Prevalence of *Acinetobacter Species* in Intensive Care Units

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Abstract

Background The rising incidence of Acinetobacter infection in the ICU and in patients with immature or defective body defense system cause a great concern to all clinicians worldwide due to their extraordinary ability to develop resistance to multiple classes of antibiotics which limit array of the therapeutic options.

Objective Is to determine the prevalence of Acinetobacter infection in ICUs of Kasr EL-Aini Hospital, its demographic features, speciation and antibiotic sensitivity pattern.

Methods Samples collected from infected patients in ICUs were subjected to direct microscopic examination and culture on blood, MacConkey and Herellea media. Microbact (12A) Gram-negative identification system was used. Susceptibility patterns were done by Modified Kirby Bauer disc-diffusion methods.

Results Out of 140 inpatients suffering from infections, 21.4 % (no=30) were found to be infected with Acinetobacter spp. It was responsible for 26.3% of LRTIs, 20% of wound infections and 16.2% of UTIs. *A. baumannii* was the most predominant species (93.3%). Prolonged stay in ICU (p=0.03) and stroke (p=0.005) were significantly associated with Acinetobacter infections. Other risk factors include previous antibiotic treatment (OR=1.07). The most effective antibiotics were cefoperazone/sulbactam (40%), imipinem (36.7%) and amikacin (30%). Totally 43.3% (13/30 isolates) were found to be MDR Acinetobacter isolates.

Conclusions Infection due to *A.baumannii* has become a significant challenge to healthcare systems. 21.4% of the studied patients suffered from Acinetobacter infections. Invasive procedures, prolonged stay in ICU as well as previous antibiotic treatment are associated with higher rate of infection. Eradication of Acinetobacter spp. requires adherence to good infection control practices and prudent antibiotic use.

Keywords: Acinetobacter spp., ICUs, mechanical ventilation, LRTIs, UTIs.

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List of Abbreviations

Abbreviation	Full term
A.baumannii	*Acinetobacter baumannii*
ABC efflux pump	ATP binding cassette efflux pump
ADCs	Acinetobacter-Derived Cephalosporinases.
Ade	Adenine deaminase
ADP	Adenine diphosphate
AFLP	Amplified Fragment Length Polymorphism
API 20NE	Analytic Profile Index 20 Non Enteric Gram-negative rods
ARDRA	Amplified Ribosomal DNA Restriction Analysis
ARI-1	*Acinetobacter* Resistant to Imipenem-1
ATCC	American Type Culture Collection
ATPase	Adenine triphosphatase
BAL	Bronchoalveolar lavage
BD4	Butanediol 4
BJ	Bouvet and Jean jean
bla Oxa	beta lactam Oxacillinases
bp	Base pairs
BSI	Blood Stream Infection
bv.	Biovar
CD	Cluster of Determination
CDC	Center for Disease Control and Prevention
cDNA	complementary Deoxyribonucleic Acid
CLaI	*Caryophanon latumI*
CLSI	Clinical and Laboratory Standards Institute
CMS	Colistin Methane Sulfonate
CNS	Central nervous system
COPD	Chronic Obstructive Pulmonary Disease
Cpn60	Chrophoblast protein 60
CSF	Cerebrospinal fluid
CTX-M	Cefotaxime-M
CVC	Central venous catheter
dhfr	dihydrofolate reductase
DM	Diabetes mellitus
DNA	Deoxyribonucleic Acid
E. coli	*Escherichia coli*
EcoR1	*E.coli* Restriction1
EDTA	Ethylene Diamine Tetraacetic Acid
ESBLs	Extended-Spectrum Beta-Lactamases
ETT	Endo Tracheal Tube
EUCAST	European Committee on Antimicrobial Susceptibility Testing
FDA	Food and Drug Administration
G+C	Guanine+Cytosine
gpI	Glucose phosphate isomerase I
gyrB	gyrase B
HMP	Heat-Modifiable Protein
hrs	Hours

ICU	Intensive Care Unit
IMP	Imipenem
IS	Insertion Sequence
***int* gene**	Integrase gene
IV	Intravenous
KDa	kilodalton
K.oxytoca	*Klebsiella oxytoca*
K.pneumonia	*Klebsiella pneumonia*
LAM	Leeds *Acinetobacter* Medium
LPS	Lipopolysaccharide
LRTI	Lower Respiratory Tract Infection
MATE	Multidrug And Toxic compound Extrusion
MBLs	Metallo-Beta-Lactamases
MDR	Multi Drug Resistant
MICs	Minimal Inhibitory Concentrations
MLST	Multi Locus Sequence Typing
µg	Microgram
µl	Micro litter
mm	millimeter
ml	milliliter
NI	Nosocomial Infection
NCCLS	National Committee for Clinical Laboratory Standards
no	number
Nov.	novel
Oligo-Aks	Oligo-Arginine kinases
OMP	Outer Membrane Protein
OR	Odd Ratio
ORFs	Open Reading Frames
OXA	Oxacillinases
PBPs	Penicillin-Binding Proteins
PCR	Polymerase Chain Reaction
PCR-ESI-MS	PCR-Electro Spray Ionization -Mass Spectrometry
PDR	Pan Drug Resistant
PFGE	Pulsed-Field Gel Electrophoresis
Ps.aeruginosa	*Pseudomonas aeruginosa*
qac	quaternary ammonium compound-resistance protein
Rec gene	Recall gene
REP	Repetitive Extragenic Palindromic
RND	Resistance-Nodulation-Division
rRNA	ribosomal Ribonucleic Acid
SaII	*Streptomyces albus*II
Sec.	Seconds
S. aureus	*Staphylococcus aureus*
SD	Standard Deviation
SHV	Sulphydral variables
SPP.	Species
SPSS	Statistical Package for the Social Sciences
sul	sulfatase

TEM	Temoniera
Tet	Tetracycline
TLR	Toll-Like Receptor
tRNA	transfer Ribonucleic Acid
Tu	Tjernberg and Ursing
U.S.	United States
UTIs	Urinary Tract Infections
UTP	Uridine 5'-Triphosphate
VAP	Ventilator-Associated Pneumonia
VIM	Verona integrone encoded metalo β lactamases

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Introduction

Acinetobacter are aerobic Gram-negative coccobacilli that emerged during the last 3 decades as significant nosocomial pathogens in the hospital setting and are responsible for intermittent outbreaks ***(Dima et al., 2007)***.

Infections caused by Acinetobacter usually include pneumonia, especially ventilator associated pneumonia (VAP), septicemia, wound sepsis, urinary tract infection (UTI), endocarditis and meningitis. In addition to hospitalized patients, community–acquired *Acinetobacter* infection is increasingly reported these days ***(Leung et al., 2006)***.

The infection caused by Acinetobacter is difficult to control due to multidrug resistance (MDR) which limits therapeutic options in critically ill and debilitated patients especially from intensive care units (ICUs), where their prevalence is most noted. *Acinetobacter baumannii (A.baumannii)* is currently the third commonest isolate from Gram-negative sepsis in immunocompromised patients, posing risk for prolonged hospital stay, higher health care cost and high mortality ***(Lee et al., 2007)***.

Once introduced into a hospital, Acinetobacter often has an epidemiologic pattern of serial or overlapping outbreaks caused by various MDR strains, with subsequent endemicity of multiple strains and a single endemic strain predominating at any one time ***(Marchaim al., 2007).***

Aim of the work

The aim of this study is to determine prevalence of Acinetobacter infection in ICUs, their clinical demography and antibiogram.

Acinetobacter

Members of the genus Acinetobacter are classified in the family Moraxellaceae within the Order: Pseudomonadales, Class: Gammaproteobacteria which includes the genera Moraxella, Acinetobacter, Psychrobacter and related organisms ***(Rossau et al., 1991)***. Acinetobacter (from the Greek [akinetos] i.e. nonmotile), was initially proposed by ***Brisou and Prévot*** in ***1954*** to separate the nonmotile from the motile microorganisms within the genus Achromobacter. The genus known as Acinetobacter has undergone significant taxonomic modification over the last 30 years. Its most important representative, *A. baumannii*, has emerged as one of the most troublesome pathogens for health care institutions globally. Its clinical significance, especially over the last 15 years, has been propelled by its remarkable ability to up-regulate or acquire resistance determinants, making it one of the organisms threatening the current antibiotic era. *A.baumannii* can survive for prolonged periods throughout a hospital environment, thus potentiating its ability for nosocomial spread ***(Glew et al., 1977)***. Hospital-acquired pneumonia is still the most common infection caused by this organism. However, infections involving the central nervous system (CNS), skin and soft tissue and bone have emerged as highly problematic for certain institutions ***(Peleg et al., 2008)***.