

2220 Genetic 'shuffling' of Oral *C. albicans* isolates in HIV disease

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Objectives: Although human immunodeficiency virus (HIV) infected individuals harbour multiple strains of oral *C. albicans* little is known of their micro-evolution over time. Therefore, a prospective study was conducted with 16 HIV-infected ethnic Chinese individuals with (Gp A) and without (Gp B) symptoms of oropharyngeal candidiasis to evaluate the genotype distribution of oral *C. albicans* isolates during HIV disease progression.

Methods: Oral rinse samples were obtained from all individuals and upto five *C. albicans* colonies selected per each visit, during a 12 month period of multiple visits. After identification of isolates using standard mycological methods the genetic similarities of yeast isolates within and between sequential clones of *C. albicans* were assessed by DNA fingerprinting through random amplification of polymorphic DNA (RAPD). The results of RAPD gel profiles were further analysed using the Dendron® 3.0 software programme (Solltech Inc., Oakdale, IA).

Results: RAPD studies revealed the prevalence of upto four different genotypes per individual during the study, with multiple genotypes simultaneously isolated from a single oral rinse. When analysed by Dendron software, yeasts isolated between sequential visits from Gp A (symptomatic) demonstrated a striking level of relatedness compared with Gp B isolates. Genetically identical *C. albicans* strains also formed "loosely" connected sub-clusters spanning more than one visit indicating a genetic "shuffling" that occur in these isolates during disease progression.

Conclusions: Our data point to varying evolutionary genetic profiles in *Candida* associated with symptomatic oral candidiasis and asymptomatic carriage, in HIV disease.

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[Seq #203 - Candida II](#)

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