

Cystic Fibrosis Research News

Title:

Use of *nrdA* gene sequence clustering to estimate the prevalence of different *Achromobacter* species among Cystic Fibrosis patients in the UK

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What was your research question?

Bacteria of the *Achromobacter* group are isolated from 16-23% of people with cystic fibrosis (CF). It is not clear whether they have a negative impact on an individual's health, though some studies suggest they may have. We aimed to examine the proportion and prevalence of different *Achromobacter* species among people with CF in the UK.

Why is this important?

As the UK reference laboratory, our role is to help hospitals to accurately identify bacteria from CF sputum. This is important as it can be correlated with clinical data about an individual's health and may provide information about whether certain species or strains may be linked to poorer outcome or a better capacity for survival in the lung. It also helps doctors to identify strains of bacteria that might be better able to spread between people. Similar studies have been conducted in other countries, but there has not been a recent UK study since the addition of eight new *Achromobacter* species.

What did you do?

We used a single gene (*nrdA*) to determine the prevalence of different *Achromobacter* species among 96 people with CF received from hospitals over 18 months. All *Achromobacter* bacteria have this gene but each species has a slightly different DNA sequence. *nrdA* DNA sequencing therefore allowed us to accurately identify the different species isolated from sputum. We also used a technique called "DNA fingerprinting" to examine the numbers of strains shared between CF individuals in 27 hospitals. This allowed us to estimate whether

Cystic Fibrosis Research News

these strains were likely to have been passed from person to person, or acquired by individuals separately.

What did you find?

We found that the majority (61%) of people with CF had one species, "*Achromobacter xylosoxidans*" isolated from their lungs. We also found that four people attending one CF unit had the same strain of "*Achromobacter insuavis*", and were able to show that this was unlikely to have been passed from person to person as the differences in the DNA sequences between these bacteria were too great. It seemed most likely that this strain was a common type, likely to have been derived from the environment. We also identified three different "clusters", possibly representing new species.

What does this mean and reasons for caution?

Our study has shown that *Achromobacter xylosoxidans* is more common among UK individuals with CF than was found in recent parallel studies in other countries, and that most other species were isolated infrequently. It also showed that within hospitals there was not much evidence of people transmitting strains to each other, suggesting that the infection control measures are generally successful for these bacteria. However, our study only examined specimens over an 18-month period so it is possible that a study examining samples over a longer period of time might reveal trends that were not obvious in this study.

What's next?

As hospitals only send certain bacterial isolates to us, we are also conducting a survey requesting participating hospitals to submit every *Achromobacter* isolate from each individual with CF over a period of six months. This study will provide additional insight into species prevalence and highlight the existence of any common strains.

Original manuscript citation in PubMed

<http://www.ncbi.nlm.nih.gov/pubmed/?term=Use+of+nrdA+gene+sequence+clustering+to+estimate+the+prevalence+of+different+Achromobacter+species+among+Cystic+Fibrosis+patients+in+the+UK>