

The genetic influence on recurrent vulvovaginal candidiasis

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ABSTRACT

Candidiasis is an infection of the vulva that generates one of the main clinical complaints in gynecology: discharge. It can present itself in a recurring way, having a picture with 3 or more episodes in the year. This study aims to analyze the genetic influence on recurrent vulvovaginal candidiasis (CVVR). This is a descriptive study, carried out through a bibliographic review on the PubMed and Scielo platforms. Candidiasis is a fungal infection caused by *Candida albicans* and its clinical presentation progresses with lumpy discharge, like cottage cheese, adhered to the vaginal walls, without odor and with intense vulvar itching, in addition to skin rash, burning, and negative amine test, the pH is acidic and has pseudohyphae under the microscope. The epidemiology is characterized by approximately 75% of women having at least one episode of vulvovaginal candidiasis (CVV) during their lifetime, and about 5-8% of women having episodes of CVVR. In addition, no distinct strain of *C. albicans* has been described in the patients, giving arguments against microbiological factors as a determinant of CVV. Thus, we hypothesize that genetic factors of the host may be an important component that determines susceptibility to RVVC. Recent studies reveal that it may be due to mutations in the CARD9 gene. This gene encodes a protein of the CARD group, which is related to cell apoptosis and the role of the fungal cellular response, activating the immune cascade. Therefore, mutations in the CARD9 gene may be a cause of predisposition to fungal infections in patients without known immunodeficiencies and who present with cases of recurrent vulvovaginal candidiasis.

Keywords: Candidiasis, Vulvovaginal, Recurrent, Genetics.

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