

THE INFLUENCE OF COVID-19 ON THE VAGINAL MICROBIOTA IN WOMEN, CONSIDERING THE WARTIME CONDITIONS IN UKRAINE

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The COVID-19 pandemic caused by SARS-CoV-2 has become an unprecedented challenge, as the virus exerts a systemic impact on the human body, affecting nearly all organ systems. Numerous studies have demonstrated that SARS-CoV-2 infection adversely influences the respiratory, intestinal, and genital microbiota.

The combination of the previous coronavirus infection and the severe stress induced by martial law in Ukraine significantly amplifies disturbances in immune and endocrine regulation, thereby aggravating alterations in the vaginal microbiota.

The aim of our study was to investigate the features of the vaginal microbiota in women who had recovered from the coronavirus infection, taking into account the impact of wartime conditions in Ukraine.

Bacteriological examinations of vaginal samples were performed on 20 women who had recovered from COVID-19 before the onset of full-scale military aggression (Group I) and 20 women infected during martial law (Group II). The control group consisted of 30 healthy women examined before the beginning of hostilities.

Cultures were obtained by the sectoral streaking method on solid nutrient media. Microorganisms were identified according to their cultural, morphological, and biochemical characteristics using an automated bacteriological analyzer Vitek 2 Compact 15 (bioMérieux, France). *Ureaplasma urealyticum* infection was diagnosed by culture on urea–arginine broth LIO-2 (bioMérieux, France). Statistical analysis was performed using Student's t-test ($p < 0.05$).

Microbiological analysis revealed that in Group I, the most frequently isolated species were *S. epidermidis* (hem+), *S. aureus*, *S. haemolyticus*, *S. pyogenes*, and *S. agalactiae*, occurring in 25–30% of samples at concentrations $> \lg 4.0$ CFU/mL. Vaginal colonization by *E. coli* (hem+) (15%) and *Klebsiella* spp. (25%) was also observed, with bacterial loads ranging from $\lg 4.2$ to $\lg 4.8$ CFU/mL. Fungi of the genus *Candida* were isolated in 30% of women ($\lg 4.6$ CFU/mL). *Lactobacillus* spp. were present in 85% of Group I participants, though in 45% of cases their concentration did not exceed $\lg 3.8$ CFU/mL.

In Group II, the spectrum of isolated cocci (phylum *Firmicutes*) was broader. In addition to *S. epidermidis* (hem+) (30%), *S. aureus* (20%), *S. haemolyticus* (30%), *S. agalactiae* (25%), *S. pyogenes* (20%), and *Enterococcus* spp. (35%), *S. lentus* (25%) and *Kocuria kristinae* (30%) were also detected at concentrations of $\lg 4.0$ – $\lg 6.2$ CFU/mL. Among *Enterobacteriaceae*, *E. coli* (30%), *E. coli* (hem+), and *Klebsiella* spp. (35%) predominated, with loads between $\lg 4.3$ and $\lg 5.8$ CFU/mL. Vaginal colonization by *Candida* spp. was more pronounced (45%, $\lg 5.7$ CFU/mL), accompanied by a marked reduction in *Lactobacillus* spp. (65%, $\lg 2.8$ CFU/mL).

Excessive stress is known to disrupt the balance of the vaginal microbiome—particularly through stress hormones such as cortisol—leading to depletion of protective *Lactobacillus* spp. and the proliferation of opportunistic microorganisms.

The incidence of bacterial vaginosis (55%) and nonspecific vaginitis (35%) was higher in Group II compared with Group I (35% and 25%, respectively).

Women who had recovered from the coronavirus infection during the military conflict in Ukraine exhibited a significantly higher frequency (80%) of multi-component (2–4 species) bacterial associations, often in combination with infectious agents such as *Ureaplasma urealyticum* and HSV-1/2, compared with those infected prior to the war (45%).

