Biotypes and randomly amplified polymorphic DNA (RAPD) profiles of subgingival Candida albicans isolates in HIV infection

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A group of subgingival isolates of C. albicans recovered from Italian HIV-positive (HIV+) subjects were characterized both phenotypically and genotypically. Phenotyping of the isolates was carried out by a biotyping method based on the enzyme profiles, carbohydrate assimilation patterns and boric acid resistance of the yeasts. Genotyping was performed through randomly amplified polymorphic DNA (RAPD) analysis.

Five biotypes were found among the 29 subgingival C. albicans strains examined. The predominant biotypes were A1R (55.17%), A1S (24.14%), and A2R (13.79%), while the biotypes A11R and A13R were represented by a single isolate each. RAPD profiles identified 15 genotypes among the 29 isolates. Almost every individual harboured his/her own specific isolate and in three out of the six subjects with multiple isolates (two to six each) more than one genotype (two to six) was found.

The biotype distribution we found is consistent with previous reports on C. albicans isolates from other oral sources, whereas the resistance to boric acid was highly frequent in subgingival strains. RAPD analysis showed high genetic heterogeneity within subgingival isolates, also when isolates were phenotypically identical. These findings, obtained from HIV+ subjects living in Southern Italy, may be useful as baseline information on subgingival C. albicans colonization in the Mediterranean area.

KEY WORDS: Candida albicans; biotypes; RAPD; HIV infection; subgingival microflora; Italy