TITLE: IDENTIFICATION AND DIFERENCIATION OF *Candida parapsilosis* COMPLEX SPECIES FROM ARGENTINIAN MEDICAL PATIENTS.

AUTHORS: SOSA¹, V.M.E.; SEÑUK¹; I.A.; ASKENAZI¹, M.V.; MADRASSI¹ L.M.; FONSECA² M.I.; VEDOYA¹, M.C.

INSTITUTION: ¹LABORATORIO DE MICOLOGIA DE LA CÁTEDRA DE MICROBIOLOGÍA, LABORATORIO "DRA. MARTHA MEDVEDEFF. MÓDULO DE BIOQUÍMICA Y FARMACIA, FACULTAD DE CIENCIAS EXACTAS QUÍMICAS Y NATURALES, AV. MARIANO MORENO 1375 – UNAM –3300- POSADAS, MISIONES, ARGENTINA.

²LABORATORIO DE BIOTECNOLOGÍA MOLECULAR, INSTITUTO DE BIOTECNOLOGÍA MISIONES, CONICET, FACULTAD DE CIENCIAS EXACTAS QUÍMICAS Y NATURALES, UNAM, RUTA 12 KM 7,5 – CAMPUS UNIVERSITARIO UNAM – 3304. POSADAS, MISIONES, ARGENTINA.

ABSTRACT:

Candida parapsilosis complex is integrated by three genetically different species called C. parapsilosis sensu stricto, C. orthopsilosis y C. metapsilosis which vary in their virulence and anti-fungal sensibility. To identify this disease agents up to species category is necessary the use of both, classical phenotypical identification trough microbiological assays and molecular identification through genetic approaches. In the context of poor or none knowledge about the main in Argentina, the aid of this work was to verify the existence and identify of any of these three species in a set of at least 40 strains, previously characterized as C. parpsilosis only by microbiological assays. Molecular studies where based on ITS 1- 5.8S- ITS2 region. The primers used in the PCR reaction where ITS 1 and ITS 4. The resulting sequences included both regions ITS1 and ITS 2 partially, and the 5.8S region completely. The sequences where evaluated using Chromaslite 2.01 which allows both visualization and edition of chromatograms. The alignments and phylogenetical analysis where made in Mega 7. The chosen statistical method was maximum likelihood. Results revealed that about 84% of the samples where C. parapsilosis sensu stricto, 8% percent where C. orthopsilosis and 8% where C. metapsilosis. The results of these studies are very important because the right identification of *C. parasilosis* complex species is required to archive efficient treatments, since they differ in susceptibility to drugs profiles.

Keywords: Candida parapsilosis complex, Candida parapsilosis sensu stricto, Candida metapsilosis, Candida orthopsilosis, molecular identification, phylogenetical analysis.

Develop Agency: Secretaría de Ciencia y Tecnología de la Universidad Nacional de Misiones (UNaM). Secretaría de Investigación y Posgrado de la Facultad de Ciencias Exactas Químicas y Naturales. Proyecto Especial16Q594.