

Research Article

Microbiological Spectrum of Maternal Genital and Urinary Tract Infections in Spontaneous Preterm Labour and Its Association With Clinical Characteristics

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Abstract

Background

The microbiology of maternal genital tract and urinary tract infection in spontaneous preterm labor varies with population, geography and diagnostic methodology. Identification of clinical patterns that are specific to organisms may aid in identifying women who need focused microbiological assessment.

Objective

To describe the microbiological spectrum of genital and urinary tract infections in women with spontaneous preterm labor and to evaluate the association of identified microorganisms with maternal clinical characteristics.

Materials and Methods

The present hospital-based case-series study was conducted on 100 women with singleton pregnancy who presented with spontaneous pre-term labor between 28 and 36+6 weeks of gestation at a tertiary-care hospital in Bagalkot, Karnataka during August 2022 to February 2024. The clinical characteristics, maternal comorbidities and presenting complaints were noted. High vaginal swabs and urine specimens

were examined by microscopy and culture and identified and tested for antimicrobial susceptibility according to institutional microbiological procedures. Associations between microorganisms and clinical characteristics were analyzed with appropriate categorical statistical tests. A p-value of less than 0.05 was taken as statistically significant.

Results

Candida species was the most commonly isolated microorganism, representing 39% of the microbiological results, followed by Escherichia coli (28%) and Gardnerella vaginalis (9%). Candida spp. were responsible for 60% of isolates in women with genital infection, followed by E. coli and G. vaginalis (10.91% each). The most prevalent organism in urinary infections was E. coli (48.48%) followed by insignificant bacteriuria (24.24%) and Klebsiella spp. (15.15%). In combined genitourinary infection G. vaginalis was responsible for 25% and E. coli for 75% of identified organisms. There was a significant association between the distribution of microorganisms and maternal comorbidities ($p=0.045$) and presenting complaints ($p=0.005$). Abdominal pain was the most

common complaint for women with *E. coli* and *G. vaginalis* infection, and was also most commonly associated with *Candida*.

Conclusion

In women with spontaneous preterm labor the microbiological spectrum was dominated by *Candida* species in genital specimens and *E. coli* in urinary and combined genitourinary infections. The important associations between microorganisms and maternal comorbidities and clinical complaints suggest that clinical presentation may provide useful clues to the underlying microbiological profile. More multicentre studies using standardized molecular and culture-based methods are required to determine whether specific organisms are independently associated with spontaneous preterm labor.

Keywords: preterm labour; genital infection; urinary tract infection; *Candida*; *Escherichia coli*; *Gardnerella vaginalis*; vaginal microbiota; pregnancy

Introduction

Spontaneous pre-term labor is a multifactorial obstetric condition where infection and inflammation are considered to be important biological pathways. Maternal genital and urinary tract microorganisms may contribute to inflammatory activation, although the strength and direction of the associations varies between populations and individual organisms [1,2].

The vaginal microbiome is a complex ecosystem of microbes, often dominated in many women by *Lactobacillus* species. Community composition changes, in particular, reduced *Lactobacillus* dominance and increased presence of organisms related to dysbiosis have been studied in relation to spontaneous preterm birth [3]. But the link between the vaginal microbial composition and preterm birth is not uniform. For example, a case-control study in Kenya found no significant overall difference in vaginal microbial composition between women with

preterm and term deliveries, emphasizing the significance of geographical and population-specific variation [4].

The attention has been directed to particular individual organisms, *Gardnerella vaginalis* and other organisms associated with bacterial vaginosis. Meta-analyses have shown an association between bacterial vaginosis and preterm delivery, particularly when diagnosed early in pregnancy [5,6]. Conversely, evidence from systematic reviews indicates that vulvovaginal yeast infection itself may not be strongly associated with preterm birth, although *Candida* is frequently detected during pregnancy [7]. Thus, isolation of an organism should not be taken as evidence of a causal role in preterm labor.

Another important aspect of maternal genitourinary infection is Urinary Tract Infection (UTI). *E. coli* is a common isolate in urine cultures of pregnant women, and studies of women with preterm labor have also found *E. coli* to be the predominant urinary pathogen [8]. Also there is a chance of concomitant genital and urinary infection which can cause a higher inflammatory burden.

The clinical picture of infection of the genitourinary tract is diverse. Abdominal pain, vaginal discharge, leakage of fluid per vagina and dysuria may occur either singly or in combination. The relationship between specific symptoms and individual microorganisms is not well defined in women presenting with spontaneous preterm labor.

Thus, the present study specifically investigated clinical correlations at the organism level in the study cohort. The objective of the study was to characterize the microbiological spectrum of genital and urinary infections and determine whether the identified microorganisms were associated with maternal comorbidities or clinical complaints presented.

Materials and Methods

Study design and setting

A hospital-based case-series study was conducted at S. Nijalingappa Medical College and HSK Hospital & Research Centre, Bagalkot, Karnataka, India, from August 2022 to February 2024.

The study included 100 women with spontaneous preterm labour and singleton pregnancies. The original thesis identified the study design as a case series and recruited women presenting to the labour room and inpatient department.

Eligibility criteria

Women were eligible if they had:

- gestational age between 28 and 36+6 weeks;
- spontaneous onset of preterm labour;
- singleton pregnancy; and
- premature rupture of membranes of less than 12 hours.

Preterm labour was diagnosed on the basis of regular uterine contractions together with cervical dilatation >1 cm and cervical effacement >80%.

Women with uterine malformations, multifetal gestation, polyhydramnios, gestational or pre-existing diabetes mellitus, cervical length <25 mm on first- or second-trimester ultrasonography, hypertensive disorders of pregnancy, in-vitro fertilization conception, intrauterine fetal demise or immunodeficiency were excluded.

Sample size

Sample-size estimation was performed using OpenEpi version 2.3.1. Based on an estimated prevalence of vaginal infection of 33%, 95% confidence and 10% absolute precision, the calculated sample size was 88; 100 women were ultimately included.

Clinical assessment

Maternal demographic and obstetric characteristics were recorded from case records. Particular attention was given to:

- maternal age;
- gravidity;
- gestational age;
- maternal comorbidities;
- abdominal pain;
- vaginal discharge;
- per-vaginal fluid leak;
- dysuria; and
- microbiological findings.

The study classified microorganisms according to their source and also evaluated organism-specific clinical presentation.

Microbiological assessment

High vaginal swabs were collected and examined by microscopy and culture. The thesis reports that 100 vaginal specimens were evaluated, with *Candida*, *E. coli*, *G. vaginalis*, *Staphylococcus* species, *Acinetobacter baumannii* complex, Group B Streptococcus, Klebsiella and Streptococcus species. identified among the reported findings.

Urine specimens were subjected to culture and organism identification. Among the 33 women classified as having urinary infection, *E. coli*, Group B Streptococcus, insignificant bacteriuria, Klebsiella and *Staphylococcus haemolyticus* were reported.

Microbiological classification

For the purpose of this manuscript, microorganisms were analyzed according to:

1. overall microbiological findings;
2. genital infection;
3. urinary infection;
4. combined genitourinary infection;

5. maternal comorbidity; and
6. presenting clinical complaint.

This focus distinguishes the present manuscript from Manuscript 1, which primarily described the overall clinical and microbiological distribution of infection categories.

Statistical analysis

Categorical variables were expressed as frequencies and percentages. Associations between categorical microbiological and clinical variables were assessed using the appropriate chi-square-based analysis. A two-

sided $p < 0.05$ was considered statistically significant.

Results

Overall microbiological spectrum

The overall microbiological analysis demonstrated that *Candida* spp. was the most frequent microorganism, accounting for 39% of findings, followed by *E. coli* (28%) and *G. vaginalis* (9%). The thesis specifically reports *Candida* as the most common microorganism across the clinical-comorbidity analysis and *E. coli* as the second most common organism.

Table 1. Overall distribution of major microorganisms

Microorganism	n	%
<i>Candida</i> spp.	39	39.0
<i>Escherichia coli</i>	28	28.0
<i>Gardnerella vaginalis</i>	9	9.0
Klebsiella spp.	7	7.0
<i>Acinetobacter</i> spp.	6	6.0
Insignificant bacteriuria	5	5.0
Group B Streptococcus	3	3.0
Staphylococcus spp.	3	3.0
Other/remaining organisms	—	—

Genital microbiological profile

Among the 55 women classified as having genital infection, *Candida* was the predominant isolate, identified in 33 women (60%). *E. coli* and *G. vaginalis* were each identified in 6 women (10.91%). Staphylococcus spp. accounted for 9.09%, *Acinetobacter baumannii* complex for 5.45%, and Group B Streptococcus and Klebsiella species for 1.82% each.

Table 2. Microbiological spectrum among women with genital infection

Microorganism	n	%
<i>Candida</i> spp.	33	60.00
<i>E. coli</i>	6	10.91
<i>G. vaginalis</i>	6	10.91
Staphylococcus spp.	5	9.09
<i>Acinetobacter baumannii</i> complex	3	5.45
Group B Streptococcus	1	1.82
Klebsiella spp.	1	1.82
Total	55	100.00

Urinary microbiological profile

Among the 33 women with urinary infection, *E. coli* was the predominant organism (48.48%), followed by insignificant bacteriuria (24.24%), Klebsiella spp. (15.15%), Group B Streptococcus (6.06%) and *Staphylococcus haemolyticus* (6.06%).

Table 3. Microorganisms isolated from urine cultures

Microorganism	n	%
<i>E. coli</i>	16	48.48
Insignificant bacteriuria	8	24.24
Klebsiella spp.	5	15.15
Group B Streptococcus	2	6.06
<i>Staphylococcus haemolyticus</i>	2	6.06
Total	33	100.00

The predominance of *E. coli* was consistent with previous Indian studies. Yarlagadda et al. reported urinary tract infection in 27.58% of women with preterm labour, with *E. coli* being the most commonly isolated urinary organism [8].

Combined genitourinary infection

Twelve participants had concurrent genital and urinary infection. *E. coli* was identified in 9 cases (75%), whereas *G. vaginalis* was identified in 3 cases (25%).

Table 4. Microorganisms identified in combined genitourinary infection

Microorganism	n	%
<i>E. coli</i>	9	75.0
<i>G. vaginalis</i>	3	25.0
Total	12	100.0

Association Between Microorganisms and Maternal Comorbidities

A statistically significant association was observed between microorganism distribution and maternal comorbidities ($p=0.045$).

Candida was the most frequent microorganism overall (39%). Among women with *Candida*, 41.67% had no recorded comorbidity, 37.50% had anaemia and 37.14% had hypothyroidism. *E. coli* was the second most frequent organism (28%); 37.14% of women with *E. coli* had hypothyroidism, 27.08% had no comorbidity and 12.50% had anaemia.

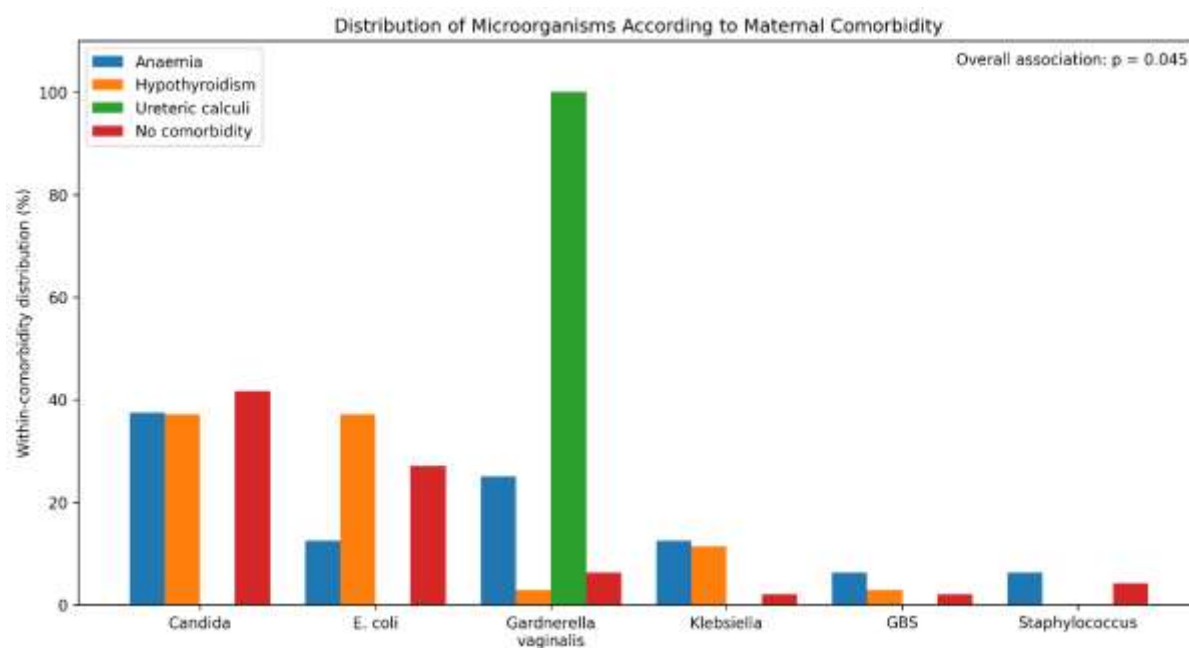
Table 5. Distribution of microorganisms according to maternal comorbidity

Microorganism	Anaemia n (%)	Hypothyroidism n (%)	Ureteric calculi n (%)	No comorbidity n (%)	Total n (%)
<i>Acinetobacter</i> spp.	0 (0.0)	0 (0.0)	0 (0.0)	6 (12.50)	6 (6.0)
<i>Candida</i> spp.	6 (37.50)	13 (37.14)	0 (0.0)	20 (41.67)	39 (39.0)
<i>E. coli</i>	2 (12.50)	13 (37.14)	0 (0.0)	13 (27.08)	28 (28.0)
<i>G. vaginalis</i>	4 (25.00)	1 (2.86)	1 (100.0)	3 (6.25)	9 (9.0)

Group B Streptococcus	1 (6.25)	1 (2.86)	0 (0.0)	1 (2.08)	3 (3.0)
Insignificant bacteriuria	0 (0.0)	3 (8.57)	0 (0.0)	2 (4.17)	5 (5.0)
Klebsiella spp.	2 (12.50)	4 (11.43)	0 (0.0)	1 (2.08)	7 (7.0)
Staphylococcus spp.	1 (6.25)	0 (0.0)	0 (0.0)	2 (4.17)	3 (3.0)
Total	16 (100)	35 (100)	1 (100)	48 (100)	100 (100)

Overall association: $p=0.045$.

Because only one participant had ureteric calculi, the apparent association involving this subgroup should be interpreted cautiously.



Association Between Microorganisms and Presenting Complaints

The distribution of clinical complaints differed significantly according to microorganism ($p=0.005$).

***Candida* spp.**

Candida was the most frequently identified organism (39%). Abdominal pain was the predominant complaint among women with *Candida* (33.33%), followed by abdominal pain with vaginal discharge (20.51%) and abdominal pain with per-vaginal fluid leak (12.82%).

E. coli

E. coli was the second most common organism (27% in the clinical-complaint analysis). Abdominal pain was again the most frequent complaint (37.04%), followed by abdominal pain with vaginal discharge (18.52%). Abdominal pain with dysuria and vaginal discharge and abdominal pain with per-vaginal fluid leak each accounted for approximately 11%.

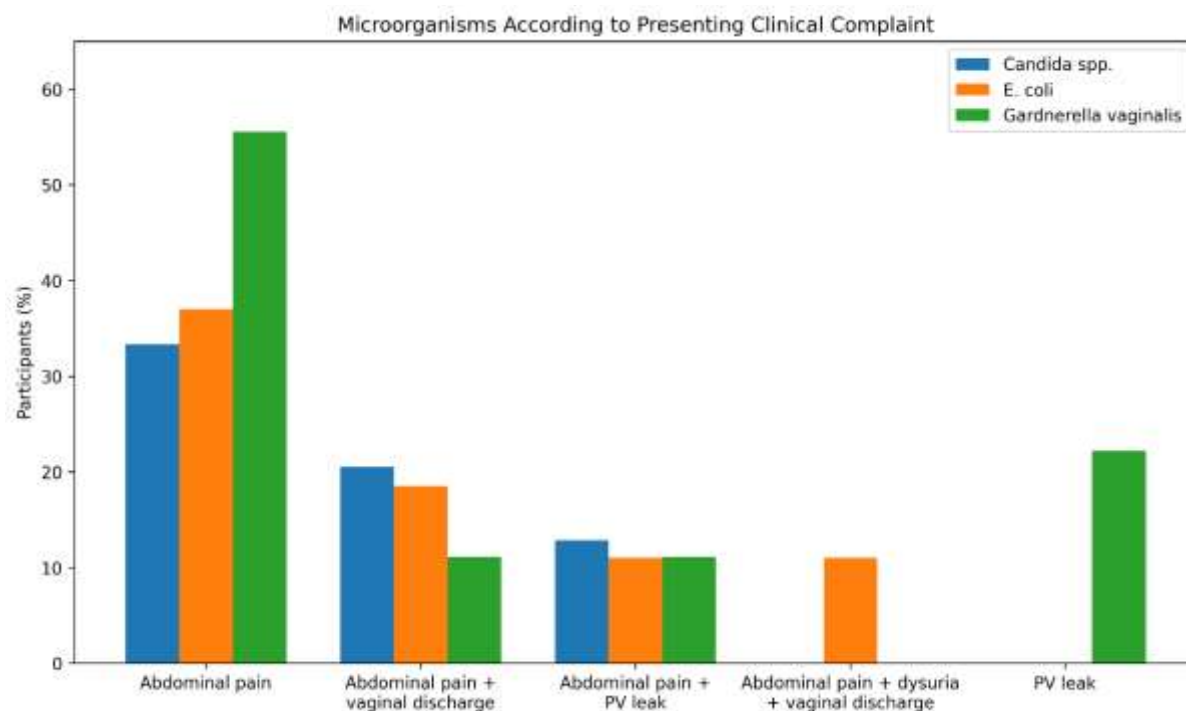
Gardnerella vaginalis

Among women with *G. vaginalis*, abdominal pain was the predominant complaint (55.56%), followed by per-vaginal fluid leak (22.22%). Abdominal pain with per-vaginal fluid leak and abdominal pain with vaginal discharge each accounted for 11.11%.

Table 6. Principal presenting complaints according to major microorganism

Microorganism	Most frequent complaint	Frequency (%)
<i>Candida</i> spp.	Abdominal pain	33.33
<i>Candida</i> spp.	Abdominal pain + vaginal discharge	20.51
<i>Candida</i> spp.	Abdominal pain + PV leak	12.82
<i>E. coli</i>	Abdominal pain	37.04
<i>E. coli</i>	Abdominal pain + vaginal discharge	18.52
<i>E. coli</i>	Abdominal pain + dysuria + vaginal discharge	11.00
<i>E. coli</i>	Abdominal pain + PV leak	11.00
<i>G. vaginalis</i>	Abdominal pain	55.56
<i>G. vaginalis</i>	PV leak	22.22
<i>G. vaginalis</i>	Abdominal pain + PV leak	11.11
<i>G. vaginalis</i>	Abdominal pain + vaginal discharge	11.11

Overall microorganism–complaint association: $p=0.005$.



Microorganisms and Birth Weight

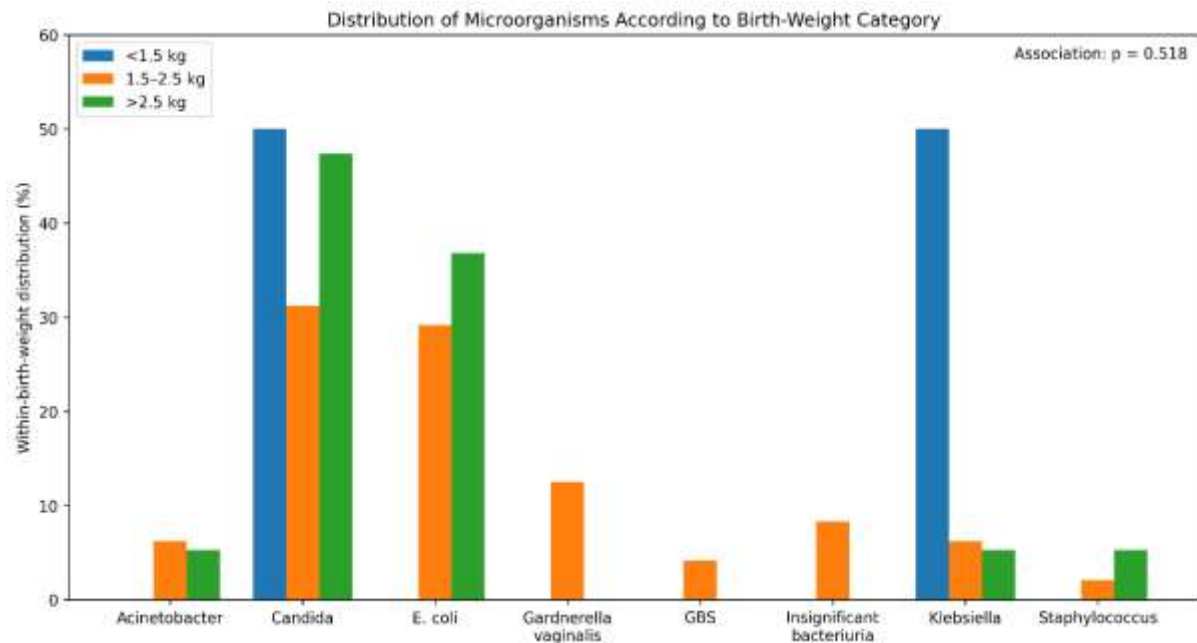
Birth-weight data were available for 69 infants. *Candida* was the most frequent microorganism across birth-weight categories (36.23%), followed by *E. coli* (30.43%). However, there was no statistically significant association between microorganism and birth-weight category ($p=0.518$).

Table 7. Distribution of microorganisms according to birth-weight category

Microorganism	<1.5 kg n (%)	1.5–2.5 kg n (%)	>2.5 kg n (%)	Total n (%)
<i>Acinetobacter</i>	0 (0.0)	3 (6.25)	1 (5.26)	4 (5.80)
<i>Candida</i>	1 (50.0)	15 (31.25)	9 (47.37)	25 (36.23)
<i>E. coli</i>	0 (0.0)	14 (29.17)	7 (36.84)	21 (30.43)
<i>G. vaginalis</i>	0 (0.0)	6 (12.50)	0 (0.0)	6 (8.70)
Group B Streptococcus	0 (0.0)	2 (4.17)	0 (0.0)	2 (2.90)
Insignificant bacteriuria	0 (0.0)	4 (8.33)	0 (0.0)	4 (5.80)
Klebsiella	1 (50.0)	3 (6.25)	1 (5.26)	5 (7.25)
Staphylococcus spp.	0 (0.0)	1 (2.08)	1 (5.26)	2 (2.90)
Total	2 (100)	48 (100)	19 (100)	69 (100)

$p=0.518$.

The absence of a statistically significant association suggests that, within this cohort, the presence of particular microorganisms was not demonstrably related to the infant's birth-weight category.



Discussion

This study specifically investigated the relationship of individual microorganisms with clinical features in women presenting with spontaneous preterm labor. Three findings are of special note: Candida was the most frequent genital organism, E. coli was the most frequent urinary organism and the distribution of organisms was significantly related to both maternal comorbidities and presenting complaints.

Our results showing Candida as the predominant organism in genital specimens are in agreement with previous Indian studies. Genital infections in the present cohort were due to Candida in 60%. Yarlagadda et al [8] also found that Candida was the commonest organism in high vaginal swab cultures of women with preterm labor. Fernandes and Chandra also reported Candida albicans as the most common organism in women with vaginal infection [9]. But other populations have shown different dominant organisms such as coagulase-negative staphylococci, indicating

that genital microbiological profiles vary by setting.

The biological significance of Candida in preterm labor should be interpreted with caution. Vulvovaginal yeast infection can cause local inflammation, but a recent systematic review and meta-analysis of 57 studies of pregnant women found no strong statistical evidence of an association between vulvovaginal yeast infection and risk of preterm birth [7]. Hence, the high rate of Candida in this study indicates the high prevalence of Candida among women with preterm labor but does not establish that Candida was the cause of labor.

The second main finding was the predominance of E. coli in urinary infections. E. coli was responsible for nearly half of the urinary infections (48.48%). This finding is in accordance with previous observations in Indian. Yarlagadda et al reported E. coli as the most common urinary organism isolated in women with preterm labor [8]. Thus the current finding seems to be a reproducible phenomenon

of urinary microbiology in this clinical population.

The combined genitourinary group showed an even larger predominance of *E. coli*, representing 75% of the identified organisms. Remaining 25% was *G. vaginalis*. This pattern suggests that urinary pathogens may play an important role in the concurrent genitourinary infection in women with spontaneous preterm labor.

The study also found a significant association between microorganism and maternal comorbidity ($p=0.045$). The organisms most frequently represented among the comorbidity categories were *Candida* and *E. coli*. A large proportion of women with *Candida* had no comorbidity documented, but anemia and hypothyroidism were also represented. Hypothyroidism was the most represented comorbidity among women with *E. coli*.

The biological explanation for this association is not derivable from the present study. The study design was observational. Comorbidity categories were of different size. In particular, one patient had ureteric calculi. Thus, although the overall chi-square test was statistically significant, the result should be interpreted as exploratory rather than suggestive of a particular comorbidity predisposing to a particular organism.

More clinically interesting was the significant association between organism and presenting complaint ($p=0.005$). Abdominal pain was the most frequent complaint among the major organisms, but the relative distribution of associated symptoms differed. For women with *Candida*, abdominal pain was followed by abdominal pain plus vaginal discharge. In infection with *E. coli* abdominal pain and combinations with vaginal discharge or dysuria were observed. In women with *G. vaginalis*, abdominal pain was noted in more than half of the cases.

The link between *G. vaginalis* and preterm birth is especially complicated. *Gardnerella* is classically linked with bacterial vaginosis type dysbiosis and previous meta-analyses have

demonstrated an association between bacterial vaginosis and preterm delivery [5,6]. However, culture of *G. vaginalis* alone does not confirm bacterial vaginosis. Recent microbiome research has demonstrated that the association of certain organisms with preterm birth is a function of the larger microbial community, not just the detection of a single organism [3,4]. Gudnadottir et al. highlighted variation in associations between vaginal community-state types and preterm birth, while Gulavi et al. did not find any significant overall difference in vaginal community composition between preterm and term groups in their Kenyan population.

An important negative finding is given by the analysis of birth-weight. *Candida* and *E. coli* were the most common microorganisms in all birth weight categories but their distribution did not significantly differ relative to the birth weight category ($p=0.518$). This demonstrates that in this dataset the presence of a specific microorganism was not significantly associated with birth-weight category.

This finding is contrasted to some studies that found lower birthweight in infants born to women with bacterial vaginosis or other infections. The thesis refers to an Indian study in Assam where 89.28% of infants born after preterm labor with bacterial vaginosis were underweight and a Malaysian study which found lower birth weight among women with bacterial vaginosis [10,11]. Inconsistent findings may be due to differences in study design, definitions of infection, gestational age and microbiological methodology.

Thus the present study usefully distinguishes between microbial frequency and microbial association with clinical outcome. *Candida* was common but no association was shown between its presence and birth-weight category. Similarly, *E. coli* was common in urinary and combined genitourinary infections but the study design does not demonstrate that it alone caused preterm labor or adverse neonatal outcomes.

Clinical Implications

These findings support a selective approach to microbiological assessment of women presenting with spontaneous preterm labor. Genital and urinary symptoms should be assessed in a systematic manner and microbiological testing should be considered where the clinical picture is compatible with infection.

Relevant local surveillance information is available from the dominant organisms in genital specimens being *Candida* and in urinary specimens being *E. coli*. However, empiric antimicrobial therapy should not be guided solely by the organism frequencies observed in this study. The treatment should be based on the culture results, antimicrobial susceptibility testing, clinical findings, and established pregnancy-specific treatment recommendations.

Strengths:

The main strength of this manuscript is its focus on organism-specific clinical correlations, rather than just the prevalence of infection. The study evaluated genital and urinary microbiology and associations with maternal comorbidity and presenting symptoms at the same time.

Limitations

First, this was a single-centre case series of 100 women and thus has limited external validity. Secondly, there was no term-control group. Therefore, it was not possible to determine whether certain microorganisms were more prevalent than in women with term labor. Third, conventional culture-based methods cannot characterize the entire vaginal microbial community and can underestimate fastidious or nonculturable organisms.

Conclusion

In the microbiological spectrum of women with spontaneous preterm labor, *Candida* spp. were predominant in genital infections and *E. coli* in urinary and combined genitourinary infections. *G. vaginalis* was another important genital organism.

The distribution of microorganisms was significantly associated with maternal

comorbidities ($p=0.045$) and clinical complaints at presentation ($p=0.005$). However, the observed associations should be interpreted as correlations, not as proof of causation. No significant association was found between microorganism and birth-weight category ($p=0.518$).

These findings support appropriate clinical and microbiological assessment and highlight the heterogeneity of maternal genitourinary microbiology in spontaneous preterm labor. Further prospective multicentre studies using molecular microbiome techniques and appropriate term controls are required to determine whether specific organisms or patterns of microbial communities independently contribute to spontaneous preterm labor and adverse perinatal outcomes.

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