Population levels of autochthonous obligate and major representatives of intestinal microbiocenosis and multifunctional according to bacterial significance of genera *Bifidobacterium* and *Lactobaccilus* are considerably decreased, and in 38,70 % of patients these bacteria are totally eliminated. On the other hand, population levels of *Proteus, Klebsiella, Enterobacteria, Citrobacter, Serratia, Hafnia, Pseudomonas*, hemolytic and lactase-negative *Escherichia, Staphylococci* and yeast-like fungi of genus *Candida* are significantly increased. The majority of strains of *Klebsiella, Enterobacter, Psuedomonas, E. coli Hly+, E. coli Lac-, S. aureus* has high adhesive property and shows anti-lysozime activity.

In 17,02 % patients with RA and accompanied dysbiosis of IV stage adaptive-compensatory processes were in stress zone. In most of the patients adaptive index was in training zone, and nobody was in higher activity zone.

So, rheumatoid arthritis is often accompanied with deep changes of intestinal microflora, which are represented by elimination of some part of autochthonous bacteria and contamination with opportunistic microbes. Investigated population levels of intestinal microbiota confirm the presence of developed dysbacteriosis/dysbiosis of I-IV stages.

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SYSTEMIC PERSISTENCE OF OBLIGATE INTRACELLULAR MICROORGANISMS AND INFERTILITY OF II TYPE

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Today every tenth couple in Ukraine is sterile [G.M. Drannyk, 2010]. Family fertility of equally depends on the reproductive potential of a man and a woman. The reason of secondary infertility in a couple is often recurrent or lasting chronic inflammation processes of the reproductive organs. A special value in infertility belongs to continuous persistence of obligate intracellular pathogenic and opportunistic microorganisms: viruses, mycoplasma, ureoplasma, chlamidia, toxoplasma etc. Persistence of intracellular infection in the human organism forms immunodeficiency status that assists in higher colonization of the reproductive organs with opportunistic microorganisms (bacteria, fungi etc.) that finally may result in infertility.

The aim of the investigation was to define the level of persistence of obligate intracellular microorganisms in women suffering from secondary infertility by retrospective diagnostics.

By means of enzyme-linked immunoassay the investigation of blood sera of 67 women (19-34 years old) with infertility of II type it has been conducted. Retrospective diagnostics of persistence infection was made by detection of the titer of specific immunoglobulins (IgM and IgG). Antigens of obligate intracellular microorganisms were detected by solid-phase enzyme-linked immunoassay.

In 35 (52,24 %) women with infertility of II type there is persistence of *Herpes simplex viruses* type 1 and 2, *Cytomegalovirus* in 39 (58,21 %) of patients. These viruses are dominant and persist in all women with infertility of II type. *T. gondii* and *C. trachomatis* occurs frequently. *Rubella virus* and mycoplasma rarely persist in women with infertility of II type.

In the peripheral blood of 67 women with infertility of II type it any high (diagnostic) level of IgM was not detected that testifies the absence of acute inflammation process caused by persistent viruses, chlamidia, toxoplasma etc. Diagnostic titers of IgG in the peripheral blood to viral antigens of herpes group, chlamidia and toxoplasma give the evidence chronic of character of the persistence infection.

In 50 women with infertility of II type it has been found the persistent of one, two or three intracellular microorganisms that are referred to 6 different taxonomic groups. That testifies possible persistence of several taxons in one organism. By quantitive characteristics single causative agent was isolated in 15 women with infertility of II type. In other 35 cases there was persistence of associations of intracellular microorganisms: in 12 cases associations were composed of 2 taxons, in 8 of 3 taxons and in 15 women there was simultaneous persistence of 4 taxons of intracellular microorganisms.

Among the qualitative composition of associations more often (in 19,40 %) associations of different taxons of *Herpesviruses* (*Cytomegalovirus* with *Herpes simplex viruses* type 1 and 2) occurred. Among 4-component associations in 10 women there was the association composed of *Cytomegalovirus, Herpes simplex virus, Rubella virus* and *Toxoplasma* and in 8 (11,94 %) association composed of *Cytomegalovirus, Herpes simplex* and *Chlamidia*.

So, infertility of II type may be accompanied with persistence of obligate intracellular microorganisms, which form associations of 2-4 taxons.

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AUTOCHTHONOUS OBLIGATE AND FACULTATIVE MICROFLORA OF VULVOVAGINAL CONTENT IN WOMEN WITH II TYPE OF INFERTILITY

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Infertility is a dramatic problem of not only a single family but also a social challenge. In the majority of women, infertility is based on the tube-peritoneal form that testifies prior inflammation process of the uterus or uterine adnexa caused by pathogenic or opportunistic microorganisms. Thus, the study of microecological interrelations in vulvovaginal microbiota is necessary for paraclinical diagnostics and formation of therapeutic tactics.

The aim of the study was to investigate vulvovaginal microflora in women with infertility of II type.

With the help of microscopic, bacteriological and mycological methods there has been conducted the survey of vulvovaginal content of 67 women (age: 19-34 years old; average age: 27,33±2,73 years old) with diagnosed II type of infertility. To detect the mechanisms of colonization of the vaginal cavity there has been used the ecological method, which anables to form a concept of coexistence of representatives of ecological system "microbiota – macroorganism (host)" and to trace direction of dynamic changed of vulvovaginal microecology by the destabilization of microbiocenosis. There have been studied indices of species diversity (Wittaker index), species richness (Margalef index), species domination (Berger-Parker and Simpson indexes), and also indices of taxon consistency and frequency of occurrence.

Microbiological investigations it has been conducted to determine taxonomic composition and population level of autochthonous obligate anaerobic bacteria of genera *Bifidobacterium, Propionibacterium*; autochthonous anaerobic opportunistic bacteria of genera *Bacteroides, Peptostreptococcus, Peptococcus, Clostridium, Eubacterium*; facultative anaerobic and aerobic *Enterobacteria (E. coli, E. coli Hly+, E. coli lac-, Proteus, Klebsiella, Enterobacter* etc.) and yeast-like fungi of genus *Candida*. Received results testify that II type of infertility is accompanied with the dynamic changes of taxonomic content of vulvovaginal microbiota in the form of partial elimination of autochthonous obligate *Lactobacteria, Bifidobacteria* and *Propionibacteria*. Against this background there is colonization of biotope with pathogenic and conditionally pathogenic yeast-like fungi of genus *Candida, S. aureus, T. vaginalis*, bacteria of genus *Peptosteptococcus, Enterobacteria (E. coli, K. pneumoniae), E. faecalis, N. gonorrhoeae, B. fragilis* etc. They reach average in biotope constancy index, frequency of occurrence, Wittaker, Margalef, Berger-Parker and Simpson indices.

Pathogenic and opportunistic microbes of vulvovaginal content of women with infertility of II type are generally represented in the form of association, which consist of 2 taxons (35,82 % of women), 3 taxons (40,30 %) or 4 taxons (13,44 %).

So, microbiological investigations of vulvovaginal microflora in women with infertility of II type show changes in taxonomic composition and population level of autochthonous obligate and facultative bacteria with formation of associations of pathogenic and opportunistic microbes.

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STATE OF CAVITARY MICROBIOTA OF COLON IN PATIENTS WITH CHRONIC VIRAL HEPATITIS C

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Hepatitis C is an ubiquitous infectious disease caused by the hepatitis C virus (HCV). Number of chronic carriers of HCV in the world is from 150 millions to 500 millions. And their number is growing and there is no reducing trend. Traditionally, main role in protection of macroorganism against foreign bodies belongs to the enzymatic processes that take place in the liver, and the role of intestinal microbiota in processes of detoxification is ignored or given a secondary role.

To determine taxonomic composition and population level of colon microbiota in patients with chronic hepatitis C.

Content of the colon was studied by bacteriological examination and prior was taken with a sterile spatula from median portions of faeces. Identification of pure cultures of *Enterobacteriaceae* (*Escherichia, Citrobacter, Proteus* and other *Enterobacteriaceae*) was made by W. Ewing, using 30 basic tests recommended by the International Committee of *Enterobacteriaceae*.

By indices of species diversity (Wittaker index), species richness (Margalef index), species domination (Berger-Parker and Simpson indexes), indices of taxon consistency and frequency of occurrence main microbiota of colon in patients with chronic hepatitis C consist of bacteria from genera *Bacteroides, Escherchia, Bifidobacterium, Lactobacillus*, pathogenic and opportunistic *Enterobacteria* of genus *Proteus*, hemolytic *E. coli* (*E. coli Hly* +), opportunistic *P. niger* and anaerobic spore-forming bacteria from genus *Clostridium*.

Additional microbiota of colon in patients with chronic hepatitis C is represented by opportunistic *Staphylococci*, related to them *Peptostreptococi* and yeast-like fungi of genus *Candida*. A characteristic feature of the formation and course of chronic hepatitis C is contamination of colon with pathogenic and opportunistic *Enterobacteria* (*E. coli Hly+*, EPEC, *E. coli Lac-*, *Proteus*, *C. freundii*, *S. marcescens*, *E. aeregenes*), *Peptostreptococci*, *Peptococci*, anaerobic spore-forming *Clostridium* and yeast-like fungi of genus *Candida* (*C. albicans*).

Thus, in patients with chronic hepatitis C there is formation of a trend towards the elimination of (reduction of constancy index by 9,94 % and frequency of occurrence - by 57.14 %) *Bifidobacteria* and *Lactobacilli*, *Eubacteria* (by 3.88 and 2 times, respectively) and growth of persistence of *Peptostreptococci*, *Clostridia*, *Proteus*, *Staphylococci* and yeast-like fungi of genus *Candida*, which creates conditions for contamination and persistence of pathogenic and opportunistic *Enterobacteriaceae* (EPEC, *E. coli Hly+*, *E. coli Lac-*, *Citrobacter*, *Enterobacter*, *Serratia*), *Peptococcus*.

There is formation of distinct reduction of indigenous obligate multifunctional *Bifidobacteria* by 41.28 % (three orders), lactic acid bacteria - by 42.15 % (three orders) in cavity of colon in patients with chronic hepatitis C; increasing concentrations of *Bacteroides* in biotope (by 65.01 %), *Peptostreptococci* - by 57.43 %, *Clostridia* - by 2.03