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SAP Expression in *Candida albicans* Strains Isolated from Mexican Patients with Vaginal Candidosis

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ABSTRACT

To determine the frequency and expression of the ten *SAP* (secreted aspartyl protease) genes in a group of *Candida albicans* strains isolated from Mexican women suffering from vaginal candidosis, a group of 264 women (age 18 - 57 years) with vaginal infections, predisposed by diabetes mellitus or contraceptive consumption, were evaluated. *C. albicans* was identified using PCR to amplify the rRNA internal transcribed spacer regions ITS1 and ITS2. The presence of the *SAP* genes was determined using conventional PCR, and their expression levels were determined using real-time PCR after the *C. albicans* strains had been grown in reconstituted human vaginal epithelium (RHVE). *C. albicans* was identified in the samples from 50 women (18.9%). The genotyping frequencies of the *SAP* genes were as follows: *SAP1*, 94%; *SAP2*, 98%; *SAP3*, 80%; *SAP4*, 100%; *SAP5*, 100%; *SAP6*, 100%; *SAP7*, 63%; *SAP8*, 96%; *SAP9*, 70%; and *SAP10*, 88%. The most frequently expressed genes in the strains harboring all of the genes were *SAP1*, 90%; *SAP2*, 90%; *SAP3*, 90%; *SAP4*, 100%; *SAP5*, 90%; *SAP6*, 90%; *SAP7*, 100%; *SAP8*, 90%; *SAP9*, 100%; and *SAP10*, 100%. *SAP* genes were expressed in the RHVE, suggesting that the Sap proteins play an important role in the pathogenesis of infection.

KEYWORDS

Candida albicans; RHVE; SAP Expression

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