

Genes and cellular processes that contribute to the pathogenesis of RVVC found

June 13 2019, by Bob Yirka



Candida albicans. Credit: Wikipedia.

An international team of researchers has identified some of the genes and cellular processes that contribute to the pathogenesis of recurrent vulvovaginal candidiasis (RVVC)—a *Candida albicans* fungal infection. In their paper published in the journal *Science Translational Medicine*, the group describes their study of the infection in women and what they learned about it.

RVVC infects approximately 8 percent of women worldwide, generally leading to serious discomfort and often pain. The fungus targets the lining of the vagina, which results in inflammation. And while it is very rarely deadly, it is resistant to traditional treatments, which means women in less developed parts of the world are left to suffer. Prior research has shown that some women are more prone to the infection than others, but until now, it was not known why. In this new effort, the researchers undertook a genealogical study of the infection in European women to find out if the reason might be genetic in nature. As part of their effort, the researchers collected [tissue samples](#) from 327 European women—155 who were RVVC patients and 172 controls. All of the samples were sequenced and studied for differences.

The researchers report that they found abnormalities in genes in the RVVC patients that were related to processes involved in metabolism and cell structure. They also found a difference in a gene called SIGLEC15, which is involved in producing regulating effects in certain cells. And they found that one type of immune cell called PMBC had an alteration that results in the release of unusually high amounts of molecules involved in instigating inflammation when exposed to the fungus *C. albicans*. The researchers suggest this indicates that [women](#) with RVVC are more prone to infections because their immune systems respond differently to the fungus, resulting in the inflammation that typically accompanies RVVC infections and the discomfort that results.

The researchers also found that expression by SIGLEC15 increased in mouse models when they were exposed to *C. albicans*. The researchers suggest that more study is required to learn more about how the pathways they identified might be targeted in patients with RVVC to treat their symptoms.

More information: M. Jaeger et al. A systems genomics approach identifies SIGLEC15 as a susceptibility factor in recurrent vulvovaginal

candidiasis, *Science Translational Medicine* (2019). DOI: [10.1126/scitranslmed.aar3558](https://doi.org/10.1126/scitranslmed.aar3558)

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