

The incidence of *Stenotrophomonas maltophilia* infection appears to be on the increase and this is bad news for those affected by cystic fibrosis. Clearly, selective isolation of the organism would be advantageous, as Galina Crawford explains.

S. maltophilia in cystic fibrosis patients

In microbiology, little attention is paid to *Stenotrophomonas maltophilia*, formerly known as *Bacterium bookeri*, *Pseudomonas maltophilia* and *Xanthomonas maltophilia*.^{1,2}

Currently, scientific attention is focused on microorganisms such as methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant enterococci (VRE) or avian viruses responsible for bird influenza. Thus, it is not surprising that little was known about *S. maltophilia* until isolation rates started to increase in the early 1970s.² Since then, studies have reported numerous clinical cases involving *S. maltophilia* infection.

Ubiquitous in nature, *S. maltophilia* is an environmental Gram-negative bacillus with a preference for aqueous environments that are widespread in the home and hospital environments.^{3,4} The respiratory tract of hospitalised patients is the most common site for isolation of *S. maltophilia*, although the majority of patients with *S. maltophilia*-positive respiratory tract cultures are colonised rather than infected with the organism.² The inability to distinguish between colonisation and infection has resulted in the perception that *S. maltophilia* is an organism of limited pathogenicity. So, where does one draw the line between colonisation and infection? At what point does a colonised individual become infected?

Ventilated patients are known to become colonised with *S. maltophilia* but usually this does not manifest as a clinical disease. However, reported isolation of *S. maltophilia* from the sputa of cystic fibrosis (CF) patients has become a cause for concern in the CF community,² as the organism is resistant to many of the antibiotics prescribed in the management of CF (Table 1). Ironically, the primary risk factor associated with colonisation and possible infection by *S. maltophilia* is antibiotic use.⁵

This introduces a number of questions. What is so special about the lungs of CF sufferers? Is *S. maltophilia* a pathogen or non-pathogen? If it is a pathogen, is it a selective pathogen? How virulent is *S. maltophilia*?

Cystic fibrosis is a genetic disorder in which salt and water movement in and out of the cells is abnormally. The most important effect of this abnormality is felt in the lungs. Here, thick mucus builds up, leading to progressive blockage, infection and eventual permanent lung damage.

Two somewhat alarming facts are known about *S. maltophilia*. First, being aquatic in origin, the organism has a tendency to form biofilms, which reportedly increase bacterial resistance to phagocytic killing.⁶ Second, *S. maltophilia* produces DNase enzymes, which hydrolyse DNA to nucleotides. Currently, it is not known whether these

enzymes play a role in damaging human cells; however, they are present in the bacterium's periplasmic space and apparently are not released into the outside environment.

At this point it is worth noting that organisms such as *Staphylococcus aureus* and *Streptococcus pyogenes* produce DNases as virulence factors, and such factors assist invasion by the microorganism. However, little is known about *Stenotrophomonas maltophilia* virulence factors or why it should produce them if it is not an invader.

Unlike the established pathogenic roles of *Pseudomonas aeruginosa* and *Burkholderia cepacia* in the pathogenesis of CF,^{1,5} the significance of *S. maltophilia* remains to be recognised in the clinical context.⁷ In CF patients, *P. aeruginosa* and *B. cepacia* are a major health risk for children and young adults. *P. aeruginosa* and *B. cepacia* infect



Fig 1. *Stenotrophomonas maltophilia* growing on the selective medium.

Table 1. Antimicrobial susceptibility of *S. maltophilia* (ref 5).

	Susceptible (%)	Resistant (%)
Ceftriaxone	2.1	91.7
Ceftazidime	52.9	34.0
Cefepime	27.6	44.7
Piperacillin	8.9	70.7
Piperacillin/tazobactam	20.1	54.7
Ticarcillin/clavulanate	55.7	16.1
Aztreonam	7.7	88.3
Imipenem	0.9	98.7
Meropenem	3.8	92.7
Ciprofloxacin	30.9	39.6
Gatifloxacin	69.6	14.1
Levofloxacin	86.1	6.5
Amikacin	16.8	73.3
Gentamycin	13.9	78.9
Tobramycin	13.7	78.4
Tetracycline	8.6	69.7
Trimethoprim/sulphamethoxazole	95.3	4.7

these patients and this is associated with deterioration in lung function. In contrast, patients with *S. maltophilia* tend to be older, show only mild to moderate change in the lung function, and are commonly co-infected with *P. aeruginosa*.⁸

Culture of the organism from body fluids and proper identification from the microbiology laboratory confirms the presence of *S. maltophilia*. However, as there is no selective medium for isolation of *S. maltophilia*, misidentification can have

important clinical and psychosocial implications. In a survey of 32 *B. cepacia* strains isolated from CF patients and sent to the Canadian Pseudomonas Repository Laboratory, three were identified subsequently as *S. maltophilia*.² This gives rise to concern that it might be *S. maltophilia* rather than *B. cepacia* that causes deterioration in lung function.

Lack of a selective medium for *S. maltophilia* may affect the ability of clinical laboratories to demonstrate the presence of the bacterium in sputum. This is because the organism cannot be identified easily among *Pseudomonas* species growing on the same plate. Pseudomonads grow rapidly and tend to spread slightly, whereas *S. maltophilia* is a slow-growing non-lactose fermentor, with no tendency to spread. Therefore, the presence of pseudomonads can mask the presence of *S. maltophilia*, unless, of course, the former are present in very small numbers and the latter are present in large numbers.

Nonetheless, the reported isolation rate from various studies implies that the frequency of *S. maltophilia* detection is increasing in the CF population. However, an analysis of baseline data from trials suggests that under-reporting of this organism from CF respiratory samples may occur because of inadequate culture techniques.⁷ Thus, it seems that there is a need for a selective medium on which to isolate *S. maltophilia*.

Furthermore, a selective medium for *S. maltophilia* would enable the assessment of how frequently *S. maltophilia* is isolated and allow the amount of growth to be quantified. If *S. maltophilia* is present over extended periods of time then it would suggest the possibility of its involvement in the deterioration of CF patients seen in cases where no other potential pathogens are found.

It is easy to prepare a selective medium for the isolation of *S. maltophilia*, as the

organism is unusually DNase-positive, unlike other Gram-negative bacilli which are DNase-negative. On DNase agar containing 100 mg/L toluidine blue as an indicator, *S. maltophilia* appear as dark blue colonies surrounded by pink-violet zones after three days' incubation at 37°C (Fig 1). All other Gram-negative bacilli, which are DNase-negative, are pale blue (Fig 2). The medium can be made selective for *S. maltophilia* by the addition of antibiotics to which the organism is intrinsically resistant, such as imipenem or meropenem.

There remains much speculation about the pathogenicity of *S. maltophilia* and therefore more research is needed to find out more about this microorganism and its virulence factors. With the growth of the CF at-risk population and the increase in the incidence of *S. maltophilia* infection, failure to recognise this organism as a potential pathogen could lead to many deaths that could be avoided if it was caught and treated in time. ■

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Fig 2. *Escherichia coli*, the negative control.

Galina Crawford is a trainee biomedical scientist at St George's Hospital, London