Prevalence and polymicrobial patterns of genital tract microorganisms among women with genital symptoms in Northern Cyprus: a cross-sectional study

Prevalência e padrões polimicrobianos de microrganismos do trato genital em mulheres com sintomas genitais no Norte do Chipre: um estudo transversal

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ABSTRACT

Introduction: Recent advances in molecular diagnostics have shown that interactions between polymicrobial infections are increasingly influencing the epidemiology of sexually transmitted and genital infections. Despite the evident importance of this information to world health, no specific information is available regarding Northern Cyprus. **Objective:** To analyse the presence of multi-microbial pathogens and classic sexually transmitted infections in the genitourinary system. **Methods:** A total of 1,000 vaginal swab samples from symptomatic women were included in this study and analysed for 12 different sexually transmitted and genital tract-associated microorganisms by multiplex real-time polymerase chain reaction. Prevalence, co-detection, and age distribution were investigated. **Results:** At least one microorganism was detected in 39.0% (390/1,000) of the study population. Microbiota-associated organisms were the most prevalent, including *Gardnerella vaginalis* (28.2%), *Ureaplasma parvum* (17.7%), and *Candida albicans* (11.6%), followed by *Mycoplasma hominis* (3.3%) and *Ureaplasma urealyticum* (1.5%). Classical sexually transmitted infections, such as *Chlamydia trachomatis* (2.3%) and *Neisseria gonorrhoeae* (0.6%) were found at lower rates, while *Mycoplasma genitalium* (0.7%), herpes simplex virus type 2 (0.3%), *Treponema pallidum* (0.1%), and *Trichomonas vaginalis* (0.1%) were detected at very low rates; herpes simplex virus type 1 was not detected. Infections were most frequently observed in women aged 20–29 years, though no statistically significant age difference was found between microbiota-associated and classical sexually transmitted pathogen groups (p=0.95). Co-detection of multiple microorganisms was frequent, occurring in 49.5% of positive cases, particularly among *G. vaginalis*, *U. parvum*, and *C. albicans*, which showed the strongest pairwise associations (phi coefficients 0.27–0.40, all p<0.001), highlighting strong polymicrobial interactions. **Conclusion:** Genital tract infection for this demographic group is mainly mediated by microbiota-associated pathogens, with a substantial tendency toward co-detection. This first comprehensive molecular data set from Northern Cyprus underscores the importance of microbiota-focused diagnostic approaches and encourages a paradigm shift beyond traditional STI-centric frameworks.

Keywords: Sexually transmitted infections. PCR. Genital microbiota. Epidemiology.

RESUMO

Introdução: Avanços recentes no diagnóstico molecular têm mostrado que as interações entre infecções polimicrobianas estão influenciando cada vez mais a epidemiologia das infecções sexualmente transmissíveis e genitais. Apesar da importância evidente dessa informação para a saúde mundial, não há informações específicas disponíveis sobre o Norte de Chipre. **Objetivo:** Analisar a presença de patógenos multimicrobianos e infecções sexualmente transmissíveis clássicas no aparelho geniturinário. **Métodos:** Um total de 1.000 amostras de esfregaços vaginais de mulheres sintomáticas foi incluído neste estudo e analisado para 12 diferentes microrganismos sexualmente transmissíveis e associados ao trato genital, por meio da reação em cadeia da polimerase multiplex em tempo real. Prevalência, codetecção e distribuição etária foram investigadas. **Resultados:** Pelo menos um microrganismo foi detectado em 39,0% (390/1.000) da população estudada. Os organismos associados à microbiota foram os mais prevalentes, incluindo *Gardnerella vaginalis* (28,2%), *Ureaplasma parvum* (17,7%) e *Candida albicans* (11,6%), seguidos por *Mycoplasma hominis* (3,3%) e *Ureaplasma urealyticum* (1,5%). Infecções sexualmente transmissíveis clássicas, como *Chlamydia trachomatis* (2,3%) e *Neisseria gonorrhoeae* (0,6%), foram encontradas em taxas mais baixas, enquanto *Mycoplasma genitalium* (0,7%), vírus herpes simplex tipo 2 (0,3%), *Treponema pallidum* (0,1%) e *Trichomonas vaginalis* (0,1%) foram detectados em taxas muito baixas; o vírus herpes simplex tipo 1 não foi detectado. As infecções foram observadas com mais frequência em mulheres com idade de 20–29 anos, embora nenhuma diferença estatisticamente significativa de idade tenha sido encontrada entre os grupos de patógenos associados à microbiota e às infecções sexualmente transmissíveis clássicas (p=0,95). A codetecção de múltiplos microrganismos foi frequente, ocorrendo em 49,5% dos casos positivos, particularmente entre *G. vaginalis, U. parvum* e *C. albicans*, que mostraram as associações pares mais fortes (coeficientes phi 0,27–0,40, todos p<0,001), destacando fortes interações polimicrobianas. **Conclusão:** A infecção no trato genital para este grupo demográfico é mediada principalmente por patógenos associados à microbiota, com uma tendência substancial à codetecção. Este primeiro conjunto abrangente de dados moleculares do Norte de Chipre ressalta a importância das abordagens de diagnóstico centradas na microbiota e incentiva uma mudança de paradigma para além dos quadros tradicionais centrados nas infecções sexualmente transmissíveis.

Palavras-chave: Infecções sexualmente transmissíveis. PCR. Microbiota genital. Epidemiologia.

INTRODUCTION

According to the World Health Organization, more than one million new cases of sexually transmitted infections (STIs) occur every day worldwide, and the major pathogens responsible for these infections are T*richomonas vaginalis, Chlamydia trachomatis, Neisseria gonorrhoeae,* and *Treponema pallidum*[1,2]. Various factors may influence the transmission of infectious diseases, including

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behaviours, individual characteristics, and microorganisms responsible for causing the diseases. Individuals may be unaware that they have the disease, which is a particular concern in women. Some of the complications associated with STIs include infertility and pelvic inflammatory disease[3].

Recent molecular diagnostic techniques have improved the detection capability of microorganisms that cause STIs by making it possible to detect fastidious and hitherto neglected organisms, including *Mycoplasma genitalium, Ureaplasma parvum,* and *Mycoplasma hominis*[3,4]. This improvement raises questions about the conventional approach to diagnosing STIs, which is based on the pathogen-centric view. This issue poses significant problems in terms of how to understand the presence of these organisms since they may occur as opportunists or commensals within the genital tract.

Vaginal flora typically includes large amounts of lactobacilli that assist in keeping the vaginal pH acidic and providing defence against the invasion of pathogens. Dysbiosis may occur when the normal flora becomes imbalanced, allowing anaerobes such as *G. vaginalis* to grow excessively[5]. Bacterial vaginosis is a condition that is quite common across the globe, and its prevalence may put individuals at greater risk of contracting various other illnesses, such as STIs and poor reproductive health conditions[6]. The advent of molecular technology has made the detection of such dysbiosis conditions easier than before.

The connection between STIs and the vaginal microbiome is intricate and mutually related; vaginal dysbiosis increases the risk of acquiring an STI, and sexual contact per se may change the microbial composition[7]. Thus, infection of the genitourinary system should not be explained by one pathogen alone, since it always implies polymicrobial interaction occurring in a disrupted microbial environment. Although much research has been conducted on this issue, current information on the molecular epidemiology of classic STIs and microbiota-associated microbes is very limited and lacks a geographical focus. In this study, symptomatic status was defined clinically by the presence of one or more of the following signs at presentation: abnormal vaginal discharge, malodour, pruritus, or erythema, which are the most common presenting features of genital tract infection in outpatient gynaecological practice[3].

OBJECTIVE

The objective of this study is to conduct a comprehensive analysis of the microorganisms in the genitourinary system, taking into consideration the presence of polymicrobial pathogens and classic STIs.

METHODS

Study design and population

This cross-sectional observational study was conducted among 1,000 female patients presenting to outpatient clinics in Northern Cyprus. Participants were women aged 18 and older who attended the clinics with symptoms suggestive of genital tract infection. The most commonly reported symptoms included abnormal vaginal discharge, malodour, pruritus, and erythema, with symptom duration of at least 3 days before clinical evaluation, as required for study inclusion.

Patients who were pregnant or had received antibiotic treatment before sample collection were excluded from the study to minimise potential confounding effects on microbial detection. Samples deemed inadequate or improperly collected were also excluded from the analysis. Ethical approval for the study was obtained from the Near East University Ethics Committee (Approval No. YDU/2026/144-2100), and all procedures were conducted in accordance with the Declaration of Helsinki.

Sample collection and deoxyribonucleic acid extraction

Vaginal swab samples were collected using sterile Copan swab collection systems under standard clinical conditions. Following collection, samples were transported to the laboratory and processed under appropriate biosafety conditions.

Genomic deoxyribonucleic acid (DNA) was extracted using the QIAamp DNA Mini Kit (Qiagen, Germany) according to the manufacturer's instructions. The quality and integrity of extracted DNA were ensured before downstream molecular analysis.

Multiplex real-time polymerase chain reaction analysis

The detection of pathogens in the genital tract was performed with the use of the CareGENE™ STD-12 Detection Kit (Wells Bio, South Korea), which enables the simultaneous identification of 12 bacterial, viral, fungal, and protozoan microorganisms from vaginal swab specimens, including *C. trachomatis*, *N. gonorrhoeae*, *Ureaplasma urealyticum*, *U. parvum*, *M. genitalium*, *M. hominis*, *T. pallidum*, *Gardnerella vaginalis*, *T. vaginalis*, herpes simplex virus type 1 (HSV-1), herpes simplex virus type 2 (HSV-2), and *Candida albicans*.

The process of amplification was carried out for 40 cycles, with the Rotor-Gene Q real-time polymerase chain reaction (PCR) instrument (Qiagen, Germany). For amplification of the target pathogen, a Ct (cycle-threshold) value of ≤39.0 was regarded as positive; whereas a Ct value of >39.0 or the absence of amplification was considered negative. Three separate reaction sets were conducted during the amplification process and termed Reaction Set A, Reaction Set B, and Reaction Set C. These three reaction sets included four targets per reaction set, each of which contained an internal control. During the amplification process, fluorescence was determined in multiple channels, including FAM, HEX, Cy5, and Quasar 705. However, to amplify the internal control, the ROX channel was used to assess the quality of nucleic acid extraction and PCR. The absence of amplification of both the target pathogens and the internal control was treated as an invalid sample and was not considered in data interpretation. The sensitivity of this test is estimated at 0.5–5,0 copies/µL, and it can detect trace quantities of microbial DNA.

Statistical analysis

Statistical analyses were conducted using Python (v3, pandas and SciPy libraries). Summary statistics were employed to describe the frequency of microorganisms identified in this study, expressed as frequencies and percentages with their respective 95% confidence intervals (95%CI), calculated using the Wilson score method.

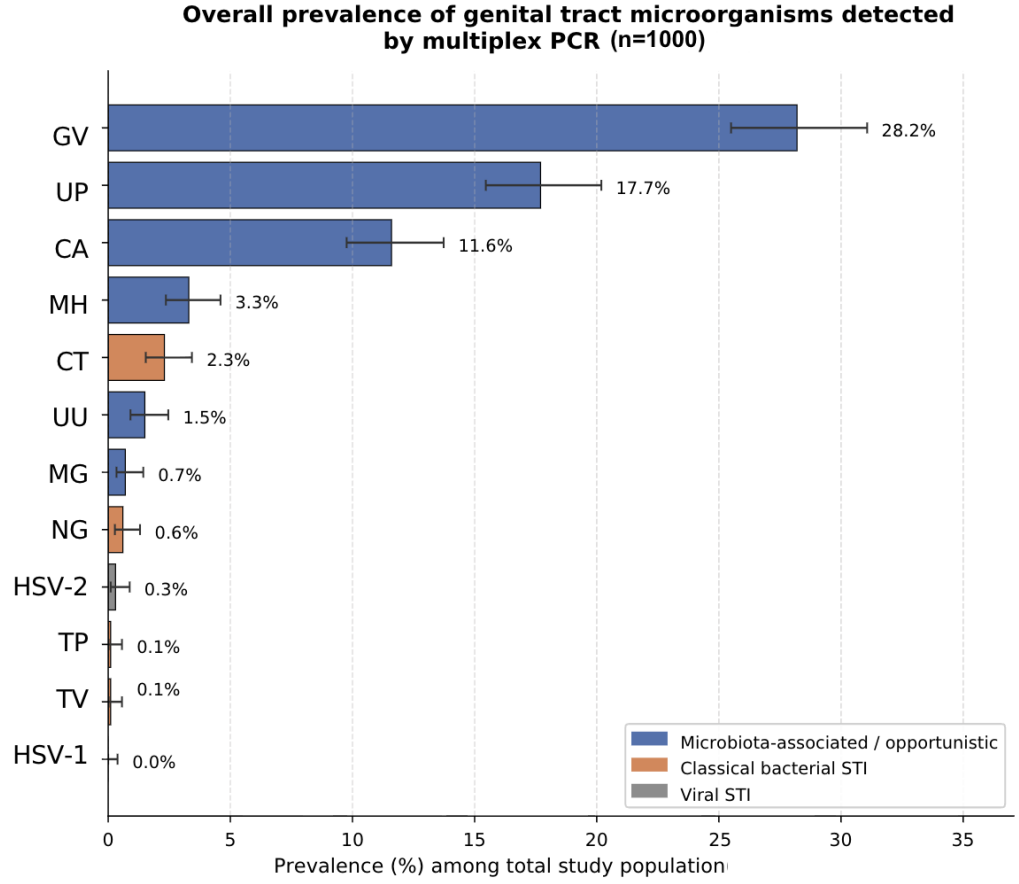
Correlations between different microorganisms were assessed through the phi coefficient (Pearson correlation applied to binary presence/absence data) and tested for statistical significance using chi-square tests of independence, with the results visualised in a correlation matrix. Age distributions across pathogens were compared using independent-samples t-tests. A significance level of $p<0.05$ was applied in all cases.

RESULTS

Overall, 1,000 clinical specimens collected from women with symptoms of genital tract infection were analysed, and microorganisms were found in 390 samples (39.0%; 95%CI 36.0–42.1) (Figure 1). Table 1 shows that *G. vaginalis* had the highest prevalence, being observed in 28.2% (95%CI 25.5–31.1) of the total number of samples; further, *U. parvum* was found in 17.7% (95%CI 15.5–20.2) and *C. albicans* in 11.6% (95%CI 9.8–13.7). As for the classical STIs, 2.3% (95%CI 1.5–3.4) of samples contained *C. trachomatis*, and 0.6% (95%CI 0.3–1.3) of samples contained *N. gonorrhoeae*. Other organisms were detected at low frequencies: *M. hominis* in 3.3% (95%CI 2.4–4.6), *U. urealyticum* in 1.5% (95%CI 0.9–2.5), *M. genitalium* in 0.7% (95%CI 0.3–1.4), and *T. vaginalis* and *T. pallidum* each in 0.1% (95%CI 0.02–0.6). HSV-2 was found in 0.3% (95%CI 0.1–0.9) of samples, and HSV-1 was not detected in any specimen.

As with the original framing, a distinction can be drawn between classical STI pathogens and microbiota-associated organisms. Classical pathogens (*C. trachomatis*, *N. gonorrhoeae*, *T. vaginalis*, *T. pallidum*) were collectively uncommon, while the vast majority of positive cases involved the microbiota-associated species *G. vaginalis*, *U. parvum*, and *C. albicans* — consistent with most symptomatic infections reflecting vaginal dysbiosis rather than classical STI acquisition (Figure 1).

Interestingly, there are co-infections when two or even more organisms occur in tandem (Figure 2). These include both species that form part of the normal microbiota and opportunistic pathogens. Of the 390 positive cases, 193 (49.5%) involved two or more organisms simultaneously (mean 1.70 organisms per positive case). The correlation matrix confirmed this pattern statistically — the



PCR: polymerase chain reaction; GV: Gardnerella vaginalis; UP: Ureaplasma parvum; CA: Candida albicans; MH: Mycoplasma hominis; CT: Chlamydia trachomatis; UU: Ureaplasma urealyticum; MG: Mycoplasma genitalium; NG: Neisseria gonorrhoeae; HSV-2: Herpes simplex virus type 2; TP: Treponema pallidum; TV: Trichomonas vaginalis; HSV-1: Herpes simplex virus type 1; STI: sexually transmitted infection.
Source: Authors' own elaboration, 2026.

Figure 1 – Overall prevalence of genital tract microorganisms detected by multiplex PCR among 1,000 symptomatic women. Bars represent the percentage of the total study population (n=1,000) positive for each organism, with error bars indicating 95% Wilson score confidence intervals. Organisms are ordered by prevalence and colour-coded by category: microbiota-associated/opportunistic organisms (blue), classical bacterial STI pathogens (orange), and viral STI pathogens (grey).

strongest and most significant pairwise associations were between *U. parvum* and *G. vaginalis* (φ=0.40, p<0.001), *G. vaginalis* and *C. albicans* (φ=0.30, p<0.001), and *M. hominis* and *G. vaginalis* (φ=0.27, p<0.001). Additional significant associations included *U. parvum–C. albicans* (φ=0.18), *U. parvum–M. hominis* (φ=0.16), *M. hominis–C. albicans* (φ=0.16), and *C. trachomatis–G. vaginalis* (φ=0.11). *N. gonorrhoeae*, *T. pallidum*, and *T. vaginalis* were too rare (n≤6) for reliable correlation testing. These findings reinforce that co-detections predominantly involve microbiota-associated organisms rather than classical STIs.

Finally, age-related patterns in organism prevalence were examined among the 346 positive cases with recorded age (Table 2). Microbiota-associated organisms — *G. vaginalis*, *U. parvum*, and *C. albicans* — were most prevalent in women aged 20–29 years (accounting for 47–56% of each organism's positive cases in this band), with all three organisms detected across a wide age span extending from 18 up to the mid-to-late 70s (and, for *U. parvum*, to 86 years). *G. vaginalis* had the broadest distribution (18–77 years, median 30), while *C. albicans* was somewhat more concentrated in younger women (median 27, interquartile range [IQR] 23.0–35.5) without being confined to a narrow band. *U. parvum* showed a comparable pattern to *G. vaginalis*, with prevalence spread across reproductive age and no single sharply defined peak.

The classical sexually transmitted pathogens did not show a markedly narrower or younger age distribution than the microbiota-associated organisms in this dataset. *C. trachomatis* cases ranged 18–48 years (median 28), with a fairly even split between women in their 20s (47.6%) and a secondary concentration in the 40–49 band (23.8%), rather than being confined to the late teens/early twenties. *N. gonorrhoeae*, though based on only 6 cases, was detected in comparatively older women (median 35, range 21–41 years), consistent with the pattern seen for other low-frequency pathogens. Overall, comparing microbiota-associated organisms (mean age 32.0 years) with classical STI pathogens (mean age 31.9 years) showed no statistically significant difference (independent-samples *t*-test, p=0.95), indicating that in this cohort, age alone does not clearly distinguish the two pathogen categories — unlike the sharper separation suggested in some prior reports.

DISCUSSION

This study presents a molecular epidemiological analysis of genital microorganisms in symptomatic women reporting vaginal discharge, malodour, pruritus, and erythema. The findings indicate a clear preponderance of microbiota-associated organisms over classical STIs: 39.0% of the total study population (390/1,000) tested positive for at least one organism, with *G. vaginalis* (28.2%), *U. parvum* (17.7%), and *C. albicans* (11.6%) accounting for the vast majority of positive detections, compared with just 2.3% for *C. trachomatis* and 0.6% for *N. gonorrhoeae*. These findings support a paradigm in which polymicrobial infection and vaginal dysbiosis are considered alongside — rather than instead of — the classical single-pathogen model of genital tract infection[8,9].

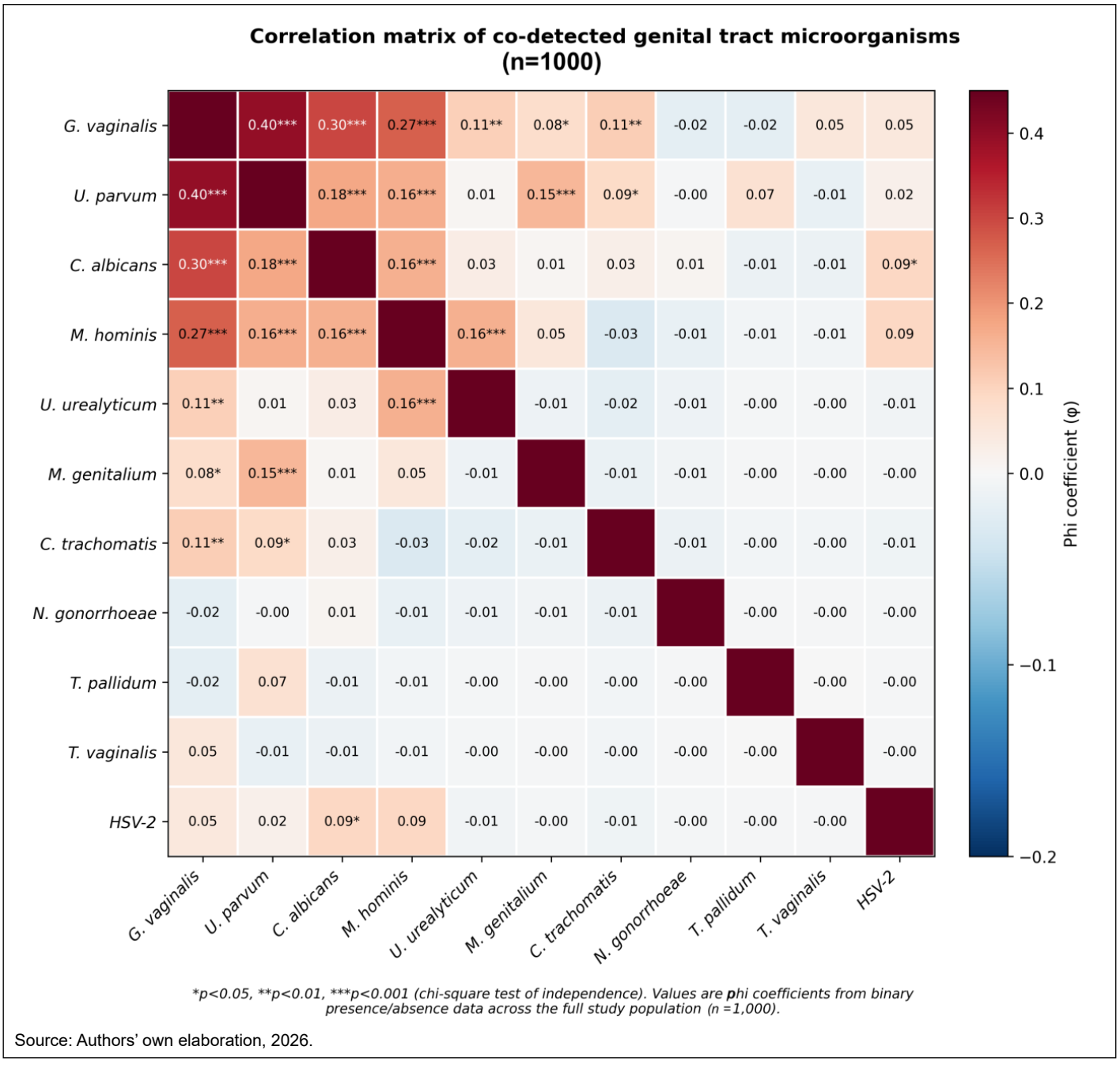
The high prevalence of *G. vaginalis* noted above correlates with the known importance of this organism as a prominent marker and cause of bacterial vaginosis, a disease characterised by disturbances in the normal *Lactobacillus* vaginal microflora[8]. Likewise, the high frequency of *U. parvum* and *M. hominis* (3.3%) correlates with the known significance of these bacteria as causative agents in dysbiotic conditions and their increasingly recognised significance as opportunistic pathogens[3]. While formerly classified as commensals, *Ureaplasma* species have recently been associated with several reproductive problems, including infertility, premature delivery, and chronic genitourinary infections[4]. Beyond their individual prevalence, the clinical significance of *U. parvum* and *M. hominis* in this cohort is best understood through their co-detection patterns rather

Table 1 – Prevalence of genital tract pathogens detected among 1,000 symptomatic female patients, presented as frequency (n), percentage, and 95% Wilson score confidence interval. Percentages are calculated using the total study population (n=1,000) as denominator; values do not sum to 100% due to polymicrobial co-detections.

Code	Organism	n positive	Prevalence (%)	95%CI	% of positive cases
GV	*Gardnerella vaginalis*	282	28.2	25.5–31.1	72.3
UP	*Ureaplasma parvum*	177	17.7	15.5–20.2	45.4
CA	*Candida albicans*	116	11.6	9.8–13.7	29.7
MH	*Mycoplasma hominis*	33	3.3	2.4–4.6	8.5
CT	*Chlamydia trachomatis*	23	2.3	1.5–3.4	5.9
UU	*Ureaplasma urealyticum*	15	1.5	0.9–2.5	3.9
MG	*Mycoplasma genitalium*	7	0.7	0.3–1.4	1.8
NG	*Neisseria gonorrhoeae*	6	0.6	0.3–1.3	1.5
HSV-2	Herpes simplex virus type 2	3	0.3	0.1–0.9	0.8
TP	*Treponema pallidum*	1	0.1	0.02–0.6	0.3
TV	*Trichomonas vaginalis*	1	0.1	0.02–0.6	0.3
HSV-1	Herpes simplex virus type 1	0	0.0	—	—
Any pathogen	Overall positivity	390	39.0	36.0–42.1	—

CI: confidence interval.
Source: Authors' own elaboration, 2026.

than in isolation. Both organisms showed their strongest associations with *G. vaginalis* (φ=0.40 and φ=0.27, respectively) rather than with each other or with classical STI pathogens, suggesting that their pathogenic relevance in this population is closely tied to a broader dysbiotic vaginal environment rather than representing independent infectious events. This supports the view that *U. parvum* and *M. hominis* often act as facilitators or markers of microbial imbalance rather than as sole causative agents of symptomatic disease[3,4].



Source: Authors' own elaboration, 2026.

Figure 2 – Correlation matrix illustrating pairwise co-detection patterns among the 11 genital tract microorganisms identified in the study population (n=1,000). Values represent phi coefficients (φ), calculated as Pearson correlations on binary presence/absence data for each organism pair. Cell colour reflects the strength and direction of association (red=positive, blue=negative), and asterisks denote statistical significance from chi-square tests of independence (*p<0.05; **p<0.01; ***p<0.001). Organisms are ordered to group microbiota-associated/opportunistic species (G. vaginalis, U. parvum, C. albicans, M. hominis, U. urealyticum, M. genitalium) separately from classical and viral STI pathogens (C. trachomatis, N. gonorrhoeae, T. pallidum, T. vaginalis, HSV-2). The strongest co-detections were observed among microbiota-associated organisms, particularly between U. parvum and G. vaginalis (φ=0.40, p<0.001), G. vaginalis and C. albicans (φ=0.30, p<0.001), and M. hominis and G. vaginalis (φ=0.27, p<0.001), whereas classical STI pathogens showed weak and largely non-significant associations with one another and with microbiota-associated species.

Table 2 – Age distribution of positive cases by pathogen with recorded age ≥18 years. Values are presented as median age, interquartile range (IQR), full range, and modal age band (5-year intervals). Pathogens with fewer than five age-recorded cases (*Treponema pallidum*, *Trichomonas vaginalis*, herpes simplex virus type 2) were excluded from age-band interpretation due to insufficient sample size.

Organism	n (age known)	Median age	IQR	Range	Modal age band (%)
Candida albicans	111	27	23–35.5	18–77	20–24 (31.5)
Mycoplasma hominis	32	26	23.8–36.3	20–52	20–24 (34.4)
Gardnerella vaginalis	252	30	24–39	18–77	20–24 (26.6)
Ureaplasma parvum	167	29	24–40	18–86	20–24 (24.6)
Chlamydia trachomatis	21	28	24–39	18–48	tied 20–24 and 25–29 (23.8% each)
Ureaplasma urealyticum	14	30	23.3–36.8	18–61	tied 20–24 and 35–39 (35.7% each)
Mycoplasma genitalium	7	28	26.5–36	21–53	25–29 (42.9)
Neisseria gonorrhoeae	6	35	26.8–38.8	21–41	35–39 (33.3)

IQR: interquartile range.
Pathogens with fewer than five age-recorded cases (*Treponema pallidum*, *Trichomonas vaginalis*, herpes simplex virus type 2) were excluded from age-band interpretation due to insufficient sample size.
Source: Authors' own elaboration, 2026.

In contrast to the low prevalence of *C. trachomatis* and *N. gonorrhoeae*, the latter correlates with large-scale European surveillance data, in which these pathogens, although medically important, are found less frequently than microbiota-related organisms[10-12]. Notably, the 2.3% prevalence of *C. trachomatis* observed here among symptomatic women is comparable to — rather than substantially higher than — prevalence figures reported among asymptomatic women in some European surveillance studies[10,11], suggesting that symptom status alone may not reliably predict *C. trachomatis* positivity and reinforcing the case for broader molecular screening independent of clinical presentation.

With respect to age, the most prevalent age range for detecting microbiota-associated organisms (*G. vaginalis, U. parvum*, and *C. albicans*) was 20–29 years. However, the range of ages among the women infected with any one of these organisms was wide and extended up to the age of 86 years (in the case of *U. parvum*) and included even older women who were up to 70 years old. In contrast to expectations, classical STI pathogens in this cohort were found to have no narrower age distribution; rather, there was no statistically significant difference between the mean age of patients positive for microbiota-associated organisms (32.0 years) and that of patients positive for classical STI (31.9 years) ($p=0.95$). This suggests that, at least in this population, age alone does not clearly distinguish between the two pathogen categories — a finding worth noting explicitly, since it differs from patterns reported in some other cohorts[13,14].

The high rate of co-infection observed further supports the polymicrobial nature of genital infections in this population: 49.5% of positive cases (193/390) involved two or more organisms simultaneously. Correlation analysis (phi coefficients, chi-square tested) confirmed that co-detection was concentrated among microbiota-associated organisms rather than occurring at random — the strongest associations were between *U. parvum* and *G. vaginalis* ($\varphi=0.40$, $p<0.001$), *G. vaginalis* and *C. albicans* ($\varphi=0.30$, $p<0.001$), and *M. hominis* and *G. vaginalis* ($\varphi=0.27$, $p<0.001$). Classical STI pathogens showed weak and largely non-significant associations both with each other and with microbiota-associated species. This pattern is consistent with the current understanding of bacterial vaginosis as a polymicrobial condition involving biofilm formation and complex inter-organism interactions rather than the action of a single pathogen[15]. The synergistic detection of *G. vaginalis*, *U. parvum*, and *C. albicans* in particular may reflect a shared ecological niche or facilitative relationship between these organisms, though causality cannot be established from cross-sectional co-detection data alone.

The epidemiological trends identified in this study are broadly consistent with results from other Mediterranean and European populations. Studies conducted in Türkiye, Greece, and Italy have similarly documented a high prevalence of bacterial vaginosis-associated microorganisms such as *G. vaginalis*, *Ureaplasma* spp., and *Mycoplasma* spp., in some cases exceeding the prevalence of classical STIs[16-18]. This may point to a shared regional pattern in microbiota-mediated genital tract infections, potentially shaped by environmental, behavioural, or sociocultural factors. The very low prevalence of *T. vaginalis* observed in the present study (0.1%, 1 case) likely reflects geographic and population-specific factors affecting genital tract microbiology[19]. This study provides new epidemiological data specific to the Northern Cyprus region, where such information has previously been limited.

In summary, this study has shown that genital tract infections in symptomatic women in this population are mainly caused by microbe-associated infections and have a high co-infection tendency compared to classical sexually transmitted infections. The results have indicated that the microbiome-based approach should be integrated into the diagnosis of genital tract infections along with traditional STI screening.

Strengths

This study represents the first comprehensive molecular dataset on genital tract microorganisms from Northern Cyprus. The use of multiplex real-time PCR to simultaneously detect 12 bacterial, viral, fungal, and protozoan organisms allowed the identification of polymicrobial profiles and co-detection patterns that would not have been captured by single-target testing[13].

Limitations

Several limitations should be considered. First, the study population was restricted to symptomatic women, which establishes clinical relevance but limits generalisability to asymptomatic carriers. Second, Ct (cycle-threshold) values were used only to define positivity and were not analysed further, so the data do not allow estimation of microbial burden or load[20]. Third, the cross-sectional design precludes any causal interpretation of the observed co-detection patterns between microorganisms. Additionally, this study relied exclusively on physician-collected vaginal swabs; self-collection methods, shown to be a viable alternative in resource-limited settings, were not evaluated[21]. Finally, symptom duration before sampling was not captured with sufficient precision to allow stratified analysis by symptom chronicity.

CONCLUSION

The analysis of genital tract infections among women with genital symptoms in Northern Cyprus revealed important differences in the epidemiological profile of detected microorganisms, with a marked predominance of microbiota-associated organisms over classical sexually transmitted pathogens, in addition to distinct patterns of co-detection among specific organism groups. *G. vaginalis* (28.2%), *U. parvum* (17.7%), and *C. albicans* (11.6%) accounted for the vast majority of positive cases, while classical sexually transmitted pathogens were *C. trachomatis* (2.3%) and *N. gonorrhoeae* (0.6%). Co-detection of two or more organisms was observed in 49.5% of positive cases, with the strongest associations found between *U. parvum* and *G. vaginalis*, *G. vaginalis* and *C. albicans*, and *M. hominis* and *G. vaginalis* (all $p<0.001$), indicating that polymicrobial patterns were concentrated among microbiota-associated organisms rather than classical pathogens. No significant age difference was found between women positive for microbiota-associated organisms and those positive for classical STI pathogens. These findings highlight the importance of microbiota-focused diagnostic strategies, considering the distinct prevalence and co-detection patterns of each pathogen group.

Approval by the Human Research Ethics Committee

Ethical approval for the study was obtained from the Near East University Ethics Committee (Approval No. YDU/2026/144-2100), and all procedures were conducted in accordance with the Declaration of Helsinki.

Participation of each author

BK: Conceptualization, Data curation, Formal Analysis, Methodology, Writing – original draft, Writing – review & editing. EY: Data curation, Investigation, Writing – review & editing. MCE: Data curation, Writing – review & editing.

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Use of AI in manuscript construction

No AI instruments were used in the preparation of this manuscript.

Data confidentiality

The authors declare having followed the protocols in use at their working centre regarding patients' data publication.

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The funder had no role in the preparation, review, or approval of the manuscript or the decision to submit the manuscript for publication

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