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Clinical Profile of opportunistic bacterial and fungal pathogens in HIV/AIDS patients of Thuraiyur region of Tiruchirappalli District, Tamil Nadu, India

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Abstract

Human Immunodeficiency Virus (HIV) infection is leading to AIDS and it is a major threat to human beings. The HIV is not an only thereat but due to associated opportunistic pathogens the major cause of morbidity and mortality is occurring in such patients. Twenty five positive symptomatic patients who are coming to ART centre of Thuraiyur region, Government Hospital of Trichy were included in the present study for finding the profile of opportunistic bacterial and fungal pathogens. Hundred biosamples were collected from 25 clinically symptomatic HIV+ patients during the month of June - December, 2014.Blood serum, sputum, oral swabs and urine samples were collected with taking all aseptic precautions. A total of 73 isolates were identified from 25 HIV infected patients. Among them, seventeen types of bacterial and four types of fungal species were identified. The predominant bacteria isolated in the study were *Escherichia coli* RV412 and *Klebsiella pneumonia* DSM and Staphylococcus haemolyticus CHB. Similarly in fungal species the most predominant fungus is *Candida tropicalis* followed by *Candida glabrata*

Introduction

Human Immunodeficiency Virus (HIV) is one of the major threats to mankind. HIV infection is a global pandemic with numerous cases reported from many countries (Fauci and Lane, 2008). Globally these were 35.3 million people infected with HIV in 2012. In India 0.27% as reported in 2011, that is about 2.5 million of people are survive with this virus (Dabla *et al.*, 2015). A gradual increase of HIV/AIDS cases were reported in resource poor countries like India despite the many successful AIDS control programmes. This could be attributed to the decreased level of immunity and leads to progressive fall in the level of CD cells (<200/µl

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to $<50 / \mu$ l). Thus, these patients become prone to various opportunistic pathogens, particularly those caused by bacteria and fungi (Gradon,*et al.*, 1992; Jain, *et al.*, 2014). The major threat to their life is not by the virus but due to these opportunistic pathogens and associated complications. The clinical microbial profile of AIDS in India is different from the other countries especially in the developed world, since our environment reported with high prevalence of many infectious diseases (Kaur *et al.*, 2016). Hence, early identification of such pathogena and rapid treatments are very much essential to manage the HIV/AIDS cases. Considering this fact, the present study was carried out to find out the opportunistic bacterial and fungal associated with

HIV/AIDS patients of the Thuraiyur region of Tiruchirappalli District of Tamil nadu.

Materials and Methods

The present investigation was carried out on 25 HIV seropositive patients at the Department of Botany, St. Joseph S College, Trichy, Tamil Nadu, India. Their HIV status was confirmed by two ELISA/simple tests performed in the ART centre itself. Necessary pre and post-test counseling of the patients was carried out and relevant data was collected. All the samples were collected taking all aseptic precautions. The collected biosamples were inoculated on Mac conkey agar, blood agar, chocolate agar, Bismuth sulphate agar, Candida agar and Hi chrome agar. The isolates obtained were characterized by their colony characters, staining morphology and biochemical characters as per standard techniques (Collee et al., 1989) the oral swabs and sputum were also cultured on potato dextrose agar. The growth obtained was identified by standard procedures (Chakrabarti et al., 1998)

Results and Discussion

The morphology and staining results revealed that 17 types of bacterial species which were identified. Among the identified pathogens, Escherichia coli RV412, Escherichia coli DH5 alpha, Klebsiella pneumonia DSM, Klebsiella pneumonia CHB, Enterobacter cloacae DSM, Enterobacter cloacae MB, Enterobacter faecalis DSM, Enterobacter faecalis CHB, Pseudomonas lutea, and Citrobacter sedlakii were Gram negative rods. Staphylococcus haemolyticus DSM, Staphylococcus haemolyticus CHB Staphylococcus saprophyticus DSM, Staphylococcus hominis DSM and Staphylococcus hominis MB were gram positive cocci. Corynebacterium aurimucosum is gram positive rod. Corynebacterium Klebsiella aurimucosum, pneumoniae, Citrobacter sedlakii, **Staphylococcus Staphylococcus** aureus. epidermidis, *Staphylococcus* saprophyticus and Staphylococcus haemolyticus were non-motile and others were motile bacteria.

The biochemical tests revealed that all the bacterial pathogens were catalase positive except, *Enterobacter cloacae* DSM, *Enterobacter cloacae* MB, *Enterobacter faecalis* DSM, *Enterobacter faecalis* CHB, *Pseudomonas lutea and Staphylococcus haemolyticus DSM*, Staphylococcus saprophyticus DSM, Staphylococcus hominis DSM and

Staphylococcus hominis MB showed positive result for oxidase test. Escherichia coli RV412, Escherichia coli DH5 alpha, Klebsiella pneumonia DSM, Klebsiella pneumonia CHB gave positive results to indole test. Escherichia coli RV412, Escherichia coli DH5 alpha, Klebsiella pneumonia DSM, Klebsiella pneumonia CHB Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus saprophyticus, Citrobacter sedlakii and Staphylococcus haemolyticus showed positive results to MR test and Klebsiella pneumonia DSM, Klebsiella pneumonia CHB, Staphylococcus haemolyticus DSM, Staphylococcus haemolyticus CHB Staphylococcus saprophyticus DSM, Staphylococcus hominis DSM and Staphylococcus hominis MB, Enterobacter cloacae DSM, Enterobacter cloacae MB, Enterobacter faecalis DSM and, Enterobacter faecalis CHB gave positive results to VP test. and Escherichia coli RV412, Escherichia coli DH5 alpha, Staphylococcus haemolyticus DSM, Staphylococcus haemolyticus CHB Staphylococcus saprophyticus DSM, Staphylococcus hominis DSM and Staphylococcus hominis MB were citrate negative and others are citrate positive. For urease test, Klebsiella pneumonia DSM, Klebsiella pneumoniae CHB, Pseudomonas lutea Staphylococcus haemolyticus DSM, Staphylococcus haemolyticus CHB, Staphylococcus saprophyticus DSM, Staphylococcus hominis DSM and Staphylococcus hominis MB were positive. Most of the bacteria showed positive results for carbohydrate fermentation. All the bacteria showed both the acid and gas production where as Staphylococcus aureus and pseudomonas lutea showed acid production only. In some cases the samples were identified through MALDITOF

A total of 73 isolates were identified from 25 HIV infected patients. Out of 50 bacterial isolates, seventeen types of bacterial species were isolated. The predominant bacteria isolated in the study were Escherichia coli RV412 and Klebsiella pnemoniae (11.1%), Escherichia coli DH5 alpha, Enterobacter cloacae MB, Klebsiella pneumonia DSM and Staphylococcus haemolyticus CHB (7.4%), where as other organisms like Enterobacter cloacae DSM, Citrobacter sedlakii, Staphylococcus haemolyticus DSM, Staphylococcus saprophyticus DSM, Pseudomonas lutea, Enterobacter faecalis DSM, Staphylococcus hominis DSM, Staphylococcus hominis MB, Corynebacterium aurimucosum, Lechlerchia adecarboxylate and Enterobacter faecalis CHB were found to be very low such as 3.7%. Out of all pathogens isolated bacterial isolates constituted 92.6%. Among the isolated bacterial pathogens 52% of bacteria responsible for urinary tract infections and 24% cause respiratory

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infections and 24% causes blood borne infections. Among HIV positive patients, the most prevalent urinary tract pathogen is *Escherichia coli* (11.1%) (Table -1; Figure-1).The studies made by Ayyagari *et al.*, (1999) found such result in their study. The present study result is also supported by Aggarwal (2005) where they reported the similar kind of results whereas the other bacterial pathogens isolated in our study were varying from the study of other workers (Afessa and Grren, 2000) who have reported *Pseudomonas aeruginosa*, *Streptococcus pneumoniae* and *Haemophilus influenzae* to be predominant isolates.

Table.1 Opportunistic bacterial pathogens isolated from HIV Positive patients

S. No	Name of the organism	Number of isolates	Percentage (%)
1	Escherichia coli RV ₄₁₂	6	11.1
2.	Escherichia coli DH5 alpha	4	7.4
3.	Enterobacter cloacae DSM	2	3.7
4.	Enterobacter cloacae MB	4	7.4
5.	Klebsiella pneumonia	4	7.4
6.	Citrobacter sedlakii	2	3.7
7.	Staphylococcus haemolyticus DSM	2	3.7
8.	Staphylococcus saprophyticus DSM 20038	2	3.7
9.	Pseudomonas lutea	2	3.7
10.	Lechlerchia adecarboxylata	2	3.7
11.	Enterobacter faecalis DSM	2	3.7
12.	Staphylococcus hominis DSM	2	3.7
13.	Staphylococcus hominis MB	2	3.7
14.	Corynebacterium aurimucosum	2	3.7
15.	Klebsiella pneumonia CHB	6	11.1
16.	Staphylococcus haemolyticus CHB	4	7.4
17.	Enterobacter faecalis CHB	2	3.7

Table.2 Opportunistic fungal pathogens isolated from 2 HIV Positive patients

S. No	Name of the yeast	Number of isolates	Percentage (%)
1	Candida tropicalis	6	26.5%
2.	Candida glabrata	5	21.7%
3.	Candida albicans	5	21.7%
4.	Candida krusei	4	17.3%

Fig.1 Percentage of opportunistic bacterial pathogens in HIV/AIDS patients





Fig.2 Percentage of opportunistic fungal pathogens in HIV/AIDS patients

Using the colony morphology, spore formation and the nature of colonies on various selective and differential media the bacterial isolates were identified. Similarly, there are four types of fungal pathogens were identified from the twenty three yeast fungal isolates were known to found among the 25 HIV positive patients. The present study suggest that multiple parts happen to HIV/AIDS patients of opportunistic fungal infections and a variety of pathogenic fungi are overlapping infected, which are mainly distributed in the respiratory tract, parts of it in the digestive tract and minority in the urinary tract. Out of all pathogens isolated, fungal isolates constituted 31.5 %. In our study, Candida species were the most common isolates. Among them Candida tropicalis (26.5%) was the most predominant isolate followed by Candida glabrata (21.7 %), Candida albicans (21.7 %.), Candida krusei (17.3%) (Table 2; Figure 2).In contrast to the present study, Gandham et al., (2013) reported that Candida albicans (75.8%) was the most prevalent species followed by C. tropicalis and other Candida species whereas the studies made by Picardi et al., (2012) in USA between 2004 and 2009, reported that Candida non-albicans strains were more frequently isolated in HIV/AIDS patients.

Thus the present study proved that the spectrum of opportunistic bacterial and fungal pathogens among various patient groups varies significantly. Moreover, this is the first study to assess cumulative data on opportunistic pathogens among HIV/AIDS patients on active care from Thuraiyur region of Tiruchirappalli District showing the real time distribution from Middle part of Tamil nadu and would thus serve as matrix for future evaluation.

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