 13/08/2021
Place: Belagavi

Your's Faithfully,


Mrs. Heikham Gineta Chanu

Guide:


Dr. Sudha A Raddi
Principal, KAHER INS,
Belagavi


Medical Superintendent
K.L.E. Dr. P. K. Charitable Hospital,
BELGAUM - 580010

LETTER SEEKING PERMISSION TO CONDUCT RESEARCH STUDY**From,**

Mrs. Heikham Gineta Chanu
Asst. Professor & Ph.D Scholar,
Department of OBG Nursing
KAHER INS, Belagavi

To,

The HOD
Department of OBG
KLE's Dr. Prabhakar Kore Charitable Hospital
Nehru Nagar, Belagavi

(Through Proper Channel)

Subject: Request for permission to conduct research study

Respected Madam,

With reference to the subject cited above, I would like to request you to kindly grant me permission to conduct a research study for my Ph.D work. I am pursuing my Ph.D at KLE Academy of Higher Education and Research, Belagavi under the guidance of Dr. Sudha A Raddi, Principal, KAHER Institute of Nursing Sciences, Belagavi. The topic of my study is "**Study of vaginal microbiome in women admitted for delivery to a tertiary care hospital**". Samples for my study are mothers delivering baby with gestation of 28 weeks or more. The data collected will be kept confidential and used only for my Ph.D study work. Hence I request you to kindly permit me to conduct the research study at your esteemed hospital.

Kindly do the needful.

Thanking You,

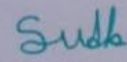
(Enclosure: Ethical Clearance Letter)

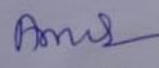
Date: 14/08/2021
Place: Belagavi

Your's Faithfully,


Mrs. Heikham Gineta Chanu

Guide:


Dr. Sudha A Raddi
Principal, KAHER INS,
Belagavi


14/8/21
To seek MS permission

ANNEXURE III

INFORMATION SHEET AND CONSENT FORM

STUDY OF VAGINAL MICROBIOME IN WOMEN ADMITTED FOR DELIVERY TO A TERTIARY CARE HOSPITAL

Research Scholar: Mrs. Heikham Gineta Chanu

Supervisor: Prof (Dr.) Sudha A. Raddi

Co-Guide: Dr. Prof. Anita Dalal

INFORMATION SHEET:

Introduction:

We are requesting you to agree to participate in the study entitled “Study of vaginal microbiome in women admitted for delivery to a tertiary care hospital” at KLE Hospital. I am Mrs. Heikham Gineta Chanu, Research Scholar, KAHER, doing a research on this study. The study includes mothers delivering in KLE Hospital.

Explanation of the procedure:

In this study you have to answer few questions about information of mother in pregnancy, during delivery & outcome of pregnancy (your baby), reports related to your newborn like weight, Apgar score at one minute and five minute will be recorded. A vaginal swab will be taken to check the presence of any abnormal micro- organisms with the help of cotton swab stick. It is a non invasive procedure. This entire procedure will take 20-30 minutes.

Possible Benefits:

There will be no immediate and direct benefit to you (your baby), but your participation is likely to help in studying the vaginal micro-organisms to check its effect on gestational age, maternal and neonatal health. Although there may not be extra benefits to your baby by being part of the project, the project will help in planning other programs that may benefit other babies who are born in developing countries.

Possible Risks:

The procedure for conducting the study is safe and as such is not likely to cause any harm to you.

Confidentiality:

Your identity will not be revealed and all the information will be collected and coded so that no one will know your identity.

Withdrawal:

Participation in study is voluntary. If you don't wish to participate in the study at any point you can refuse. You do not have to be in the research study in order to receive health care during your delivery.

Cost of participation:

The cost of the study will be borne by the researcher. There will be no additional cost to you for participating in this study.

Payment of participation:

There will be no incentives to you (or your baby) for participating this study.

Contact information

At this venture I have provided you the information about the research which I am interested to do. I have also given information about participation, dangers and benefits of participating in the study. Your participation is not mandatory. You can quit at any given time. If you have any doubts or questions you can contact any time to Mrs. Heikham Gineta Chanu, Research Scholar, KAHER, Mobile No: 9036694478.

I am giving my consent to participate in the study by signing below.

_____	_____	_____
Sign of Participant	Name	Date

_____	_____	_____
Sign of Investigator	Name	Date

CONSENT FORM

I have read this consent form and I have understood it. I have been given the opportunity to ask my query regarding the study & I have got satisfactory answers for them. I consent voluntarily to participate as a participant in this research.

Signature of participant: _____

Signature of Researcher: _____

Date:

Place:

If Illiterate

I have witnessed the accurate reading of the consent form to the potential participant, and the individual has had the opportunity to ask questions. I confirm that the individual has given consent freely.

Name of witness _____

Signature of witness _____

Date:

Place:

Thumb print of participant

**Statement by the researcher**

I have accurately read out the information sheet to the potential participant, and to the best of my ability made sure that the participant understands above mentioned procedure.

I confirm that the participant was given an opportunity to ask questions about the study, and all the questions asked by the participant have been answered correctly and to the best of my ability. I confirm that the individual has not been coerced into giving consent, and the consent has been given freely and voluntarily.

A copy of this Informed Consent Form has been provided to the participant.

Name of Researcher / person taking the consent _____

Signature of Researcher / person taking the consent _____

Date _____

\

टेस्टीयरी केअर हॉस्पिटल मध्ये डिलीवरी साठी अॅडमीट केलेल्या स्त्रीयांवर
वॅजीनल मायक्रोबायोम अभ्यास.

संशोधक स्कॉलर : श्रीमती हायकम जिनेटा चानू

सुपरवाईजर : प्रोफेसर (डॉक्टर) सुधा ए. रेड्डी

को गार्ड : (मदतनीस) डॉ. प्रोफेसर अनिता दलाल

माहिती पत्र

माहिती ओळख :

ज्या बायका के.एल.ई. हॉस्पिटलच्या टेस्टीयरी हॉस्पिटल मध्ये प्रसुतीसाठी हजर झाल्या आहेत त्यांना वॅजीनल मायक्रोबायोम जिनेटा चानू रिसर्च स्कॉलर, कहर या अभ्यासावर संशोधन करत आहे. के.एल.ई. हॉस्पिटल मध्ये बाळंत होणाऱ्या बायकांचा यात समावेश आहे.

पध्दतीवर सविस्तर सांगणे:

या अभ्यासामध्ये तुम्हाला कांही प्रश्नांची उत्तरे द्यायची आहेत. तुम्हाला आईची गर्भधारणा बदल माहिती द्यायची व जन्मावेळेला बाळाचे वजन घ्यायचे व अपगर स्कोर (एक ते पाच मिनिटाच्या आतले) हे नोंद केले जातील. कापूसाच्या बोळ्याच्या काठीने वॅजीनल (योनी) स्वॅब हे असामान्य सूक्ष्म ऑर्गॅनीजम प्रत्यक्ष आहेत का ते पाहण्यासाठी नमुने घेतले जातील. ही एक आक्रमक पध्दत आहे. ही पूर्ण पध्दती ही 20-30 मिनिटे घेते.

संभावीत फायदे :

प्रत्यक्ष व लवकर फायदे हे तुमच्या बाळाला नसतील पण तुमचे सहभाग हे जेस्टेशनल (एज) गर्भधारणा, वय, आईचे व निऑनटल (द्रव) प्रकृती तपास करण्यासाठी वॅजीनल मायक्रो ऑर्गॅनिजमचा अभ्यासात मदत करेल. जरी तुमच्या बाळाला कांही जास्तीचे फायदे या अभ्यासात भाग

..2..

घेण्याने नसले तरी, हा प्रोजेक्ट, हा डेवलपिंग देशातून जन्मनाच्या बाळांसाठी प्रोगॅम करण्यासाठी मदत करेल.

नुकसानीची शक्यता :

हा अभ्यास करण्याची पध्दती ही अगदी सुरक्षीत आहे व ही पध्दत तुम्हाला कोणतीही इजा पोहचवणारा नाही.

गोपनीयता :

तुमची ओळखही गुप्त ठेवली जाईल व तुमच्या ओळखीच्या गोपनीयतेसाठी सर्वजन केलेली माहिती ही कोड केली जाईल.

माघार घेणे :

सहभाग घेणे हा पूर्णपणे तुमच्या मर्जिवर असेल. जरी केंव्हाही या अभ्यासात सहभाग होण्याची इच्छा नसेल तर तुम्ही नाही म्हणू शकता. प्रस्तुती वेळेच्या व्यवस्थेच्या काळजीसाठी तुम्ही या संशोधन अभ्यासात राहण्याची कांही गरज नाही.

सहभागाचा खर्च :

या अभ्यासाचा खर्च हा संशोधक घेतील या अभ्यासात सहभागी होण्यासाठी तुम्हाला जास्तीचा खर्च हा लागणार नाही.

सहभागासाठीचा पगार, भत्ता :

तुम्हाला किंवा तुमच्या बाळाला या अभ्यासात सहभागी होण्यासाठी कोणताही पगार, भत्ता दिला जाणार नाही.

करार माहिती (कॉन्ट्रॅक्ट इन्फॉर्मेशन)

यावेळी मी तुम्हाला मी करू इच्छीनाऱ्या संशोधनाबद्दल पूर्ण माहिती दिली आहे. मी तुम्हाला या सहभागाबद्दल माहिती व त्याचे धोके व फायदे या बद्दल सांगितले आहेत. तुमचा सहभाग हा जबरदस्तीचा (मँडेटरी) नाही. तुम्ही कधीही हे सोडू शकता. जर तुम्हाला कांही शंका किंवा प्रश्न विचारायचे असतील तर तुम्ही कधीही श्रीमती हेईखान जीनेटा चानु रिसर्च स्कॉलर कहर मोबाईल नं. 9036694478 यांच्याशी संपर्क साधू शकता.

खाली सही करून मी माझी संमती या अभ्यासात सहभागासाठी देत आहे.

सहभागीदाराची सही

नांव

तारीख

संशोधकाची सही

नांव

तारीख

संमती पत्र (1)

मी हे संमती पत्र वाचून पाहिले आहे व मला हे समजले आहे. मला अभ्यासाबद्दल प्रश्नावली विचारण्याची संधी दिली गेली आहे. व मला समाधानकारक उत्तरे मिळाली आहेत. मी माझ्या स्व इच्छेने या संशोधनामध्ये सहभागी होण्यासाठी संमती देत आहे.

सहभागीदाराची सही _____

संशोधकाची सही _____

तारीख :

स्थळ :

असुशिक्षित असल्यास

समक्ष सशक्त सहभागासाठी मी हे संमती पत्र माझ्या साक्षी समक्ष अगदी बरोबर वाचून घेतले आहे व स्वतः होवून प्रश्न विचारण्याची संधी मिळाली. मी हे निश्चित करतो की, मी स्वतःहून ही संमती पूर्णपणे स्वतः होवून साक्षीनीशी देतो.

साक्षीदाराचे नांव _____

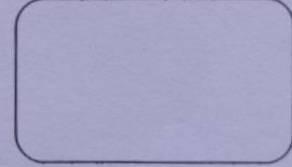
सहभागी दाराचा डाव्या हाताचा अंगठा

सही _____

तारीख :

सही :

संशोधकाचे विधान, वक्तव्य :



मी अगदी बरोबर संमतीपत्र हे सहभागीदाराला वाचून दाखविली आहे. व माझ्यापूर्ण बुद्धीने ही खात्री केली की सहभागीदाराला या पद्धतीबद्दल पूर्णपणे समजले आहे.

मी हे सुनिश्चित करतो की सहभागीदाराला अभ्यासाबद्दल प्रश्न विचारण्याची संधी दिली गेली आहे. व सर्व प्रश्न विचारल्याबद्दलची सहभागीदाराला समर्पक उत्तरे दिली गेली आहेत. व मी हे सुनिश्चित करतो की, व्यक्तीला (इंडीवीज्युअल) कोणत्याही प्रकारचे संमती देण्यासाठी भयोत्पन्न केलेले नाही. व संमतीही पूर्णपणे स्व इच्छेने व स्वातंत्र्यपणे दिली गेली आहेत.

या माहिती पत्राची प्रत ही सहभागीदाराला दिली गेली आहे.

संशोधकाचे नांव / संमती घेणारा व्यक्ती _____

संशोधकाची सही/ संमती घेणारा व्यक्ती _____

तारीख : _____

ಟೀರಟೀಯರಿ ಕೇಯರ್ ಆಸ್ಪತ್ರೆದಲ್ಲ ಪ್ರಸೂತಿ ಸಲುವಾಗಿ ದಾಖಲ ಆಗಿರುವ

ಸ್ತ್ರೀಯವರ ಮೇಲೆ ಅಭ್ಯಾಸ

ಸಂಶೋಧಕ ಸ್ಕಾಲರ್ : ಶ್ರೀಮತಿ ಹೈಕಮ್ ಜೆನೇತಾ ಚಾನು

ಸುಪರ್‌ವಾಯಜರ್ : ಪ್ರೊಫೆಸರ್ (ಡಾಕ್ಟರ್) ಸುಧಾ ಎ. ರೆಡ್ಡಿ

ಕೋ-ಗೈಡ್ : ಡಾ ಪ್ರೊಫೆಸರ್ ಅನಿತಾ ದಲಾಲ

ಮಾಹಿತಿ ಪತ್ರ

ನಾನು ಯಾವು ಸ್ತ್ರೀಗಳು ಕೆ.ಎಲ್.ಇ. ಆಸ್ಪತ್ರೆಯ ಟೀರಟೀಯರಿ ಆಸ್ಪತ್ರೆದಲ್ಲ ಪ್ರಸೂತಿ ಹಾಜರ ಆಗಿದ್ದಾರೆ ಅವರಿಗೆ ವ್ಯಾಜಿನಲ್ ಮಾಯೋಕ್ರೋಬಾಯೋಮ್ ಅಭ್ಯಾಸದಲ್ಲ ಭಾಗವಹಿಸುವ ಸಲುವಾಗಿ ವಿನಂತಿ ಪಡಿಸಿಕೊಳ್ಳುತ್ತೇನೆ. ನಾನು ಶ್ರೀಮತಿ ಜೀನಿಟಾ ಚಾನು ರಿಸರ್ಚ್ ಸ್ಕಾಲರ್ ಕಹರ್ ಈ ಅಭ್ಯಾಸ ಮೇಲೆ ಸಂಶೋಧನ ಪಡಿಸುತ್ತಿದ್ದೇನೆಂದರೆ ಕೆ.ಎಲ್.ಇ. ಆಸ್ಪತ್ರೆದಲ್ಲ ಪ್ರಸೂತಿ ಆಗುವ ಸ್ತ್ರೀಯರ ಇದರಲ್ಲ ಸಮಾವೇಶವಿದೆ.

ಪದ್ಧತಿಯ ಮೇಲೆ ಸವಿಸ್ತಾರ ಮಾಹಿತಿ :

ಈ ಅಭ್ಯಾಸದಲ್ಲ ನಿಮಗೆ ಕೆಲವೊಂದು ಪ್ರಶ್ನೆ ಒಂದು ಉತ್ತರಗಳು ಕೊಡಬೇಕಾಗಿದೆ ನಿಮಗೆ ತಾಯಿಯ ಗರ್ಭಧಾರಣ ಬಗ್ಗೆ ಮಾಹಿತಿ ಕೊಡಬೇಕಾಗಿದೆ. ಮತ್ತು ಜನ್ಮದ ವೇಳೆಯಲ್ಲಿ ಮಗುವ ತೂಕ ಕೊಡಬೇಕಾಗಿದೆ, ಅಪಗರ್ (1 ರಿಂದ 5 ನಿಮಿಷ ಒಳಗಿಂದ) ನೋಂದನಿ ಮಾಡುತ್ತಾರೆ ಅಲ್ಟ್ರಾ ಕಟಗಿಯಿಂದ ವ್ಯಾಜಿನಲ್ (ಯೋನಿ) ನ್ನಾಬ್ ಆ ಸಮಸ್ಯೆ ಸೂಕ್ಷ್ಮ ಆ ರೋಗ್ಯನೀಜವು ಪ್ರತ್ಯಕ್ಷದಲ್ಲ ಇದಾರೂ ಇಲ್ಲ ನೋಡುವ ಸಲುವಾಗಿ ನಮೂನೆ ತೆಗೆದುಕೊಳ್ಳುತ್ತಾರೆ. ಇದು ಒಂದು ಅಆಕ್ರಮಕ ಪದ್ಧತಿ ಇದೆ ಈ ಪದ್ಧತಿ 20 ರಿಂದ 30 ನಿಮಿಷ ತೆಗೆದುಕೊಳ್ಳುತ್ತದೆ.

ಸಂಭಾವಿತ ಫಾಯದೆಗಳು :

ಪ್ರತ್ಯಕ್ಷ ಮತ್ತು ತುರ್ತು ನಿಮ್ಮ ಮಗುವಿಗೆ ಫಾಯದೆಗಳು ಇರುವುದಿಲ್ಲ. ನಿಮ್ಮ ಸಹಭಾಗ (ಜೇಸ್ಟೆಶನಲ್ ಎಜ್) ಗರ್ಭಧಾರಣಾ ಕಾಲ, ವಯಸ್ಸು, ತಾಯಿಯ ಮತ್ತು ನಿಅನಟಲ್ (ದ್ರವ) ಪ್ರಕೃತಿ ತಪಾಸನೆ ಮಾಡುವ ಸಲುವಾಗಿ ವ್ಯಾಜಿನಲ್ ಮೈಕ್ರೋ ಆಗೋನೀಜಮ್ ಅಭ್ಯಾಸದಲ್ಲ ಸಹಾಯ ಇದೆ. ನಿಮ್ಮ ಮಗುವಿಗೆ ಯಾವುದೇ ಹೆಚ್ಚಿನ ಫಾಯದೆಗಳು ಈ ಅಭ್ಯಾಸದಲ್ಲ ಭಾಗವಹಿಸು ಸಲುವಾಗಿ ನಿಗದಿದ್ದರೆ ಈ ಫೋಜೆಕ್ಟ್

ಡೆವೆಲಪಿಂಗ್ ದೇಶಗಳಲ್ಲಿ ಜನ್ಮ ಆಗುವ ಮಗುಗಳಿಗೆ ಪ್ರೋಗ್ರಾಮ್, ಮಾಡು ಸಲುವಾಗಿ ಸಹಾಯ ಮಾಡುತ್ತಿದ್ದೆ.

ನೂಕಸಾನದ ಸಂಭಾವಿತಾ :

ಈ ಅಭ್ಯಾಸ ಮಾಡುವ ಪದ್ಧತಿ ಬಹಳ ಸುರಕ್ಷಿತ ಇದೆ. ಮತ್ತು ಈ ಪದ್ಧತಿ ನಿಮಗೆ ಯಾವುದೇ ತರಹದ ಗಾಯ ಕೊಡುವುದಿಲ್ಲ.

ಗೋಪನಿಯತಾ :

ನಿಮ್ಮ ಗುರ್ತು ಗುಪ್ತ ಇಡಬಹುದು ಮತ್ತು ನಿಮ್ಮ ಗುರ್ತು ಗೋಪನಿಯತೆ ಸಲುವಾಗಿ ಸರ್ವ ಜಮಾಮಾಡಿದ್ದು ಮಾಹಿತಿ 'ಕೋಡಿ' ಮಾಡಬಹುದು.

ಹಿಂದೆಪಡೆಯುವ ಸಲುವಾಗಿ :

ಸಹಭಾಗ ಪಡೆಯುವುದು ಪೂರ್ಣವಾಗಿ ನಿಮ್ಮ ಮರ್ಜೆಮೇಲೆ ಇದೆ. ನಿಮಗೆ ಯಾವತ್ತು ಈ ಅಭ್ಯಾಸದಲ್ಲಿ ಸಹಭಾಗ ಆಗುವುದು ಇಚ್ಛಾ ಇರಲಿಲ್ಲ ಅಂದರೆ "ಇಲ್ಲಾ" ಅನ್ನಬಹುದು ಪ್ರಸೂತಿ ವೇಳೆಗೆ ತಬ್ಬೀಯತದ ಕಾಳದ ಸಲುವಾಗಿ ನೀವು ಈ ಸಂಶೋಧನ ಅಭ್ಯಾಸದಲ್ಲಿ ಇರುವುದು ಯಾವುದು ಅವಶ್ಯಕತೆ ಇಲ್ಲ.

ಸಹಭಾಗದ ಖರ್ಚು :

ಈ ಅಭ್ಯಾಸದ ಖರ್ಚು ಸಂಶೋಧಕ ತೆಗೆದುಕೊಳ್ಳುತ್ತಾರೆ. ಈ ಅಭ್ಯಾಸದಲ್ಲಿ ಸಹಭಾಗದ ಸಲುವಾಗಿ ನಿಮಗೆ ಯಾವುದೇ ಹೆಚ್ಚಿನ ಖರ್ಚು ಬರುವುದಿಲ್ಲ.

ಸಹಭಾಗ ಸಲುವಾಗಿ ಸಂಬಳ, ವೇತನ :

ನಿಮಗೆ ಅಥವಾ ನಿಮ್ಮ ಮಗುವಿಗೆ ಈ ಅಭ್ಯಾಸದಲ್ಲಿ ಭಾಗಪಡಿಸುವ ಸಲುವಾಗಿ ಯಾವುದೇ ಸಂಬಳ ವೇತನ ಕೊಡಲುಕೆ ಆಗುವುದಿಲ್ಲ.

ಕರಾರ ಮಾಹಿತಿ (ಕಾನ್ಟ್ರಾಕ್ಟ್ ಇನ್‌ಫಾರ್ಮೇಶನ್)

ಈ ವೇಳೆ ನಾನು ನಿಮಗೆ ಮಾಡುವ ಸಂಶೋಧನ ಬಗ್ಗೆ ಪೂರ್ಣ ಮಾಹಿತಿ ಕೊಟ್ಟಿದ್ದೇನೆ. ನಾನು ನಿಮಗೆ ಈ ಸಹಭಾಗದ ಬಗ್ಗೆ ಮಾಹಿತಿ ಮತ್ತು ಅದರ ಆಪತ್ತು ಮತ್ತು ಫಾಯ್ದೆಗಳ ಬಗ್ಗೆ ಹೇಳಿದ್ದೇನೆ. ನಿಮ್ಮ ಸಹಭಾಗ ಒತ್ತಾಯ (ಮ್ಯಾನಡೇಟರಿ) ಇಲ್ಲ. ನಿವು ಯಾವಾಗೂ ಇದು ಬಿಡಬಹುದು ನಿಮಗೆ ಯಾವುದೇ ಶಂಖಾ ಅಥವಾ ಪ್ರಶ್ನೆ ಕೇಳಬೇಕಾದರೆ ನೀವು ಯಾವತ್ತು ಶ್ರೀಮತಿ ಹೇಇಕಾಮ್ ಜೀನೆಟಾ ಚಾನು ರಿಸರ್ಚ್ ಸ್ಕಾಲರ್, ಕಹರ ಮೋಬಾಯಿಲ್ ನಂ. 903669478 ಇವರಿಗೆ ಸಂಪರ್ಕ ಮಾಡಬಹುದು.

ಕೆಳಗೆ ಸಹಿ ಮಾಡಿ ನಾನು ನನ್ನ ಸಮ್ಮತಿ ಈ ಅಭ್ಯಾಸದಲ್ಲಿ ಸಹಭಾಗ ಸಲುವಾಗಿ ಕೋಡುತ್ತೇನೆ.

ಸಹಭಾಗಿದಾರರ ಸಹಿ

ಹೆಸರು

ತಾರೀಖು

ಸಂಶೋಧಕರರ ಸಹಿ

ಹೆಸರು

ತಾರೀಖು

ಸಮ್ಮತಿ ಪತ್ರ

ನಾನು ಈ ಸಮ್ಮತಿ ಪತ್ರ ಓದಿದ್ದೇನೆ. ಮತ್ತು ಇದು ನನಗೆ ತಿಳಿದಿದೆ. ನನಗೆ ಈ ಅಭ್ಯಾಸದ ಬಗ್ಗೆ ಪ್ರಶ್ನೆ ಕೆಳುವ ಸಂಧಿ ಕೊಟ್ಟಿದ್ದೆ ಮತ್ತು ನನಗೆ ಸಮಾಧಾನಕಾರಕ ಉತ್ತರಗಳು ಸಿಕ್ಕಿದ್ದಾರೆ. ನಾನು ನನ್ನ ಸ್ವ ಇಚ್ಛೆಯಿಂದ ಈ ಸಂಶೋಧನದಲ್ಲ ಸಹಭಾಗ ಪಡಿಸುವಸಲುವಾಗಿ ಸಮ್ಮತಿ ಕೊಟ್ಟಿದ್ದೇನೆ.

ಸಹಭಾಗಿದಾರರ ಸಹಿ :-----

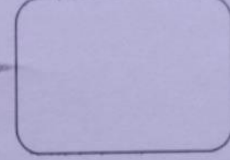
ಸಂಶೋಧಕರ ಸಹಿ :-----

ಸಹಭಾಗಿದಾರರ ಹೆಬ್ಬಟು

ತಾರೀಖು :

ಸ್ಥಳ :

ಅನುಸ್ಥಿತತಾ ಇದ್ದರೆ :



ಸಶಕ್ತ ಸಹಭಾಗ ಸಲುವಾಗಿ ನಾನು ಈ ಸಮ್ಮತಿ ಪತ್ರ ಸಾಕ್ಷಿ ಸಮಕ್ಷ ಸರಿಯಾಗಿ ಓದಿ ತೋರಿಸಿದ್ದಾನೆ. ಮತ್ತು ನಾನು ಸ್ವತವಾಗಿ ಪ್ರಶ್ನೆ ಕೆಳುವ ಸಂಧಿ ನನಗೆ ಸಿಕ್ಕಿದೆ. ನಾನು ಇದು ಸಿಕ್ಕಿವವಾಗಿ ನಾಸ್ತತ ಆಗಿ ಈಸಮ್ಮತಿ ಪೂರ್ಣ ಸ್ವತಾ ಆಗಿ ಸಾಕ್ಷಿದಾರರ ಸಮಕ್ಷ ಕೋಡುತ್ತೇನೆ.

ಸಾಕ್ಷಿದಾರರ ಹೆಸರು : -----

ಸಾಕ್ಷಿದಾರರ ಸಹಿ : -----

ಸಂಶೋಧಕರ ವಿದಾನ ವಕ್ತವ್ಯ :

ನಾನು ಸರಿಯಾಗಿ ಈ ಸಮ್ಮತಿ ಪತ್ರ ಸಹಭಾಗಿದಾರರಿಗೆ ಓದಿ ತೋರಿಸಿದ್ದೇನೆ. ಮತ್ತು ನನ್ನ ಪೂರ್ಣ ಬುದ್ಧಿಯಿಂದ ನಾನು ಇದು ಖಾತ್ರಿ ಪಡಿಸಿದ್ದುನೆಂದರೆ, ಸಹಭಾಗಿದಾರರಿಗೆ ಈ ಪದ್ಧತಿ ಬಗ್ಗೆ ಪೂರ್ಣ ತಿಳಿದಿದೆ. ನಾ ಇದು ಸುನಿಶ್ಚಿತ ಮಾಡಿತೋಂದರೆ ಸಹಭಾಗಿದಾರರಿಗೆ ಅಭ್ಯಾಸದ ಬಗ್ಗೆ ಕೆಳುವುದು ಸಂಧಿ ಕೊಟ್ಟಿದ್ದಾರೆ. ಮತ್ತು ಸರ್ವ ಹೇಳುವ ಪ್ರಶ್ನೆದ ಉತ್ತರಗಳು ಸಹಭಾಗಿದಾರರಿಗೆ ಸಮರ್ಪಕವಾಗಿ ಕೊಟ್ಟಿದ್ದಾರೆ ಮತ್ತು ನಾನು ಈ ಸುನಿಶ್ಚಿತ ಮಾಡಿತೋಂದರೆ ವ್ಯಕ್ತಿಗೆ (ಇಚಡಿವಿಜಲ್) ಗೆ ಯಾವುದೇ ತರಹದ ಸಮ್ಮತಿ ಸಲುವಾಗಿ ಭಯೋತ್ಪನ್ನ ಮಾಡಿಲ್ಲ ಮತ್ತು ಇದು ಸಮ್ಮತಿ ಪೂರ್ಣತಹ ಸ್ಪಷ್ಟ ಮತ್ತು ಸ್ವಾತಂತ್ರ್ಯದಿಂದ ಕೊಟ್ಟಿದ್ದೇನೆ.

ಈ ಮಾಹಿತಿ ಪತ್ರದ ಪ್ರತ ಸಹಭಾಗಿದಾರರಿಗೆ ಕೊಟ್ಟಿದ್ದಿದೆ.

ಸಂಶೋಧಕರ ಹೆಸರು / ಸಮ್ಮತಿ ತೋಗುಳುವ ವ್ಯಕ್ತಿ :-----

ಸಂಶೋಧಕರ ಸಹಿ / ಸಮ್ಮತಿ ತೋಗುಳುವ ವ್ಯಕ್ತಿ :-----

ತಾರೀಖು :

ANNEXURE IV

DATA COLLECTION PROFORMA

PERFORMA

A. SOCIODEMOGRAPHIC PROFILE

Sr. No	Variables with Code	Responded Code
1	Name, Address and IP No	
2	Age of the mother 1. 18-23 years 2. 24-29 years 3. 30 years and above	
3	Religion – 1. Hindu 2. Muslim 3. Christian 4. Others	
4	Education level of the Mother 1. No formal education 2. Primary 3. Secondary 4. PUC 5. Graduation 6. Post Graduation and above	
5	Occupation of Woman 1. Home maker 2. Govt. Service 3. Pvt Service 4. Self employed	
6	Type of Marriage 1. Consanguineous 2. Non Consanguineous	
7	Diet 1. Vegetarian 2. Non-Vegetarian	

B. QUESTIONNAIRE ON MATERNAL AND NEONATAL HEALTH OUTCOME

Sr. No	Variables with Code	Responded Code
1.	Gestational Age 1. 28-32 weeks 2. 33-37 weeks 3. 38 weeks and above	
2.	If preterm, which sub category 1. Extremely preterm (<28 weeks) 2. Very preterm (28-32 weeks) 3. Moderate to late preterm (32-37 weeks)	
3.	Date of Delivery	
4.	Mode of delivery 1. Vaginal delivery 2. Cesarean section	
5.	Parity - 1. Primipara 2. Multipara	
6.	Total No of Pregnancies including present 1. One 2. Two 3. Three 4. Four +	
7.	Outcome of Previous pregnancy 1. Total No of Live Birth 2. Total No of Still Birth 3. Total No of Miscarriages 4. Total No of MTP 5. No. of preterm delivery 6. Total No of early Neonatal Death (0-7days) 7. Total No of late Neonatal Death (8-28 days) 8. No. of Living children 9. NA	

8.	Did the mother undergo HIV Test – 1. Yes 2. No	
9.	Pre existing medical problems 1. Hypertensive disorders 2. Thyroid disorders 3. Diabetes Mellitus 4. Tuberculosis 5. <u>Anemia</u> 6. Other conditions 7. NA	
10.	No. of Antenatal Visits 1. 1-3 visits 2. 4-6 Visits 3. 7-10 visits 4. 11-13 visits	
11.	What is the mother diagnosed in present pregnancy 1. Hypertensive disorders 2. Thyroid disorders 3. Diabetes Mellitus 4. <u>Anemia</u> 5. Other conditions 6. NA	
12.	If underwent C-section/ Forceps/Vacuum delivery, what is the indication 1. Maternal Cause 2. <u>Fetal Cause</u>	
13.	<u>Fetal/Neonatal Outcome</u> – 1. Alive 2. Dead	
14.	Was it Singleton pregnancy – 1. Yes 2. No	
15.	Was it twin delivery – 1. Yes 2. No	
16.	Birth Weight – 1. Very Small (<1000g)	
	2. Small (1000-1499g) 3. Small to Normal (1500-2499g) 4. Normal (>2500g)	
17.	Head Circumference	
18.	Chest Circumference	
19.	Length	
20.	Apgar Score – 1. At 1 Minute _____ 2. At 5 Minute _____	
21.	Did baby breastfed within 1 hour after birth – 1. Yes 2. No	
22.	Was baby resuscitated with bag and mask – 1. Yes 2. No	
23.	Is baby admitted to NICU- 1. Yes 2. No	
24.	Reason for NICU admission Immediately after birth 1. Prematurity 2. Asphyxia 3. Congenital Anomaly 4. Others 5. NA	
25.	Is baby treated with Oxygen – 1. Yes 2. No	
26.	If Death, reason – 1. Asphyxia 2. Preterm 3. Respiratory Arrest 4. Other 5. NA	

ಪರಫಾಮಾ

ಅ) ನೋಡಿಯೇ ಡೆಮಾಗ್ರಾಫಿಕ್ ಪೋಫಾಯಿಲ / ಲೇಖ

ಅ.ಕ್ರ	ನೋಡ ಸಹಿತ ವೆರಿಯೆಬಲ್	ರಿಸಪಾಂಡೆಡ್ ನೋಡ
೧	ಹೆಸರು ವಿಳಾಸ ಮತ್ತು ಆಯ್.ಪಿ.ನಂ.	
೨	ತಾಯಿಯ ವಯಸ್ಸು 1) 18-23 ವರ್ಷ 2) 24-29 ವರ್ಷ 3) 30 ಮತ್ತು ಮೇಲೆ	
೩	ಧರ್ಮ 1) ಹಿಂದೂ 2) ಮೀನಾಂ 3) ಕ್ರೈಸ್ತ 4) ಇಸ್ಲಾಂ	
೪	ತಾಯಿಯ ಶೈಕ್ಷಣಿಕ ಪಾತ್ರತೆ 1) ಪರಿಪೂರ್ಣ ಶಿಕ್ಷಣ ವಿಲ್ಲ 2) ಪ್ರಾಥಮಿಕ 3) ಮಾಧ್ಯಮಿಕ 4) ಪಿ.ಯು.ಸಿ 5) ಪದವಿಧರ 6) ಉಚ್ಚ ಪದವಿಧರ / ಜಾಸ್ತಿ	
೫	ಸ್ತ್ರೀಯ ವ್ಯವಸ್ಥಾಪನಾ 1) ಮನೆಯ ಕೆಲಸ 2) ಸರಕಾರಿ ನೋಕರ 3) ಖಾಸಗಿ ನೋಕರ 4) ಸ್ವ ವ್ಯವಸ್ಥಾಪನಾ	
೬	ಮದಮಿಯ ಪ್ರಕಾರ 1) ರಕ್ತ ಸಂಬಂಧಿಕ 2) ರಕ್ತ ಸಂಬಂಧಿಕ ವಿಲ್ಲ	
೭	ಪ್ರತಿಮಾಹ ಪ್ರಾಪ್ತಿ 1) < ರೂ. 5000/- 2) ರೂ. 5001-10000/- 3) ರೂ. 10001-15000/- 4) ರೂ. 15000 ಕ್ಕಿಂತ ಹೆಚ್ಚು	

ಬ) ಮಾತೃತ್ವ ಮತ್ತು ಜನ್ಮದ ಪ್ರಥಮ ತಿಂಗಳಿಂದ ಆರೋಗ್ಯಮೇಲಿಂದ ಪರಿಣಾಮರ ಬಗ್ಗೆ ಪ್ರಶ್ನಾವಳಿ

ಅ.ಕ್ರ	ಕೋಡ್ ಸಹಿತ ವರಿಯೆಬಲ್	ರಿಸಪಾಂಡೆಡ್ ಕೋಡ್
೧	ಗರ್ಭಧಾರಣೆಯ ಕಾಲಾವಧಿ 1) 28-32 ವಾರಗಳು 2) 33-37 ವಾರಗಳು 3) 38 ವಾರಗಳು ಮತ್ತು ಮೇಲೆ	
೨	ಸಮಯದ ಮೇದಲು/ ಅಪರಿಪಕ್ವ ಇದ್ದರೆ ಯಾವದೆ ಸಬ್ ಕ್ಯಾಟಗರಿ 1) ಅತಿಶಯ ಮೇದಲು/ಅಪರಿಪಕ್ವ (<28 ವಾರಗಳು) 2) ಅತಿ ಮೋದಲು/ ಅಪರಿಪಕ್ವ (24-32 ವಾರಗಳು) 3) ಮರ್ಯಾದದಿಂದ ಲೇಟ ಮೋದಲು/ ಅಪರಿಪಕ್ವ (32-37 ವಾರಗಳು)	
೩	ಪ್ರಸೂತಿಯ ದಿನಾಂಕ	
೪	ಪ್ರಸೂತಿಯ ಮಾರ್ಗ 1) ಯೋನಿ ಮಾರ್ಗ 2) ಸಿಜರಿನ್	
೫	ಪ್ಯಾರಿಸಿ 1) ಪ್ರಿಮಿಪ್ಯಾರಾ 2) ಮಲ್ಟಿಪ್ಯಾರಾ	
೬	ಸದೆಯ ಗರ್ಭಧಾರಣೆ ಸಹಿತ ವಜ್ಜು ಗರ್ಭಧಾರಣೆ 1) ವಂದು 2) ಎರಡು 3) ಮೂರು 4) ನಾಲ್ಕು +	
೭	ಹಿಂದಿನ ಗರ್ಭಧಾರಣೆಯ ಪರಿಣಾಮ 1) ವಜ್ಜು ಲಾಯುವ ಜನ್ಮ 2) ವಜ್ಜು ಸ್ಥಿಲ ಜನ್ಮ 3) ವಜ್ಜು ಗರ್ಭಪಾತ 4) ವಜ್ಜು ಎಮ್. ಟಿ.ಪಿ 5) ವೇಳೆಯ ಮೋದಲನ/ಅಪರಿಪಕ್ವ ಪ್ರಸೂತಿ ಅರಳಿ ನಿಯಂಟರ ಮೃತ 6) ಸ್ಕೆದ ಸಂಖ್ಯೆ (೦-7-ದಿನ) 7) ಲೇಟ ನಿಯಂಟರ ಮೃತ್ಯು ಸಂಖ್ಯೆ (8-28 ದಿನ) 8) ಜವಂತ ಮಕ್ಕಳದ ವಜ್ಜು ಸಂಖ್ಯೆ 9) ಮೇಲಿಂದ ಯಾವದೆ ಇಲ್ಲ	
೮	ತಾಯಿ ಎಚ್. ಆರ್. ವಿ ಟೆಸ್ಟದಿಂದ ಹೋಗಿದ್ದಾರೇ ? 1) ಹೌದು 2) ಇಲ್ಲ	

೯	ಮೊದಲಿಂದ ಕೇರುವ ಆರೋಗ್ಯದ ಸಮಸ್ಯೆ 1) ಅತಿ ಉಜ್ಜ್ವಲತೆ ಹೊಂದಿರುವ ಆರೋಗ್ಯ (ಆರೋಗ್ಯಕರ) 2) ಧಾರ್ಮಿಕತೆಯಿಂದ ಹೊಂದಿರುವ ಆರೋಗ್ಯ (ಆರೋಗ್ಯಕರ) 3) ಧಾರ್ಮಿಕತೆಯಿಂದ ಹೊಂದಿರುವ ಆರೋಗ್ಯ 4) ಧಾರ್ಮಿಕತೆಯಿಂದ ಹೊಂದಿರುವ ಆರೋಗ್ಯ 5) ಆರೋಗ್ಯಮಯ 6) ಆರೋಗ್ಯ ಸ್ಥಿತಿ 7) ಮೊದಲಿಂದ ಯಾವುದೇ ಇಲ್ಲ	
೧೦	ಆರೋಗ್ಯದಿಂದ ಹೊಂದಿರುವ ಸಮಸ್ಯೆ 1) 1-3 ಭೇದಗಳು 2) 4-6 ಭೇದಗಳು 3) 7-10 ಭೇದಗಳು 4) 11-13 ಭೇದಗಳು	
೧೧	ಸದ್ಯಕ್ಕೆ ಗರ್ಭಧಾರಣೆಯಿಂದ ಹೊಂದಿರುವ ತಾಯಿಯನ್ನು ಹೊಂದಿರುವ ಆರೋಗ್ಯ 1) ಹೊಂದಿರುವ ಟೆನಿಸಿವ (ಅತಿ ಉಜ್ಜ್ವಲ) ಹೊಂದಿರುವ ಆರೋಗ್ಯ 2) ಧಾರ್ಮಿಕತೆಯಿಂದ ಹೊಂದಿರುವ ಆರೋಗ್ಯ 3) ಧಾರ್ಮಿಕತೆಯಿಂದ ಹೊಂದಿರುವ ಆರೋಗ್ಯ 4) ಆರೋಗ್ಯಮಯ 5) ಅರೋಗ್ಯ ಸ್ಥಿತಿ 6) ಮೊದಲಿಂದ ಯಾವುದೇ ಇಲ್ಲ	
೧೨	ಎಂದರೆ ಸಿ-ಸೇಕ್ವೆನ್ಸ್/ಮೋರಿಸೆಪ್ಪ ವ್ಯಾಖ್ಯಾನ ಪ್ರಕಾರ ಇದ್ದರೆ ಎನ ತೋರಿಸುತ್ತದೆ 1) ತಾಯಿಯ ಕಾರಣ 2) ಗರ್ಭ ಕಾರಣ	
೧೩	ಗರ್ಭದ / ಜನ್ಮದ ಪರಿಣಾಮ 1) ಜೀವಂತ 2) ಮೃತ	
೧೪	ವಂದ ಮಗುವಿನ ಜನ್ಮ 1) ಹೌದು 2) ಇಲ್ಲ	
೧೫	ಎರಡು ಮಗುವಿನ ಜನ್ಮ 1) ಹೌದು 2) ಇಲ್ಲ	
೧೬	ಜನ್ಮದ ಸಮಯ ತುಕ 1) ಅತಿ ಸ್ವಲ್ಪ (<1000 ಗ್ರಂ) 2) ಸ್ವಲ್ಪ (1000-1499 ಗ್ರಂ) 3) ಸ್ವಲ್ಪಕ್ಕಿಂತ ಸಾಮಾನ್ಯ (1500-2499 ಗ್ರಂ) 4) ಸಾಮಾನ್ಯ (>2500 ಗ್ರಂ)	

೧೭	ಹೆಡ (ತೆಲ) ಸರಕಮಫರಸ್ತ	
೧೮	ಎದೆಯ (ಬೇಷ್) ಸರಕಮಫರಸ್ತ	
೧೯	ಹಾಯಿಟ (ಉದ್ದ)	
೨೦	ಅಪಗಾರ ಸ್ಥೋರ 1) ವಂದೆ ನಿಮಿಶಕ್ಕೆ-- 2) ಐದು ನಿಮಿಶಕ್ಕೆ	
೨೧	ಮಗುವೆ ಜನ್ಮದ ಬಂದತಾನಲ್ಲಿ ಸ್ಥನಪಾನ ಮಾಡಲಾಗಿದೆ ? 1) ಹೌದು 2) ಇಲ್ಲ	
೨೨	ಮಗುವ ಪುನರುತ್ಥಾನ (ರೇಜುಸ್ಟಿಟೆಡ) ಬ್ಯಾಗ ಮತ್ತು ಮಾಸ್ಕ್ ಸಹಿತ ಆಯಿತು ? 1) ಹೌದು 2) ಇಲ್ಲ	
೨೩	ಮಗುವೆ ಏನ ಆಯ. ಸಿ. ಯು. ದಲ್ಲಿ ದಾಖಲ ಮಾಡಿದ್ದಾರೆ ? 1) ಹೌದು 2) ಇಲ್ಲ	
೨೪	ಹುಟ್ಟಿದತಕ್ಷಣಾ ಮಗುವಿಗೆ ಏನ ಆಯ. ಸಿ ಯು ದಲ್ಲಿ ದಾಖಲ ಮಾಡುವ ಕಾರಣ 1) ಸಮಯ ಮೋದಲ/ಅಪರಿಪಕ್ವ (ಪ್ರಿಮೆಚುರಿಟಿ) 2) ಆಸ್ಪತ್ರೆಯಾ 3) ಕೋಂಜೇನಿಂಟಲ ಆನಾಮಾಲ 4) ಮೇಲಂದ ಬದಲು 5) ಮೇಲಂದ ಯಾವದೆ ವಿಲ್ಲ	
೨೫	ಮಗುವೆ ಆಕ್ಸಿಜನ ಕೋಡಲಾಗಿದೆ ? 1) ಹೌದು 2) ಇಲ್ಲ	
೨೬	ಮೃತ ಇದ್ದರೆ - ಕಾರಣ 1) ಆಸ್ಪತ್ರೆಯಾ 2) ಪ್ರಿಮರ್ಮ/ ಅಪರಿಪಕ್ವ 3) ರೆಸ್ಪರಿಟರಿ ಅರೆಸ್ಟ್ 4) ಇತರೆ 5) ಮೇಲಂದ ಯಾವದೆ ಇಲ್ಲ	

परफॉर्म

अ) सोशियोडेमोग्राफीक प्रोफाईल /लेख

अ.क्र.	कोड सहित वेरीएबल	रिस्पॉंडेंट कोड
१	नांव पत्ता व आई.पी.नं.	
२	आईचे वय १) १८-२३ वर्षे २) २४-२९ वर्षे ३) ३० वर्षे व वरील	
३	धर्म १) हिंदू २) मुस्लिम ३) ख्रिश्चन ४) अन्य	
४	आईची शैक्षणिक पात्रता १) औपचारिक शिक्षण नाही २) प्राथमिक ३) माध्यमिक ४) पी.यु.सी. ५) पदवीधर ६) उच्च पदवी व वरील	
५	स्त्रीचा व्यवसाय १) घरगूती २) सरकारी नोकरी ३) खाजगी नोकरी ४) स्वतःचा व्यवसाय	
६	लग्नाचा प्रकार १) एकारक्तातले जवळ नसलेले	
७	प्रतीमाह आय (मिळकत) १) <रु. ५०००/- २) रु. ५००१- रु. १०,००० ३) रु. १०००१ – रु. १५,००० ४) रु. १५,००० – व वरील	

परफॉर्म

ब) मातृत्व व जन्माच्या प्रथम महिन्याच्या तबीयती परिणामाबद्दल प्रश्नावली

अ.क्र.	कोड सहित वेरीएबल	रिस्पॉडेंट कोड
१	गर्भधारणेचा कालावधी १) २८-३२ आठवडे २) ३३-३७ आठवडे ३) ३८ आठवडे व वरील	
२	जर अवकाळी असल्यास, कोणती सब केटेगरी १) अतिशय अवकाळी / परिपक्वतेच्या आधी (<२८ आठवडे) २) अति अवकाळी / परिपक्वतेच्या आधी (२८-३२ आठवडे) ३) (मॅडरेट मयदितील) लेट अवकाळी/ परिपक्वतेच्या आधी (३२-३७ आठवडे)	
३	प्रसूतीची तारीख	
४	प्रसूतीचा मार्ग १) योनी मार्ग २) सिझरीयन	
५	पॅरीटी १) प्रिमीपॅरा २) मल्टीपॅरा	
६	सध्याची गर्भधारणा सहित एकूण गर्भधारणा १) एक २) दोन ३) तीन ४) चार +	
७	मागिल गर्भधारणेचे परिणाम १) एकूण लाईव जन्म (लाईव बर्थ) २) एकूण आतापावेता जन्म (स्टील बर्थ) ३) एकूण गर्भपात ४) एकूण एम. टी. पी ५) अवकालीन (परिपक्वतेच्या आधी) प्रसूती एकूण ६) अर्ली (निऑन्टल) मृत्युची एकूण संख्या (०-७ दिवस) ७) लेट (निऑन्टल) मृत्यु एकूण संख्या (८-२८ दिवस) ८) जिवंत मुलांची एकूण संख्या ९) वरील कोणतीही नाही	

८	आई.एच.आई. ती टेस्ट मधून गेली आहे का? १) होय २) नाही	
९	आधीपासून असणाऱ्या तबीयतीचे तक्रार १) अतिउच्चपणाचे डिसऑर्डर (अराजकता) २) थायरॉईड डिसऑर्डर (अराजकता) ३) डायबेटीक मेलीटस ४) टायबर कुलॉसीस ५) अनेमिया ६) अन्य स्थिती ७) वरील कोणतीही नाही	
१०	अंटेनेटल विजीटचे संख्या (गर्भवतीच्या भेटीची संख्या) १) १-३ भेट २) ४-६ भेट ३) ७-१० भेट ४) ११-१३ भेट	
११	सध्या गर्भधारणेत मातेचे काय डायग्रॉजड झाले. १) हायपरटेनसिव (आतिउच्च) डिसऑर्डर(अराजकता) २) थायरॉईड डिसऑर्डर(अराजकता) ३) डायबेटीक मेलीटस ४) अनेमिया ५) अन्य स्थिती ६) वरील कोणतीही नाही	
१२	जर का सी-सेक्शन / फॉरसेप्स / वॅक्यूम प्रसुती असल्यास काय दर्शविते. १) आईची कारणे २) गर्भ कारण	
१३	गर्भाचे जन्माचे परिणाम १) जीवंत २) मृत	
१४	एक बाळाचा जन्म १) होय २) नाही	
१५	दोन बाळाचा जन्म होय नाही	
१६	जन्मावेळी वजन १) अति लहान (<१००० ग्रॅम) २) लहान (१०००-१४९९ ग्रॅम)	

	३) लहान ते सामान्य (१५००-२४९९ ग्रॅम) ४) सामान्य (> २५०० ग्रॅम)	
१७	हेड (डोके) सरकमफरन्स	
१८	(छाती) चेस्ट	
१९	लांबी	
२०	अपगार स्कोर १) एका मिनीटाला २) पाच मिनीटाला	
२१	बाळाला जन्माच्या एका तासात स्थनपान केले ? १) होय २) नाही	
२२	बाळाचे पुनरुत्थान बॅग (रेज्युस्किटेड) बॅग व मास्क सकट झाले १) होय २) नाही	
२३	बाळाला एन. आय. सी. यू मध्ये दाखल केले १) होय २) नाही	
२४	जन्माबरोबरच बाळाला एन.आय.सी.यू मध्ये दाखल करण्याचे कारण १) अवकालीन / परिपक्वते आधी (प्रीमॅट्यूरीटी) २) ऍस्फीक्सीया ३) कॉन्टेनीटल अनॉमाली ४) याखेरीज ५) वरील कोणतेही नाही	
२५	बाळाला ऑक्सीजन दिले गेले? १) होय २) नाही	
२६	जर मृत कारण १) ऍस्फीक्सीया २) प्रीटर्म- अवकालीन ३) रेस्परीटोरी अरेस्ट ४) इतर ५) वरील कोणतेही नाही	

ANNEXURE V PUBLICATIONS



Home / About the Journal

About the Journal

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- Book reviews and event summary etc
- Short and summarized biography of Modern India Builders
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RESEARCH ARTICLE

Association between the socio-demographic variables of women admitted for delivery to a Tertiary Care Hospital and their maternal and neonatal outcome - A cross-sectional study

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Abstract

The adverse outcome of pregnancy, either on the mother or fetus, remains to be still high despite improvements in healthcare services. This is due to various factors, including medical, environmental or socioeconomic factors. A cross-sectional study was conducted among 300 women admitted for delivery to a tertiary care hospital at Belagavi to find the association between socio-demographic variables and their maternal and neonatal outcomes. Data was collected using tools on socio-demographic profiles and questionnaires on Maternal and neonatal health outcomes. Descriptive statistics, Chi-square test and multiple logistic regression analysis analyzed data. Majority (47%) of the mothers belonged to the age group of 24 to 29 years, 79% are Hindu, 48.67% completed Pre-University course, 98.33% are homemakers, 67.33% had a non-consanguineous marriage and 62.33% are non-vegetarian. In the study, 62.33% had a vaginal delivery, 58% were primipara and 52.67% of them were pregnant for the first time. There was a significant association between the mother's age and education level and maternal and neonatal outcome, and there was no significant association between the preterm and term with demographic characteristics. Multiple logistic regression analysis showed that women who had delivered vaginally, those pregnant for the third time had good maternal outcomes and women who had 11 to 13 antenatal visits have good neonatal outcomes. Also, women with either maternal or fetal conditions have an equal chance of undergoing Cesarean section. Birth weight and length of the baby is associated with the mother's gestational age at the time of delivery.

Keywords: Maternal outcome, Neonatal outcome, Low birth weight, Preterm birth, Associations.

Introduction

The effect of the fertilization process, which takes place from the time the embryo is formed till the first few weeks of life, either to the mother or the fetus, is considered a

pregnancy outcome. These outcomes can include live birth, which may be full-term or preterm birth, stillbirth, spontaneous abortion, induced abortion and early neonatal mortality (Yeshialem E. *et al.*, 2017). During antepartum, intrapartum and postpartum period, health issues that affect the mother or baby, or both can fall under the category of adverse pregnancy outcomes like antepartum hemorrhage, hyperemesis gravidarum, postpartum hemorrhage, stillbirth, low birth weight, premature rupture of membranes, obstructed labor, hypertensive disorders of pregnancy, prematurity, uterine rupture and puerperal sepsis (CDC 24/7: saving lives, protecting people, 2016).

In low- and middle-income nations, the burden of unfavorable pregnancy outcomes is still significant and is the primary contributor to maternal and newborn morbidity and mortality as well as long-term physical and psychological consequences. Negative pregnancy outcomes are also found to be influenced by age, occupation, place of residence, and the absence of prenatal care (Tadese M. *et al.*, 2022).

Hereditary and environmental factors, current health and nutritional status, inter-pregnancy interval, maternal age, genitourinary or general disorders in women,

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How to cite this article: Chanu, H. G., Raddi, S. A., Dalal, A., Kharde, S. N., Tendulkar, S. (2024). Association between the socio-demographic variables of women admitted for delivery to a Tertiary Care Hospital and their maternal and neonatal outcome - A cross-sectional study. *The Scientific Temper*, **15**(1):58-64.

Doi: 10.58414/SCIENTIFICTEMPER.2024.15.1.09

Source of support: Nil

Conflict of interest: None.

socioeconomic level, and educational attainment influence pregnancy outcomes (Naik JD. *et al.*, 2016).

Approximately 810 women worldwide die every day from issues that could have been avoided during pregnancy, childbirth or the postpartum period (U. WHO & B. W. UNFPA, 2019).

Worldwide, 4.6 million children died before turning one, with 50% dying during the first day and over 75% within the first week. Each year, there are an additional 2.6 million stillbirths, 25% of which occur during labor. The majority of stillbirths and early neonatal fatalities are caused by birth-related problems that might be avoided. If sufficient prenatal, intrapartum, and neonatal services were accessible, the majority of the 6.3 million perinatal fatalities that take place yearly in underdeveloped nations could be prevented (Anggondowati T. *et al.*, 2017).

Many studies have demonstrated that when gestational age decreases, newborn mortality increases significantly. Due to myometrial stretching from previous pregnancies, high parity may increase the chance of preterm delivery (Wagura, P., *et al.*, 2018).

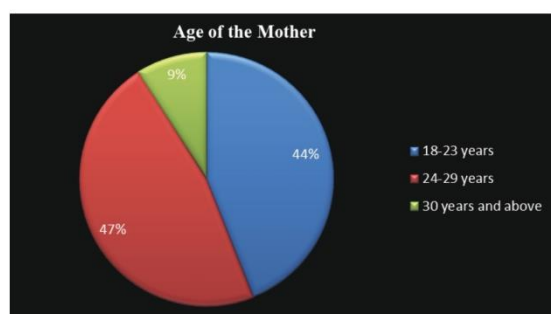
Preterm birth is a leading cause of perinatal morbidity and mortality in both developed and also developing countries (Goldenberg R. L. *et al.*, 2008).

Grand multiparity can have adverse effects on the mother and fetus, including antepartum and postpartum hemorrhage, gestational diabetes, hypertension, anemia, and preterm birth (Abdelmageed E. *et al.*, 2022).

Hence this study was undertaken to determine the association between the socio-demographic variables of women admitted for delivery and their maternal and neonatal outcomes.

Materials And Methods

The study used a cross-sectional research design with an evaluative approach. The study was conducted at a selected Tertiary care hospital of Belagavi city. Consecutive mothers with gestation of 28 weeks or more admitted for delivery in selected tertiary care hospitals of Belagavi city were included in the study. The sample size was 300 mothers.



Graph 1: A pie graph showing percentage distribution of age of the mother.

The study included all mothers with or more than 28 gestational weeks delivering in tertiary care hospitals of Belagavi city. The study excluded the mothers with use of vaginal antimicrobials or antibiotics and women associated with medical conditions (hypertensive disorders in pregnancy, diabetes, heart disease, antepartum hemorrhage).

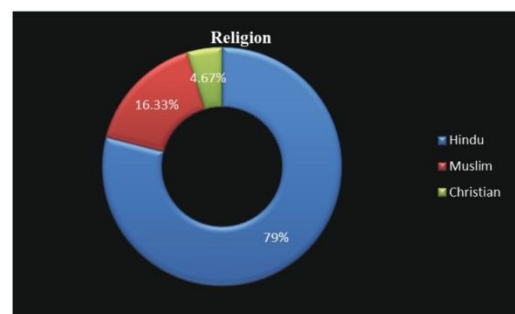
Data collection

After obtaining ethical clearance and formal permission from the Institutional ethical committee and also from the Medical Director and Medical Superintendent of the selected tertiary care hospital, the purpose of the study was explained to mothers and relatives and written consent was taken from every subject to collect the data. Data was collected using the Socio-demographic profile and Questionnaire on Maternal and neonatal health outcomes. Data was analyzed using Descriptive statistics, Chi-square test and multiple logistic regression analysis.

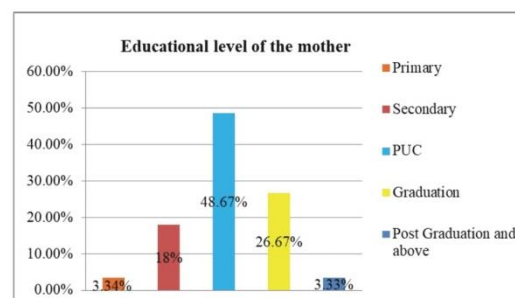
Results

Demographic Characteristics of Respondents

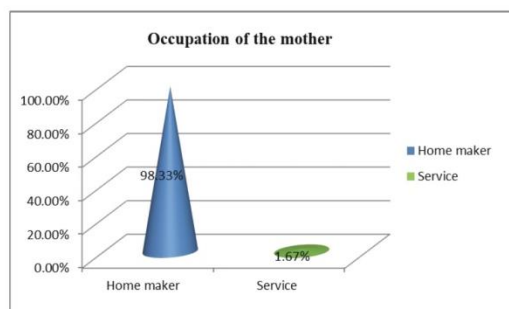
Graph 1-6 depicts that among the 300 respondents, majority (47%) of the mothers belongs to the age group of 24-29 years, 79% of them are Hindu, 48.67% have completed Pre-University Course, 98.33% are home maker, 67.33% had a non consanguineous marriage and 62.33% are non vegetarian.



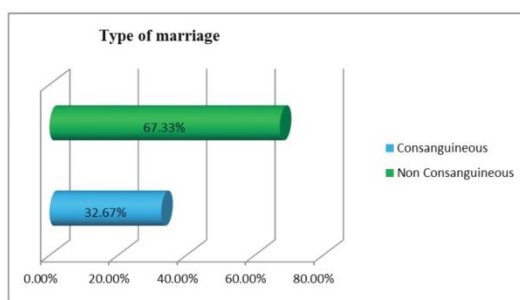
Graph 2: A doughnut graph showing percentage distribution of religion of the mother.



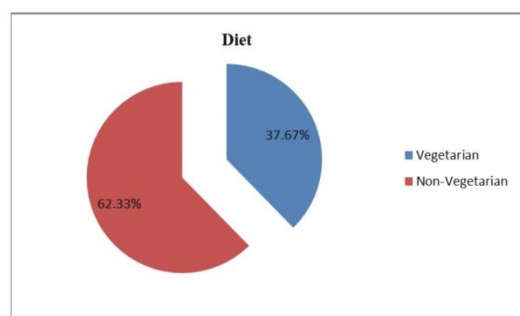
Graph 3: A column graph showing percentage distribution of the mother's educational level.



Graph 4: A column graph showing the percentage distribution of the mother's occupation.



Graph 5: A bar graph showing percentage distribution of type of marriage of the mother.



Graph 6: A pie graph showing percentage distribution of diet of the mother.

Maternal Characteristics of Respondents

Table 1 shows that among the 300 respondents, 62.33% had vaginal delivery, 58% were primipara and 52.67% of them were pregnant for the first time.

Association between socio-demographic variables with maternal and neonatal outcome

Table 2 indicates that there is a significant association between the age and education level of the mother along with maternal and neonatal outcome; which means that there is no significant association between the religion,

Table 1: Maternal characteristics of respondents

n = 300

Maternal characteristics	No of respondents	% of respondents
Mode of delivery		
Vaginal delivery	187	62.33
Cesarean section	113	37.67
Parity -		
Primipara	174	58.00
2	107	35.67
3	19	6.33
Gravida		
One	158	52.67
Two	89	29.67
Three	46	15.33
Four +	7	2.33
Total	300	100.00

occupation, type of marriage and diet of the mother along with maternal and neonatal outcome ($p < 0.05$).

Association between gestational age (Preterm and term) with demographic characteristics

Table 3 shows that there is no significant association between gestational age (Preterm and term) with demographic characteristics ($p < 0.05$).

Multiple logistic regression analysis of gestational age by maternal outcomes

Table 4 shows that the women who had delivered vaginally and those who were pregnant for the third time had good maternal outcomes ($p < 0.05$).

Multiple logistic regression analysis of gestational age by neonatal outcomes

Table 5 indicates that the women who had 11 to 13 antenatal visits had good neonatal outcomes, and those with maternal or fetal conditions had an equal chance of undergoing Cesarean section ($p < 0.05$).

Multiple logistic regression analysis of gestational age by other parameters

Table 6 shows that the Birth weight and length of the baby is associated with the mother's gestational age at the time of delivery ($p < 0.05$).

Comparison of gestational age (Preterm and term) with birth weight, head circumference, chest circumference and length by independent t-test

Table 7 shows that there is a significant association between gestational age (Preterm and term) with birth weight, head circumference, chest circumference and length by independent t-test ($p < 0.05$).

61 Association of socio-demographic variables and maternal & neonatal outcome of women admitted for delivery

Table 2: Association between socio-demographic variables with maternal and neonatal outcome

Table 2: Association between socio-demographic variables with maternal and neonatal outcome												
	Age of the mother					Education level of the mother						
Health outcome	18-23 years	24-29 years	30 years+	%	χ^2 test, p-value	Primary	Secondary	PUC	Degree	PG	%	χ^2 test, p-value
Mode of delivery												
Vaginal delivery	84	86	17	62.33	0.208, 0.901	7	39	96	40	5	62.33	9.058, 0.06
Cesarean section	48	55	10	37.67		3	15	50	40	5	37.67	
Parity												
Primipara	103	62	9	58	45.232, 0.0001*	6	23	87	51	7	58	13.25, 0.104
2	28	66	13	35.67		4	23	53	25	2	35.67	
3	1	13	5	6.33		0	8	6	4	1	6.33	
Gravida												
One	91	61	6	52.67	43.262, 0.0001*	6	16	85	44	7	52.67	26.569, 0.0090*
Two	33	47	9	29.67		0	20	41	26	2	29.67	
Three	8	29	9	15.33		3	16	18	8	1	15.33	
Four +	0	4	3	2.33		1	2	2	2	0	2.33	
No. of antenatal visits												
4-6 Visits	6	12	1	6.33	2.5, 0.645	3	6	9	1	0	6.33	17.23, 0.0280*
7-10 visits	29	28	7	21.33		1	12	33	17	1	21.33	
11-13 visits	97	101	19	72.33		6	36	104	62	9	72.33	
If underwent CS/ forceps/ vacuum delivery, what is the indication												
No	82	82	18	60.67	5.916, 0.206	8	39	93	37	5	60.67	14.721, 0.065
Maternal Cause	9	22	3	11.33		1	2	17	12	2	11.33	
Fetal Cause	41	37	6	28		1	13	36	31	3	28	
Is baby admitted to NICU-												
Yes	26	18	3	15.67	2.945, 0.229	0	8	30	6	3	15.67	10.114, 0.0390*
No	106	123	24	84.33		10	46	116	74	7	84.33	
Reason for NICU admission Immediately after birth												
Prematurity	3	1	0	1.33	8.667, 0.193	0	1	2	1	0	1.33	39.729, 0.0001*
Asphyxia	2	6	0	2.67		0	1	4	0	3	2.67	
Others	21	11	3	11.67		0	6	24	5	0	11.67	
NA	106	123	24	84.33		10	46	116	74	7	84.33	
Is baby treated with Oxygen												
Yes	8	7	0	5	1.734, 0.42	1	3	7	1	3	5	16.101, 0.0030*
No	124	134	27	95		7	51	139	79	7	95	
Total	132	141	27	100		10	54	146	80	10	100	

*p<0.05

Table 3: Association between gestational age (Preterm and term) with demographic characteristics

Characteristics	Preterm	%	Term	%	Total	%	χ^2 test, p-value	p-value
<i>Age of the mother</i>								
18-23 years	22	53.66	110	42.47	132	44.00	2.2130	0.3310
24-29 years	17	41.46	124	47.88	141	47.00		
30 years & above	2	4.88	25	9.65	27	9.00		
<i>Religion</i>								
Hindu	31	75.61	206	79.54	237	79.00	0.8000	0.6700
Muslim	7	17.07	42	16.22	49	16.33		
Christian	3	7.32	11	4.25	14	4.67		

<i>Education level of the mother</i>								
Primary	0	0.00	10	3.86	10	3.34	6.3775	0.2711
Secondary	11	26.83	43	16.60	54	18.00		
PUC	22	53.66	124	47.88	146	48.67		
Graduation	8	19.51	72	27.80	80	26.67		
Post Graduation & above	0	0.00	10	3.86	10	3.33		
<i>Occupation of Woman</i>								
Homemaker	41	100.00	254	98.07	295	98.33	0.8050	0.3700
Service	0	0.00	5	1.93	5	1.67		
<i>Type of Marriage</i>								
Consanguineous	10	24.39	88	33.98	98	32.67	1.4790	0.2240
Non-consanguineous	31	75.61	171	66.02	202	67.33		
Diet	41	100.00	259	100.00	300	100.0		
Vegetarian	15	36.59	98	37.84	113	37.67	0.0240	0.8780
Non-Vegetarian	26	63.41	161	62.16	187	62.33		
Total	41	100.00	259	100.00	300	100.0		

*p < 0.05

Table 4: Multiple logistic regression analysis of gestational age by maternal outcomes

	Maternal outcomes			
Maternal outcomes	Adjusted OR	95% CI for OR		p-value
		Lower	Upper	
Mode of delivery				
Vaginal delivery	0.32	0.19	0.54	0.0001*
Cesarean section	Ref.			
Parity				
Primipara	Ref.			
2	1.03	0.20	5.23	0.9690
3	0.82	0.05	13.68	0.8880
Gravida				
One	Ref.			
Two	0.25	0.06	1.16	0.0760
Three	0.10	0.01	0.75	0.0250*
Four +	0.19	0.01	2.84	0.2290

*p < 0.05

Comparison of gestational age (Preterm and term) with APGAR scores at 1 min and 5 min by independent t-test

Table 8 shows that there is a significant association between the gestational age (Preterm and term) of the mother with APGAR scores of the newborn at 1 min and 5 min by independent t-test (p < 0.05).

Discussion

In the study, the majority (47%) of the mothers belong to the age group of 24 to 29 years, 79% of them are Hindu, 48.67% completed Pre-University Course, 98.33% are homemaker,

Table 5: Multiple logistic regression analysis of gestational age by neonatal outcomes

Neonatal outcomes				
Neonatal outcomes	Adjusted OR	95% CI for OR		p-value
		Lower	Upper	
No. of antenatal visits				
4-6 Visits	Ref.			
7-10 visits	2.08	0.69	6.30	0.1950
11-13 visits	0.51	0.27	0.96	0.0360*
If underwent CS/ forceps/ vacuum delivery. What is the indication				
No	Ref.			
Maternal Cause	0.10	0.03	0.34	0.0001*
Fetal Cause	0.18	0.09	0.33	0.0001*
Is baby admitted to NICU-				
No	Ref.			
Yes	1.83	0.80	4.20	0.1540
Reason for NICU admission: Immediately after birth				
Prematurity	Ref.			
Asphyxia	-	-	-	-
Others	0.52	0.03	8.04	0.6380
Is baby treated with Oxygen				
No	Ref.			
Yes	3.61	0.37	35.48	0.2710

*p < 0.05

67.33% had a non-consanguineous marriage and 62.33% are non-vegetarian.

Table 6: Multiple logistic regression analysis of gestational age by other parameters

Others	Adjusted OR	95% CI for OR		p-value
		Lower	Upper	
Birth weight	0.07	0.03	0.18	0.0001*
Head circumference	0.78	0.56	1.08	0.1310
Chest circumference	0.97	0.68	1.37	0.8490
Length	1.43	1.16	1.77	0.0010*
APGAR Score at 1 min.	1.07	0.67	1.73	0.7730

*p<0.05

Table 7: Comparison of gestational age (Preterm and term) with birth weight, head circumference, chest circumference and length by independent t-test

Parameters	Preterm		Term		t-value	p-value
	Mean	Std.Dev.	Mean	Std.Dev.		
Birth weight	3.32	0.47	3.87	0.37	-8.6333	0.0001*
Head circumference	33.29	1.05	34.71	1.77	-4.9743	0.0001*
Chest circumference	31.39	1.26	32.70	1.79	-4.4943	0.0001*
Length	45.71	1.42	47.51	1.72	-6.3746	0.0001*

*p<0.05

Table 8: Comparison of gestational age (Preterm and term) with APGAR scores at 1 min and 5 min by independent t-test

Parameters	Preterm		Term		t-value	p-value
	Mean	Std.Dev.	Mean	Std.Dev.		
APGAR Score at 1 min.	7.24	0.83	7.57	0.78	-2.4431	0.0151*
APGAR Score at 5 min.	8.22	0.79	8.68	0.64	-4.1213	0.0001*

*p<0.05

Among the 300 respondents, 62.33% had a vaginal delivery, 58% were primipara and 52.67% of them were pregnant for the first time.

The study showed that i) there is a significant association between the age and education level of the mother along with maternal and neonatal outcome ($p<0.05$); ii) there is no significant association between the gestational age (Preterm and term) with demographic characteristics ($p<0.05$).

Similar findings are seen in the study conducted by Naik, J.D., *et al.* (2016) where most subjects (57.71%) were from urban areas and 66.66% were Hindu. There was a significant association between pregnancy outcome with education, nature of work, socioeconomic status, age at marriage, and consanguineous marriage, a significant association was observed with maternal age, and residence and no significant association was observed with type of family transport facilities.

Multiple logistic regression analysis of gestational age by maternal outcomes showed that the women who had delivered vaginally and those who were pregnant for the third time have good maternal outcome ($p<0.05$); women who had 11 to 13 antenatal visits have good neonatal outcomes, and those women with either maternal or fetal

conditions have equal chance of undergoing Cesarean section; and it has also shown that birth weight and length of the baby is associated with the gestational age of the mother at the time of delivery ($p<0.05$).

In the study conducted by Harrison, M.S., *et al.* (2020), there is reduced adverse maternal outcomes among the women with ≥ 4 antenatal visits; and those women with malpresenting fetuses, obstetrically high-risk women, less education, and those with maternal or obstetric indication have increased odds of adverse outcomes.

The comparison of gestational age (Preterm and term) with birth weight, head circumference, chest circumference and length by independent t-test showed that there is a significant association between gestational age (Preterm and term) with birth weight, head circumference, chest circumference and length by independent t-test ($p<0.05$).

A similar finding is shown in the study conducted by Babilu *et al.* (2022) which showed a significant correlation between foot length with GA and other anthropometric parameters in preterm babies and in term AGA and LGA babies.

Also the comparison of gestational age (Preterm and term) with APGAR scores at 1 and 5 minutes by independent

t-test showed a significant association between the gestational age (Preterm and term) of the mother with APGAR scores of the newborn at 1 and 5 minutes by independent t-test at 0.05 level of significance.

Conclusion

The study provides a general overview of the association between the socio-demographic variables of the women and their maternal and neonatal outcomes. This study will also help prevent adverse maternal and neonatal outcomes by identifying it as soon as possible.

Acknowledgment

I express my heartfelt gratitude to my Guide and Co-guide for their guidance in conducting the study. I also express my sincere thanks to all the Department of OBG Nursing, KAHER Institute of Nursing Sciences, Belagavi faculty for their constant support in conducting the study. Special thanks to all my study subjects who have actively participated in this study.

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RESEARCH

O&G Forum 2024; 34 – 3s: 945-952

EXPLORATION OF THE VAGINAL MICROBIOME COMPOSITION IN PARTURIENT WOMEN ADMITTED TO A TERTIARY CARE HOSPITAL: A COMPREHENSIVE INVESTIGATION

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Abstract

Background: Vaginal microbiome is the microorganism that colonizes the vagina and has a significant impact on women's health and disease conditions. Microbiome starts to develop from the uterus and is further influenced by various factors like timing of birth, environmental exposures, diet, inflammatory immune responses, clinical infection, and sexual and hygiene practices. Anaerobic bacteria replace the lactobacillus, the usual vaginal flora, in bacterial vaginosis. About 20% of expectant mothers have it, and most of them have no symptoms. It is associated with premature rupture of membranes, preterm delivery, chorioamnionitis, and intra-uterine death. It also leads to adverse neonatal outcomes like assisted ventilation or respiratory distress at birth, neonatal Intensive care unit admission, fetal and infant mortality, neonatal sepsis, chronic lung disease and delayed development.

Methods: A case series study was conducted among 300 women to study the vaginal microbiome in women admitted for delivery to a tertiary care hospital at Belagavi. Vaginal swabs were collected from the posterior vaginal fornix and then placed in a sterile tube which was stored immediately until the sample is tested at -70°C. The samples were smeared onto MRS agar plates and left in an anaerobic room for a whole day at 37°C. A biochemical test (Gram staining and IMViC test) was performed for the samples followed by DNA extraction using QIAamp® DNA Mini Kit. After the amplification, the samples were analyzed by Sanger Sequencing.

Results: Gram staining was performed for all the samples followed by IMViC test. Out of all samples, 106 were Voges-Proskauer test positive and 69 were citrate test positive. In the study, 18 samples (6%) were gram negative and 282 samples (94%) were gram positive. After identifying the samples with similar characteristics, representatives were selected for DNA isolation and then sanger sequencing was performed. The result showed that the women who had full term delivery showed more abundance of *L. crispatus* (39.3%), *L. jensenii* (27.8%), *L. iners* (26.3%), *Bacillus cereus* (6.6%); and the women who had preterm delivery showed the presence of *Lactobacillus iners* (48.8%), *L. Gasseri* (7.3%), *Atopobium vaginae* (4.9%) and *Enterococcus faecalis* (39%).

Conclusion: Women who may benefit from interventions targeted at restoring a normal vaginal flora and who are at risk of premature delivery can be identified with the aid of early detection of aerobic vaginitis and bacterial vaginosis in pregnancy. A large population study will be needed to ascertain whether treating vaginal dysbiosis in asymptomatic pregnant women will have a meaningful impact on the onset of premature labour. The study suggests imparting awareness to health care professionals and all women of reproductive age group regarding the importance of maintaining healthy vaginal microbiome

Keyword: Child birth, Full-term labour, low birth weight, preterm labour, vaginal microbiome.

INTRODUCTION

Reproductive health of a women is important not only for her health but also for her partner/husband and child. Bacterial

infections may affect pregnant women from the time of implantation of fertilized ovum till delivery and also during the postpartum period.¹

The vaginal microbiome or vaginal flora is the micro-organisms that colonize the vagina. It is thought to have a significant impact on women's health and illness states. A woman in the reproductive age range secretes between 1 and 4 milliliters of vaginal fluid, each of which has 106–108 bacteria per milliliter. The vaginal microbiome is dynamic due to the composition that changes during pregnancy, menstruation and diseases like bacterial vaginosis.^{2,3}

The development of the microbiome begins in utero and is further impacted by several factors, including the time of birth (i.e., immediately after or at the gestational age), the mode of delivery, the use of antibiotics, the use of breast milk,⁴ exposure to the environment, nutrition and diet, inflammatory immune responses, clinical infections, disease state⁵, and sexual and hygiene practices.⁶ During pregnancy, *Lactobacillus lactis* lowers the presence of common bacterial species due to the intravaginal cleansing effect. In some women, there may be some microorganisms other than the normal microorganisms that can cause complications.^{7,8}

Anaerobic bacteria such as *Gardnerella vaginalis* and *Mycoplasma hominis* replace the typical *Lactobacillus vaginalis* flora in cases of bacterial vaginosis. About 20% of pregnant women have it, and most of them have no symptoms. It is associated with premature rupture of membranes, preterm delivery, chorioamnionitis and intra-uterine death. Studies have shown that poor pregnancy outcomes are higher among pregnant women with bacterial vaginosis and urinary tract infections. Bacterial vaginosis can lead to adverse neonatal outcomes like assisted ventilation or respiratory distress at birth, neonatal Intensive care unit admission, fetal and infant mortality, neonatal sepsis, chronic lung disease and delayed development.^{1,9}

Vaginal microbiome varies among the asymptomatic women belonging to reproductive age group.^{10, 11} The frequency of bacterial vaginosis ranges from 4% to 64% worldwide. In women who are of reproductive age, it is the most prevalent lower vaginal tract infection.¹²

Although there is no conclusive data, studies have indicated that treating bacterial vaginosis during pregnancy to lessen the related problems is not very beneficial.^{13, 14}

Many studies have been done on the vaginal microbiome (microorganisms) and their links to preterm birth, but considerably less research has been done on the changes that occur in the vaginal microbiome during late pregnancy and childbirth. Despite much investigation, the underlying causes of the triggering of labour remain unknown. Thus, an interesting area of study is the potential correlations between the vaginal microbiome in late pregnancy, shortly before childbirth, and at the commencement of labour. The mother's vaginal microbiome appears to alter during childbirth and following the rupture of the membranes, and the technique of delivery is known to impact the composition of the baby's future microbiome. But the scope and associated relationships are still mostly unclear.¹⁵

Hence this study is planned to find out the effect of vaginal microbiome on gestational age and outcomes of vaginal microbiome on mother and the baby. This will also help to make a protocol and educate the women on prevention of vaginal infection so that further complications will be prevented to the mother and fetus. This study will also help mothers to understand the importance of maternal reproductive health for positive pregnancy outcomes.

MATERIALS AND METHODS

The study's research methodology was an evaluative method. Utilising a case series research design, consecutive mothers admitted for delivery in selected tertiary care hospital of Belagavi city were incorporated into the research. The formula used to determine the sample size was:

$$N = Z_{1-\alpha/2}^2 \frac{pq}{(10\%p)^2} \times 1.1$$

Where,

$Z_{1-\alpha/2}$ = one tail standard normal variate assuming sample size at 95% confidence interval;

P = Prevalence;

Q = 1-p and Attrition = 15%

Considering the above formula, the sample size is calculated as 300.

The study included mothers with or more than 28 gestational weeks delivering in tertiary care hospitals of Belagavi city. The study excluded mothers using vaginal antimicrobials or antibiotics and those associated with medical conditions (hypertensive disorders in pregnancy, diabetes, heart disease, antepartum hemorrhage).

Ethical clearance and formal permission were obtained from the Institutional ethical committee and also from Medical Director and Medical Superintendent of the selected tertiary care hospital. Written consent from each participant was acquired. Mothers and family members were informed of the study's goal during the data collection process. The tools used were: Socio-demographic profile, Identification of bacteria by: Collection of sample (vaginal swabs), morphology testing, bio-chemical test, isolation of DNA, PCR (Polymerase chain Reaction) test.

After collecting vaginal swabs from the posterior vaginal fornix, they were promptly preserved at -70°C in a sterile tube until analysis. The samples were smeared onto MRS agar plates and left in an anaerobic room for 24 hours at 37°C. These specimens underwent a biochemical examination (Gram staining and IMViC test).

Using the QIAamp® DNA Mini Kit, DNA extraction was carried out by following the instructions below: Samples were put into a 1.5 millilitre microcentrifuge container. Following a thorough vortex to mix in 20 µl of Proteinase K and 180 µl of Buffer ATL, the mixture was incubated at 56 °C for three hours, or until fully lysed. After adding 200 µl of Buffer AL, mix well by vortexing for 15 seconds. Next, it was incubated for ten minutes at 70°C. A short centrifugation of the tube was used to remove the drips from the lid. Add 200 µl of 96–100% ethanol, and vortexed for 15 seconds. Centrifuging the tube for a short while extracted the drops from the cap. After being pipetted onto the QIAamp Mini spin column (in a 2 ml collection tube), the liquid was spun for one minute at 6000 x g (8000 rpm). After that, the flow-through and collection tube was thrown away. 500 µl of Buffer AW1 was introduced to a fresh 2 ml collection tube containing the QIAamp Mini spin column. The tube was centrifuged at 6000 x g (8000 rpm) for a duration of one minute. Once more, the collecting and flow-through tube was thrown away. 500 µl of Buffer AW2 was once more added to a fresh 2 ml collection tube containing the QIAamp Mini spin column. After that, the tube was centrifuged for three minutes at maximum speed (20,000 x g; 14,000 rpm). The tube used for collection and flow-through was disposed of. A fresh 1.5 ml microcentrifuge tube was filled with the QIAamp Mini spin column and distilled water. To elute the DNA, the tube was centrifuged at 6000 x g (8000 rpm) for 1 minute after being incubated for 1 minute at room temperature. A single band of

RESEARCH

O&G Forum 2024; 34 – 3s: 945-952

high-molecular weight DNA was seen on a 1.0% agarose gel used to assess the purity of the isolated DNA.

Table no.1: Primers used for PCR Amplification

S.No	Primer Name	Sequence 5' to 3'	Length
1)	16S rRNA- F	F (5'-AGAGTTTGATCCTGGCTCAG-3')	20
2)	16S rRNA- R	R (5'-GGTTACCTTGTTACGACTT-3')	19

The primers used for PCR Amplification are mentioned in (Table 1). 16SrRNA-F and 16SrRNA-R primers were used to amplify a fragment of the 16S rRNA gene. A single distinct 1500 bp PCR amplicon band was seen on an agarose gel. The PCR amplicon was purified to remove contaminants. Utilising the BDT v3.1 Cycle sequencing kit on an ABI 3730xl Genetic Analyzer, the forward and reverse DNA sequencing reactions of the PCR amplicon were performed using 16SrRNA-F and 16SrRNA-R primers. Using aligner software, a consensus sequence for the 16S rRNA gene was produced from forward and reverse sequence data. BLAST was performed using the 16S rRNA gene sequence and the NCBI GenBank database's "nr" database. Based on the maximum identity score, the first ten sequences were selected and aligned using the multiple alignment software Clustal W. Using MEGA 10, a distance matrix and phylogenetic tree were created.

The sequence obtained from the sequencing analysis was subjected to BLAST on NCBI. A nucleotide blast was conducted. The accession portion contained the forward and reverse nucleotide sequences. The organism was added in the allotted section and later clicked on blast. Similarly, in the same section, we also found the distance between the trees. Operational definitions

- **Vaginal microbiome:** In the present study vaginal microbiome are the microorganisms present in the vagina that may or may not affect the gestational age or health status or of the women and also the health of the fetus and newborn.
- **Bacterial vaginosis:** In the present study, bacterial vaginosis means any imbalance of normal vaginal flora or microorganisms.
- **Preterm birth:** In the present study, preterm birth means delivery of babies before 37 full weeks of gestation.
- **Vaginal smear:** In the present study, vaginal smear means the vaginal sample collected in the cotton swab.
- **PCR (Polymerase chain reaction) Test:** It is a test to find genetic material from a particular organism, such as bacteria or a virus.
- **Lactobacilli:** In the present study, lactobacilli mean the normal vaginal flora.

RESULTS

Gram staining was performed for all the samples followed by IMViC test. The analysis results of the biochemical test are mentioned in Table no. 2 and Table no.3.

Table no. 2: Biochemical Test (Gram Staining and IMViC Test) result for selected samples

Sample	Gram Staining		IMViC Test				
	Colour	Shape	Gram Reaction	Indole test	Methyl red test	Voges-Proskauer test	Citrate utilization test
1.	Violet	Rod	Gram +	-	-	-	-
2.	Blue	Rod	Gram +	-	-	-	-
3.	Blue	Rod	Gram +	-	-	-	-
4.	Purple	Rod	Gram +	-	-	-	-
5.	Blue	Rod	Gram +	-	-	-	-
6.	Purple	Rod	Gram +	-	-	+	+
7.	Purple	Rod	Gram +	-	-	+	+
8.	Blue	Oval	Gram +	-	-	+	-
9.	Blue	Oval	Gram +	-	-	+	-
10.	Blue	Oval	Gram +	-	-	+	-
11.	Blue	Rod	Gram +	-	-	-	-
12.	Blue	Rod	Gram +	-	-	-	-
13.	Blue	Rod	Gram +	-	-	-	-

14.	Blue	Rod	Gram +	-	-	-	-
15.	Violet	Rod	Gram +	-	-	-	-

Table no. 3: Biochemical Test (Gram Staining) Result for all samples

Bacteria	n	%
Gram Negative	18	6
Gram Positive	282	94
Total	300	100

Out of all samples, **106** were Voges-Proskauer test positive and **69** were citrate test positive.

16S rRNA Amplification and Sequencing:

After identifying the samples with similar characteristics, representatives were selected for DNA isolation and sent for sanger sequencing. The 16SrRNA amplicon of selected samples are shown in Figure no.1.

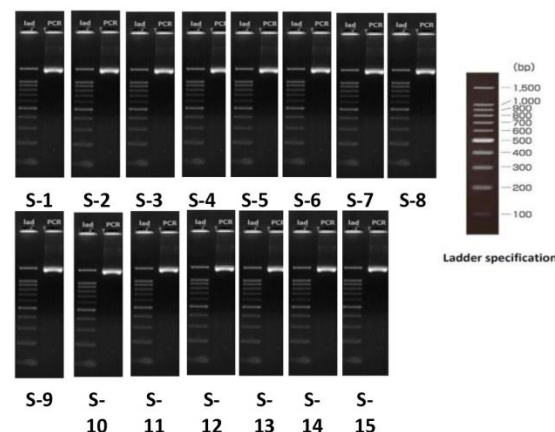


Fig no.1: 16SrRNA amplicon of selected samples

Table no. 4: Showing results of PCR amplification

Preterm	n	%	Term	n	%
L. iners	20	48.8	L.iners	68	26.3
L.gasseri	3	7.3	L. crispatus	102	39.3
Atopobium vaginae	2	4.9	L. jensenii	72	27.8
E. faecalis	16	39	Bacillus cereus	17	6.6
Total	41	100	Total	259	100

After the amplification, the samples were analyzed by Sanger Sequencing. The samples showed the presence of *Lactobacillus Crispatus*, *Lactobacillus jensenii*, *Lactobacillus inners*, *L. Gasseri*, *Bacillus cereus*, *Bacillus sp. Firmi*, *Bacillus sp. Strain*, *Atopobium vaginae*, *Enterococcus sp. Strain* and *Enterococcus faecalis*.

In the study, as mentioned in Table No. 4, the women who had full term delivery showed more abundance of *L. crispatus*, *L. jensenii*, *L. iners*, *Bacillus cereus*, *Bacillus sp. Firmi* and *Bacillus sp. Strain*; and the women who had preterm delivery showed the presence of *Lactobacillus iners*, *L. Gasseri*, *Atopobium vaginae*, *Enterococcus sp. Strain* and *Enterococcus faecalis*.

Phylogenetic tree: Phylogenetic tree of selected samples are shown in Figure no.2 to Figure no.16.

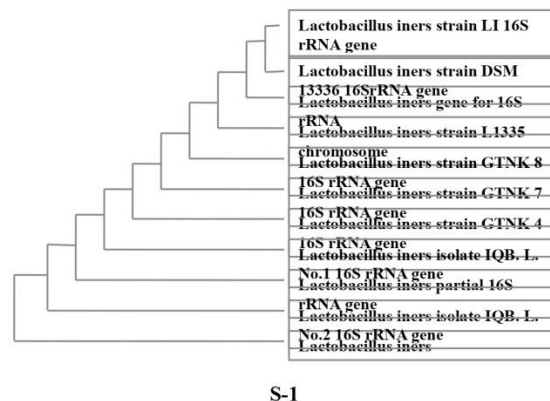


Fig no.2: Phylogenetic tree of Sample no.1

RESEARCH

O&G Forum 2024; 34 – 3s: 945-952

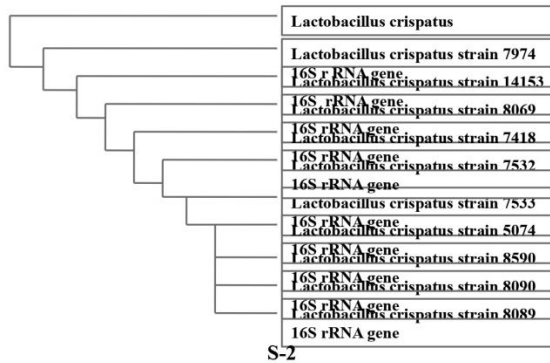


Fig no.3: Phylogenetic tree of Sample no.2

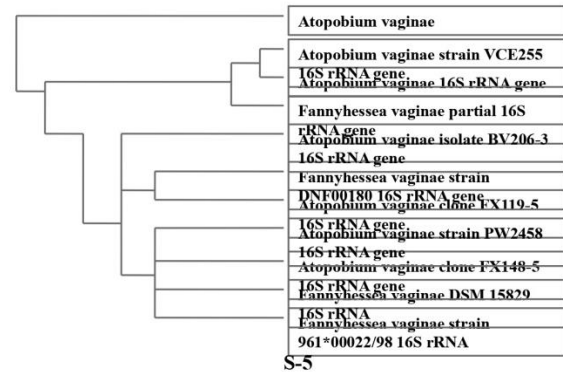


Fig no.6: Phylogenetic tree of Sample no.5

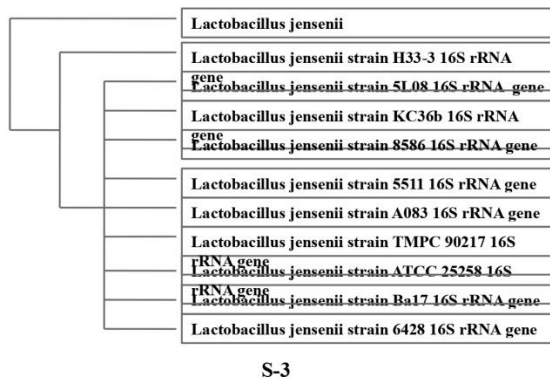


Fig no.4: Phylogenetic tree of Sample no.3

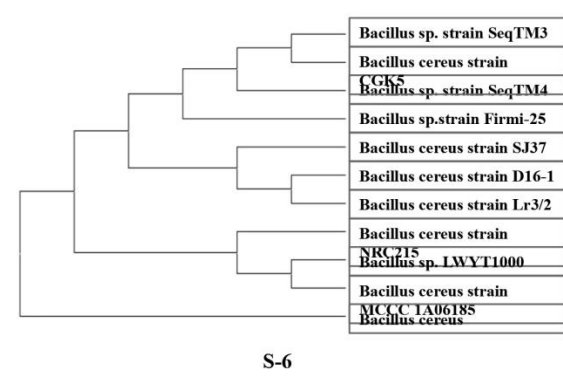


Fig no.7: Phylogenetic tree of Sample no.6

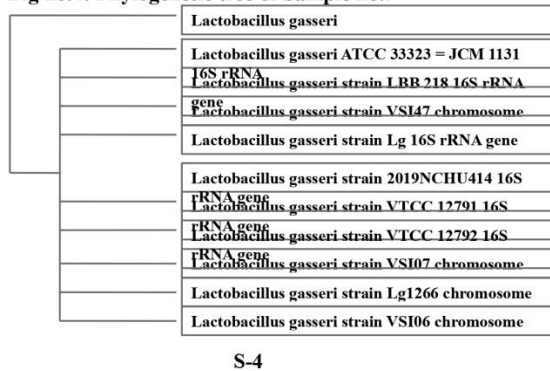


Fig no.5: Phylogenetic tree of Sample no.4

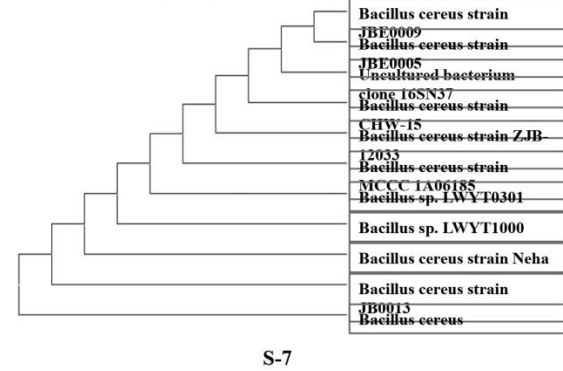
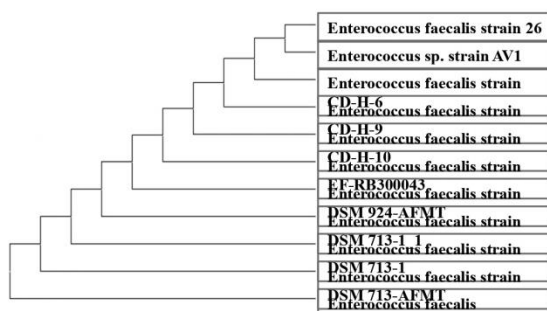


Fig no.8: Phylogenetic tree of Sample no.7

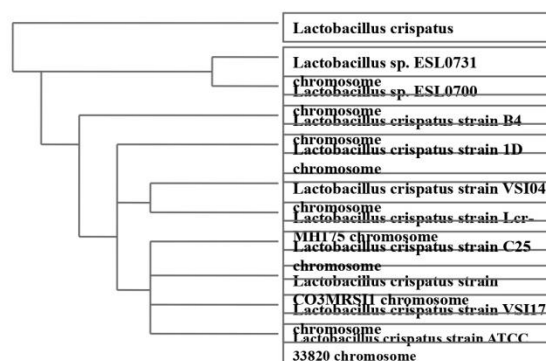
RESEARCH

O&G Forum 2024; 34 – 3s: 945-952



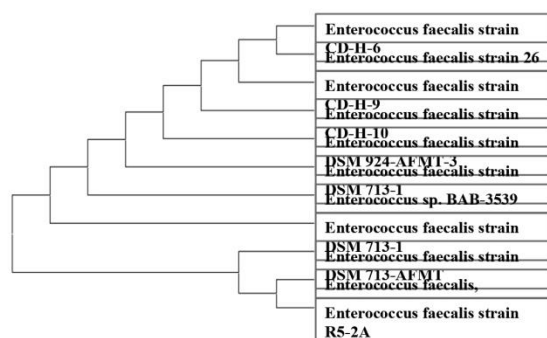
S-8

Fig no.9: Phylogenetic tree of Sample no.8



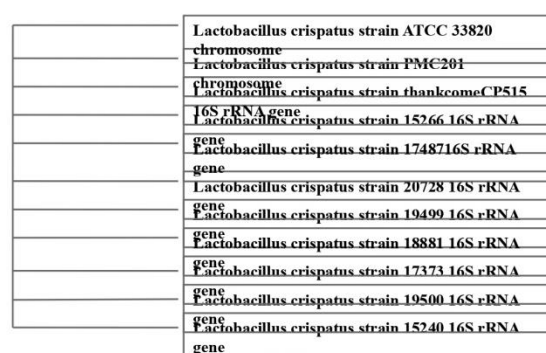
S-11

Fig no.12: Phylogenetic tree of Sample no.11



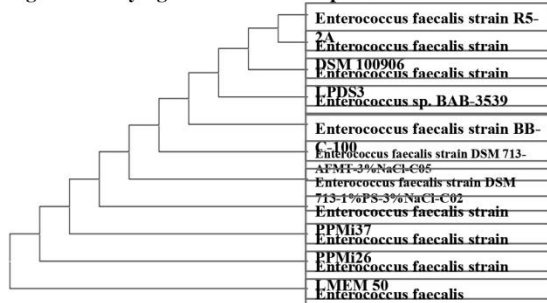
S-9

Fig no.10: Phylogenetic tree of Sample no.9



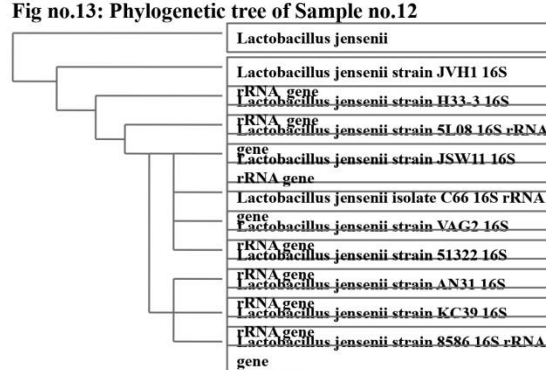
S-12

Fig no.13: Phylogenetic tree of Sample no.12



S-10

Fig no.11: Phylogenetic tree of Sample no.10



S-13

Fig no.14: Phylogenetic tree of Sample no.13

RESEARCH

O&G Forum 2024; 34 – 3s: 945-952

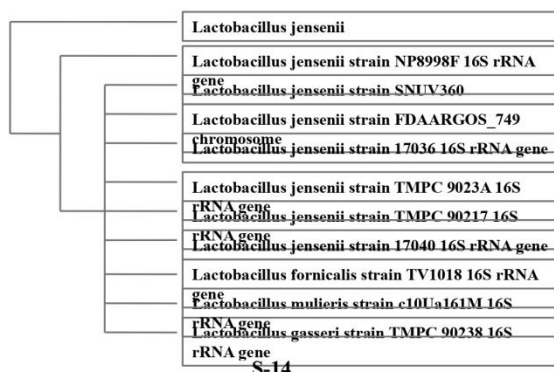


Fig no.15: Phylogenetic tree of Sample no.14

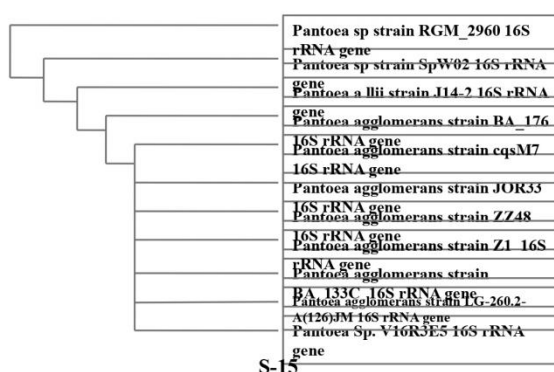


Fig no.16: Phylogenetic tree of Sample no.15

DISCUSSION

Lactobacillus species predominate in a healthy or ecologically stable vaginal microbiome, which regulates the pH of the vagina to help avoid genital infections. On the other hand, an imbalance in the microbial makeup of the vagina is known as an aberrant vaginal microbial composition, and it is linked to a higher risk of trichomoniasis, bacterial vaginosis, STDs, premature labour, and other birth abnormalities. Race, ethnicity, pregnancy, hormonal fluctuations, sexual activity, cleanliness habits, and other factors all have an impact on this microbial diversity.¹⁶ It's also possible that variations in the prevalence of different Lactobacillus strains in the vaginal microbiome are just the result of ethnic variances.¹⁷

The predominant *Lactobacillus Acidophilus*, *Lactobacillus Crispatus*, *Lactobacillus Gasseri*, *Lactobacillus Jensenii*, and *Lactobacillus Iners* species found in the vaginal flora. A change in the vaginal flora can cause anaerobic species such *Gardnerella*, *Mobiluncus*, *Bacteroides*, *Prevotella*, and *Peptostreptococcus* to predominate, along with *Streptococcus*, *Staphylococcus*, and *Escherichia coli*. This can lead to either an aerobic vaginitis or a bacterial vaginosis. It is common for fertile women to contract bacterial vaginosis. A vaginal discharge that has the characteristic "fishy" smell is a sign that it is present. This is brought on by the amines that bacteria create during metabolism.¹⁸

In this study, the women who had full-term delivery showed more abundance of *L. crispatus*, *L. jensenii*, *L. iners* and *Bacillus cereus*; and the women who had preterm delivery showed the presence of *L. iners*, *L. Gasseri*, *Atopobium vaginae* and

Enterococcus faecalis. Sakabe Y et al. conducted a similar investigation and discovered that Lactobacillus was generally plentiful, with *L. crispatus* and *L. iners* being particularly common, whereas the population of *L. gasseri* was low in samples of preterm deliveries.¹⁹ It was discovered that *L. crispatus* dominated the vaginal microbiota of healthy women before or during pregnancy. However, during the puerperium, the situation changed, resulting in a drop in the number of disease-fighting Lactobacillus species, making the vaginal microecological barrier vulnerable to illnesses.²⁰ In another study, it was discovered that term-delivering mothers have one or more Lactobacillus species like *L. crispatus* followed by *L. jensenii* and *L. gasseri* whereas 40% of preterm-delivering mothers lack Lactobacillus species.²¹

Randomization could not be done in the present study which stands out as the limitation of our study. The following future recommendations can be considered: To enable a wider generalization of the findings, a comparable study with a bigger sample size might be conducted. A similar study can be conducted in different settings and also by using a randomization sampling technique.

CONCLUSION

Each woman admitted to the hospital for early labor had a diagnosis of the altered normal vaginal microbiota. Women who may benefit from interventions targeted at restoring normal vaginal flora and who are at risk of premature delivery can be identified with the aid of early detection of aerobic vaginitis and bacterial vaginosis in pregnancy. A large population study will be needed to ascertain whether treating vaginal dysbiosis in asymptomatic pregnant women will have a meaningful impact on the onset of premature labor. The study highlights the common vaginal microbiome present during the time of delivery and its effect on maternal and neonatal health outcomes. The study suggests imparting awareness to healthcare professionals and all women of reproductive age groups regarding the importance of maintaining a healthy vaginal microbiome.

ACKNOWLEDGEMENT

I express my heartfelt gratitude to my Guide and Co-guide for their guidance in conducting the study. I also sincerely thank Dr. Ramesh S. Paranjape, In-Charge Director, and all the faculty of Dr. Prabhakar Kore's Basic Science Research Laboratory, KAHAR, Belagavi for the support and cooperation during the study. My acknowledgment will never be complete without thanking my study participants who actively participated in this study.

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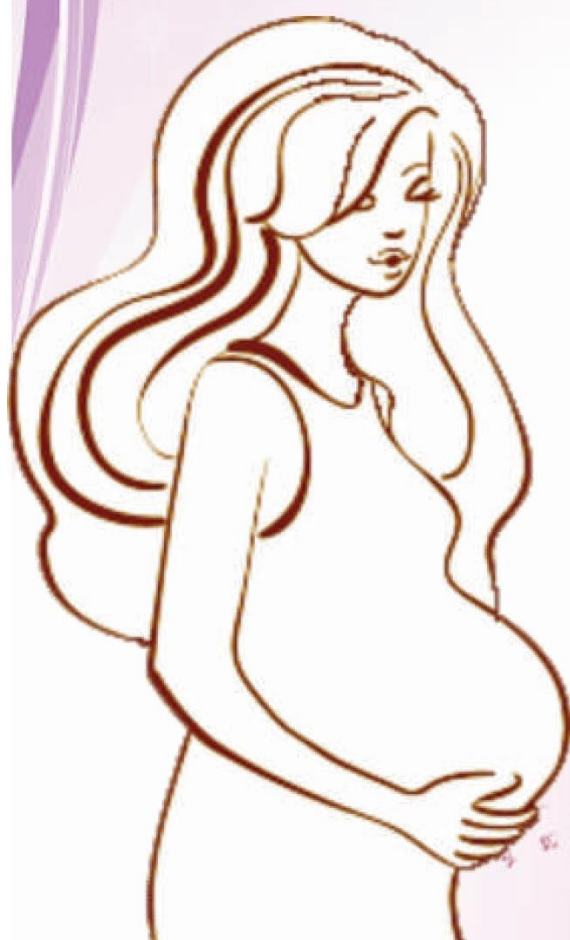
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RESEARCH

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Antenatal Hygiene



ANTENATAL HYGIENE

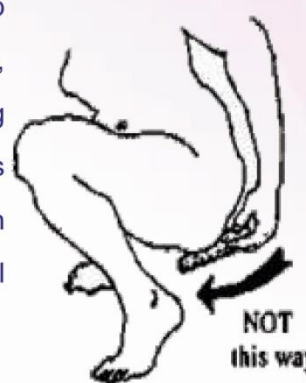
VAGINAL HYGIENE:

During pregnancy, women experience hormonal changes that result in increased blood circulation in the pelvic area and, frequently, an increase in vaginal discharge. In fact, this discharge helps keep germs and other microbes from migrating from the vagina to the uterus and is usually safe. It normally has no smell, but when dried, it could look yellow. An infection, however, can be indicated by an unusual or foul-smelling discharge.

1. Use a mild soap and lukewarm water to cleanse: Hot water can irritate skin and upset the vagina's natural bacterial balance. Strong soaps and creams with strong scents should be avoided since they might irritate the vaginal area and change its pH values.



2. Wipe from front to back: To stop bacteria from entering the vagina, always wipe the area after using toilets from front to back. This procedure lowers the risk of infection and helps maintain vaginal cleanliness.



3. Avoid douching: Douching involves the use of a liquid solution to wash the interior of the vagina. It is not recommended during pregnancy as it can disrupt the fragile balance of microorganisms within the vagina, increasing the likelihood of infections. The vagina has its own natural cleaning mechanism, so douching is unnecessary for maintaining hygiene.





4. Select breathable, clean underwear: Keeping the intimate area healthy can be achieved by choosing cotton underwear. Avoid wearing clothes that are too tight or synthetic since they might trap moisture and bacteria, increasing the risk of illnesses.

5. Avoid using feminine hygiene products: Wipes and sprays are not necessary during pregnancy. These products contain chemicals that have the potential to irritate skin and upset the normal balance of microorganisms in the vagina.



6. Focus on the perineum: Throughout pregnancy, the skin surrounding the vagina, known as the perineum, may stretch and become more susceptible to irritation. To prevent infections, keeping this area clean and dry is essential. After using the restroom, softly pat the perineum dry with a fresh, gentle towel.



7. Opt for pads instead of tampons while pregnant: It is generally advised to use pads rather than tampons during pregnancy. Tampons may heighten the risk of toxic shock syndrome (TSS), a rare yet serious condition that can arise during this time.

ORAL HYGIENE:

As the mouth serves as the entry point to the entire body, maintaining the health of gums and teeth becomes increasingly important, especially due to the many changes occurring in the body during pregnancy.

1. It's important to visit the dentist as soon as possible during pregnancy to have any cavities, gum disease, and other dental issues examined and treated. Avoid eating foods that could raise the chances of getting cavities.



2. Ensure to use fluoride containing toothpaste to brush the teeth twice a day.

3. Delay extensive dental procedures, such as dental surgery, until after giving birth to prevent the use of anaesthetics that may impact the growing foetus.



SKIN & HAIR HYGIENE:

Throughout pregnancy, a woman's body generates increased amounts of sweat, oils, and sebum, which can notably affect the look and feel of her skin and hair.

1. It's important to apply sunscreen and also to use umbrella that guards against both UV rays; as the skin tends to be more sensitive during this time.



2. Avoid scrubbing your skin too vigorously to prevent inflammation and irritation.

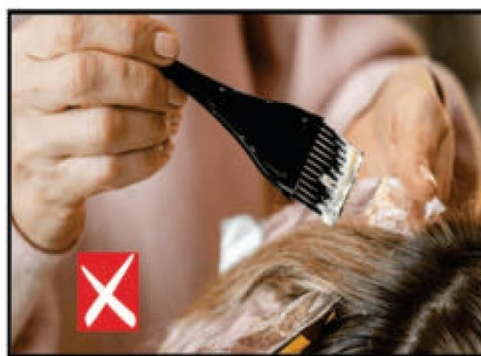


3. Maintain skin hydration to prevent cracking, peeling, or bleeding. Regularly apply moisturizer to the skin on the hips, thighs, and abdomen to reduce the appearance of stretch marks.



4. Choose fragrance-free skincare products to avoid irritating your skin.

5. Pregnant women should avoid getting highlights or colouring done at the hair salon because many of the chemicals used in these treatments are detrimental to the skin. Rather, concentrate on keeping up a consistent hair care regimen that uses conditioner and shampoo.



BREAST CARE AND HYGIENE:

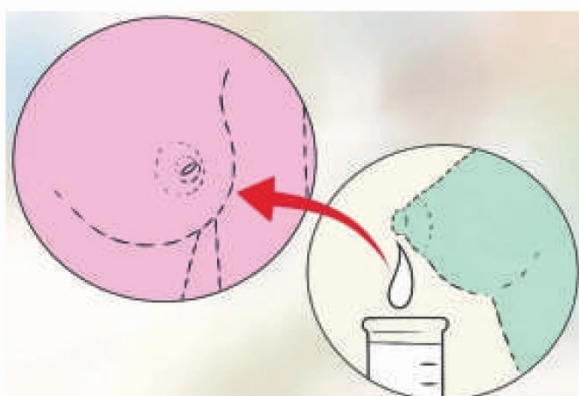
As the mouth serves as the entry point to the entire body, maintaining the health of gums and teeth becomes increasingly important, especially due to the many changes occurring in the body during pregnancy.

1. Ensure to remain properly hydrated to keep the skin on breasts well-moisturized.



2. Ensure to get enough sleep to help the skin heal and renew itself, which can lower the likelihood of developing stretch marks on breasts.

3. To cure sore or cracked nipples- nipple cream, coconut oil or few drops of breast milk may be applied on the nipple.



4. Avoid using strong cleaning agents if colostrum (the thick initial milk produced by the breasts during pregnancy and shortly after childbirth) is present; simply cleanse them with warm water.

ಪ್ರಸವಪೂರ್ವ ನೈರ್ಮಲ್ಯ

ಯೋನಿಯ ನೈರ್ಮಲ್ಯ:

ಗರ್ಭಾವಸ್ಥೆಯಲ್ಲಿ, ಮಹಿಳೆಯರು ಹಾರ್ಮೋನುಗಳ ಬದಲಾವಣೆಗಳನ್ನು ಅನುಭವಿಸುತ್ತಾರೆ, ಇದು ಶ್ರೇಣಿಯ ಪ್ರದೇಶದಲ್ಲಿ ರಕ್ತ ಪರಿಚಲನೆ ಹೆಚ್ಚಾಗುತ್ತದೆ ಮತ್ತು ಆಗಾಗ್ಗೆ ಯೋನಿ ಡಿಸ್ಚಾರ್ಜ್ ಹೆಚ್ಚಾಗುತ್ತದೆ. ವಾಸ್ತವವಾಗಿ, ಈ ವಿಸರ್ಜನೆಯು ಸೂಕ್ಷ್ಮಜೀವಿಗಳು ಮತ್ತು ಇತರ ಸೂಕ್ಷ್ಮಜೀವಿಗಳನ್ನು ಯೋನಿಯಿಂದ ಗರ್ಭಾಶಯಕ್ಕೆ ವಲಸೆ ಹೋಗದಂತೆ ಸಹಾಯ ಮಾಡುತ್ತದೆ ಮತ್ತು ಸಾಮಾನ್ಯವಾಗಿ ಸುರಕ್ಷಿತವಾಗಿರುತ್ತದೆ. ಇದು ಸಾಮಾನ್ಯವಾಗಿ ವಾಸನೆಯನ್ನು ಹೊಂದಿರುವುದಿಲ್ಲ, ಆದರೆ ಒಣಗಿದಾಗ, ಅದು ಹಳದಿಯಾಗಿ ಕಾಣುತ್ತದೆ. ಆದಾಗ್ಯೂ, ಸೋಂಕನ್ನು ಅಸಾಮಾನ್ಯ ಅಥವಾ ದುರ್ವಾಸನೆಯ ಸ್ವಾವದಿಂದ ಸೂಚಿಸಬಹುದು.

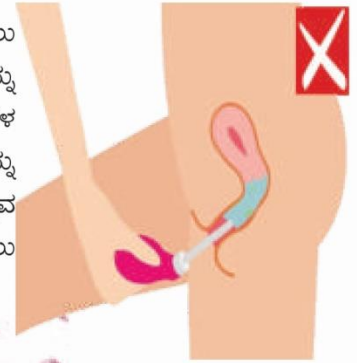
1. ಶುದ್ಧೀಕರಿಸಲು ಸೌಮ್ಯವಾದ ಸೋಪ್ ಮತ್ತು ಉಗುರುಬೆಚ್ಚನೆಯ ನೀರನ್ನು ಬಳಸಿ: ಬಿಸಿನೀರು ಚರ್ಮವನ್ನು ಕೆರಳಿಸಬಹುದು ಮತ್ತು ಯೋನಿಯ ನೈಸರ್ಗಿಕ ಬ್ಯಾಕ್ಟೀರಿಯಾದ ಸಮತೋಲನವನ್ನು ಕೆಡಿಸಬಹುದು. ಬಲವಾದ ಪರಿಮಳವನ್ನು ಹೊಂದಿರುವ ಬಲವಾದ ಸಾಬೂನುಗಳು ಮತ್ತು ಕ್ರೀಮ್‌ಗಳನ್ನು ತಪ್ಪಿಸಬೇಕು ಏಕೆಂದರೆ ಅವು ಯೋನಿ ಪ್ರದೇಶವನ್ನು ಕೆರಳಿಸಬಹುದು ಮತ್ತು ಅದರ pH ಮೌಲ್ಯಗಳನ್ನು ಬದಲಾಯಿಸಬಹುದು.



2. ಮುಂಭಾಗದಿಂದ ಹಿಂದಕ್ಕೆ ಒರೆಸಿ: ಬ್ಯಾಕ್ಟೀರಿಯಾಗಳು ಯೋನಿಯೊಳಗೆ ಪ್ರವೇಶಿಸುವುದನ್ನು ತಡೆಯಲು, ಯಾವಾಗಲೂ ಮುಂಭಾಗದಿಂದ ಹಿಂಭಾಗಕ್ಕೆ ಶೌಚಾಲಯಗಳನ್ನು ಬಳಸಿದ ನಂತರ ಆ ಭಾಗ ಒರೆಸಿ. ಈ ವಿಧಾನವು ಸೋಂಕಿನ ಅಪಾಯವನ್ನು ಕಡಿಮೆ ಮಾಡುತ್ತದೆ ಮತ್ತು ಯೋನಿ ಶುಚಿತ್ವವನ್ನು ಕಾಪಾಡಿಕೊಳ್ಳಲು ಸಹಾಯ ಮಾಡುತ್ತದೆ.



3. ಡೌಚಿಂಗ್ ಅನ್ನು ತಪ್ಪಿಸಿ: ಡೌಚಿಂಗ್ ಯೋನಿಯ ಒಳಭಾಗವನ್ನು ತೊಳೆಯಲು ದ್ರವ ದ್ರಾವಣವನ್ನು ಬಳಸುವುದನ್ನು ಒಳಗೊಂಡಿರುತ್ತದೆ. ಗರ್ಭಾವಸ್ಥೆಯಲ್ಲಿ ಇದನ್ನು ಶಿಫಾರಸು ಮಾಡುವುದಿಲ್ಲ ಏಕೆಂದರೆ ಇದು ಯೋನಿಯೊಳಗಿನ ಸೂಕ್ಷ್ಮಜೀವಿಗಳ ದುರ್ಬಲ ಸಮತೋಲನವನ್ನು ಅಡ್ಡಿಪಡಿಸುತ್ತದೆ, ಸೋಂಕಿನ ಸಾಧ್ಯತೆಯನ್ನು ಹೆಚ್ಚಿಸುತ್ತದೆ. ಯೋನಿಯು ತನ್ನದೇ ಆದ ನೈಸರ್ಗಿಕ ಸ್ವಚ್ಛತೆ ಕಾಪಾಡಿ ಕೊಳ್ಳುವ ಕಾರ್ಯವಿಧಾನವನ್ನು ಹೊಂದಿದೆ, ಆದ್ದರಿಂದ ನೈರ್ಮಲ್ಯವನ್ನು ಕಾಪಾಡಿಕೊಳ್ಳಲು ಡೌಚಿಂಗ್ ಅನಗತ್ಯವಾಗಿದೆ.





4. ಉಸಿರಾಡುವ, ಸ್ವಚ್ಛವಾದ ಒಳಉಡುಪುಗಳನ್ನು ಆಯ್ಕೆಮಾಡಿ: ಹತ್ತಿ ಬಟ್ಟೆ ಒಳಉಡುಪುಗಳನ್ನು ಆರಿಸುವ ಮೂಲಕ ನಿಕಟ ಪ್ರದೇಶವನ್ನು ಆರೋಗ್ಯಕರವಾಗಿರಿಸಿಕೊಳ್ಳಬಹುದು. ತುಂಬಾ ಬಿಗಿಯಾದ ಅಥವಾ ಸಂಶ್ಲೇಷಿತ ಬಟ್ಟೆಗಳನ್ನು ಧರಿಸುವುದನ್ನು ತಪ್ಪಿಸಿ ಏಕೆಂದರೆ ಅವು ತೇವಾಂಶ ಮತ್ತು ಬ್ಯಾಕ್ಟೀರಿಯಾವನ್ನು ಹಿಡಿದಿಟ್ಟುಕೊಳ್ಳಬಹುದು, ಅನಾರೋಗ್ಯದ ಅಪಾಯವನ್ನು ಹೆಚ್ಚಿಸಬಹುದು.

5. ಸ್ಪ್ರೇಯಿಂಗ್ ನೈರ್ಮಲ್ಯ ಉತ್ಪನ್ನಗಳನ್ನು ಬಳಸುವುದನ್ನು ತಪ್ಪಿಸಿ: ಗರ್ಭಾವಸ್ಥೆಯಲ್ಲಿ ವೈಪ್ಸ್ ಮತ್ತು ಸ್ಪ್ರೇಗಳು ಅಗತ್ಯವಿಲ್ಲ. ಈ ಉತ್ಪನ್ನಗಳು ಚರ್ಮವನ್ನು ಕೆರಳಿಸುವ ಸಾಮರ್ಥ್ಯವನ್ನು ಹೊಂದಿರುವ ರಾಸಾಯನಿಕಗಳನ್ನು ಒಳಗೊಂಡಿರುತ್ತವೆ ಮತ್ತು ಯೋನಿಯ ಸೂಕ್ಷ್ಮಜೀವಿಗಳ ಸಾಮಾನ್ಯ ಸಮತೋಲನವನ್ನು ಅಸಮಾಧಾನಗೊಳಿಸುತ್ತವೆ.



6. ಮೂಲಾಧಾರದ ಮೇಲೆ ಕೇಂದ್ರೀಕರಿಸಿ: ಗರ್ಭಾವಸ್ಥೆಯ ಕೆಲಗಿನ ಭಾಗ ವನ್ನು ಪೆರಿನಿಯಮ್ ಎಂದು ಕರೆಯಲ್ಪಡುವ ಯೋನಿಯ ಸುತ್ತಲಿನ ಚರ್ಮವು ವಿಸ್ತರಿಸಬಹುದು ಮತ್ತು ಕೆರಳಿಕೆಗೆ ಹೆಚ್ಚು ಒಳಗಾಗಬಹುದು. ಸೋಂಕುಗಳನ್ನು ತಡೆಗಟ್ಟಲು, ಈ ಭಾಗವನ್ನು ಸ್ವಚ್ಛವಾಗಿ ಮತ್ತು ಶುಷ್ಕವಾಗಿರಿಸುವುದು ಅತ್ಯಗತ್ಯ. ಶೌಚಾಲಯ ಅನ್ನು ಬಳಸಿದ ನಂತರ, ತಾಜಾ, ಮೃದುವಾದ ಟವೆಲ್ನಿಂದ ಪೆರಿನಿಯಮ್ ಅನ್ನು ಮೃದುವಾಗಿ ಒಣಗಿಸಿ.



7. ಗರ್ಭಿಣಿಯಾಗಿದ್ದಾಗ ಟ್ಯಾಂಪೂನ್‌ಗಳ ಬದಲಿಗೆ ಪ್ಯಾಡ್‌ಗಳನ್ನು ಆರಿಸಿಕೊಳ್ಳಿ: ಗರ್ಭಾವಸ್ಥೆಯಲ್ಲಿ ಟ್ಯಾಂಪೂನ್‌ಗಳ ಬದಲಿಗೆ ಪ್ಯಾಡ್‌ಗಳನ್ನು ಬಳಸಲು ಸಾಮಾನ್ಯವಾಗಿ ಸಲಹೆ ನೀಡಲಾಗುತ್ತದೆ. ಟ್ಯಾಂಪೂನ್‌ಗಳು ವಿಷಕಾರಿ ಅಪಯಕಾರಿ ಯಾಗಿ ರತ್ತವೇ. ಈ ಉತರ ಉಪಯೋಗದಿಂದ ಸಂಕ್ರಮಣವು ಉದ್ಭವಿ ಕೊಳ್ಳುತ್ತದೆ.

ಮೌಖಿಕ ನೈರ್ಮಲ್ಯ:

ಬಾಯಿ ಇಡೀ ದೇಹಕ್ಕೆ ಪ್ರವೇಶ ಬಿಂದುವಾಗಿ ಕಾರ್ಯನಿರ್ವಹಿಸುವುದರಿಂದ, ಒಸಡುಗಳು ಮತ್ತು ಹಲ್ಲುಗಳ ಆರೋಗ್ಯವನ್ನು ಕಾಪಾಡಿಕೊಳ್ಳುವುದು ಹೆಚ್ಚು ಮುಖ್ಯವಾಗಿದೆ, ವಿಶೇಷವಾಗಿ ಗರ್ಭಾವಸ್ಥೆಯಲ್ಲಿ ದೇಹದಲ್ಲಿ ಸಂಭವಿಸುವ ಅನೇಕ ಬದಲಾವಣೆಗಳಿಂದಾಗಿ..

1. ಗರ್ಭಾವಸ್ಥೆಯಲ್ಲಿ ಯಾವುದೇ ಕುಳಿಗಳು, ವಸಡು ಕಾಯಿಲೆ ಮತ್ತು ಇತರ ಹಲ್ಲಿನ ಸಮಸ್ಯೆಗಳನ್ನು ಪರೀಕ್ಷಿಸಲು ಮತ್ತು ಚಿಕಿತ್ಸೆ ನೀಡಲು ಸಾಧ್ಯವಾದಷ್ಟು ಬೇಗ ದಂತವೈದ್ಯರನ್ನು ಭೇಟಿ ಮಾಡುವುದು ಮುಖ್ಯ. ಕುಳಿಗಳನ್ನು ಪಡೆಯುವ ಸಾಧ್ಯತೆಯನ್ನು ಹೆಚ್ಚಿಸುವ ಆಹಾರವನ್ನು ಸೇವಿಸುವುದನ್ನು ತಪ್ಪಿಸಿ.



2. ದಿನಕ್ಕೆ ಎರಡು ಬಾರಿ ಹಲ್ಲುಜ್ಜಲು ಟೂತ್‌ಪೇಸ್ಟ್ ಫ್ಲೋರೈಡ್ ಹೊಂದಿರುವ ಅನ್ನು ಬಳಸುವುದನ್ನು ಖಚಿತಪಡಿಸಿಕೊಳ್ಳಿ.

3. ಬೆಳೆಯುತ್ತಿರುವ ಭ್ರೂಣದ ಮೇಲೆ ಪರಿಣಾಮ ಬೀರುವ ಅರಿವಳಿಕೆಗಳ ಬಳಕೆಯನ್ನು ತಡೆಗಟ್ಟಲು ಜನ್ಮ ನೀಡುವವರೆಗೆ ವ್ಯಾಪಕವಾದ ಹಲ್ಲಿನ ಕಾರ್ಯವಿಧಾನಗಳನ್ನು, ಅಂತಹ ಹಲ್ಲಿನ ಶಸ್ತ್ರಚಿಕಿತ್ಸೆಯನ್ನು ವಿಳಂಬಗೊಳಿಸಿ.



ಚರ್ಮ ಮತ್ತು ಕೂದಲಿನ ನೈರ್ಮಲ್ಯ:

ಗರ್ಭಾವಸ್ಥೆಯ ಸಮಯದಲ್ಲಿ, ಮಹಿಳೆಯ ದೇಹವು ಹೆಚ್ಚಿನ ಪ್ರಮಾಣದಲ್ಲಿ ಬೆವರು, ಎಣ್ಣೆಗಳು ಮತ್ತು ಮೇದೋಗ್ರಂಥಿಗಳ ಸ್ರಾವವನ್ನು ಉತ್ಪಾದಿಸುತ್ತದೆ, ಇದು ಅವಳ ಚರ್ಮ, ಕೂದಲಿನ ನೋಟ, ಮತ್ತು ಭಾವನೆಯನ್ನು ಗಂಭೀರವಾಗಿ ಪರಿಣಾಮ ಬೀರುತ್ತದೆ.

1. ಸನ್‌ಸ್ಟೀನ್ ಅನ್ನು ಅನ್ವಯಿಸುವುದು ಮತ್ತು ಗರಿ ಕಿರಣಗಳ ವಿರುದ್ಧ ರಕ್ಷಿಸುವ ಛತ್ರಿಯನ್ನು ಬಳಸುವುದು ಮುಖ್ಯವಾಗಿದೆ; ಈ ಸಮಯದಲ್ಲಿ ಚರ್ಮವು ಹೆಚ್ಚು ಸೂಕ್ಷ್ಮವಾಗಿರುತ್ತದೆ.



2. ಉರಿಯೂತ ಮತ್ತು ಕಿರಿಕಿರಿಯನ್ನು ತಡೆಗಟ್ಟಲು ನಿಮ್ಮ ಚರ್ಮವನ್ನು ತುಂಬಾ ಬಲವಾಗಿ ಸ್ಕರ್ಟ್ ಮಾಡುವುದನ್ನು ತಪ್ಪಿಸಿ.

3. ಬಿರುಕುಗಳು, ಸಿಪ್ಪೆಸುಲಿಯುವುದು ಅಥವಾ ರಕ್ತಸ್ರಾವವನ್ನು ತಡೆಗಟ್ಟಲು ಚರ್ಮದ ಜಲಸಂಚಯನವನ್ನು ಕಾಪಾಡಿಕೊಳ್ಳಿ. ಹಿಗ್ಗಿಸಲಾದ ಗುರುತುಗಳನ್ನು ಕಡಿಮೆ ಮಾಡಲು ಸೊಂಟ, ತೊಡೆಗಳು ಮತ್ತು ಹೊಟ್ಟೆಯ ಮೇಲೆ ಚರ್ಮಕ್ಕೆ ನಿಯಮಿತವಾಗಿ ಮಾಯಿಶ್ಚರೈಸರ್ ಅನ್ನು ಅನ್ವಯಿಸಿ.



4. ನಿಮ್ಮ ಚರ್ಮವನ್ನು ಕೆರಳಿಸುವುದನ್ನು ತಪ್ಪಿಸಲು ಸುಗಂಧ-ಮುಕ್ತ ತ್ವಚೆ ಉತ್ಪನ್ನಗಳನ್ನು ಆಚ್ಛೇದಿಸಿ.

5. ಗರ್ಭಿಣಿಯರು ಹೇರ್ ಸಲೂನ್‌ನಲ್ಲಿ ಮುಖ್ಯಾಂಶಗಳು, ಬಣ್ಣ ಅಥವಾ ಹೈಡ್ರೆಟ್ ಅಥವಾ ಎತ್ತರೆ ಕೆಮಿಕಲ್‌ಗಳ ಬಳಕೆ ಮಾಡುವುದನ್ನು ತಪ್ಪಿಸಬೇಕು ಏಕೆಂದರೆ ಈ ಚಿಕಿತ್ಸೆಗಳಲ್ಲಿ ಬಳಸಲಾಗುವ ಅನೇಕ ರಾಸಾಯನಿಕಗಳು ಚರ್ಮಕ್ಕೆ ಹಾನಿಕಾರಕವಾಗಿದೆ. ಬದಲಿಗೆ, ಕಂಡಿಷನರ್ ಮತ್ತು ಶಾಂಪೂ ಬಳಸುವ ಸ್ಥಿರವಾದ ಕೂದಲ ರಕ್ಷಣೆಯ ನಿಯಮವನ್ನು ಇಟ್ಟುಕೊಳ್ಳುವುದರ ಮೇಲೆ ಕೇಂದ್ರೀಕರಿಸಿ.



ಸ್ತನ ಆರೈಕೆ ಮತ್ತು ನೈರ್ಮಲ್ಯ:

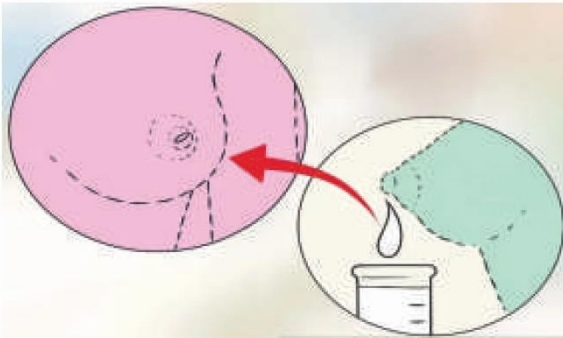
ಗರ್ಭಧಾರಣೆ ಮತ್ತು ಹಾರ್ಮೋನುಗಳ ಬದಲಾವಣೆಯಿಂದ ದೇಹವು ವಿವಿಧ ಬದಲಾವಣೆಗಳಿಗೆ ಒಳಗಾಗುತ್ತದೆ, ಸ್ತನಗಳು ಹೆಚ್ಚಾಗಿ ಗಾತ್ರದಲ್ಲಿ ಹೆಚ್ಚಾಗುತ್ತವೆ. ಕೆಲವು ಮಹಿಳೆಯರು ತಮ್ಮ ನಿಗದಿತ ದಿನಾಂಕಕ್ಕೆ ಹಲವಾರು ವಾರಗಳು ಅಥವಾ ತಿಂಗಳುಗಳ ಮೊದಲು ಹಾಲು ಅಥವಾ ಕೊಲೊಸ್ಟಮ್ ಅನ್ನು ಉತ್ಪಾದಿಸಲು ಪ್ರಾರಂಭಿಸಬಹುದು.

1. ಸ್ತನಗಳ ಮೇಲೆ ಚರ್ಮವನ್ನು ಚೆನ್ನಾಗಿ ತೇವಗೊಳಿಸುವಂತೆ ಸರಿಯಾಗಿ ನಿರನು ಕುಡಿವುದನ್ನು ಖಚಿತಪಡಿಸಿಕೊಳ್ಳಿ.



2. ಸ್ತನಗಳ ಮೇಲೆ ಹಿಗ್ಗಿಸಲಾದ ಗುರುತುಗಳನ್ನು ಅಭಿವೃದ್ಧಿಪಡಿಸುವ ಸಾಧ್ಯತೆಯನ್ನು ಕಡಿಮೆ ಮಾಡುವ ಚರ್ಮವು ಗುಣವಾಗಲು ಮತ್ತು ಸ್ವತಃ ನವೀಕರಿಸಲು ಸಹಾಯ ಮಾಡಲು ಸಾಕಷ್ಟು ನಿದ್ರೆ ಪಡೆಯಲು ಖಚಿತಪಡಿಸಿಕೊಳ್ಳಿ.

3. ನೋಯುತ್ತಿರುವ ಅಥವಾ ಒಡೆದ ಮೊಲೆತೊಟ್ಟುಗಳನ್ನು ಗುಣಪಡಿಸಲು - ಮೊಲೆತೊಟ್ಟುಗಳ ಕೆನೆ, ತೆಂಗಿನ ಎಣ್ಣೆ ಅಥವಾ ಕೆಲವು ಎದೆಹಾಲುಗಳ ಹನಿಯನ್ನು ಮೊಲೆತೊಟ್ಟುಗಳ ಮೇಲೆ ಅನ್ವಯಿಸಬಹುದು.



4. ಕೊಲೊಸ್ಟಮ್ (ಗರ್ಭಧಾರಣೆಯ ಸಮಯದಲ್ಲಿ ಮತ್ತು ಹೆರಿಗೆಯ ನಂತರ ಸ್ತನಗಳಿಂದ ಉತ್ಪತ್ತಿಯಾಗುವ ದಪ್ಪ ಆರಂಭಿಕ ಹಾಲು) ಇದ್ದರೆ ಬಲವಾದ ಶುಚಿಗೊಳಿಸುವ ಏಜೆಂಟ್‌ಗಳನ್ನು ಬಳಸುವುದನ್ನು ತಪ್ಪಿಸಿ; ಸರಳವಾಗಿ ಬೆಚ್ಚಗಿನ ನೀರಿನಿಂದ ಅವುಗಳನ್ನು ಸ್ವಚ್ಛಗೊಳಿಸಿ.

प्रसवपूर्व स्वच्छता

योनि स्वच्छता:

गर्भावस्था के दौरान, महिलाओं को हार्मोनल परिवर्तनों का अनुभव होता है जिसके परिणामस्वरूप श्रोणि क्षेत्र में रक्त परिसंचरण में वृद्धि होती है और अक्सर, योनि स्राव में वृद्धि होती है। वास्तव में, यह नखिलन कीटाणुओं और अन्य रोगाणुओं को योनि से गर्भाशय में पलायन करने से रोकने में मदद करता है और आमतौर पर सुरक्षित होता है। इसमें आमतौर पर कोई गंध नहीं होती है, लेकिन सूखने पर, यह पीला दूख सकता है। एक संक्रमण, हालांकि, एक असामान्य या दुर्गंधयुक्त नखिलन द्वारा इंगित किया जा सकता है।

1. साफ करने के लिए हल्के साबुन और गुनगुने पानी का उपयोग करें: गर्म पानी त्वचा को परेशान कर सकता है और योनि के प्राकृतिक जीवाणु संतुलन को परेशान कर सकता है। मजबूत सुगंध वाले मजबूत साबुन और क्रीम से बचा जाना चाहिए क्योंकि वे योनि क्षेत्र को परेशान कर सकते हैं और इसके पीएच मान को बदल सकते हैं।



2. आगे से पीछे की ओर पोछें: बैक्टीरिया को योनि में प्रवेश करने से रोकने के लिए, शौचालय का उपयोग करने के बाद हमेशा सामने से पीछे तक योनि क्षेत्र को पोछ लें। यह प्रक्रिया संक्रमण के जोखिम को कम करती है और योनि को साफ रखने में मदद करती है।



3. डूशिंग से बचें: डूशिंग में योनि के अंदरूनी हिस्से को धोने के लिए एक तरल घोल का उपयोग शामिल है। गर्भावस्था के दौरान इसकी सफाई नहीं की जाती है क्योंकि यह योनि के भीतर सूक्ष्मजीवों के नाजुक संतुलन को बाधित कर सकता है, जिससे संक्रमण की संभावना बढ़ जाती है। योनि का अपना प्राकृतिक सफाई तंत्र होता है, इसलिए स्वच्छता बनाए रखने के लिए डूशिंग हानिकारक है।



4. सांस लेने योग्य, साफ अंडरवियर का चयन करें: अंतरंग क्षेत्र को स्वस्थ रखने के लिए सूती अंडरवियर चुनकर प्राप्त किया जा सकता है। ऐसे कपड़े पहनने से बचें जो बहुत तंग या सख्ती हों क्योंकि वे नमी और बैक्टीरिया को फँसा सकते हैं, जिससे बीमारियों का खतरा बढ़ जाता है।

5. स्त्री स्वच्छता उत्पादों का उपयोग करने से बचें: गर्भावस्था के दौरान पोछ और स्प्रे आवश्यक नहीं है। इन उत्पादों में ऐसे रसायन होते हैं जिनमें त्वचा को परेशान करने और योनि में सूक्ष्मजीवों के सामान्य संतुलन को परेशान करने की क्षमता होती है।



6. पेरनिम पर ध्यान दें: गर्भावस्था के दौरान, योनि के नीचे की त्वचा, जसि पेरनिम के रूप में जाना जाता है, खचाव कर सकती है और जलन के प्रति अधिक संवेदनशील हो सकती है। संक्रमण को रोकने के लिए, इस क्षेत्र को साफ और सूखा रखना आवश्यक है। टॉयलेट का उपयोग करने के बाद, एक ताजा, कोमल तौलिया के साथ पेरनिम को धीरे से थपथपाकर सुखाएं।



7. गर्भवती होने पर टैम्पोन के बजाय पैड का चयन करें: आमतौर पर गर्भावस्था के दौरान टैम्पोन के बजाय पैड का उपयोग करने की सलाह दी जाती है क्योंकि इसे संक्रमण बरता है।

मौखिक स्वच्छता :

चूंक मुंह पूरे शरीर में प्रवेश बटु के रूप में कार्य करता है, इसलिए मसूड़ों और दांतों के स्वास्थ्य को बनाए रखना तेजी से महत्वपूर्ण हो जाता है, खासकर गर्भावस्था के दौरान शरीर में होने वाले कई परिवर्तनों के कारण।

1. गर्भावस्था के दौरान जितनी जल्दी हो सके दंत चिकित्सक के पास जाना महत्वपूर्ण है ताकि किसी भी गुहाओं, मसूड़ों की बीमारी और अन्य दंत मुद्दों की जांच और उपचार किया जा सके। उन खाद्य पदार्थों को खाने से बचे जो कैवटि होने की संभावना को बढ़ा सकते हैं।



2. दैनिक दो बार दांतों को ब्रश करने के लिए फ्लोराइड युक्त टूथपेस्ट का उपयोग अवश्य करें।

3. व्यापक दंत प्रक्रियाओं में देरी करें, जैसे कि दंत शल्य चिकित्सा, जन्म देने के बाद तक एनेस्थेटिक्स के उपयोग को रोकने के लिए जो बढ़ते भ्रूण को प्रभावित कर सकती है।



त्वचा और बालों की स्वच्छता:

गर्भावस्था के दौरान, एक महिला का शरीर पसीना, तेल और सीबम की बड़ी हुई मात्रा उत्पन्न करता है, जो उसकी त्वचा और बालों के रंगरूप को वंशिक रूप से प्रभावित कर सकता है।

1. सनस्क्रीन लगाना और छाते का उपयोग करना महत्वपूर्ण है जो यूवी किरणों से बचाता है; क्योंकि इस दौरान त्वचा अधिक संवेदनशील हो जाती है।



2. सूजन और जलन को रोकने के लिए अपनी त्वचा को बहुत सख्ती से स्क्रब करने से बचें।

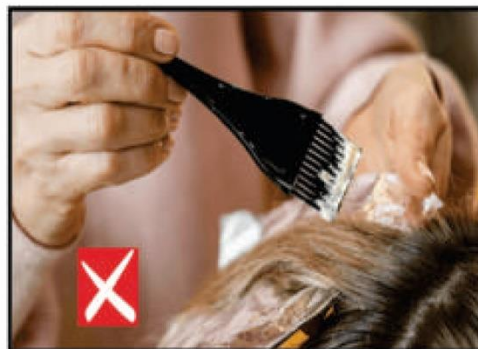


3. त्वचा के फटने, छलिन या रक्तस्राव को रोकने के लिए त्वचा में नमी बनाए रखें। स्ट्रेच मार्क्स की उपस्थिति को कम करने के लिए कूल्हों, जांघों और पेट की त्वचा पर नियमित रूप से क्रीम लगाएं।



4. अपनी त्वचा को परेशान करने से बचने के लिए खुशबू मुक्त क्रीम उत्पादों का चयन करें।

5. गर्भवती महिलाओं को हेयर सैलून में हाइलाइट्स या कलरिंग करवाने से बचना चाहिए क्योंकि इन उपचारों में इस्तेमाल किए जाने वाले कई रसायन त्वचा के लिए हानिकारक होते हैं। इसके बजाय, कंडीशनर और शैम्पू का उपयोग करने वाली एक सतत बाल देखभाल व्यवस्था बनाए रखने पर ध्यान केंद्रित करें।



स्तन देखभाल और स्वच्छता

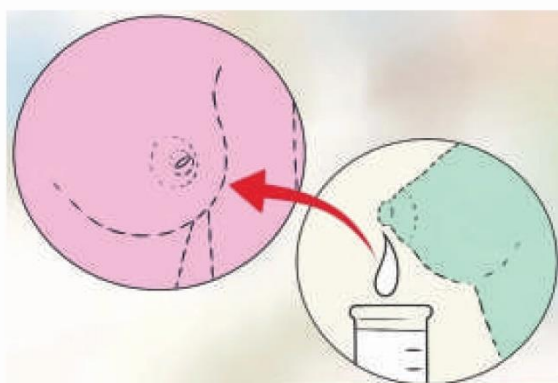
चूंकि शरीर गर्भावस्था और हार्मोनल बदलाव से वभिन्न परिवर्तनों से गुजरता है, स्तन अक्सर आकार में बढ़ जाते हैं। कुछ महिलाएं अपनी नियत तारीख से कई सप्ताह या महीने पहले दूध या कोलोस्ट्रम का उत्पादन शुरू कर सकती हैं।

1. स्तनों की त्वचा को अच्छी तरह से नमीयुक्त बनाए रखने के लिए उचित रूप से ज्यादा पानी का उपयोग करना सुनिश्चित करें।



2. त्वचा को ठीक करने और खुद को नवीनीकृत करने में मदद करने के लिए पर्याप्त नींद लेना सुनिश्चित करें, जिससे स्तनों पर खचाव के नशान विकसित होने की संभावना कम हो सकती है।

3. गले या फटे नपिल्स को ठीक करने के लिए- नपिल क्रीम, नारियल तेल या स्तन के दूध की कुछ बूंदों को नपिल पर लगाया जा सकता है।



4. मजबूत सबून या अन्या चीजों के उपयोग करने से बचे यदि कोलोस्ट्रम (गर्भावस्था के दौरान और बच्चे के जन्म के तुरंत बाद स्तनों द्वारा उत्पादित गाढ़ा प्रारंभिक दूध) मौजूद है; बस उन्हें गर्म पानी से साफ करें।

प्रसूतीपूर्व स्वच्छता

योनीस्वच्छता:

गर्भधारणेदरम्यान, स्त्रियांना हार्मोनल बदल ाचा अनुभव येतो ज्यामुळे पेल्विक भागात रक्ताभसिरण वाढते आणि बऱ्याचदा योनीतून स्त्राव वाढतो. खरं तर, हा स्त्राव जंतू आणि इतर सूक्ष्मजंतूंना योनीतून गर्भाशयात स्थलांतरित होण्यापासून रोखण्यास मदत करतो आणि सहसा सुरक्षित असतो. त्याला सामान्यतः गंध नसतो, परंतु वाळल्यावर तो पविळा दिसू शकतो. संसर्ग, तथापि, असामान्य कवा दुर्गंधीयुक्त स्त्रावद्वारे दर्शवला जाऊ शकतो.

1. स्वच्छ करण्यासाठी सौम्य साबण आणि कोमट पाण्याचा वापर करा: गरम पाण्यामुळे त्वचेला त्रास होऊ शकतो आणि योनीचे नैसर्गिक बॅक्टेरियाचे संतुलन बिघडू शकते. मजबूत सुगंध असलेले साबण आणि क्रीम टाळले पाहजे कारण ते योनिमार्गाच्या भागात चडिचडि करू शकतात आणि त्याचे पीएच मूल्य बदलू शकतात.



2. समोरून मागे पुसणे : योनीत बॅक्टेरिया प्रवेश करू नयेत म्हणून नेहमी समोरून मागच्या बाजूस टॉयलेट वापरल्यानंतर तो भाग पुसून टाकावा. या प्रक्रियेमुळे संक्रमणाचा धोका कमी होतो आणि योनीची स्वच्छता राखण्यास मदत होते



3. डोचिंग टाळा : डोचिंगमध्ये योनीचे आतील भाग धुण्यासाठी द्रव द्रावणाचा वापर केला जातो. गर्भधारणेदरम्यान याची शफारस केली जात नाही कारण यामुळे योनीतील सूक्ष्मजीवांचे नाजूक संतुलन बिघडू शकते, ज्यामुळे संक्रमणाची शक्यता वाढते. योनीची स्वतःची नैसर्गिक स्वच्छता यंत्रणा आहे, म्हणून स्वच्छता राखण्यासाठी डोचिंग अनावश्यक आहे.



4. श्वास घेण्यायोग्य, स्वच्छ अंतर्वस्त्रांची नविड करा : कॉटन अंडरवेअर ची नविड करून जव्हाळ्याचा भाग नरिगी ठेवणे साध्य केले जाऊ शकते. खूप घट्ट कवा सधितक असलेले कपडे घालणे टाळा कारण ते ओलावा आणि बॅक्टेरिया अडकवू शकतात, ज्यामुळे आजारांचा धोका वाढतो.

5. स्त्रीस्वच्छता उत्पादने वापरणे टाळा: गरोदरपणात वाइप्स आणि स्प्रे आवश्यक नसतात. या उत्पादनांमध्ये अशी रसायने असतात ज्यात त्वचेला त्रास देण्याची आणि योनीतील सूक्ष्मजीवांचे सामान्य संतुलन बिघडवण्याची क्षमता असते.



6. पेरिनियमवर लक्ष केंद्रित करा: गर्भधारणेदरम्यान, योनीच्या सभोवतालची त्वचा, ज्याला पेरिनियम म्हणून ओळखले जाते, ताणले जाऊ शकते आणि चडिचडि होण्याची शक्यता जास्त असते. संसर्ग टाळण्यासाठी हा भाग स्वच्छ आणि कोरडा ठेवणे आवश्यक आहे. टॉयलेट वापरल्यानंतर, ताज्या, सौम्य टॉवेलने पेरिनियम कोरडे हळूवारपणे थाप द्या.



7. गरोदर असताना टॅम्पोनऐवजी पॅडची नविड करा : गरोदरपणात टॅम्पोनऐवजी पॅड वापरण्याचा सल्ला दिला जातो. करण होजाने संक्रमण वडला जातो.

तोडी स्वच्छता:

तोड संपूर्ण शरीरात प्रवेश बद्धि म्हणून काम करत असल्याने हरिड्या आणि दातांचे आरोग्य राखणे दविसेदविस महत्वाचे ठरते, वशिषतः गरोदरपणात शरीरात होणाऱ्या अनेक बदलांमुळे.

1. गर्भधारणेदरम्यान कोणत्याही पोकळी, हरिड्यांचा रोग आणि इतर दंत समस्यांची तपासणी आणि उपचार करण्यासाठी शक्य तितक्या लवकर दंतचिकित्सकांकडे जाणे महत्वाचे आहे. पोकळी होण्याची शक्यता वाढवणारे पदार्थ खाणे टाळा.



2. दविसातून दोनदा दात घासण्यासाठी फ्लोराइडयुक्त टूथपेस्टचा वापर करावा.

3. वाढत्या गर्भावर परणाम करू शकणाऱ्या ॲनेस्थेटिक्सचा वापर टाळण्यासाठी दंत शस्त्रक्रियेसारख्या वसित दंत प्रक्रियेस जन्म देईपर्यंत उशीर करा.



त्वचा आणि केसांची स्वच्छता:

गर्भधारणेदरम्यान, एखाद्या महिलेचे शरीर घाम, तेल आणि सीबमचे प्रमाण वाढवते, ज्यामुळे तर्च्या त्वचेच्या आणि केसांच्या दसिण्यावर आणि भावनांवर लक्षणीय परणाम होऊ शकतो.

1. गर्भधारणेदरम्यान, एखाद्या महिलेचे शरीर घाम, तेल आणि सीबमचे प्रमाण वाढवते, ज्यामुळे तर्च्या त्वचेच्या आणि केसांच्या दसिण्यावर आणि भावनांवर लक्षणीय परणाम होऊ शकतो.



2. जळजळ आणि चडिचडि टाळण्यासाठी आपली त्वचा जास्त जोमाने घासणे टाळा.

3. कर्कगि, सोलणे कवि रक्तसूत्राव टाळण्यासाठी त्वचेचे हायड्रेशन टकिवून ठेवा. स्ट्रेच मार्क्सचे स्वरूप कमी करण्यासाठी नतिंब, मांडी आणि ओटीपोटावरील त्वचेला नयिमतिपणे मॉइश्चरायझर लावा.



4. आपल्या त्वचेला त्रास होऊ नये म्हणून सुगंध-मुक्त क्रीम चा उपयोग करा.

5. गरोदर महिलांनी हेअर सलूनमध्ये हायलाइट्स, कलर गि कवि पर्म करणे टाळावे कारण या उपचारांमध्ये वापरली जाणारी अनेक रसायने त्वचेसाठी हानिकारक असतात. त्याऐवजी, कंडशिनर आणि शॅम्पू वापरणारी केसांची सातत्यपूर्ण काळजी घेण्यावर लक्ष केंद्रित करा.



स्तनांची काळजी आणि स्वच्छता :

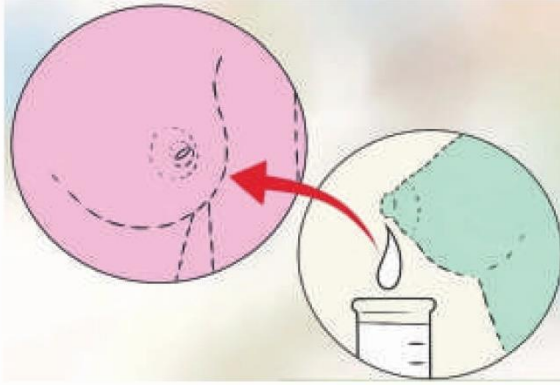
गरोदरपणात आणि हार्मोनल बदलांमुळे शरीरात विविध बदल होत असल्याने स्तनांचा आकार अनेकदा वाढतो. काही स्त्रिया त्यांच्या देय तारखेच्या कित्येक आठवडे क्वि महिन्यांपूर्वी दुध क्वि कोलोस्ट्रम तयार करण्यास सुरवात करू शकतात.

1. स्तनांवरील त्वचा चांगल्या प्रकारे कोमल ठेवण्यासाठी योग्य प्रकारे ज्येष्ठ पाणी पनियाचा खात्री करा.



2. त्वचेला बरे होण्यास आणि स्वतःचे नूतनीकरण करण्यास मदत करण्यासाठी पुरेशी झोप घेण्याची खात्री करा, ज्यामुळे स्तनांवर स्ट्रेच मार्क्स होण्याची शक्यता कमी होऊ शकते.

3. खवखवलेले क्वि फाटलेले स्तनाग्र बरे करण्यासाठी नप्पल क्रीम, नारळाचे तेल क्वि आईच्या दुधाचे काही थेंब स्तनाग्रवर लावावे.



4. कोलोस्ट्रम (गरोदरपणात आणि बाळंतपणानंतर लगेचच स्तनांनी तयार केलेले जाड प्रारंभिक दुध) असल्यास मजबूत सफाई एजंट वापरणे टाळा; फक्त त्यांना कोमट पाण्याने स्वच्छ करा.



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