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Clinical Microbiology 2015: Effects of select chemicals on the opportunistic multidrug-resistant bacterial pathogen, Stenotrophomonas maltophilia and its bio-film- Joanna S Brooke- DePaul University

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Abstract
Stenotrophomonas maltophilia may be a global human opportunist which is related to infections that include those of the tract , bloodstream, soft tissue and bone, eye, heart and brain. S. maltophilia infection is of serious concern in immunocompromised patients and a high deathrate has been reported. This bacterium is found in water, washed foods, plant roots and soils and animals. Hospital-acquired and community-acquired infections of S. maltophilia have been reported. Antimicrobial resistance surveillance monitoring networks worldwide report a steady rise in the number of drug-resistant strains of S. maltophilia recovered from patients. S. maltophilia is resistant to a wide range of antimicrobials, including beta-lactams, fluoroquinolones, aminoglycosides, polymyxins, macrolides, carbapenems, tetracycline's, chloramphenicol and trimethoprim-sulfamethoxazole. Intrinsically drug-resistant strains of S. maltophilia are recovered from environments outside of the clinical setting. New strategies are needed to prevent/challenge S. maltophilia infections. S. maltophilia forms biofilms on medical devices and on living tissues. One of the goals of our laboratory is to study the molecular mechanisms used by this pathogen to form biofilms and subsequently identify suitable targets for treatment strategies to prevent/inhibit S. maltophilia growth, biofilms, and cell survival. We have observed that S. maltophilia is in a position to make biofilms on PVC, polystyrene and glass. We have screened various chemicals and observed that the growth and biofilm formation of S. maltophilia can be hindered. We will report on recent studies that examine the consequences of select chemicals on the expansion, biofilm development and survival of S. maltophilia.

INTRODUCTION

Clinical microbiologists have long recognized the importance of identifying infectious microbial pathogens as the cause of disease in humans. The emergence of new multiple-drug-resistant (MDR) organisms (MDROs) found in nonclinical environments, the increasing reports of community-acquired infections, and the spread of these pathogens in the clinical setting have all underscored the need to monitor these organisms. The increase in reported cases of MDRO-associated infections has resulted in efforts to examine possible sources of these pathogens, assess the current antimicrobial strategies used for the treatment of infections, and elucidate the molecular mechanisms used by these pathogens during infection and disease.

Gram-negative bacterial pathogens have received much attention, as they're often MDROs thanks to multidrug resistance pumps, plasmids harboring antibiotic resistance genes, and various gene transfer mechanisms involved within the acquisition of antimicrobial resistance. Pseudomonas aeruginosa is an example of such an MDRO that causes respiratory infections in patients, particularly those with CF (CF) or those with chronic lung diseases. P. aeruginosa has been reported to survive for months on dry surfaces (180), and it is able to persist and grow in contaminated antimicrobial hand soap containing triclosan, making it a significant issue of concern for hospital staff.

Stenotrophomonas maltophilia is an environmental global emerging Gram-negative MDRO that's most ordinarily related to respiratory infections in humans. It can cause various serious infections in humans. This current review focuses on the strategies used or being developed to treat infections associated with S. maltophilia; the cellular and molecular mechanisms important for its survival, persistence, and pathogenesis; and its multiantibiotic resistance and provides a comparison of clinical and environmental S. maltophilia isolates.

MICROBIOLOGY

Characteristics of S. maltophilia

S. maltophilia is a Gram-negative obligate aerobe that is rod shaped and motile with a few polar flagella. It is able to persist in nutrient-poor aqueous environments. The growth characteristics of S. maltophilia. Standard microbiology reference data currently indicate that S. maltophilia is an oxidase-negative bacterium. Recent data, however, suggest that some S. maltophilia isolates are oxidase positive.

Burdge et al. reported the misidentification of S. maltophilia as Pseudomonas cepacia. In that study, 3 (9%) of 32 clinical isolates were incorrectly identified as being P. cepacia isolates as a result of a delayed reading (3 min instead of within 1 min) of the oxidase test and not holding the tests for DNase

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production 72 h prior to observation of the results. The misinterpretation of those tests has clinical importance, as P. cepacia is a significant pathogen in CF patients.

S. maltophilia has been coisolated with other microorganisms (e.g., Pseudomonas aeruginosa, Burkholderia species, Staphylococcus aureus, methicillin-resistant S. aureus, Acinetobacter baumannii, Escherichia coli, Klebsiella species, Enterobacter species, Enterococcus species, Bacteroides species, Corynebacterium species, and Candida albicans) in samples recovered from patients. The non-fermenting Gram-negative bacteria P. aeruginosa, A. baumannii, and S. maltophilia are all pathogens of the human tract . The reader is directed to recent publications for further information about the relationship of S. maltophilia to P. aeruginosa and A. baumannii. Selective agar media are designed to enhance the isolation of S. maltophilia from polymicrobial cultures.

To improve the isolation of S. maltophilia from CF patient sputum samples, VIA medium, containing vancomycin, imipenem, and amphotericin B, was developed. VIA medium consists of a mannitol agar base with a bromthymol blue (BTB) indicator, 5 mg/liter vancomycin, 32 mg/liter imipenem, and 4 mg/liter amphotericin B. A comparison of S. maltophilia colony counts recovered from sputum samples on VIA medium with counts on bacitracin (10,000 U/liter) chocolate (BC) medium revealed that VIA medium detected a better ($P < 0.0001$) number of S. maltophilia-positive samples than BC medium with an imipenem disk on its surface. VIA medium was particularly useful for the detection of low colony counts (102 to 106 CFU/ml) (77).

Gram-negative selective agar (GNSA) medium was later developed by Moore et al. to detect Gram-negative microflora in CF patient sputa. GNSA medium contains novobiocin (5 mg/liter), cycloheximide (100 mg/liter), amphotericin (2 mg/liter), nisin (48 mg/liter), and crystal violet (2 mg/liter) and detects 6.70 × 103 CFU of S. maltophilia/ml sputum. Other Gram-negative organisms recovered from adult CF patients and ready to grow on this selective medium include P. aeruginosa, Burkholderia cepacia, E. coli, and Alcaligenes xylosoxidans. This medium is beneficial for high-throughput specimen screening, because it is compatible with semiautonumeration using digital image capture and processing with transilluminal white light.

Culture media are developed to differentiate between the bacterial species present in mixed culture samples (e.g., colony color differences between S. maltophilia and P. aeruginosa reflect their different metabolic abilities). The production of acid from maltose but not from glucose by S. maltophilia has been wont to distinguish it from P. aeruginosa, as P. aeruginosa produces acid from glucose and does not use maltose or lactose to a great extent. Colonies of S. maltophilia appear yellow and blue on BTB-containing medium containing maltose and glucose, respectively, in contrast to P. aeruginosa colonies, which appear blue on BTB medium containing maltose and yellow green on medium containing glucose. A selective and differential agar medium, SM2i, contains Mueller-Hinton agar supplemented with maltose, dl-methionine, vancomycin, imipenem, amphotericin B, and bromthymol blue. S. maltophilia colonies are smooth, round, and green, with an green center with a peripheral lighter green area or a dark green center with an green peripheral area surrounded by a blue-green halo. The colony appearance of S. maltophilia is definitely distinguished from those of other Gram-negative bacteria, such as P. aeruginosa, which appears white or colored but very often silver, or E. faecium, which appears minute and colorless. In one study, this medium was successfully used to recover S. maltophilia from water samples and cotton swab samples of cold water taps. Another study using this medium resulted in an increased awareness by health care workers of the importance of strict adherence to hand hygiene measures, the use of point-of-use (POU) water filtration, and regular maintenance of swan-necked faucets with a regimen of descaling, disinfection, and drying.

S. maltophilia could also be related to polymicrobial infections or grow slowly within the host, leading to some difficulty in isolating this bacterium. Various molecular biology techniques have been used to identify different strains of S. maltophilia. PCR amplification of the 16S rRNA gene has been used to detect S. maltophilia in blood samples of patients undergoing chemotherapy for leukemia or myelodysplastic syndrome. That study suggested that PCR analysis of blood would be useful for cases where the bacterial species grows poorly in blood culture medium.

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