Cystic fibrosis

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 immunocompromised 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.[1]

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 with CF,[2] cross infection between patients attending hospital as inpatients or outpatients was rightly considered to be rare outside CF siblings. In addition to the acquisition of *P aeruginosa* by previously non-colonised subjects, patients with CF who are already colonised may contract hypertransmissible strains.[3] There were reports of transmission of an antibiotic resistant strain of *P aeruginosa* in the Copenhagen CF centre in the 1980s, but the methods used then for strain definition lacked discriminatory power and perhaps indicated widespread cross infection when there was none. The technique most widely used today for genotyping bacteria is DNA macrorestriction profiling by pulsed field gel electrophoresis (PFGE) which gives an overview of the architecture of 70–80% of the genome. It is widely recognised as the gold standard for strain definition because of its superior discrimination and reproducibility over other methods so far evaluated for *P aeruginosa*.[4]

The first report from Liverpool in 1996 of a ceftazidime resistant strain of *P aeruginosa* defined by PFGE in children with CF served to raise awareness of a potential problem.[5] Other communications followed which documented clusters of single strains in some clinics in Melbourne and Wisconsin and culminated in the reports last year from the Liverpool and Manchester adult CF centres.[3 6] 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 with centres. For example, in one centre the proportion of patients with strains also found in another individual compared with the proportion with unique strain genotypes varied from 2:11 to 5:12, 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 in 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.[7] 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.[8] 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.

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