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Review about virulence factor of Stenotrofomonus . maltophiliaisolation of plural fluid in uppar respiratory tract infection

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ABSTRACT
Stenotrofomonus . maltophilia, bacteria solely found in humans, are the only known cause of causes Infectious processes including bacteria, viruses, tuberculosis, atypical mycobacterium, fungus, as well as parasites account for a substantial percentage of these effusions causes Infectious processes including bacteria, viruses, tuberculosis, atypical mycobacterium, fungus, as well as parasites account for a substantial percentage of these effusions,S. maltophiliais nonfermentative rod Gram negative bacteria and aerobic , slightly small in size (0.7–1.8 × 0.4–0.7 μm) than other members of the genus, they are motile with polar flagella, non-capsulated and non-sporulation grow well on MacConkey agar non-producing pigmented colonies, S. maltophilia is catalase-positive, oxidase-negative (which distinguishes it from most other members of the genus) and has a positive reaction for extracellular DNase, it is an uncommon bacterium and human infection is difficult to treat. Bacteria can develop antibiotic resistance through genetic variety as well as adaptation to the physiologically unique biofilm mode of development, even when neither mutation nor the acquisition of fresh DNA has taken place

I. INTRODUCTION

In the pleural cavity of normal human being, there is a small amount of fluid known as a pleural fluid which lubricates the lining of the cavity. Pleural effusion is always abnormal and indicates the presence of an underlying disease (Saladin and Kenneth et al., 2011). Pleural fluid accumulates when pleural fluid formation exceeds pleural fluid absorption. Normally, fluid enters the pleural space from the capillaries in the parietal pleura and is removed via the lymphatics situated in the parietal pleura. Fluid can also enter the pleural space from the interstitial spaces of the lung via the visceral pleura or from the peritoneal cavity via small holes in the diaphragm. The lymphatics have the capacity to absorb twenty times more fluid than is normally formed (Saladin and Kenneth et al., 2011). Pleural effusion is defined as an abnormal, excessive collection of fluid in the Pleural space. Two types of effusions can develop, transudative and exudative. Various kinds of pleural effusion, depending on the nature of the fluid and what caused its entry into the pleural space, are hydrothorax (serous fluid), hemothorax (blood), chylothoraxpyothorax (pus) Bacterial infection of the pleura was first described in ancient Greece by Hippocrates (Light et al., 2007). Pleural effusions are produced by a wide variety of causes Infectious processesincluding bacteria, viruses, tuberculosis, atypical mycobacterium, fungus, as well as parasites account for a substantial percentage of these effusions. The etiologies of pleural effusions as a whole, and then more specifically the various specific findings of pleural effusions resulting from infectious diseases (Light et al., 2007). S. maltophiliais non fermentative rod Gram negative bacteria and aerobic, they are motile, non-capsulated and non-sporulation grow well on MacConkey agar non-producing pigmented colonies, S. maltophiliais catalase-positive, oxidase-negative (which distinguishes it from most other members of the genus) and has a positive reaction for extracellular DNase, it is an uncommon bacterium and human infection is difficult to treat (Neela et al., 2014). Naturally the bacterium S. maltophilia is widely distributed in aqueous environments, soil, plants and it has also been used in biotechnology applications (Norton and Dachsetal et al., 2015). S. maltophilia can be morbidity and mortality rates among immune compromised patients with multi antibiotics resistant (Chang et al., 2015). S. maltophilia can lead to the nosocomial infections, it is also an emerging nosocomial pathogen associated with opportunistic infections in patients with cystic fibrosis, cancer, and immune compromised the patients, S. maltophiliais responsible for causing various infections which included bacteremia, endocarditis, pneumonia, meningitis, ocular infections, urinary tract infection, enteritis, and skin/soft tissue infections (Senol et al., 2004; Abbott et al., 2011). The invading pathogen must be able to produce various

virulence factors inorder to establish infections and this largely depends on environmental conditions and level of micronutrients within the hospital environment (Sritharanet al.,2006). In such circumstances, S. maltophilia is known to exhibit its pathogenicity through (1) pili/flagella/fimbrial/adhesins which contributes to adherence, auto-aggregation, colonization of biotic and abiotic surfaces, (2) outer membrane lipopolysaccharide (LPS) plays a role in biofilm formation and resistance to antibiotic as well as complement-mediated cell killing, (3) diffusible signal factor (DSF) plays a huge role in quorum sensing, which in turn mediate motility, extracellular enzymes production, LPS synthesis, micro colony formation, and tolerance toward antibiotics and heavy metal ions and (4) Extracellular enzymes production such as elastase, gelatinase, hyaluronidase, proteases, lipases, DNase, RNase and mucinase, (Looney et al., 2005; Abbott et al., 2011; Brooke et al., 2012)Thenewlyisolation and identification of S. maltophiliaand limitation of virulence factors of it, the study aims to determine the biofilm formation among the clinical isolates from pleural fluid infections

Characteristics and identification of Stenotrophomonasmaltophilia

S. maltophiliais nonfermentative rod Gram negative bacteria and aerobic , slightly small in size (0.7–1.8 × 0.4–0.7 μm) than other members of the genus, they are motile with polar flagella, non-capsulated and non-sporulation grow well on MacConkey agar non-producing pigmented colonies, S. maltophiliais catalase-positive, oxidase-negative (which distinguishes it from most other members of the genus) and has a positive reaction for extracellular DNase, it is an uncommon bacterium and human infection is difficult to treat (Neela,Naturally the bacterium S.maltophiliais widely distributed in aqueous environments, soil, plants and it has also been used in biotechnology applications (Norton and Dachsetal., 2015)

Pathogenicity and Virulence Factor Stenotrophomonasmaltophilia

S. maltophiliacan be considered as a ―newly emerging pathogen of concern‖ that is being isolated more frequently , it is also recognized as one of the underestimated important multi-drug resistant organisms in hospitals by the World Health Organization (WHO), it was ranked as the ninth most important one per British microbiologists and one of the challenging pathogens in the infectious disease community and studies, it is widely known as an opportunistic organism associated with high morbidity and mortality rates among immune compromised patients (Chang et al.,2015)

S. maltophiliacan lead to the nosocomial infections, it is also an emerging nosocomial pathogen associated with opportunistic infections in patients with cystic fibrosis, cancer, and immune compromised the patients , adherence of this organism to abiotic surfaces such as medical implants and S. maltophilia is responsible for causing various infections which included bacteremia, endocarditis, pneumonia, meningitis, ocular infections, urinary tract infection, enteritis, and skin/soft tissue infections (Senol, 2004; Abbott et al., 2011). The bacterium was recently reviewed to gain acces into the clinical settings, thus recognized as an important multi-drug-resistant global opportunistic nosocomial pathogen (Brooke et al., 2017).

The invading pathogen must be able to produce various virulence factors in order to establish infections and this largely depends on environmental conditions and level of micronutrients within the hospital environment (Sritharan,etal.,2006). In such circumstances, S. maltophiliais known to exhibit its pathogenicity through(1) pili/flagella/fimbrial/adhesins which contributes to adherence, auto-aggregation, colonization of biotic and abiotic surfaces, (2) outer membrane lipopolysaccharide (LPS) plays a role in biofilm formation and resistance to antibiotic as well as complement-mediated cell killing, (3) diffusible signal factor (DSF) plays a huge role in quorum sensing, which in turn mediate motility, extracellular enzymes production, LPS synthesis, micro colony formation, and tolerance toward antibiotics and heavy metal ions and (4) Extracellular enzymes production such as elastase, gelatinase, hyaluronidase, proteases, lipases, DNase, RNase, and mucinase, for tissue invasion and escaping the host immunity, lipases in particular are also believed to damage the lipid-rich lung tissues leading to focal lung necrosis and initiating strong inflammatory responses (Looney, 2005; Abbott et al., 2011; Brooke,etal.,2012)

This opportunistic pathogen can cause severe infections, such as bacteremia, sepsis, pneumonia, meningitis after neurosurgical procedures, endocarditis, urinary tract infection, septic arthritis, and endophthalmitis, in immunocompromised patients (Denton and Kerr, 1998; Park et al., 2008; Botana-Rialet al., 2016; Waite et al., 2016)

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Structural virulence factorof Stenotrophomonasmaltophilia

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Biofilm composition and stages biofilm formation

A population of bacteria adhering to a surface and to one another by an extracellular matrix released by the bacterial cells is referred to as a bacterial biofilm. Microorganisms have the ability to colonize surfaces and form biofilms, which are intricate microbial colonies embedded in exopolymeric materials including polysaccharides, proteins, and nucleic acids. There are several reasons why biofilms increase the viability and development of bacteria As they can withstand physical pressures that may dislodge attached cells, immune cell phagocytosis, or chemical penetration, biofilms first act as a sanctuary for bacteria. Second, since they may anchor microbes to surfaces with plenty of nutrients, biofilms enable microbial cells to stay in a favorable niche. Third, the development of biofilms enables the cohabitation of microorganisms. By producing and detecting extracellular signaling molecules termed autoinducers, quorum sensing, a method of bacterial cell-to-cell communication, is given improved possibilities. Additionally, intimate cell proximity enhances genetic exchange, and biofilms are the normal method of development for bacteria in nature when resources are few (Madiganetal.,2006Species and environmental factors affect how specifically biofilms grow. However, the image depicts five separate generalized phases (1). When a motile planktonic cell first colonizes a surface, the process is known as the Van der Waals interaction, which occurs at distances greater than 50 nm from the surface. Hydrophobic interactions, which occur at distances less than 0.5-2 nm from the surface, also play a role in the attachment of the cell to the surface. The bacteria begin to exhibit species-specific behaviors during this reversible attachment, including rolling, crawling, aggregation formation, and windrow creation. The bacteria that are connected use cell adhesion structures like pili and also produce exopolymeric material, a more sticky substance.

Additionally, it has been proposed that the conversion from reversible binding to permanent attachment may depend on the cells' proximity to one another or that the attached bacteria start excreting an extracellular matrix, which replaces the initial reversible binding with much stronger, irreversible covalent bonds that prevent independent cell movement. Once the bacterial attachment is formed, the bacteria start to form a microcolony. As the microcolony grows and reproduces, additional maturation takes place, and the biofilm matures into a completely three-dimensional structure with clusters of cells and channels connecting them. These pathways aid in the transport of nutrients and water to cells as well as the elimination of waste. Cell division is mostly absent in mature biofilms, and the generation of exopolysaccharides consumes the majority of energy. Cell dispersion is the final stage ofbiofilm development, during which bacteria spread out from biofilms onto new areas that are suited for colonization (Branda et al. 2005).

Antibiotic Resistance Mechanisms in Stenotrophomonas.maltophilia

The reduced susceptibility of S. maltophilia to antibiotics has been associated with intrinsic resistance factors common to all S. maltophilia strains, such as low membrane permeability, the presence of multidrug resistance (MDR) efflux pumps, antibiotic-modifying enzymes, and the quinolone resistance gene (Crossman et al., 2008; Sanchez et al., 2009) . Resistance can also be acquired via the acquisition of mutations or resistance genes through horizontal gene transfer (HGT) , microorganisms sharing the same environment can provide these exogenous genes, it has been postulated that other unknown mechanisms may also help account for the S. maltophilia antibiotic resistance phenotype

(Sánchez,etal.,2015) The intrinsic resisted has been defined as the group of chromosomal genes involved in the intrinsic resistance present in the strains of a bacterial species prior to exposure to an antibiotic and which is not due to HGT (Fajardo et al., 2006). The intrinsic resisted involves known and unknown genes related to antibiotic resistance, which might include genes involved in cell metabolism (Olivares et al., 2013).

Like all Gram negative bacteria, S. maltophiliashows low membrane permeability—the consequence of it having two cell membranes and a peptidoglycan wall, the outer membrane is an efficient barrier, mutants showing altered outer membrane permeability or which have a different Low susceptibility to antibiotics is often related to the presence of active efflux pumps ,such pumps have been identified in S. maltophilia K279a, including eight MDR efflux pumps belonging to the putative resistance nodulation cell division (RND) family, two belonging to the major facilitator superfamily (MFS), and two ATP-binding cassette (ABC) pumps (Crossman et al., 2008). In Gram negative bacteria, RND efflux pumps are composed of three proteins an inner membrane protein, which binds the substrate, an outer membrane protein (porin), and a membrane fusion protein (MFP), which binds the outer and inner proteins in the periplasmic space S. maltophiliacan manifest resistance to many commonly used antibiotics, including carbapenems, which makes infections caused by this bacterium difficult to treat (Yang et al., 2009) . Inappropriate use of broad-spectrum antibiotics like imipenem presents risk factor for S. maltophilia infections, the most important reason for this is the ability of its to hydrolyseimipenem (Okazaki and Avison,etal., 2008)S. maltophilia strains are intrinsically resistant to multiple antibiotics due to aminoglycoside acetyl-transferase and enzymes that inactivate erythromycin and genes encoding efflux pumps ,besides the S. maltophilia strains being resistant to one antibiotic, these strains can develop resistance to multiple antibiotics (multidrug resistance), due to frequent and irrational use of the broad-spectrum antibiotics, pan resistant strains have been occasionally reported in the hospitals (Huang et al., 2010 All the proteins of the efflux pumps SmeABC, SmeDEF and SmeVWX, which belong to the RND family, are encoded in the same operon following the typical genomic arrangement, the roles of these efflux pumps in intrinsic and acquired resistance have been extensively characterized (Chen et al., 2011). SmeABC is involved in acquired resistance to β-lactams, aminoglycosides and quinolones, but has no influence on intrinsic resistance, the deletion of the smeABC gene (porin) affects susceptibility to several antibiotics SmeDEF is involved in both intrinsic and acquired resistance to chloramphenicol, tetracycline and quinolones SmeVWX has a role in acquired resistance to the some antibiotics (Garcia-Leon et al., 2014)

II. CONCLUSION

The outcomes of this study revealed a great spread of S. maltophilia isolates in Najaf hospitals that produce virulence factor and are resistant to many antibiotics.

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