

REVIEW OF *ENTEROBACTER* SPP. : TAXONOMY, PATHOGENISITY AND ANTIBIOTIC RESISTANCE

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ABSTRACT : A gram negative bacteria is *Enterobacter* spp. that isolated from different environmental regions includes soil, water, plants and sewage that belongs to family Enterobacteriaceae. This genus includes many species considered opportunistic pathogens and in immunocompromised patients associated with nosocomial infections also, skin, neonates, intensive care units, soft tissue infections and emergency sections. *Enterobacter cloacae* is most isolated from human and animals. While, *E. aerogenes* and *E. cloacae* are associated with human pathogens between the genus *Enterobacter* and we can differentiate between *Enterobacter* spp. strains. Many risk factors of *Enterobacter* spp. infections represented to crowding, premature birth, poor hand hygiene, prolonged hospital stay, extended spectrum antibiotics, low birth weight, incubation, intravenous catheters and contaminated infant formula. *Enterobacter* spp. have increase in antibiotic resistance rapidly and cause different disease like bacteremia, meningitis, neonatal meningitis, pneumonitis, urinary tract infection and soft skin infection.

Key words : *Enterobacter* spp., immunocompromised patients, soft skin infection, opportunistic pathogens.

INTRODUCTION

Enterobacter was introduced by Hormaeche and Edwards (1960a) which belongs to Enterobacteriaceae family and a fermentative gram negative bacteria (Francine *et al*, 2015). These opportunistic pathogens found in respiratory tract of human and animals also in gastrointestinal microbiota (Pati *et al*, 2018; Chart *et al*, 2012). Genus *Enterobacter* have ability to survive environmental condition that cause various infections in medical settings (Chavda *et al*, 2016). The characterization of these bacteria are motile by peritrichous flagella, glucose fermentation. In the past decade, various regions in the world infections with this genus due to resistance to antibiotic (Boucher *et al*, 2009; Rice, 2010). Contaminations caused by blood products, cotton swabs, intravenous injection fluids and stethoscope associated with gram negative bacteria (Dos Santos *et al*, 2015). Most strains of Enterobacteriaceae have negative red test and positive vogas-proskauer reaction also without selective media for isolation of *Enterobacter* species available (William, 2015).

Taxonomy classification and properties

In this genus twenty two species have been detected after delimitation via DNA-DNA hybridization. Molecular methods of 16S rRNA gene, *gyr B* and *oriC* locus used to differentiate between strains of *Enterobacter* species

by Hoffmann and Roggenkamp clusters there are 12 genomic clusters 1-x11. Most of species could not be determined and *Enterobacter* has been arranged as apolyphyletic genus by 16S rRNA analysis (Mezzatesta *et al*, 2012; Ahmed *et al*, 2019).

In the past or recently identified more clinically species of this genus includes *Enterobacter aerogenes* (*E. aerogenes*), *Pantoea agglomerans* (*E. agglomerans*), *E. amnigenus*, *E. asburiae*, *Cronobacter sakazakii* (*E. sakazakii*), *E. gerovae*, *E. hormaechei*, *E. cancerogenus* (*E. tylosae*), *E. intermedium* and *E. dissolvens* (Francine *et al*, 2015; McMullan *et al*, 2018). The source and transmission in the epidemic strains determine by typing method include serotyping, pulsed-field gel electrophoresis, plasmid profile, bio typing, ribotyping, and multi-locus enzyme electrophoresis testing. While the effective methods for detection of epidemic strains that cause outbreaks which are the polymerase chain reaction (PCR)-based methods (Patel *et al*, 2016; Stump *et al*, 2005). Furthermore, twelve genetic clusters defined within the complex phylogenetically (Hoffmann *et al*, 2003; Hoffmann *et al*, 2005). A large complex of at least 13 type species, subspecies and genotypes depend on the biochemical attributes have done by clinical bacteriologists. Also, these clusters are diagnostic as *Enterobacter cloacae* complex species by using API 20 E. as commercial biochemical kits, *Enterobacter cloacae*