

Letters to the Editor

Evidence of Nosocomial *Stenotrophomonas maltophilia* Cross-Infection in a Neonatology Unit Analyzed by Three Molecular Typing Methods

To the Editor:

I read with interest the paper by García de Viedma et al¹ on *Stenotrophomonas maltophilia*. Although not the first evidence of nosocomial cross-transmission of this microorganism, the authors' use of molecular methods was thorough and contributed to what is known about this important organism. We used the molecular techniques contour-clamped homogeneous electric-field gel electrophoresis² and arbitrarily primed polymerase chain reaction³ to compare 64 hospital endemic and neonatal intensive care unit epidemic isolates of *S. maltophilia*. Additionally, we conducted a retrospective chart review to determine risk factors.⁴ Our results showed that, while nosocomial transmission does occur, most isolates are acquired independently as a consequence of risk factors such as prior antibiotic therapy.

Why is it important to know how patients become infected with this organism? So that we can make decisions on how to protect them. What should we do, for example, when two isolates of *S. maltophilia* are found on the same unit? If we assume them to be cross-transmitted, we easily become immersed in a finger-pointing war to see who can be blamed for breaking isolation technique. The doctors blame the nurses, the nurses blame the doctors, and everyone blames housekeeping. If we assume isolates to arise from diverse environmental sources, we fail to isolate properly. What is the infection control clinician to do? Should resources be utilized at all? When molecular data are available,

these questions are relatively easy to answer. Most clinicians, however, must make these decisions without the assistance of this typing technology. Although rarely seen in a modern research paper, the old standby, antibiotic susceptibility patterns, can be useful, even with a multiply resistant organism. We showed antibiograms to have a Simpson's Discriminatory Index of 0.87 when applied to 56 isolates of *S. maltophilia*.² Although analyzing variability in antibiograms becomes extremely complicated when multiple strains are involved, a single pair can often be analyzed efficiently and economically. The data may help a bedside clinician motivate others to expend resources constructively to prevent further infections.

REFERENCES

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The authors reply.

We appreciate Dr VanCouwenberghe's interest in our article. Her group has obtained solid data about *Stenotrophomonas maltophilia* noso-

comial transmission based on molecular analysis. Additionally, they have made some interesting observations, such as the hypothesis that some cases of nosocomial infections by this microorganism could be due to community-acquired isolates after the selective pressure exerted by antibiotic therapy. This would explain the high genetic variability frequently associated with nosocomial *S. maltophilia* isolates.

Regarding her observation that ours is not the first evidence of nosocomial cross-transmission due to this microorganism, we would like to make some comments. Several other authors before us have found molecular similarities among nosocomial *S. maltophilia* isolates. Nevertheless, to our knowledge, none of them have fulfilled the epidemiological conditions that allowed us to assign a role to cross-transmission (meaning patient-to-patient transmission) in the nosocomial outbreak.

The article by VanCouwenberghe et al discusses the notion that the similarities found among the molecular fingerprints of a group of isolates indicate that this microorganism can be transmitted from patient to patient. They support this conclusion because of the chronological overlap found in patients with isolates sharing fingerprints. It is worth noting that, in their study, all *S. maltophilia* isolates were obtained after several days of hospital stay for all patients. In our opinion, this leaves two possible causes for the outbreak, either patient-to-patient transmission or the participation of a unique environmental source.

On the contrary, in our study, the first isolate in the outbreak corresponded to a neonate, transferred from another institution, with an *S. maltophilia* isolate drawn from a culture taken on the very day of admission to the neonatology unit. This strongly rules out the possibility of an environmental source for this neonatal infection. Additionally, all but one of the isolates in the outbreak clustered at 96% similarity