

Original Research Article

Achromobacter: an emerging nosocomial pathogen

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ABSTRACT

Background: *Achromobacter* is a ubiquitous, non-fermenting, Gram-negative bacterium that lives in soil and aquatic environments. In recent years, many studies have shown its potential as opportunistic pathogen. It can colonize various items used in hospital and can survive various disinfectants. The infections get complicated due to its vast spectrum of intrinsic and extrinsic resistance to antimicrobial agents and disinfectants. *Achromobacter* spp. is an emerging pathogen and is becoming a reservoir for horizontal genetic transfer elements involved in spreading antibiotic resistance. This study was conducted to assess the extent of the *Achromobacter* related infection in our hospital setting and to set a baseline for future studies.

Methods: This study was conducted over a period of one year (January to December 2018) in our tertiary care hospital. All specimens submitted for aerobic culture and sensitivity were analyzed and the bacterial identification and antibiotic sensitivity of the isolates was carried out using automated method (Vitek 2 Compact, bioMerieux).

Results: *Achromobacter* species was reported from 0.46% (63/13831) specimens, 40% of them were isolated from suction tips. *Achromobacter denitrificans* amounted for 47/63 (74.6%) while *Achromobacter xylosoxidans* was identified in 16/63 (25.4%).

Conclusions: Studying the organisms in order to observe their changing trends with respect to their gaining pathogenic potential will help in designing the approach to their treatment for future.

Keywords: *Achromobacter denitrificans*, *Achromobacter xylosoxidans*, Antimicrobial drug resistance, Emerging pathogens, Nonfermenter, Nosocomial infection

INTRODUCTION

Achromobacter is a part of the gastrointestinal and respiratory tracts of some people. It has been recovered from aquatic surroundings in hospitals such as ventilators, humidifiers, sterile saline, intravenous fluids and irrigation and dialysis solutions. They have also been recovered from infant formula, children's soap bubbles, well water and swimming pools. These organisms survive many disinfectants and have been cultured from chlorhexidine, 1% eosin, alcohol and quaternary amine-containing compounds.^{1,2}

The organism was first isolated from purulent ear discharges of seven patients with chronic otitis media and the name *Achromobacter xylosoxidans* was proposed and described by Yabuuchi and Oyama in 1971, reclassified to the *Alcaligenes* genus, and more recently placed back in the *Achromobacter* genus.^{3,4}

Previously termed *Alcaligenes xylosoxidans*, the name *Achromobacter xylosoxidans* was formalized since 1998 and now encompasses two different subspecies (*A. xylosoxidans* subsp. *xylosoxidans* and *A. xylosoxidans* subsp. *denitrificans*).⁵

The organism is a motile, gram-negative asporogenous, straight rods with peritrichous flagella that produces glistening, smooth pinpoint colonies after overnight incubation at 37°C. The organism grows well on Mac-Conkey agar and is citrate, oxidase, and catalase test positive. Glucose is oxidized slowly, as is xylose, whereas other carbohydrates are not. Tests for urease, lysine decarboxylase, and arginine dihydrolase are negative.⁶

Most cases in the literature are described in patients with some form of immunosuppression, usually haematological malignancies. Primary bacteraemia represents the most common clinical presentation.^{7,8} Published reports and literature reviews have demonstrated *Achromobacter* pneumonia, bacteremia, urinary tract infections, gastrointestinal infections, endocarditis, meningitis, abscesses, osteomyelitis prosthetic valve endocarditis, peritonitis and ophthalmic disease.^{1,8-12}

Originally considered commensals, they are increasingly being recognised as important, although rare, nosocomial pathogens. Outbreaks of infection have been reported in hospitals including neonatal intensive care units. Nosocomial infections occur in association with immune suppression, malignancies, HIV infection and neonates. *Achromobacter xylosoxidans* bacteraemia is almost always a nosocomial infection.^{13,14} Reported case-fatality rates have varied from 3% for primary or catheter-associated bacteremia to 80% for neonatal infection.⁷

Infections caused by *Achromobacter* are complicated by the fact that the organisms carry both intrinsic and acquired multidrug resistance.^{15,16} They do possess intrinsic characteristics that allow survival in adverse environmental conditions that would otherwise limit distribution. Such characteristics include a large genome rich in C-G sequences, intrinsic resistance to arsenic and other toxic metals, and the ability to degrade aromatic compounds.¹⁶⁻¹⁸

These characteristics allow *Achromobacter* species to survive and flourish in environments inhospitable to other organisms and may help explain why the genus is increasingly found in the nosocomial setting. *Achromobacter* spp. is an emerging pathogen and is becoming a reservoir for horizontal genetic transfer elements involved in spreading antibiotic resistance.¹⁵ Hospital-acquired pneumonia (HAP) due to *Achromobacter* spp. has emerged as a substantial concern in recent years. Pulmonary involvement has been frequently reported in cases with underlying disease, especially in cystic fibrosis (CF).^{16,17,19,20}

Achromobacter strains are frequently resistant to aminoglycosides, ampicillin, first- and second-generation cephalosporins, chloramphenicol, and fluoroquinolones but are usually susceptible to anti-Pseudomonas third-generation cephalosporins, imipenem, and trimethoprim-

sulfamethoxazole.^{1,21,22} However, this frequency may be underestimated because this organism can be confused with *Pseudomonas aeruginosa*, *Burkholderia cepacia* complex (BCC), and *Stenotrophomonas maltophilia*, particularly in laboratories that are not specialized for evaluation.²³

The factors that predispose patients to colonization/infection have not been fully determined. Frequent exposure to antibiotics, particularly during treatment for chronic colonization with *P. aeruginosa*, may favor the emergence of this and other Gram-negative, multidrug-resistant bacteria.^{24,25}

Achromobacter spp. typically is resistant to a large number of antibiotics therefore antimicrobial susceptibility profile for each case should be taken into account for determining the therapy.²⁶ *Achromobacter* species had been historically responsive to antipseudomonal agents with various success rates depending on site of infection and complexity of the cases.²⁷

In addition, current data on this uncommon entity is mostly limited to very small series or single case reports. The present study was conducted to analyse the profile of *Achromobacter* species isolated from our hospital.

METHODS

This study was conducted over a period of one year (January to December 2018) in our tertiary care hospital. A total of 13831 specimens were submitted to the Microbiology lab of this hospital for bacterial aerobic culture and sensitivity. The decision to take samples for microbiological culture and the selection of type of samples was made by the physicians.

Inclusion criteria

All organisms identified by preliminary tests and automated method as *Achromobacter* and with complete drug susceptibility pattern were included in this study.

Exclusion criteria

All *Achromobacter* species identified by automated method but with incomplete antimicrobial susceptibility pattern and *Achromobacter* species identified beyond 2018 were excluded from the study.

Authors used commercial blood culture bottles (BacT/ALERT, bioMérieux) to assess bacteremia as well as for all sterile body fluids (CSF, pleural fluid, peritoneal fluid, synovial fluid, ant and posterior chamber fluid) and disposable sterile cotton swabs (PW003, Sterile Hiculture device, HiMedia) for superficial infections, urine samples and other specimens were collected in sterile single-use universal containers for microbiological culture.

After preliminary tests like Gram staining, motility, oxidase test and catalase test on the growth, standard culture based automated methods were used for identification of the organism and antimicrobial susceptibility testing (Vitek2 Compact, bioMérieux) and reported according to Clinical Laboratory Standards Institute (CLSI) guidelines.

The data was imported into a Microsoft Excel spreadsheet file and all important patient identifiers were properly and securely discarded. The information regarding organism isolated, phenotypic drug resistance and MIC values against a variety of antibiotics was collected from Vitek 2 Compact database.

RESULTS

A total of 13831 specimens were submitted to microbiology lab for aerobic bacterial culture and sensitivity. Growth of *Achromobacter* species was reported from 63 specimens i.e., 0.46%.

Achromobacter denitrificans amounted for 47/63 (74.6%) while *Achromobacter xylosoxidans* was identified in 16/63 (25.4%). Maximum isolates belonged to ICUs (71%) followed by High Dependency Units and various wards as depicted in Figure 1.

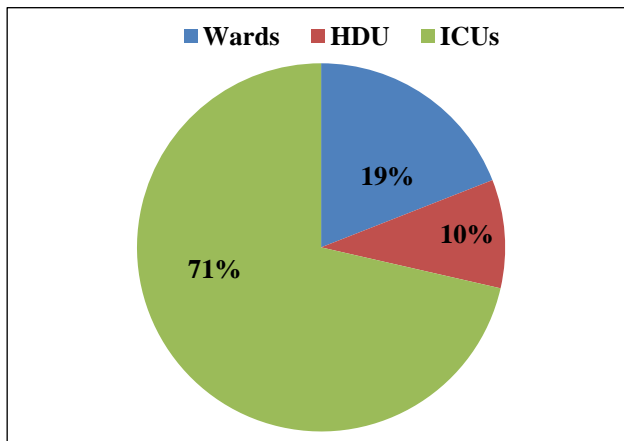


Figure 1: Location wise distribution of *Achromobacter* isolates.

Maximum isolates of *Achromobacter* species were cultured from Suction tips 40% (25/63) followed by Central Venous P tips 35% (22/63) while only 1/63 isolate was from CSF. (Figure 2).

Antimicrobial resistance of the isolates of *Achromobacter* were analysed based on the MICs against antipseudomonal antibiotics.

Resistance to reserved drugs like colistin is observed to be 7.94% while higher resistance is observed against levofloxacin (12.7%) and meropenem (11.11%) (Figure 3).

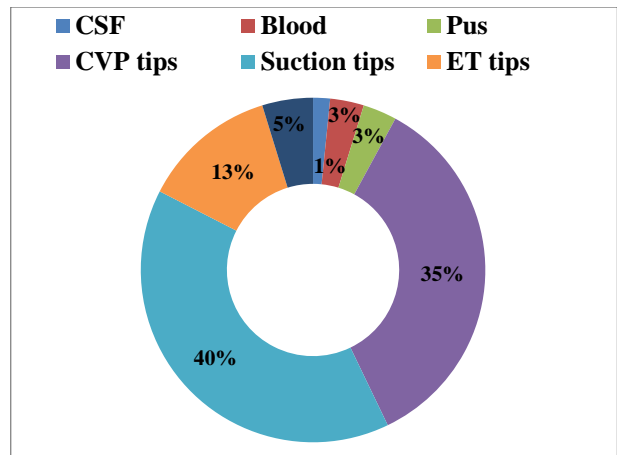


Figure 2: Specimen wise distribution of *Achromobacter* isolates.

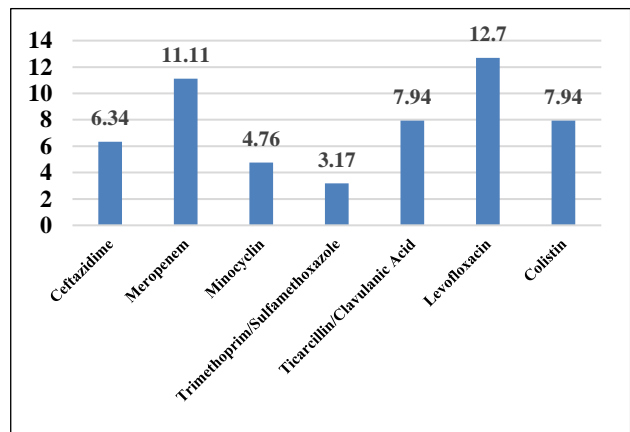


Figure 3: Resistance pattern of isolates of *Achromobacter* species (in percentage).

DISCUSSION

Lately, *Achromobacter* species are being isolated and being reported as pathogens from labs in developing countries like India also.^{2,10} The main reason behind the identification and reporting of *Achromobacter* species is the utilization of automated methods of identification and sensitivity. In the past with manual identification there was a possibility of misidentification. The frequency may be underestimated because this organism can be confused with *Pseudomonas aeruginosa*, bacteria from the *Burkholderia cepacia* complex (BCC), and *Stenotrophomonas maltophilia*, particularly in laboratories that are not specialized for evaluation.²³

Achromobacter spp. typically is resistant to a large number of antibiotics, including ampicillin, aztreonam, aminoglycosides, first- and second-generation cephalosporins, tetracyclines and rifampicin. Most are sensitive in vitro to trimethoprim-sulphamethoxazole, imipenem and in some cases to ceftazidime, piperacillin and cefoperazone. Antimicrobial susceptibility profile for

each case should be taken into account for determining the therapy.²⁶

The factors that predispose patients to colonization/infection have not been fully determined. Frequent exposure to antibiotics, particularly during treatment for chronic colonization with *P. aeruginosa*, may favor the emergence of this and other Gram-negative, multidrug-resistant bacteria.^{28,29}

CONCLUSION

With the advent of automated methods and their full utilization, it is important to keep a close watch on this emerging nosocomial pathogen. In this hospital setting a regular analysis would help in deciding the changes in treatment modalities and preventive measures required as the time goes by, based on the pattern of antimicrobial drug resistance.

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