Cross infection of cystic fibrosis patients with *Pseudomonas aeruginosa*

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Cross infection with *Pseudomonas aeruginosa* between patients with CF has been reported. If this problem becomes widespread, there may be a case for genotyping all strains of *P aeruginosa* from CF clinics on a regular basis.

It was once stated that pseudomonads are probably the most abundant and widespread life form on the planet. While this may be debatable, there is no doubt that *Pseudomonas aeruginosa* is one of the most ubiquitous of bacterial species and comprises an almost limitless number of strain populations. Excluding patients with cystic fibrosis (CF), *P aeruginosa* infections—although associated with high mortality in immuno-compromised individuals—are generally manageable. The choice of antimicrobial compounds has not been significantly diminished by resistance, and for most antibiotic groups about 90% of strains remain susceptible.

It has long been accepted that the lungs of patients with CF become colonised with *P aeruginosa* from the natural environment and this is reflected by the wide range of strain types recovered from these patients. Indeed, apart from summer camps and group holiday activities where there was good evidence of acquisition of strains from companions outside the hospital setting. However, the results last year from the Liverpool and Manchester adult CF centres. This prompted a debate as to whether cross infection is widespread in the CF community and led the CF Trust to fund a nationwide survey to determine the extent of the problem. This survey is still in progress but preliminary results suggest that most patients harbour their own strain, although the degree of clustering of strain genotypes varies between centres. For example, in one centre the proportion of patients with strains also found in another individual was 2% of all compared with the proportion with unique strain genotypes varied from 2.2% to 0.5%, suggesting that in the latter cross infection with multiple strains was more of a problem than in the first centre. Conservation of PFGE profiles between some centres was evident which may indicate the spread of these strains outside the hospital setting. However, further analysis of the genome using a DNA-based technique which samples the chromosome randomly at multiple sites (amplified fragment length polymorphism typing) revealed further heterogeneity in these strain populations.

There is therefore evidence to support the occurrence of episodes of cross infection between patients with CF, albeit restricted in scale to most treatment centres. The factors that determine transmissibility are unknown at present but, given the need for *P aeruginosa* to attach firmly to mucosal surfaces in order to establish the colonised state, one could speculate that adherence differences—perhaps in their affinity for mutant CFTR—might be significant. The paper by Jones et al in this issue of *Thorax* suggests that patients who harbour transmissible strains are more difficult to treat than those with unique strains. If these findings are reproduced elsewhere, there may be a case for genotyping all strains of *P aeruginosa* on a regular basis from CF clinics to identify and monitor their distribution in patient populations. This would be a significant undertaking with resource implications. However, the results would also inform the infection control strategy and allow more targeted segregation of patients attending clinics.

*Thorax* 2002;57:921

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**REFERENCES**


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