Reviewer's report

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

Version: 2 Date: 7 August 2006

Reviewer: Jan Schmid

Reviewer's report:

General

The authors have, I believe, misunderstood the main motivation behind my comments. I have no serious doubt that the science is sound, but thought that modifying the manuscript based on my suggestions would strengthen it and make it more accessible. The authors have provided some of the additional information I requested in their letter of response, but if I were to see the revised manuscript for the first time, my suggestions for improvement would be quite similar to those I made when reviewing the original manuscript.

I also note that some typos have to be introduced in the revision, and that the nearest neighbor method is not a phylogenetic method which requires knowledge of the number of events that bring about changes in the microsatellite length.

These are the comments that were not addressed:

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.

Methods. I believe that many readers would benefit from a more extensive explanation of the principle underlying multiple correspondence analysis.

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 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.

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

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

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Discretionary Revisions (which the author can choose to ignore)