Reviewer’s report

Title: Stability of three Candida albicans microsatellite markers in two French ICU populations supports a lack of nosocomial cross-contamination

Version: 1 Date: 1 June 2006

Reviewer: Jan Schmid

Reviewer’s report:

General

The manuscript describes the use of microsatellite markers to determine the probability of nosocomial transmission, by first assessing genetic diversity of isolates in each of two hospitals and then comparing genotype distribution between the two hospitals. The authors find that the genetic diversity in each of the hospitals does not differ from that determined in the general population in an earlier study and that the genotype distribution does not differ significantly between the two hospitals, as expected if nosocomial transmission would cause hospital-specific groups to be prevalent.

I agree with the overall conclusion that these data provide evidence, albeit indirectly, against nosocomial transmission. However I feel that my suggestions below might strengthen the argument and make the manuscript more accessible.

---------------------------------------------------------------------------------------------------

Major Compulsory Revisions (that the author must respond to before a decision on publication can be reached)

Background. Stating discriminatory power alone is not sufficient given the results the authors have obtained. If microsatellite pattern were highly irreproducible, nosocomial transmission could not be identified, because the same strain would give different patterns when analysed on different occasions. I believe that there is evidence from earlier work that the microsatellite patterns produced by the authors’ method are very reproducible. The authors should state that and/or provide a reproducibility-corrected discriminatory power. I.e. they should state how likely it is that the genotypes of two unrelated isolates are less similar to each other than the genotypes obtained in two repeat analyses of the same isolate (or, if they do not use distances, calculate the probability that two unrelated isolates have a different genotype, corrected for the probability that two analyses of the same isolates will result in a different genotype).

Results. Difference in equipment. The authors describe controls they have undertaken, but a clear statement as to the impact of the two different machines would be useful, i.e. what was the probability that two analyses of the same isolate, each carried out on a different machine, would not result in the same genotype (and/or they could give the reliability-corrected discriminatory power for comparisons involving pairs of genotypes determined on the two different machines).

---------------------------------------------------------------------------------------------------

Minor Essential Revisions (such as missing labels on figures, or the wrong use of a term, which the author can be trusted to correct)

Title. I find the title a bit misleading, because the study does not really assess the stability of markers. Maybe “Uniform distribution of microsatellite alleles” would be an improvement

Abstract. “period of hospitalization between patients” I believe the authors mean “time interval between periods of hospitalization”

Background second line: C. albicans

Methods. I believe that many readers would benefit from a more extensive explanation of the principle underlying multiple correspondence analysis. “Each plot” do the authors mean “each point”?

Results. “whose stay in the ICU differed by” Not clear. Do the authors mean that the patients were
not hospitalized at the same time and that there were 7 to 97 day intervals between the times at which pairs of patients with the same Candida genotype were hospitalised?

Figure1. The version I printed out did not contain the black circle referred to in the legend.

Discretionary Revisions (which the author can choose to ignore)

Results. Description of diversity of isolates on individual patients. It might be worth pointing out that only one colony per anatomical site was analysed and that therefore possible diversity at a given site was undetectable, as would be the presence of low levels of additional strains -possible some sort of a detection threshold could be calculated and shown.

Results. Statistical analyses. I think a more thorough explanation of the multiple correspondence analysis would be useful. Because I do not understand what is involved in this analysis, I am also not sure if it would detect hospital-specific clusters of genetically similar but nonidentical isolates, which would be a sign of nosocomial transmission (if the test will detect such clusters, the authors should state that). In any event, a neighbour-joining tree would do much to convince readers with limited statistical knowledge that the authors’ conclusions are warranted. Also the underlying genetic distances could be used to confirm lack of nosocomial separation between hospitals by nearest-neighbour analysis (Edelmann et al. 2006, Journal of Clinical Microbiology 43: 6164-6166): If there is no nosocomial transmission, isolates from a given hospital should not have isolates from the same hospitals as their closest related counterpart more often than expected by chance.

Figure1. Due to my lack of statistical expertise, I could not understand this figure, and the same may apply to readers of the manuscript. Could the legend be expanded? Also, the version I printed out did not contain the black circle referred to in the legend.

What next?: Accept after minor essential revisions

Level of interest: An article of importance in its field

Quality of written English: Needs some language corrections before being published

Statistical review: No

Declaration of competing interests:

I declare that I have no competing interests.