Case Study

COMMUNITY ACQUIRED STENOTROPHOMONAS MALTOPHILIA CAUSING EMPYEMA IN AN ADULT WITH HIV

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ABSTRACT

Introduction: *Stenotrophomonas maltophilia (S. maltophilia)* is multidrug resistant (MDR) organism usually associated with hospital acquired infections. Here we report a rare case of community acquired *S. maltophilia* empyema in a human immunodeficiency virus (HIV) positive patient.

Case Report: A 54 year old male presented with cough, breathlessness and chest pain for one month. On investigation, radiological picture was suggestive of massive right empyema. Pleural fluid culture grew *S. maltophilia* repeatedly which was treated with cotrimoxazole and levofloxacin based on antibiogram. Following improvement patient was discharged on anti-retro viral and anti-tubercular treatment.

Conclusion: Community acquired invasive *S. maltophilia* infections should be kept as differential diagnosis in immunocompromised patients. Being MDR, appropriate microbiological identification and susceptibility play an important role in treatment and outcome of these patients.

Key Words: *Stenotrophomonas,* immunocompromised, empyema, HIV

INTRODUCTION

Stenotrophomonas maltophilia (S. maltophilia) is an environmental emerging pathogen which is usually multi-drug-resistant (MDR). *S. maltophilia* is generally associated with hospital acquired infections in patients having co-morbidities or immune suppression. It may cause severe infections including pneumonia, endocarditis, meningitis, urinary tract infection, soft tissue and bone infections, peritonitis, bacteremia, multiple organ dysfunction. It is associated with substantial morbidity and mortality particularly in elderly patients with serious respiratory involvement requiring ventilatory support. However, community-acquired infections have been rarely reported. [(1)] These infections are difficult to treat as it is intrinsically resistant to many drugs including β-lactams.[(2)] Here we report a case of community acquired pneumonia with empyema caused by *S. maltophilia* in an HIV positive patient.

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CASE REPORT

A 54-year-old man presented with history of fever, breathlessness, chest pain and productive cough for one month. There was no past history of any chronic illness. General physical examination was unremarkable. On chest examination there were decreased chest movements on right side with stony dull note on percussion and absent breath sounds in right infra-mammary, infra-axillary, inter and infra scapular areas. Rest of the systemic examination was normal. On admission, white blood cell count and absolute neutrophil count were both normal (6.3x 10^3/μL, 4800/μL). An initial chest roentgenogram (Figure 1) showed massive right sided pleural effusion. Ultrasonography also revealed moderate right sided pleural effusion with multiple dense internal echoes suggestive of right loculated empyema. The patient tested positive for human immunodeficiency virus (HIV) infection as per National Aids Control Organization (NACO) guidelines.[(3)] CD4 count was 165/ mL. Antiretroviral therapy (ART) was withheld for two weeks till opportunistic infections were treated.[(3)]

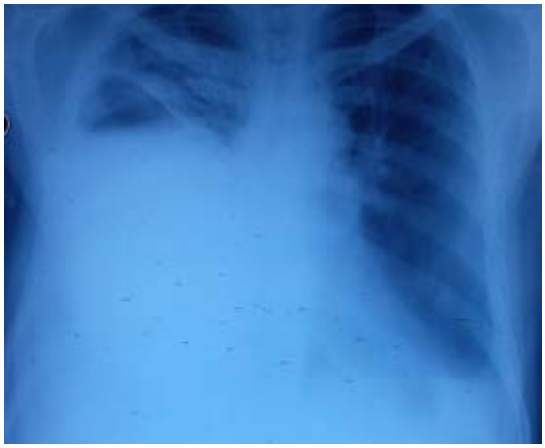

Figure 1. Massive right sided pleural effusion.

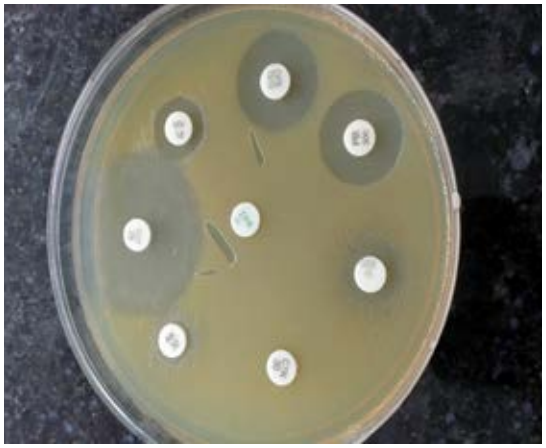

Figure 2. Antibiotic susceptibility by Kirby Bauer method

Empiric treatment with intravenous piperacillin-tazobactam, clindamycin and oral anti-tubercular drugs (ATT) was started along with co-trimoxazole prophylaxis in view of immunocompromised status. Inter-costal chest tube drainage was inserted in right 5th inter-costal space midaxillary line, which drained around one liter of thick pus. This specimen was sent for microbiological examination. Gram stain revealed many pus cells and gram negative bacilli, suggestive of pyogenic etiology. Smear for acid fast bacilli, Gene Xpert for *M. tuberculosis* complex, were negative. Pleural fluid culture grew yellow pigmented, non fermenting smooth colonies. The bacteria were gram negative and motile. Biochemical tests including catalase, citrate utilization, esculin hydrolysis were positive; oxidase, Indole, Methyl red, Voges-Proskauer reaction, Hydrogen sulfide, urea hydrolysis were negative. Based on the above findings, isolate was identified as *Stenotrophomonas maltophilia* and further confirmed by Microscan Autoscan-4 (Beckman Coulter semi automated bacterial identification and susceptibility system). Antibiotic susceptibility by Kirby Bauer method showed sensitivity to cotrimoxazole, levofloxacin, ciprofloxacin, cefoperazone-sulbactam and polymyxin-B but resistance to imipenem, gentamicin, amikacin, ceftriaxone and piperacillin (Figure 2). Following the AST report, cotrimoxazole was increased to therapeutic dose of 1500 mg once a day. The patient started improving clinically. The follow-up chest X-ray showed resolution and right lung expansion; computed tomography scan (CT scan) at day 15 showed only mild pleural collection with thick enhancing right parietal and visceral pleura associated with multiple air foci. Subpleural fibrotic streaks in right lower and right middle lung lobes was seen along with patchy areas of ground glass attenuation with ill defined nodular lesions in right upper lung lobes (Figure 3). The chest drain output decreased and repeat culture of fluid at this time also revealed growth of *S.maltophilia.* Hence intravenous levofloxacin 500mg was also added. There was further clinical and radiological improvement; drain was removed on day 20 and patient was discharged from the hospital. At discharge, patient was advised to continue cotrimoxazole for another 1 week, ATT and ART including fixed dose combination

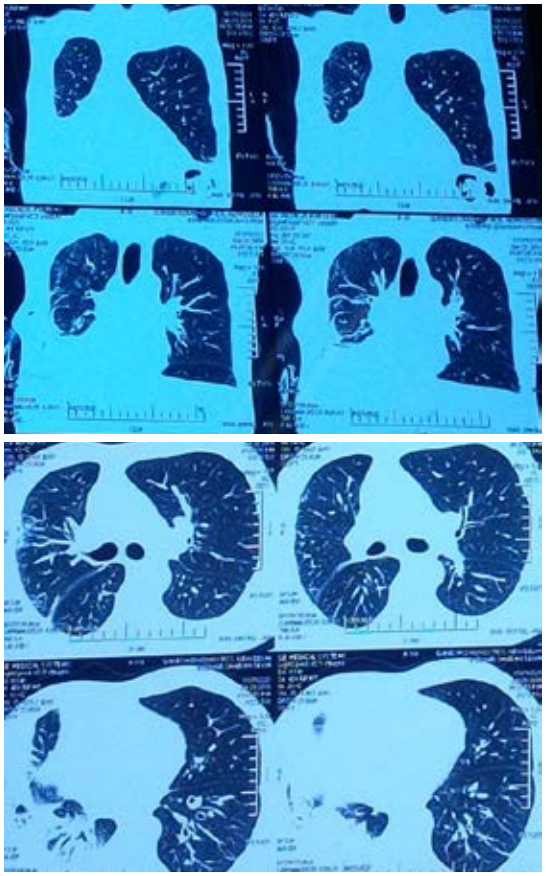

Figure 3. CT scan on day 15 of admission in hospital.

of tenofovir, lamivudine and efavirenz and was advised for further follow up at the ART and directly observed treatment short course (DOTS) centre.

DISCUSSION

S. maltophilia is an aerobic, motile, gram-negative multiple-drug-resistant organism.[4] It is an emerging pathogen which is associated with hospital-acquired infections, rarely community-acquired.[5] Our isolate was community acquired as it was isolated from pleural fluid culture from a patient with no previous history of hospitalization. These infections in community settings usually have an associated co-morbid conditions like prior hospitalization, chronic obstructive pulmonary disease (COPD), malignancy, HIV infection, or other immune suppressive conditions, trauma, prior antibiotic use.[1] It mostly causes pulmonary infections though it has also been known to cause eye, heart, brain, bone & joints and urinary tract infections. [1]

Possible community sources of infection may be water supply systems as these bacteria have been isolated from drains, water pipes, faucets, sponges, etc where they can form biofilms.[1] Biofilm formation is enhanced by *S. maltophilia* fimbriae 1 (SMF-1). Other virulence factors are lipopolysaccharides, diffusible signal factor system, flagella, extracellular hydrolytic enzymes like DNase, RNase, proteases, lipases, esterase, and fibrolysin which are encoded by *S. maltophilia* K279a genome. It can also transfer resistance genes to and fro from other MDR bacteria like *Pseudomonas, Sphingomonas, Serratia, Citrobacter, Proteus, Klebsiella* etc. Global warming is implicated with higher infection rate as the bacterial growth increases in environment which in turn increases the cell concentration leading to more chances of gene exchanges.[1]

In hospitals it has been isolated from tap water, endoscopes, suction tubings.[1] Risk factors for acquisition of this infection include HIV, malignancy, other immune suppressive conditions, COPD, central venous catheterization etc.[6] Our isolate was resistant to many drugs including carbapenems. Patients receiving long term carabapenem pose an increased threat to *S. maltophilia* infection to which it is inherently resistant[5]. Mechanism of drug resistance in *S. maltophilia* include chromosomal or plasmid encoded β lactamases, mobile elements; Class 1 integrons & insertion element common region (ISCR) elements responsible for resistance to cotrimoxazole; phosphoglucomutase (SpgM)-resistance to ceftazidime, gentamicin, nalidixic acid, polymyxin B and E, piperacillin-tazobactam, ticarcillin-clavulanic acid and vancomycin. Other mechanisms include efflux pumps, reduction in outer membrane permeability; modification of antibiotics; mutations of topoisomerase and gyrase genes. Genes for intrinsic resistance has been acquired in natural environment thus indicating the non-clinical settings for resistance transfer.

Cotrimoxazole is considered drug of choice when found to be sensitive, though the sensitivity ranges from >90% to <35%. [7,8] Alternatives being fluoroquinolones,colistin or tigecycline. [1] Our patient improved on therapeutic dose combination of cotrimoxazole with levofloxacin. In vitro pharmacodynamics studies on *S. maltophilia* have proven that combination of TMP-SMX with ciprofloxacin, ceftazidime, or tobramycin demonstrates higher bactericidal efficacy ($P < 0.0001$) than co-trimoxazole alone. [9] *S. maltophilia* being resistant to many drugs like β-lactam antibiotics including cephalosporins and carbapenems, aminoglycosides, macrolides, fluoroquinolones, chloramphenicol, tetracyclines, even TMP-SMX and polymyxins, pose difficulty in treatment leading to treatment failure or even death.[2]

Patient presenting with massive pleural effusion and being HIV positive leads to presumptive diagnosis of tuberculosis in countries like India with high tuberculosis prevalence. In turn, pulmonary tuberculosis is an independent risk factor for MDR organism co-infection like *Stenotrophomonas, Pseudomonas, Enterobacter, Proteus* etc.[10] This patient was also treated for *Mycobacterium tuberculosis* based on clinical diagnosis of Koch's disease along with *S. maltophilia* co-infection.

CONCLUSION

Community acquired invasive *S. maltophilia* infections should be kept as differential diagnosis in immune compromised patients. Being MDR, appropriate microbiological identification and susceptibility testing play an important role in treatment and outcome of these patients.

ACKNOWLEDGEMENT

We sincerely thanks our laboratory staff for their expert technical support.

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