SESSIONE 12 REVISIONE DEL PERCORSO DIAGNOSTICO PER LE VULVOVAGINITI

VAGINOSI BATTERICHE E VAGINITI AEROBIE

G. Campisciano [1], V. Petix [2], S. Morassut [2], M. Comar [1]

[1]*SSD avanzata di microbiologia traslazionale/ IRCCS Burlo Garofalo-UNITS*

[2]*SSD avanzata microbiologia traslazionale/IRCCS-Burlo Garofalo*

The alterations of vaginal microbioma can cause symptomatic conditions. The most familiar condition is bacterial vaginosis (BV), traditionally characterized as a reduction of vaginal Lactobacilli and overgrowth of facultative anaerobic bacteria. BV is not highly inflammatory and therefore often asymptomatic. Recently, the 16S ribosomal RNA gene phylogenetic analyses, have identified important vaginal bacteria that had previously been missed by culture-based methods. These bacteria included species in the Lactobacillus genus (e.g. L. iners) and bacteria associated with BV (e.g. Atopobium vaginae and BVAB1, 2, 3). Moreover, the concepts of microbiome as a dynamic population and the central role of Lactobacilli spp in orchestrating vaginal bacteria composition and host immune network, has been reported in molecular detail. All women carry Lactobacilli, regardless of their BV status by Nugent or Amsel criteria, leading to the introduction of the Community State Type (CST) classification. L. crispatus is predominantly found in BV-negative women whereas L. iners, and to a lesser extent L. gasseri, is also detected in women with intermediate microbiota or BV. Specifically, women who have a L. crispatus-dominated microbioma at baseline, are less likely to transition to a BV-microbioma than women who have a L. iners-dominated microbioma, showing a two time greater risk. Moreover, G. vaginalis and Prevotella spp. are often found as component of vaginal microflora, but their abundances increased in BV, indicating that bacterial load fluctuation, rather than presence of microorganism, represents an important marker of dysbiosis. Vaginal dysbiosis can also manifest as aerobic vaginitis (AV). It is an equally disruptive infection of the normal vaginal Lactobacillus-dominated microbiota but is characterized by overt inflammation, leukocyte and parabasal cell infiltration and proliferation of enteric aerobic bacteria. Both AV as BV have also been associated with a high risk of STIs acquisition and with women reproductive disease and sequelae.