

O0864 **Microsatellite *C. albicans* clusters causing candidaemia in neonates are supported by whole-genome sequencing**

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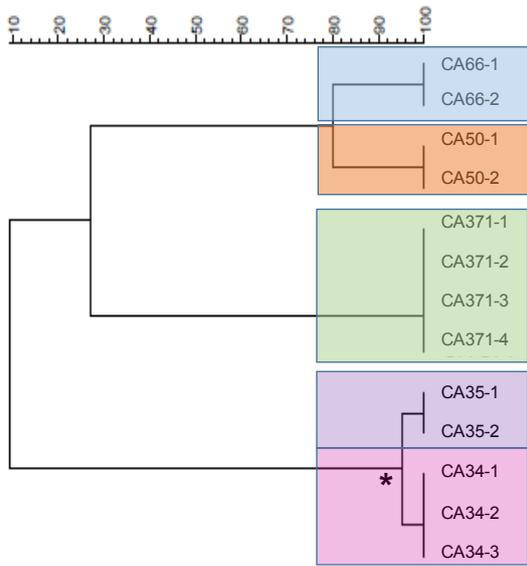
Objectives: We previously found the presence of *C. albicans* clusters (identical isolates infecting ≥ 2 patients) causing candidaemia in patients admitted to the neonatal intensive care unit (NICU) of Gregorio Marañón Hospital (Madrid, Spain). We here performed whole genome sequencing (WGS) to validate these clusters defined by microsatellite markers.

Methods: We retrospectively studied 35 neonates with candidaemia caused by *C. albicans* (one isolate per patient) admitted to the NICU (January 2007-December 2011). All isolates were genotyped by microsatellites and isolates in clusters were submitted to WGS (Illumina-MiSeq, FISABIO, Valencia). We analysed the polymorphisms between the isolates involved in each cluster. A dendrogram was performed considering only those polymorphisms which frequency was higher than 75% (referred to the coverage at that position) using R pvclust package.

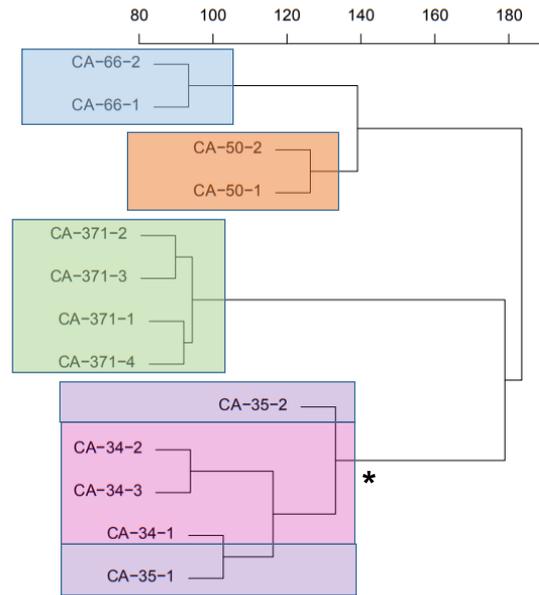
Results: According to microsatellites genotyping, 6 clusters (involving 15 patients) were found; CA34 and CA35 clusters were clonally related (genotypes with differences only in one marker, figure). We obtained reliable WGS results for 13 isolates belonging to 5/6 clusters. WGS revealed polymorphisms in the genome of isolates involved within each of the followings: clusters involving 2 patients [CA35 (124 changes), CA50 (222 changes) and CA66 (235 changes)]; a cluster involving 3 patients [CA34, 517 changes]; a cluster involving 4 patients [CA371, 614 changes]. Overall, intergenic and synonymous genomic changes were found, and minor changes resulted in missense variants. The isolates showing the lowest number of changes within a single cluster were those conforming CA35 genotype, a cluster that involved twin brothers putatively acquiring the infection during delivery. The dendrogram resulting after WGS basically mirrored that obtained using the microsatellite typing.

Conclusions: Whole genome sequencing supported *C. albicans* clusters detected by microsatellites and causing infections in neonates. Since isolates involved in clusters showed genomic differences but no consensus is available for interpretation, future criteria to define the significance of polymorphisms are warranted.

A. Microsatellite dendrogram



B. WGS dendrogram



*Clonally related genotypes